सी डी एफ डी
CDFD

वार्षिक प्रतिवेदन

अप्रैल 2012 से मार्च 2013 तक

ANNUAL REPORT

April 2012 to March 2013

डी एन ए फिंगरप्रिंटिंग एवं निदान केन्द्र

नामपल्ली, हैदराबाद - 500 001

Centre for DNA Fingerprinting and Diagnostics

Nampally, Hyderabad - 500 001

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अधिदेश

सीडीएफडी सोसाइटी के संगम ज्ञापन तथा नियम एवं विनियमों में बताए गए के अनुसार डीएनए फिंगरप्रिंटिंग एवं निदान केन्द्र की स्थापना जिन उद्देश्यों के लिए हुई वे निम्न प्रकार हैं :

i. पितृत्व विवाद, आप्रवास और अस्पतालों में नवजात शिशुओं की अदला-बदली जैसे मामलों में निजी पक्षों सहित विविध अभिकरणों के लिए पर्याप्त अदायगी पर डीएनए प्रोफाइलिंग और उससे संबंधित विश्लेषण का वैज्ञानिक अनुसंधान करना।

ii. अपराध अन्वेषण अभिकरणों को डीएनए फिंगरप्रिंटिंग और उससे संबंधित विश्लेषण तथा सुविधाएँ प्रदान करना।

iii. अपराध अन्वेषण और परिवार मामलों में डीएनए प्रोफाइल विश्लेषण और उससे संबंधित तकनीकों के साक्ष्य संबंधी मूल्य को समझने में पुलिस कर्मियों, न्यायिक वैज्ञानिकों, वकीलों तथा न्यायपालिका की सहायता करना।

iv. आनुवंशिक अव्यवस्थाओं को संसूचित करने हेतु डीएनए नैदानिक विधियाँ सिद्ध करना और इस प्रकार के संसूचन के लिए संपरीक्षाएँ विकसित करना।

v. पादप और जंतु कोशिका माल, कोशिका लाइनों के प्रामाणीकरण के लिए डीएनए फिंगरप्रिंटिंग तकनीकों का उपयोग करना और ऐसे प्रयोजनों के लिए आवश्यकतानुसार नई संपरीक्षाएँ विकसित करना।

vi. डीएनए फिंगरप्रिंटिंग तकनीकों पर प्रशिक्षण प्रदान करना।

vii. मूलभूत, अनुप्रयुक्त अनुसंधान एवं विकास कार्य करना।

viii. देश में चिकित्सा संस्थाओं, जन-स्वास्थ्य अभिकरणों और उद्योग को परामर्शी सेवाएँ प्रदान करना।

ix. केंद्र के उद्देश्यों से संगत क्षेत्रों में विदेशी अनुसंधान संस्थाओं एवं प्रयोगशालाओं और अन्य अंतर्राष्ट्रीय संगठनों के साथ सहयोग करना।

x. अनुसंधान छात्रों को स्नातकोत्तर उपाधियों के लिए पंजीकृत कर सकने के प्रयोजन हेतु उच्चतर अधिगम के मान्यता प्राप्त विश्वविद्यालयों एवं संस्थाओं के साथ संबंधन स्थापित करना।

xi. भारत सरकार, राज्य सरकारों, देश में स्थित पूर्त संस्थाओं/न्यासों, व्यक्तियों और उद्योग से नकद के रूप में या अन्य रूपों में अनुदान, दान एवं अंशदान प्राप्त करना।

xii. केंद्र सरकार के पूर्व अनुमोदन से प्रशिक्षण कार्यक्रमों, वैज्ञानिक अनुसंधान और अन्य गतिविधियों के लिए अंतर्राष्ट्रीय संगठनों सहित विदेशी स्रोतों से आर्थिक सहायता प्राप्त करना।

xiii. केंद्र की गतिविधियों को चलाने के लिए जैसा आवश्यक या सुविधाजनक हो, कोई भी संपत्ति चल या अचल या भवनों एवं निर्माणों को निर्मित करने, सुधार करने, परिवर्तित करने, गिरा देने या मरम्मत करने हेतु उपहार, क्रय, विनिमय, पट्टा, भाड़े पर लेने द्वारा या अन्यथा किसी भी तरह अर्जित करना।

xiv. केंद्र के प्रयोजन हेतु, भारत सरकार और अन्य प्रोनोटों, विनिमय पत्रों, चैक या अन्य परक्राम्य लिखतों को आहरित करना और स्वीकार करना, तैयार करना और पृष्ठांकित करना, बट्टा करना और परक्रामण करना।

xv. केंद्र को सौंपी गई निधियों या धन को निवेश करने के लिए, ऐसी प्रतिभूतियों को खोलने या ऐसे तरीके से, जो कि समय-समय पर शासी परिषद् द्वारा निर्धारित किए जाते हैं, इस प्रकार के निवेश को विक्रय या पक्षांतरण करना।

xvi. उक्त सभी उद्देश्यों या उनमें से किसी उद्देश्य की प्राप्ति के लिए सभी ऐसे अन्य विधिसम्मत कार्य, जैसा आवश्यक, प्रासंगिक या सहायक हो, करना।

xvii. केंद्र के उद्देश्यों को वास्तविक बनाने के लिए प्रोफेसरों अन्य संकाय पदों, अभ्यागत अध्येतावृत्तियों सहित अध्येतावृत्तियों, अनुसंधान एवं संवर्ग पदों, छात्रवृत्तियों आदि को संस्थापित करना।

xviii. केंद्र के वैज्ञानिक एवं प्रौद्योगिकीय कार्य के लिए प्रयोगशालाओं, कार्यशालाओं, भंडार, पुस्तकालय, कार्यालय और अन्य सुविधाओं को स्थापित करना।

xix. तकनीकी जानकारी को उद्यमकर्ताओं और उद्योगों से प्राप्त या उनको अंतरण करना; और

xx. पेटेंटों, डिज़ाइनों एवं तकनीकी जानकारी जो कि केंद्र द्वारा विकसित की गई हो, को पंजीकृत करना और केंद्र के हित में ऐसे पेटेंटों/डिज़ाइनों/तकनीकी जानकारी के किसी भाग को अंतरण करना।

MANDATE

The objectives for which the Centre for DNA Fingerprinting and Diagnostics (CDFD) was established, as enumerated in Memorandum of Association and Rules and Regulations of CDFD Society, are as follows:

i. To carry out scientific research pertaining to DNA profiling and related analysis in civil cases like paternity disputes, immigration, and exchange of newborns in hospitals, for various agencies including private parties, on appropriate payment;

ii. To provide DNA fingerprinting and related analysis and facilities to crime investigation agencies;

iii. To assist police personnel, forensic scientists, lawyers and the judiciary in understanding the evidential value of the DNA profile analysis and related techniques in crime investigation and family matters;

iv. To establish DNA diagnostic methods for detecting genetic disorders and to develop probes for such detection;

v. To use DNA fingerprinting techniques for the authentication of plant and animal cell material, cell lines and to develop new probes where necessary for such purposes;

vi. To provide training in DNA fingerprinting techniques;

vii. To undertake basic, applied and developmental R & D work;

viii. To provide consultancy services to medical institutions, public health agencies and industry in the country;

ix. To collaborate with foreign research institutions and laboratories and other international organizations in fields relevant to the objectives of the Centre;

x. To establish affiliation with recognized universities and institutions of higher learning for the purpose of enabling research scholars to register for post-graduate degrees;

xi. To receive grants, donations and contributions in cash or in other forms from the Government of India, State Governments, Charitable Institutions/Trusts, individuals and industry within the country;

xii. To receive, with the prior approval of the Central Government, monetary assistance from foreign sources including international organizations for training programmes, scientific research and other activities;

xiii. To acquire by gift, purchase, exchange, lease, hire or otherwise howsoever, any property movable or immovable or to construct, improve, alter, demolish or repair buildings and structures as may be necessary or convenient for carrying on the activities of the Centre;

xiv. For the purpose of the Centre, to draw and accept, make and endorse, discount and negotiate Government of India and other Promissory Notes, Bills of Exchange, Cheques or other Negotiable Instruments;

xv. For investing the funds of or money entrusted to the Centre, to open such securities or in such manner as may from time to time be determined by the Governing Council and to sell or transpose such investment;

xvi. To do all such other lawful acts as may be necessary, incidental or conducive to the attainment of all or any of the above objectives;

xvii. To institute Professorships, other faculty positions, fellowships including visiting fellowships, research and cadre positions, scholarships, etc. for realizing the objectives of the Centre;

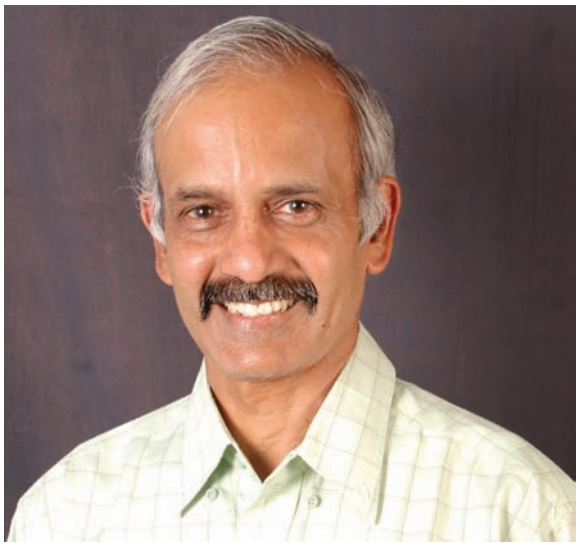
xviii. To establish, maintain and manage laboratories, workshops, stores, library, office and other facilities for scientific and technological work of the Centre;

xix. To acquire or transfer technical know-how from/to entrepreneurs and industries; and

xx. To register patents, designs & technical know-how that may be developed by the Centre and transfer any portion of such patents/designs/technical know-how in the interest of the Centre.

निदेशक का संदेश
From the Director’s Desk

निदेशक का संदेश



डीएनए फिंगरप्रिंटिंग एवं निदान केंद्र (सीडीएफडी) की स्थापना 1996 में भारत सरकार के जैव प्रौद्योगिकी विभाग (डीबीटी) के स्वायत्त संस्थान के रूप में की गई। यह देश में आण्विक जीवविज्ञान के विविध क्षेत्रों में आधुनिकतम अंतरविषयक अनुसंधान और सेवा प्रदान करने के अधिदेश के साथ बनाए गए अग्रणी अनुसंधान संस्थानों में से एक है। पिछले वर्षों में केंद्र में सभी क्षेत्रों की गतिविधियों में उल्लेखनीय वृद्धि देखी गई है और अन्वेषण के अनेक नए क्षेत्र आरंभ किए गए हैं। वर्ष 2012-13 के दौरान सीडीएफडी की उपलब्धियों और प्रगति के विवरण इस प्रगति रिपोर्ट में आगे बताए गए हैं और मैं नीचे उनमें से कुछ पर प्रकाश डालना चाहता हूं।

इस प्रतिवेदनाधीन अवधि के दौरान, डीएनए फिंगरप्रिंटिंग सेवा प्रयोगशाला में केंद्र और विभिन्न राज्य सरकारों की न्याय पालिका तथा कानून प्रवर्तन एजेंसियों द्वारा लगभग 175 मामले अग्रेषित किए गए थे। देश में डीएनए प्रोफाइलिंग सेवाओं के विस्तार के प्रति अपने प्रयासों में सीडीएफडी ने उड़ीसा और आंध्र प्रदेश की राज्य सरकारों के साथ किसी लागत के बिना डीएनए प्रोफाइलिंग सेवाएं प्रदान करने के लिए एक समझौता ज्ञापन किया है, जिसके लिए हमारा विश्वास है कि यह न्याय प्रदायगी प्रणाली में एक प्रौद्योगिकी प्रदर्शक के रूप में कार्य करेगा। उड़ीसा में समझौता ज्ञापन व्यवस्था के भाग के रूप में सीडीएफडी ने जीव विज्ञान संस्थान (आईएलएस), भुवनेश्वर के साथ मिलकर आईएलएस में डीएनए प्रोफाइलिंग की एक प्रयोगशाला स्थापित की है। नैदानिक सेवाओं के क्षेत्र में निजाम इंस्टीटच्यूट ऑफ मेडिकल साइंसिस (एनआईएमएस), हैदराबाद में चिकित्सा आनुवंशिकी विभाग की स्थापना की गई जो सफलता पूर्वक कार्यरत है और यहां लगभग 3500 रोगियों का आनुवंशिक मूल्यांकन तथा परामर्श देने का कार्य किया गया है। इस वर्ष नैदानिक प्रभाग में कार्यरत मेरे सहयोगियों ने एक्सोम सीक्वेंसिंग के माध्यम से जीन *जीजेसी2* में एक सजाति परिवार का नवीन उत्परिवर्तन अभिज्ञात किया है और बौद्धिक विकलांगता तथा दौरे के लक्षणों वाली एक महिला रोगी में -*ARHGEF9* के मानचित्रण का कार्य भी सफलता पूर्वक पूरा किया है। इस वर्ष, एपीडा-सीडीएफडी बासमती डीएनए विश्लेषण केंद्र में 200 बासमती चावल के नमूनों का परीक्षण उनकी शुद्धता के लिए किया गया।

आण्विक आनुवंशिकी की प्रयोगशाला में रेशम कीट एमएमएनपीवी अंत:क्रियाओं के अध्ययन में बीएमएनपीवी वायरस से उत्पन्न माइक्रो आरएनए को पहचानने में सफलता मिली है जो डीएनए बंधन प्रोटीन सहित वायरल लेट जीन (*सिस* लक्ष्य) की अभिव्यक्ति का नियमन करता है और बॉम्बिक्स मोरी में वायरस की लंबित अभिव्यक्ति के लिए महत्वपूर्ण है। एंथ्रिया आसमा की आनुवंशिक विविधता और आबादी की संरचना में इस समूह का अध्ययन टसर रेशम कीट के विशिष्ट इकोटाइप के परिरक्षण और असम क्षेत्र में सीमित मूंगा रेशम कीट की घटती आबादी के संरक्षण में उपयोगी रहा है। इसके अलावा, इस प्रयोगशाला के अनुसंधान कर्ताओं ने वाणिज्यिक रेशम कोकून गुणों वाले परजीनी रेशम कीट सफलता पूर्वक तैयार किए हैं जो बैकुलोवायरस प्रतिरोधक हैं और ये परजीनी लाइनें वर्तमान में बहु स्थल क्षेत्र परीक्षणों के अनुमोदन की प्रतीक्षा में हैं।

कवकी रोगजनन प्रयोगशाला के अनुसंधान कर्ताओं ने टीएचपी-1 मानव मोनोसायटिक कोशिकाओं से उत्पन्न मैक्रोफेज के साथ कैंडिडा ग्लाब्राटा के बीच अंत: क्रिया को समझा है, जिससे प्रकट होता है कि सी. ग्लाब्राटा कोशिकाओं में फेगोलाइसोसोमल परिपक्वता की रोकथाम की क्षमता होती है जो अभिक्रियात्मक ऑक्सीजन प्रजाति (आरओएस) के उच्च स्तर के साथ जीवित रह सके और पोषी कोशिकाओं की प्रतिक्रिया में आईएल - 4 स्राव आरंभ कर सकें। जीवाण्विक कोशिका जीव विज्ञान प्रयोगशाला द्वारा निर्धारण किया गया है कि माइको बैक्टीरियम ट्यूबरकुलोसिस (एमटीबी) प्रोटीन जैसे एमटीबी एचएसपी 60 के कोशिकीय स्थानीकरण के साथ मैक्रोफेज में टोल के समान ग्राहियों से अंत: क्रिया पर मैक्रोफेज की कार्यात्मकता पर प्रभाव हो सकता है और पोषी में टी - कोशिका प्रतिरक्षी प्रत्युत्तर के ध्रुवी करण से एमटीबी रोग जनकता प्रभावित हो सकती है। इस समूह ने चूहा मॉडल पर कार्य करते हुए एमटीबी की उत्तरजीविता और प्रोटीन पीपीई 18 की महत्वपूर्ण भूमिका इनवीवो दर्शाई है।

पादप सूक्ष्मजीवों की अंत: क्रिया पर हमारे अध्ययनों से XadM के लाक्षणीकरण में सहायता मिली है, जो चावल के जीवाणु रोगाणु जैंथोमोनाज़ ओरीजी पीवी ओरीजी में जैंथोमोनाज़ का एक नया आसंजन प्रोटीन है और शीघ्र संलग्नता, कॉलोनी निर्माण और बायोफिल्म निर्माण में महत्वपूर्ण भूमिका निभाता है।

आण्विक अर्बुद शास्त्र प्रयोगशाला के अध्ययनों में प्रकट हुआ है कि एआरआईडी1बी, जो एसडब्ल्यूआई/एसएनएफ क्रोमेटिन रिमॉडलिंग कॉम्प्लैक्स के एक घटक की इनकोडिंग करता है, पेनक्रियाज़ के कैंसर के लिए एक नया ट्यूमर संदमक जीन है और विशिष्ट पीएएच उत्परिवर्तन से भारत में फेनिल कीटोनूरिया पैदा करता है। स्तनी आनुवंशिकी प्रयोगशाला में किए गए अनुसंधान से कैंसर जनन और विकास में डीएनए मेथिल ट्रांसफरेज़ *डीएनएमटी3l* और *डीएनएमटी2* की भूमिका का पता चला है। इस समूह ने एमटीबी से चुनौती देने पर पोषी कोशिका में होने वाली एपिजेनेटिक बदलावों को भी अभिज्ञात किया है।

कोशिका संकेतन प्रयोगशाला के कार्य में प्रदर्शित किया गया है कि फॉस्फा इनोसिटॉल यौगिक आईपी7 द्वारा आरएनए पॉलीमरेज 1 के पाइरोफॉस्फोराइलेटिंग घटकों द्वारा ईस्ट में राइबोसोम जैव जनन का नियमन किया जाता है, और इस प्रकार आरआरएनए संश्लेषण का नियंत्रण किया जाता है। यह भी दर्शाया गया है कि इनोसिटोल पायरोफॉस्फेट का आईपी6के1 द्वारा संश्लेषण स्तनधारी कोशिकाओं में समजात पुन: संयोजन माध्यित डीएनए मरम्मत के पूरे होने में एक भूमिका निभाता है।

अनुलेखन प्रयोगशाला एसेरिशिया कोलाई में कारक आश्रित अनुलेखन समापन और समापन रोधी गतिविधि के आण्विक आधार को समझने में सक्रिय रूप से संलग्न है। जीवाण्विक आनुवंशिकी प्रयोगशाला में कारक आश्रित अनुलेखन समापन और डीएनए-आरएनए हाइब्रिड (आर-लूप्स) के निर्माण में इससे बचने में की भूमिका का अध्ययन भी किया गया है, जो अनुलेखन-द्विगुणन विवादों को बढ़ावा देता है। इस समूह ने विलेय परिवहन और नियमन तथा अलारमोन पीपी जीपीपी के अनेक कार्यों की खोज ई. कोलाई में भी की है।

अभिकलनात्मक जीव विज्ञान प्रयोगशाला में मानव वायरल सेतु प्रोटीन-प्रोटीन अंत: क्रिया नेटवर्कों के अध्ययन में दर्शाया गया है कि कुछ वायरल प्रोटीन आरटीकुलेशन बिन्दुओं के रूप में इनके बीच अन्यथा बाइकनेक्टिड मानव प्रोटीन अंत: क्रिया नेटवर्क सेतु का कार्य करते हैं। ये संयोजन मानव प्रोटीन-प्रोटीन अंत: क्रियाओं पर प्रभाव डालने के लिए वायरसों द्वारा प्रयुक्त प्रक्रियाओं को समझने में महत्वपूर्ण हैं।

तुलनात्मक रूप से केंद्र के नए संकाय सदस्यों ने विचारोत्तजक कार्य किए हैं, जो चुनौती पूर्ण है इनमें कोशिका चक्र नियमन, कोशिका मृत्यु और कोशिका उत्तर जीविता मार्ग तथा ड्रोसोफिला तंत्रिका विकास अध्ययन के क्षेत्र रहे। इसके अलावा, डॉ. देवयानी हल्दर ने हाल ही में केंद्र का

कार्य भार संभाला है और क्रोमेटिन जीव विज्ञान तथा एपिजेनेटिक्स के क्षेत्र में कार्य आरंभ किया है। मुझे विश्वास है कि हमारे युवा सहकर्मियों द्वारा आरंभ की गई इन वैज्ञानिक यात्राओं से आने वाले वर्षों में अपार लाभ मिलेंगे।

मुझे यह बताते हुए खुशी है कि हेल्डन पीठ के रूप में डॉ. डी पी कस्बेकर के आने से 'टीम सीडीएफडी' बहुत सशक्त बन गई है। न्यूरोस्पोरा आनुवंशिकी के क्षेत्र में डॉ. कस्बेकर के अग्रणी कार्य के साथ उनका संकाय और अनुसंधान वेत्ताओं के प्रति मार्गदर्शन कौशल से सीडीएफडी को अनेक प्रकार से लाभ मिलेगा। यह भी हर्ष का विषय है कि प्रतिवेदनाधीन अवधि के दौरान, नेशनल इंस्टीट्यूट ऑफ एग्रोबायोलॉजिकल साइंसिज़ (एनआईएएस), सुकुबा, जापान के प्रो. काजुई मिता, जो रेशम कीट आनुवंशिकी में अंतरराष्ट्रीय ख्याति प्राप्त व्यक्ति हैं, ने केंद्र का आमंत्रण स्वीकार किया और असाधारण विदेशी वैज्ञानिकों के लिए जैव प्रौद्योगिकी पीठ हेतु डीबीटी योजना की शर्तों के अनुसार अतिथि प्रोफेसर के रूप में यहां लगभग एक वर्ष का समय बिताया।

स्मरणीय है कि दिसंबर 2009 में सीडीएफडी तथा आईकेपी ज्ञान पार्क, हैदराबाद ने मिलकर कुछ विकसित प्रौद्योगिकियों के वाणिज्यीकरण के लिए एक महत्वकांक्षी कार्यक्रम आरंभ किया और इसे सीडीएफडी द्वारा पेटेंट कराया गया। इस कार्यक्रम के परिणाम मिलने आरंभ हो गए हैं और केंद्र में ई. कोलाई का उपयोग करते हुए एल-आर्जीनीन उत्पादन हेतु सूक्ष्म जीव प्रक्रम से संबंधित प्रौद्योगिकी को बायोनरी बाइप्रोडक्ट्स प्रा. लि. को लाइसेंस दिया गया है, जिसे डीबीटी - एसबीआईआरआई योजना से निधिकरण समर्थन प्राप्त है।

विमटा लैब्स लिमिटेड में सीडीएफडी की प्रयोगशाला जंतु सुविधा, शमीरपेट (नामपल्ली में वर्तमान परिसर से लगभग 45 किलोमीटर की दूर पर) में पूरी तरह कार्यशील है। सीडीएफडी के अनेक अनुसंधान कर्ताओं ने इस सुविधा में परियोजनाएं आरंभ की हैं, जहां वर्तमान में *आईपी6 के1*, *एनएनएटी*, सी57बीएल/6, एफओएक्सएन1$^{एनयू}$ और बाल बी/सी सहित चूहों के पांच आंतरिक रूप से प्रजनन करने वाले विभेद उपलब्ध हैं।

इस वर्ष भी सीडीएफडी के अनेक संकाय सदस्यों और अध्येताओं को प्रतिष्ठित पुरस्कार और सम्मान प्राप्त हुए हैं। इनमें शामिल हैं सीनियर इनोवेटिव यंग बायोटेक्नोलॉजिस्ट एवॉर्ड, आईसीएमआर क्षणिक ओरेशन एवॉर्ड, फेलोशिप ऑफ द इण्डियन एकेडमी, बैंगलोर, और पद्म श्री पुरस्कार। इस प्रतिवेदनाधीन अवधि के दौरान पांच अनुसंधानकर्ताओं को पीएचडी डिग्री प्रदान की गई है। सीडीएफडी द्वारा निरंतर प्रतिभाशाली, युवा और सक्रिय पीएचडी अध्येताओं, पोस्टडॉक्टरल अध्येताओं, परियोजना सहयोगियों और ग्रीष्मकालीन प्रशिक्षुओं को आकर्षित किया जाता है।

मैंने पिछले वर्ष बताया था कि सीडीएफडी उप्पल, हैदराबाद के भारतीय सर्वेक्षण विभाग की भूमि पर सरकार से वित्तीय अनुमोदन मिलने के पश्चात् स्थायी परिसर निर्मित करने का इच्छुक है। वर्तमान स्थिति यह है कि वास्तुकारों, परियोजना प्रबंधन परामर्श दाताओं और सिविल कार्य के लिए संविदाकारों का चयन पूरा हो चुका है। पुनः, भारतीय विमान पत्तन प्राधिकरण, आ. प्र. प्रदूषण नियंत्रण बोर्ड, हैदराबाद महानगर जल आपूर्ति और सीवेज बोर्ड, अग्निशमन सेवा और आ. प्र. राज्य आपदा प्रतिक्रिया सहित विभिन्न एजेंसियों से सांविधिक अनुमोदन लिए गए हैं। हमें आशा है कि भूमि कार्य जल्दी ही आरंभ होगा, ताकि केंद्र में संकाय और अन्य कार्यकर्ताओं के सामने आने वाली स्थान और मूल संरचना की कमी को जल्दी से जल्दी दूर किया जा सके।

मैं शासी परिषद, अनुसंधान क्षेत्र पैनल-वैज्ञानिक सलाहकार समिति, शैक्षिक परिषद, वित्त समिति, भवन निर्माण समिति और डीबीटी से सभी गतिविधियों के लिए प्राप्त अपार सहयोग के प्रति अपना आभार व्यक्त करता हूँ। मैं सभी सदस्यों और अधिकारियों को धन्यवाद देता हूँ , जिन्होंने हमारी गतिविधियों तथा उपलब्धियों में अपना समय और प्रयास का योगदान दिया है।

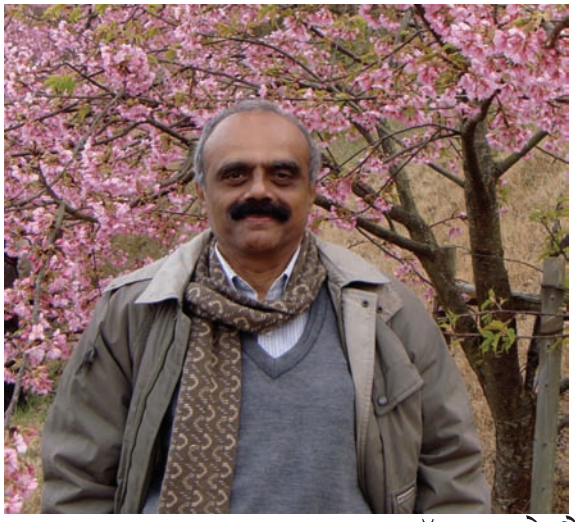
केवल इतना ही नहीं, उपरोक्त बताई गई सफलताओं के साथ मैं सीडीएफडी परिवार के सभी सदस्यों के प्रति

अपना हार्दिक आभार व्यक्त करता हूँ , मैं एक अत्यंत दुखद समाचार के साथ अपना संदेश समाप्त करने के लिए बाध्य हूँ । वर्ष 2012 के अंतिम दिन हमारे महान संकाय सदस्य और वरिष्ठ सहकर्मी, डॉ. जे नागाराजू अल्पकालीन बीमारी के बाद चल बसे। डॉ. नागराजू ने 1998 में सीडीएफडी में कार्यभार संभाला, जो आण्विक आनुवंशिकी प्रयोगशाला के प्रमुख और डीएनए फिंगरप्रिंटिंग सेवा प्रयोगशाला के समन्वयक थे। उन्हें 2011 में केंद्र की खुराना पीठ पर भी नियुक्त किया गया था। वे आनुवंशिकी के क्षेत्र में एक अंतरराष्ट्रीय रूप से जानी मानी हस्ती वाले एक वैज्ञानिक ही नहीं बल्कि रेशम कीट जीव विज्ञान और बासमती चावल में विशेष रुचि रखने के अलावा इस संस्थान में बौद्धिक और प्रशासनिक क्षमताओं के आधार थे और अनेक लोगों के सलाहकार तथा मार्गदर्शक थे। इन सब से परे वे एक नजदीकी व्यक्तिगत मित्र थे। उनकी स्मृति में सबसे अच्छी श्रृद्धांजली यही होगी कि केंद्र उन ऊंचाइयों को पाने के लिए और भी कठिन प्रयास करे, जिनके लिए डॉ. नागाराजू ने इतने जोश के साथ अपने स्वयं के अनुसंधान प्रयास आगे बढ़ाए।

ज गौरीशंकर

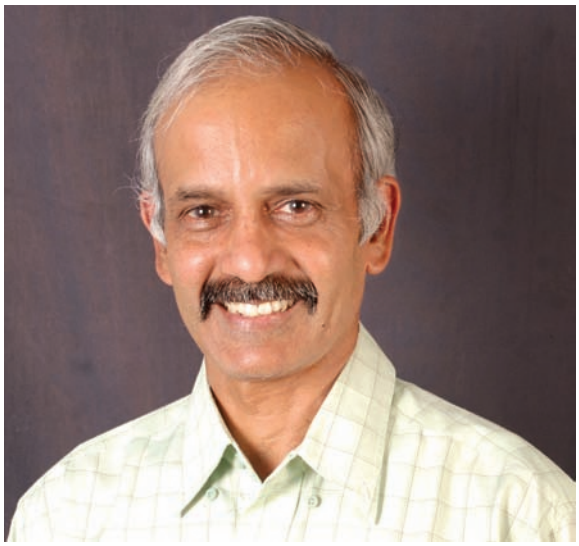
31 मार्च, 2013

स्मृति में



डॉ. जावरेगौडा नागराजु
(6 नवंबर 1954 से 31 दिसंबर 2012)

Director's Message



The Centre for DNA Fingerprinting and Diagnostics (CDFD), established in 1996 as an autonomous institute of the Department of Biotechnology (DBT) of the Government of India, is one amongst the pioneering research institutions in the country with the mandate to provide services and to undertake cutting edge interdisciplinary research in diverse areas of molecular biology. Over the years, the Centre has witnessed significant growth in all phases of activities, and several new frontiers of investigation have been initiated. The achievements and progress of CDFD's research during 2012-2013 are described in the chapters that follow in this progress report, and I would like to highlight a few of them below.

During this reporting period, the Laboratory of DNA Fingerprinting Services was forwarded about 175 cases by the judiciary and law enforcing agencies of the Union and different State Governments. In its efforts towards expansion of DNA profiling services in the country, the CDFD has entered into MoU's with the State Governments of Orissa and Andhra Pradesh to provide DNA profiling services at no cost basis, which we believe would serve as a technology demonstrator for the justice delivery system. As part of the MoU arrangement in Orissa, the CDFD has joined hands with the Institute of Life Sciences (ILS), Bhubaneshwar, to establish a DNA Profiling Laboratory at the ILS. In the area of Diagnostic services, the Medical Genetics Department established at the Nizam's Institute of Medical Sciences (NIMS), Hyderabad has been running successfully and around 3500 patients underwent genetic evaluation and counselling. My colleagues working in the Diagnostics division have identified through exome sequencing, a novel mutation in a consanguineous family in a gene *GJC2,* and have also successfully carried out mapping of *ARHGEF9* in a female patient with symptoms of intellectual disability and seizures. The APEDA-CDFD Centre for Basmati DNA Analysis tested close to 200 basmati rice samples for their purity during this year.

The Laboratory of Molecular Genetics, while studying silkworm-MmNPV interactions, has been successful in identifying BmNPV virus-derived microRNA that regulates the expression of viral late genes (*cis* targets) including DNA a binding protein which is important for the late expression of the virus in *Bombyx mori*. This group's study of the genetic diversity and population structure of *Antheraea assama* has been useful for preservation of unique ecotypes of tasar silkmoths and conservation of declining populations of muga silkmoths confined to the Assam region. In addition, the researchers in this laboratory have successfully generated transgenic silkworms resistant to baculovirus with commercial silk cocoon properties and these transgenic lines are presently awaiting approval to be taken for multi-location field trials.

Researchers in the Laboratory of Fungal Pathogenesis have deciphered the interaction between *Candida glabrata* with macrophages derived from THP-1 human monocytic cells, revealing that *C. glabrata* cells possess ability to prevent phagolysosomal maturation, to survive high levels of reactive oxygen species (ROS), and to invoke IL-4 secretion response in the host cells. The Laboratory of Molecular Cell Biology has determined that cellular localization of *Mycobacterium tuberculosis* (Mtb) proteins such as Mtbhsp60, upon interaction with Toll-like receptors in macrophages, can influence macrophage functions; and that the polarization of T-cell immune responses can affect Mtb virulence in the host. This group, while working on a mouse model, has demonstrated an important role of protein PPE18 in replication and survival of Mtb *in vivo*.

Our studies on plant-microbe interactions have helped in the characterization of XadM, which is a novel adhesion protein that plays an important role in early attachment, colonization and biofilm formation of the rice bacterial pathogen *Xanthomonas oryzae* pv. *oryzae*.

Studies in the Laboratory of Molecular Oncology have revealed that *ARID1B,* which encodes a component of the SWI/SNF chromatin remodelling complex, is a novel tumour suppressor gene for pancreatic cancers and that unique *PAH* mutations cause phenylketonuria in India. Research in the Laboratory of Mammalian Genetics has dissected out the role of DNA methyltransferases *Dnmt3l* and *Dnmt2* in carcinogenesis and development. This group has also identified epigenetic changes that the host cell undergoes when challenged with Mtb.

Work in the Laboratory of Cell Signalling has demonstrated that the phospho-inositol compound IP_7 regulates ribosome biogenesis in yeast by pyrophosphorylating components of RNA polymerase I, thereby controlling rRNA synthesis. It has also been shown that inositol pyrophosphates synthesised by IP6K1 play a role in the completion of homologous recombination-mediated DNA repair in mammalian cells.

The Laboratory of Transcription has been actively engaged in understanding the molecular basis of factor-dependent transcription termination and antitermination in *Escherichia coli.* The Laboratory of Bacterial Genetics is also studying factor-dependent transcription termination and its role in avoidance of formation of RNA-DNA hybrids (R-loops) that provoke transcription-replication conflicts. This group has also investigated the mechanisms of solute transport and regulation, as well as the multiple functions of the alarmone ppGpp in *E. coli*.

The Laboratory of Computational Biology, while studying human viral bridge protein-protein interaction networks, has shown that some of the viral proteins act as articulation points to bridge otherwise unconnected nodes in the biconnected human protein interaction network. These connections may hold keys to understand the mechanisms used by viruses for hijacking human protein-protein interactions.

The Centre's comparatively new faculty members have embarked upon exciting, yet challenging, studies in areas such as cell cycle regulation, cell death and cell survival pathways, and Drosophila neural development. In addition, Dr Devyani Haldar joined the Centre very recently and is to initiate work in the area of Chromatin Biology and Epigenetics. I am confident that these scientific journeys which have been initiated by our young colleagues would yield immense dividends in the years to come.

I am excited to report that '*Team CDFD'* has been strengthened by the joining of Dr DP Kasbekar as Haldane Chair. Dr Kasbekar's pioneering research in the area of Neurospora genetics, together with his cosmic skills in mentoring faculty and research scholars, will enrich the CDFD in numerous ways. It is a pleasure also to mention that during the period under report, Prof. Kazuei Mita, an internationally renowned authority in silkmoth genomics from the National Institute of Agrobiological Sciences (NIAS), Tsukuba, Japan, accepted the Centre's invitation and spent almost a year here as Visiting Professor, in line with terms of the DBT scheme for Biotechnology Chair for outstanding overseas scientists.

It may be recalled that in December 2009, the CDFD and IKP-Knowledge Park, Hyderabad had initiated an ambitious programme for development and commercialization of certain technologies developed and patented by CDFD. This programme has started bearing fruit, and the Centre's technology related to microbial process for L-arginine production using *E. coli* strains has been licensed to M/s Bionary Bioproducts Pvt. Ltd. with funding support secured from the DBT-SBIRI scheme.

CDFD's Laboratory Animal Facility at M/s Vimta Labs in Shamirpet (~45 kms from the current campus at Nampally) is fully operational. Several CDFD researchers have initiated projects in this facility which presently houses five inbred mouse strains including *Ip6k1*, *Nnat*, C57BL/6, *Foxn1*^{nu} and Balb/c.

This year too, several of the CDFD faculty and scholars have been recipients of prestigious awards and honours. These include the Senior Innovative Young Biotechnologist Award; ICMR Kshanika Oration Award; Fellowship of the Indian Academy of Sciences, Bangalore; and the Padma Shri award. During this reporting period, five research scholars were conferred with PhD degrees. CDFD continues to attract bright, young and dynamic PhD scholars, postdoctoral fellows, project associates and summer trainees into its midst.

I had reported last year on the intention to construct CDFD's permanent campus on land of the Survey of India at Uppal, Hyderabad, subject to final financial approvals being received from the Government. The current status is that the selection of architects, project management consultants and contractors for civil work has been completed. Further, statutory approvals of various agencies,

including the Airports Authority of India, A.P. Pollution Control Board, Hyderabad Metropolitan Water Supply and Sewerage Board, Fire Services and A.P. State Disaster Response have been taken. We do hope that the ground work would commence shortly so that the space and infrastructure constraints presently being faced by the faculty and other workers in the Centre are alleviated as soon as possible.

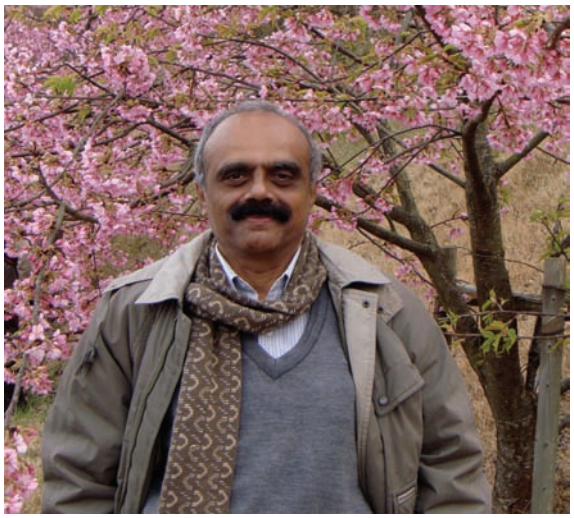
I take this opportunity also to acknowledge the unstinted co-operation which the Centre has received all along for its activities from the Governing Council, Research Area Panels-Scientific Advisory Committee, Academic / Finance / Building Committees and, of course, the DBT. I wish to thank all the members and officials for their time and effort in supporting our activities and achievements.

Notwithstanding the successes reported above, for which I extend sincere gratitude to all members of the CDFD family, I am constrained to close this message on an extremely sad note. On last day of the calendar year 2012, our illustrious faculty member and senior colleague Dr J Nagaraju passed away after a brief illness. Dr Nagaraju had joined the CDFD in 1998, was Head of the Laboratory of Molecular Genetics, and Co-ordinator of the Laboratory of DNA Fingerprinting Services; he was also appointed to the Khorana Chair of the Centre in 2011. He was not just a scientist of international renown in the area of genetics with particular reference to silkmoth biology and basmati rice, but also the backbone of this Institute in both intellectual and administrative capacities and a mentor and guiding light for many. Above all, he was a close personal friend. There can be no more fitting tribute to his memory than for the Centre to strive even harder to achieve the heights that Dr Nagaraju had so passionately cared for in his own research endeavours.

J Gowrishankar

March 31, 2013

IN MEMORIAM



Dr. Javaregowda Nagaraju

(6 November 1954 - 31 December 2012)

सेवाएँ
Services

LABORATORY OF DNA FINGERPRINTING SERVICES

Faculty	Madhusudan Reddy Nandineni	Staff Scientist
Other Members	SPR Prasad	Senior Technical Officer
	Ch V Goud	Technical Officer
	Devinder Kumar	Technical Officer
	Sanjukta Mukerjee	Technical Officer
	**DS Negi	Technical Officer
	Girnar Vijay Amrutrao	Technical Assistant
	**Chandra Shekhar Singh	Technical Assistant
	Shruti Das Gupta	Technical Assistant (Since Feb. 2013)
Coordinator	*J Nagaraju	Khorana Chair
	DP Kasbekar	Haldane Chair (Since Jan. 2013)

* deceased 31 Dec. 2012
** presently posted at DNA Profiling Laboratory of CDFD (DPL-CDFD) at the Institute of Life Sciences, Bhubaneswar, Odisha

Objectives

1. To provide DNA fingerprinting services in cases forwarded by law-enforcing agencies and judiciary of State and Federal Governments, relating to murder, sexual assault (rape), paternity, maternity, child swapping, body identification, kidney transplantation, etc.;
2. To develop human resources skilled in DNA fingerprinting, to cater to the needs of State and Federal Government agencies;
3. To impart periodical training to manpower involved in DNA fingerprinting sponsored by State and Federal Government agencies;
4. To provide advisory services to State and Federal Government agencies in establishing DNA Fingerprinting facility; and
5. To create DNA marker databases of different caste populations of India.

Summary of services provided until the beginning of this reporting year (April 1, 2011 - March 31, 2012)

A total number of 94 cases were received for DNA fingerprinting examination during this reporting period. Of these, 50 cases related to paternity/ maternity, 33 cases related to identification of deceased, 5 cases were pertaining to sexual assault (rape), 3 cases were related to murder and 3 cases pertaining to biological relationship (kidney transplantation). Seventeen States and Union Territories of India have availed DNA fingerprinting services of CDFD during this period. Andhra Pradesh forwarded the highest number of cases (33) followed by Chhattisgarh (12), Karnataka (10), Punjab (10), Kerala (6), Maharashtra (3), Uttar Pradesh (4), Bihar (3), Delhi (3), Jammu & Kashmir (2), Jharkhand (1), Madhya Pradesh (1), Orissa (1), Puducherry (1), Tamil Nadu (1) and Uttarakhand (1).

Details of services provided in the current reporting year (April 1, 2012 to March31, 2013)

Breakup of the cases during this reporting period is given below under following heads:

Biological relationship	05
Murder	13
Sexual assault (Rape)	19
Maternity/paternity	70
Identity of the deceased individuals	79
Total number of cases	**186**

A total number of 186 cases were received for DNA fingerprinting examination during the current reporting period (2012-2013). Of these, 70 cases related to paternity/maternity, 79 cases related to identification of deceased, 19 cases were pertaining to sexual assault (rape), 13 cases were related to murder and 5 cases were pertaining to biological relationship (kidney transplantation). Seventeen states and Union Territories of India have availed DNA fingerprinting services of CDFD during this period. Andhra Pradesh forwarded the highest number of cases (104) followed by Bihar (2), Chandigarh (1), Chhattisgarh (13), Delhi (1), Goa (2), Jammu & Kashmir (2), Karnataka (6), Kerala (4), Madhya Pradesh (1), Odisha (33), Puducherry (1), Punjab (10), Sikkim (1), Tamil Nadu (2), Uttar Pradesh (2) and West Bengal (1) (Figure 1).

During this reporting period, an amount of Rs. 12,39,594/- (Rupees twelve lakhs thirty nine thousand five hundred and ninety four only) has been received towards DNA fingerprinting analysis charges, which is inclusive of service charge as levied by Govt. of India.

The cases involving identification of the deceased (42%) and paternity (38%), constituted the bulk of the cases received during this reporting year (Figure 2).

Some prominent cases reported by CDFD during April 1, 2012 to March 31, 2013

1. Paternity dispute case involving a prominent politician - forwarded by Delhi High Court.
2. Identification of victims of the train accident case from Nellore district of Andhra Pradesh.
3. Identification of victims in a triple murder case by a suspected Army deserter: forwarded by CBI, Chennai branch.

Summary of the state-wise break-up of DNA fingerprinting cases:

State/Union Territory	Biological Relationship	Identity of Deceased	Maternity/ Paternity	Murder	Sexual Assault (Rape)	No. of Cases
Andhra Pradesh	04	58	34	01	07	104
Bihar	-	-	02	-	-	02
Chandigarh	-	-	01	-	-	01
Chhattisgarh	-	06	07	-	-	13
Delhi	-	-	01	-	-	01
Goa	-	-	02	-	-	02
Jammu & Kashmir	-	01	01	-	-	02
Karnataka	-	-	05	01	-	06
Kerala	-	01	03	-	-	04
Madhya Pradesh	-	-	01	-	-	01
**Odisha	-	03	08	10	12	33
Puducherry	-	-	01	-	-	01
Punjab	-	08	01	01	-	10
Sikkim	-	-	01	-	-	01
Tamil Nadu	-	01	01	-	-	02
Uttar Pradesh	-	01	01	-	-	02
West Bengal	01	-	-	-	-	01
Total number of cases	**05**	**79**	**70**	**13**	**19**	**186**

***** Among the 104 cases received from Andhra Pradesh, 56 cases were received from Andhra Pradesh State Forensic Science Laboratory (APFSL), Hyderabad under a Memorandum of Understanding (MoU) between CDFD, APFSL and the Government of Andhra Pradesh.

****** Among the 33 cases received from Odisha, 9 cases were received at CDFD from DPL-CDFD and 24 cases were received at DPL-CDFD, ILS, Bhubaneswar under an MoU between CDFD, ILS and the Government of Odisha.

4. Matching of DNA profiles in a suspected homicide case of a Pastor from Kerala: forwarded by CBI, Ernakulum, Kerala branch.

Deposition of evidence in Courts of Law

During this reporting year, the DNA experts defended their reports in 10 cases in various Hon'ble Courts throughout the country.

Training / Lectures / Workshops on DNA fingerprinting examination

Training

1. Training on DNA profiling techniques to

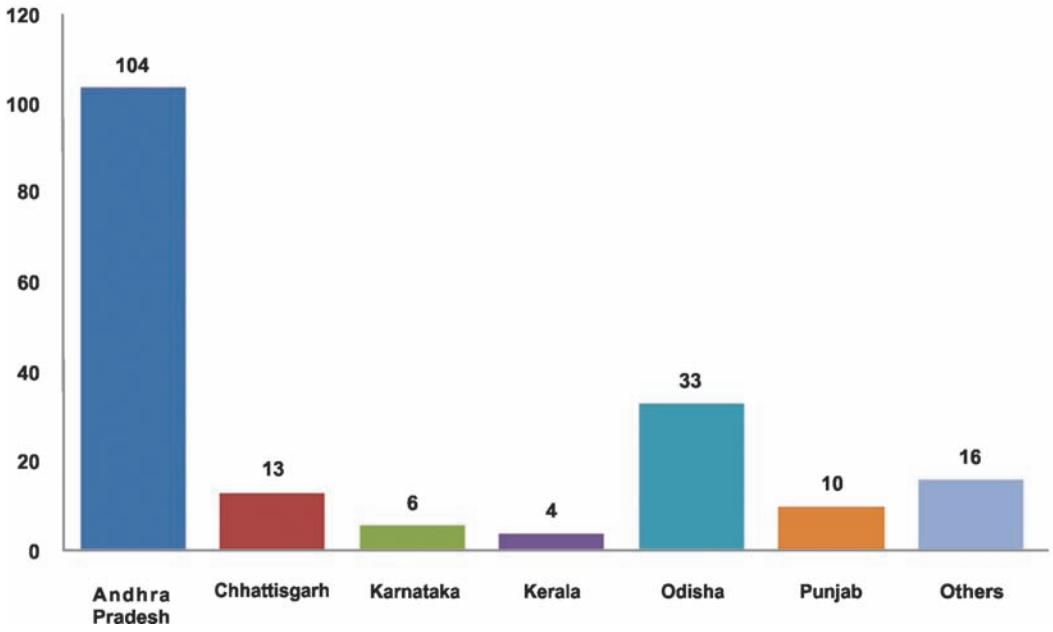


Figure 1. State-wise distribution of cases received during this reporting year

personnel from Forensic Science Laboratory, Govt. of NCT of Delhi from 14.03.2012 to 30.04.2012.

2. Training on DNA profiling techniques to scientific officer from Forensic Science Laboratory, Madhuban, Haryana from 14.07.2012 to 30.07.2012.
3. Training on DNA profiling techniques to the scientists from the State Forensic Science Laboratory, Lucknow, Uttar Pradesh during 07.05.2012 to 16.05.2012 and 26.11.2012 to 01.12.2012.
4. Training in collection, storage and transportation of biological samples for DNA profiling to Odisha Police Investigation Officers on 11.03.2013 and 25.03.2013 at DPL-CDFD, ILS Campus, Bhubaneswar.

Lectures/ Workshops

1. Delivered lecture for senior Police Officers at the Sardar Vallabhbhai Patel National Police Academy, Hyderabad on 11.05.2012.
2. Lecture at CDFD for the benefit of post-graduate biology teachers from Kendriya Vidyalaya, Hyderabad on 23.05.2012.

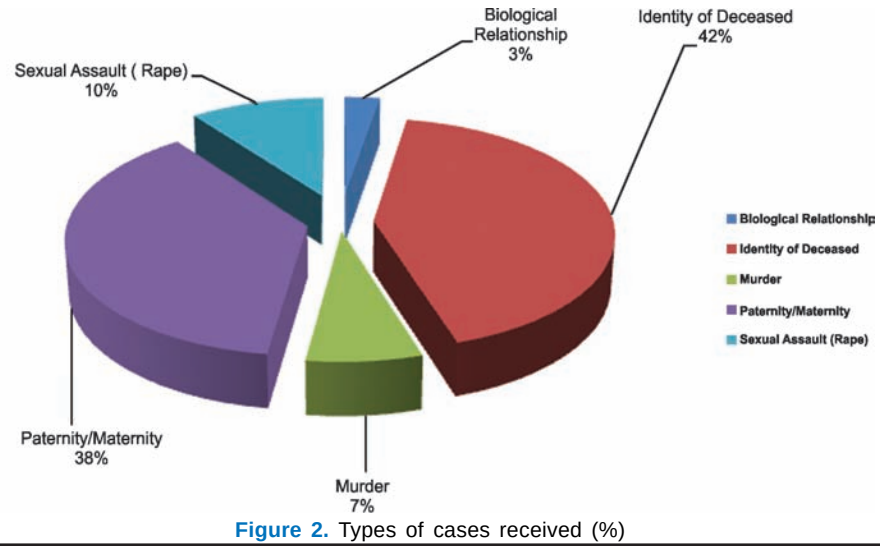


Figure 2. Types of cases received (%)

3. National Disaster Management Authority (NDMA)-CDFD Workshop on "Identification of victims of mass disasters" held on 08.06.2012 at Hyderabad.
4. Lecture for senior IPS Officers of different states of India from Administrative Staff College of India, Hyderabad on 01.08.2012.
5. Delivered lecture for students at BITS Pilani, Hyderabad Campus on 12.09.2012.
6. Delivered lecture for senior Police Officers at the Sardar Vallabhbhai Patel National Police Academy, Hyderabad on 30.01.2013.
7. Delivered lecture for Probationary IPS Officers at the Sardar Vallabhbhai Patel National Police Academy, Hyderabad on 08.02.2013.
8. Lecture for Air Force Officers from Air Force Intelligence School, Lohegaon, Pune on 12.02.2013.
9. Lecture for post-graduate students and faculty from Aurora's Degree and PG College, Hyderabad on 25.03.2013.
10. Awareness programmes on best practices for collection, storage and transportation of biological samples for DNA profiling at different District Police Head Quarters of Odisha.

Publications

1. Dalal A, Bhavani GSL, Togarrati PP, Bierhals T, Nandineni MR, Danda S, Danda D, Shah H, Vijayan S, Gowrishankar K, Phadke SR, Bidchol AM, Rao AP, Nampoothiri S, Kutsche K and Girisha KM (2012). Analysis of the *WISP3* gene in Indian families with progressive pseudorheumatoid dysplasia. ***American Journal of Medical Genetics A*** 158A: 2820-2828.
2. Ranganath P, Sharma V, Danda S, Nandineni MR and Dalal A (2012). Novel mutations in the neuraminidase-1 *(NEU1)* gene in two patients of sialidosis in India. ***Indian Journal of Medical Research*** 136: 1048-1050.

DIAGNOSTICS DIVISION

Faculty	Ashwin B Dalal	Staff Scientist
Adjunct Faculty	Prajnya Ranganath	Assistant Professor, NIMS
	Shagun Agarwal	Assistant Professor, NIMS
PhD Students	Anusha Uttarilli	Senior Research Fellow
	Anjana Kar	Junior Research Fellow
	Ashish Bahal	Junior Research Fellow (Since May 2012)
Other Members	Aneek Das Bhowmik	Research Associate
	T Nageswara Rao	Research Associate (Since Jan. 2013)
	GR Savithri	Senior Technical Officer
	Angalena R	Senior Technical Officer
	P Rajitha	Technical Officer
	Usha Rani Dutta	Technical Officer
	Jamal Md Nurul Jain	Technical Officer
	Bhagwati Sharan Sharma	Technical Assistant
	C Krishna Prasad	Technician
	R Sudheer Kumar	Technician
	Savita Wangnekar	Project Assistant (Since Jul. 2012)
	Matta Divya	Project Assistant (Since Dec. 2012)
	V Subhash	Project Assistant (Since Aug. 2012)
	Vijay Kumar Pidugu	Project Assistant (Till Jul. 2012)
	Seetalakshmi S	Project Assistant (Till Jul. 2012)
	A Sirisha	Project Assistant (Till Jan. 2013)
	Rajini Jonna	Project Assistant (Till Feb. 2013)
	Sri Lakshmi BG	Research Assistant (Till Nov. 2012)
	Sai Shruthi C	Research Assistant (Till Jun. 2012)
	CH Deepika	Research Assistant (Till Mar. 2013)

Objectives

1. To conduct genetic evaluation for patients/ families with genetic disorders;
2. To develop new methods and assays for genetic analysis and engage in research on chromosomal and single gene disorders;
3. To act as national referral center for analysis and quality control of genetic tests for few genetic diseases; and
4. To impart training in genetic evaluation of patients with genetic disorders.

(I) Details of services provided in the current reporting year (April 1, 2012 – March 31, 2013)

Clinical Genetics

A total of 3458 patient samples were analysed for genetic testing, during the year 2012-13. These consisted of patients with chromosomal disorders, monogenic disorders, mental retardation, congenital malformations, inborn errors of metabolism, and other familial disorders.

The Department of Medical Genetics established at Nizam's Institute of Medical Sciences, Hyderabad is running successfully. A total of 2310 patients were examined and counseled in the unit during 2012-13.

Genetic investigations done during 2012-13

Investigation	Total cases	Positives
Cytogenetics	1213	160 (13.2%)
Proband	1096	150 (13.6%)
Prenatal	117	10 (8.5%)
Molecular Genetics	1233	458 (37%)
Proband	1150	433 (37.6%)
Prenatal	83	25 (30%)
Biochemical Genetics	1012	272 (27%)
Proband	991	266 (26.8%)
Prenatal	21	6 (28.6%)

Cytogenetics

Disease	Abnormality	No. of cases
Down Syndrome	Trisomy 21	58
	47,SC+21	2
	46,XY,rob(21;21) +21	1
	46,XX,rob(21;21) +21	2
	46,XY,t(14;21)+21	3
	47,XY,+21,inv(9)	1
	47,X inv(Y)+21	1
	47,XX+21[42]/46,XX[8]	1
Edward Syndrome	47,SC,+18	2
Patau Syndrome	47,SC+13,9qh+,15s+	1
Turner Syndrome	Monosomy X (45,X)	2
	iso X,(46,X,i(X))	3
	Mosaic 45,X/ 46,X,i(X)	1
	Mosaic 45,X/ 46,XX	1
	46,X,del(X)(p22.2)	1
	45Y,del(X)(p22.2)	2
	46,XX/45,X,del(X)(q26→qter)	1
Klinefelter Syndrome	47,XXY	11
Sex reversal	Phenotypic female with 46,XY	6
	Phenotypic male with 46,XX	2
	47,XX+marker	2
	47,XY+marker	1

Fluorescence *in situ* Hybridization (FISH)

Disease/translocation	No. of cases	No. of positives
Prader-Willi Syndrome	SNRPN(15q11)/PML(15q24)	8
Di-George Syndrome	TUPLE(22q11.2)/ARSA(22q13)	6
Williams-Beuren	ELN(7q11)/Control(7q22)	8
Marker chromosome	WCP-15, WCP-22SE(14)/(22), SE(X)/(Y), Acro-p-arm	23
Spectral karyotyping		6

Quantitative Fluorescent PCR (QF-PCR)

QF-PCR kit	Patients	Positives
Prenatal QF-PCR	44	1
MLPA kit(P064) MR-1	42	5
MLPA kit(P064) MR-2	4	0

Structural chromosomal abnormalities

Inversions	
46,XY,inv(9)	9
46,XX,inv(9)	5
46,X,inv(Y)	1
Deletions	
46,XY,del(5)(p)1	
46,XX,del(9)(p22)	1
Translocations	
45,XY,rob(13;14)	1
45,SC,rob(13;14)pat	1
46,XX,t(1;10((q43;q24.3)	1
46.XY,t(1;5)(p36.3;q31.1)	1
46,XY,t(4;10)(q13.3;p15)	1
46,XX,t(3;15)	1
46,XX,t(4;18)(q12;q11.2)	1

46,XX,t(7;14)	1
46,XY,t(3;7)(q27;p24)	1
46,XX,t(6;13)	1
46,XX,t(1;21)(q42.1;q22.3)	1
46,XX,t (2;9)(q31;q22)	1
46,XY,t(4;5)(q34;q23.1)mat	1
46,XX,t(4;5)(q34;q23.1)	1
Polymorphic variants	
46,XX,9qh+, 46,XY,9qh+ 46,XX,9qh-, 46,XX,1qh+ 46,XY,1qh+, 46,XY,16qh+ 46,XX.22p+, 46,XY,22p+ 46,XY,21p+, 46,XX,15p+ 46,XY,15p+	15
Total	**46**

Biochemical Genetics

Disease/Test	Positives
Urine Metabolic Screening tests (340)	**87**
Amino acid disorders (N=246)	**59**
Maple syrup urine disease	2
Non Ketotic Hyperglycinemia	5
Hyperornithinemia	7
Tyrosinemia	1
Phenylketonuria	3
Other amino acid disorders	41
Lysosomal storage disorders (n=405)	**120**
Hurler syndrome (14)	6
Hunter syndrome (13)	9
Sanfilippo B (8)	1
Morquio A disease (30)	14
Arylsulphatase B (14)	5
Sly disease (10)	0
GM1-Gangliosidosis (42)	10
Fucosidosis (1)	0
Gaucher disease (37)	12

Disease/Test	Positives
Krabbe disease (32)	6
Pompe disease (11)	4
Nieman Pick disease (34)	14
Mucolipidosis (12)	11
Metachromatic Leukodystrophy (82)	20
Fabry's disease (9)	4
Mannosidase (2)	0
Hexosaminidase A/B (54)	
Tay Sachs disease	1
Sandhoff disease	3
Prenatal diagnosis (21)	**6**
Sandhoff disease (3)	1
Metachromatic Leukodystrophy (7)	1
Gaucher's disease (1)	1
Hunter syndrome (1)	0
Hurler syndrome (1)	0
MPS VI (3)	1
Morquio A disease (3)	2
GM1- Gangliosidosis (1)	0
Niemann Pick disease (1)	0

Molecular Genetics

Disorders	Cases	Positive	Negative		
DMD/BMD	225	155	70		
DMD Carrier Analysis	24	15	09		
Spinal Muscular Atrophy	101	51	50		
SMA Carrier Analysis	43	20	23		
		Normal	**Homozygous**	**Heterozygous**	**Compound Heterozygous**
β-thalassemia/Sickle cell	173	14	55	79	25
Factor V Leiden	129	126	-	03	-
Factor II mutation	88	88	-	-	-
Cystic Fibrosis	77	69	08		
Triplet Repeat Disorders		**Positive**	**Negative**		
Friedreichs Ataxia	66	22	44		
Myotonic Dystrophy	38	25	13		
Huntington Disease	45	23	22		
SCA Panel (1,2,3,6 & 7)	86	29	57		
DRPLA	03	-	03		
Fragile X Syndrome	52	05	47		

Prenatal Diagnosis					
DMD	7	1	6		
Spinal Muscular Atrophy	20	5	15		
		Normal	Homozygous	Heterozygous	Compound Heterozygous
β-thalassemia	56	10	13	27	6

Cpd Heterozygous= Compound Heterozygous

(II) Diagnostics Research

Project 1: Cloning, characterization and analysis of chromosomal rearrangements in human genetic disorders.

Summary of work done until beginning of this reporting year (Upto March 31, 2012)

Structural chromosomal rearrangements that alter the genome architecture can result in human disease phenotypes. Cloning the breakpoint can provide the quickest route to identifying the disease gene in patients with such rearrangements. This project deals with the molecular characterization of chromosomal breakpoint 46,XX,t(X;20)(q13;p13) (Figures 1B & 1C) in a patient with delayed milestones and seizures (Figure 1A).

Lymphoblastoid cell lines of the patient were established and HUMARA assay was performed, which showed a skewed X inactivation of the normal X chromosome. Array CGH studies confirmed that this translocation is not associated with any gains or losses at the breakpoints and elsewhere in the genome. We followed a positional cloning approach for mapping the chromosomal breakpoints X;20 and identified the breakpoint spanning BAC clone RP11-943J20 showing signals on normal X, and split signals on derivative X and derivative 20 (Figure 1D).

Details of progress made in the current reporting year (April 1, 2012 – March 31, 2013)

Characterization of the *ARHGEF9* gene

The breakpoint mapping results of the proband with t(X;20) translocation revealed one gene in chromosome X breakpoint (*ARHGEF9*) and 5 genes in chromosome 20 breakpoint region. We studied *ARHGEF9* expression in the patient RNA to study the existence of *ARHGEF9* transcripts. Total RNA was isolated and cDNA synthesized. Multiple *ARHGEF9* primers were designed for the 2 isoforms of the *ARHGEF9* gene. Several combinations of primers were used on control and patient cDNA with exons 1aF-1R, 1-3, 2-4, 5-6, 6-7, 6-8, and 9-11. The transcripts were present with all the combinations except 1aF-1R and 1-3 exons. This indicated that the breakpoint lies between the exon 1 and exon 2 or upstream of *ARHGEF9* gene (Figure 1E and 1F).The expression of the other exons of *ARHGEF9* gene might be due to the effect of a fused gene. The fused gene could be due to the result of fusion with other genes in the vicinity of the breakpoint region on the derivative chromosome 20 region. Hence we also checked for the fusion transcripts with 2 possible genes (*PRNP* and *PRND*) on the chromosome 20 region. No products were obtained with this combination of genes using *ARHGEF9* primers. We concluded that the *ARHGEF9* gene was disrupted in our patient causing the phenotype. There are two more reports in literature of patients with similar phenotype in whom the breakpoints disrupted this gene.

Project II: Clinical, biochemical and molecular analysis of common lysosomal storage disorders.

Summary of work done until beginning of this reporting year (Upto March 31, 2012)

Lysosomal storage disorders are a heterogenous group of disorders associated with specific lysosomal enzyme deficiency. The diagnosis in most of these disorders is based on enzyme assay. There is a large amount of overlap in enzyme levels among carriers and normal people; hence it is very difficult to detect carriers by enzyme assay. Mutation detection is helpful for carrier detection and accurate prenatal diagnosis. Our study aims to characterize the clinical features, biochemical parameters and molecular defects in common lysosomal storage disorders.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

Over last three years we have been able to identify mutations in 159 patients with different lysosomal storage diseases (LSDs) (Table 1). This study has revealed the mutation spectrum in patients with LSDs in the Indian population. Based on this work, the Indian Council of Medical Research has established a Task Force on LSDs and our centre had been chosen as one of the nodal centres to continue this work for a larger number of LSDs.

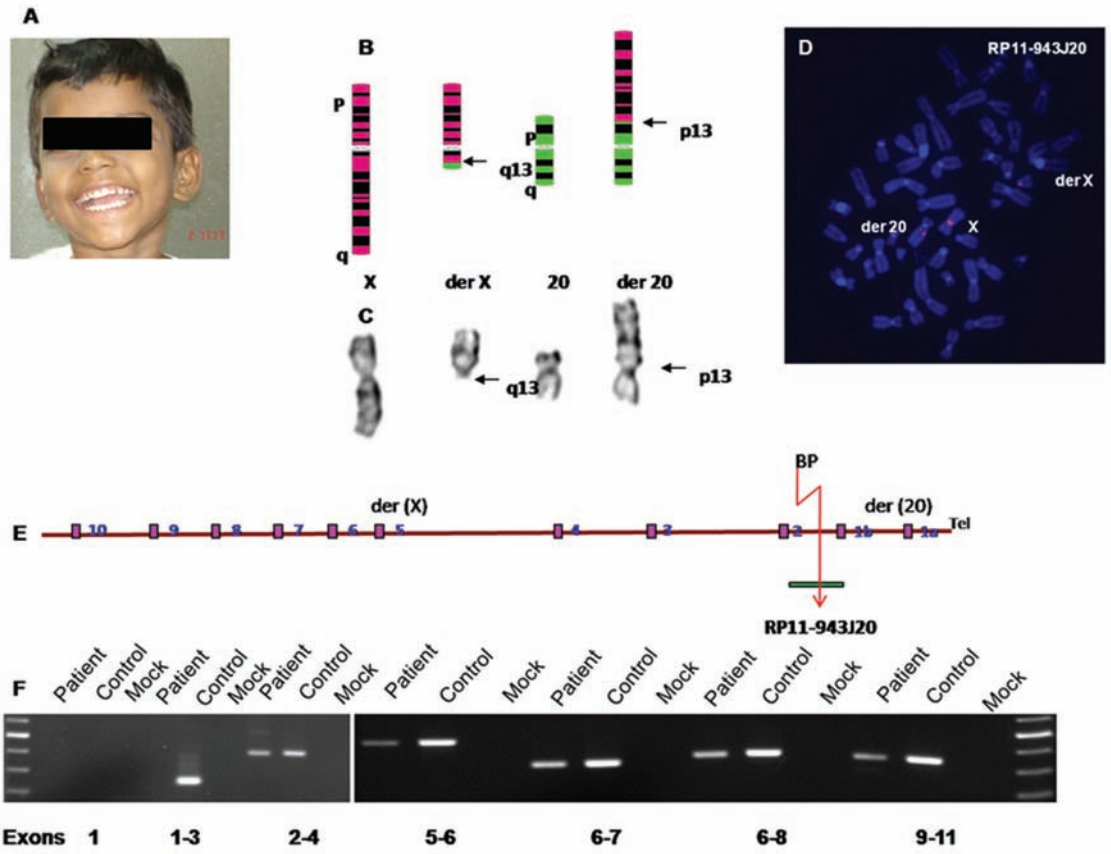


Figure 1. Breakpoint mapping in a patient with de novo translocation.(**A)** Clinical photograph of the patient.(**B)** Ideograms depicting the translocated chromosomes and their normal homologs. (**C)** Partial karyogram showing the translocation X and 20. (**D)** FISH with BAC clone RP11-943J20 showing signals on normal chromosome X and split signals on both derivative X and derivative 20. (**E)** Schematic diagram depicting *ARHGEF9* with the location of the chromosome breakpoint (arrow) as determined by FISH, breakpoint cloning, and RT-PCR experiments. The breakpoint spanning BAC RP11-943J20 is shown below the gene. (**F)** *ARHGEF9* transcript analysis in patient and control cell line RNAs.

Project III: Human exome sequencing to identify novel genes for Mendelian disorders

Summary of work done until beginning of this reporting year (Upto March 31, 2012)

Single gene disorders are rare by themselves but collectively they are an important cause of morbidity and mortality. The identification of genes for single gene disorders has value, not only in prenatal diagnosis and genetic counseling of affected families, but also in basic research towards understanding gene functions and mechanisms of disease. This in turn can help to improve our knowledge regarding the function of the proteins involved and development of new therapeutic options for both single gene and common multifactorial disorders. In spite of the robustness of classical methods of gene identification like chromosomal breakpoint mapping, linkage analysis and homozygosity mapping, these methods are laborious and require multiple families with multiple affected individuals, thus they cannot

be used for single gene disorders occurring sporadically or exhibiting phenotypic heterogeneity. Alternatively, the availability of massively parallel high throughput sequencing technologies have made it possible to identify gene for a particular disease using just a few affected individuals. This project is designed to identify mutations in such affected families using exome sequencing.

Lysosomal storage disorder	Total Patients	Number of mutations	Number of novel mutations
MPS I / Hurler syndrome	30	10	2
MPS II / Hunter syndrome	38	9	2
MPS VI / Maroteaux-Lamy syndrome	30	16	13
Niemann-Pick disease	38	30	22
Metachromatic leucodystrophy	20	20	10
Sialidosis	3	3	3
Total cases	**159**	**88**	**52**

Table 1. Data sheet showing all the mutations detected in different patients.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

We report on preliminary results of exome sequencing in one patient with presumed single gene disorder. The patient, a 5 year old girl was born out of consanguineous union and had similarly affected sibling. This patient presented with slowly progressive ataxia, optic atrophy, spasticity and normal cognition (Figure 2A).

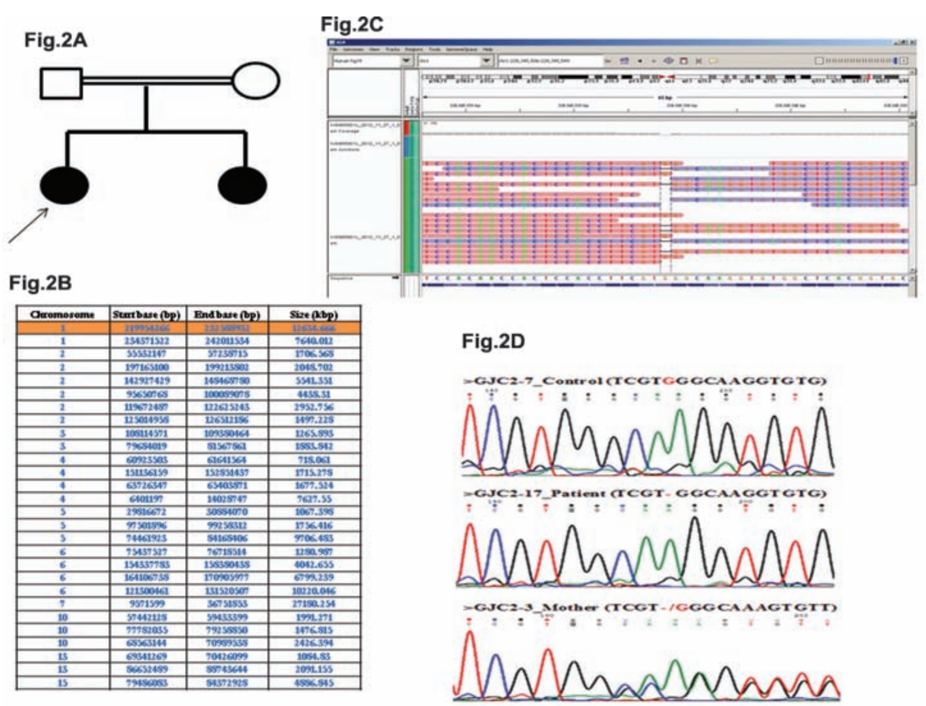


Figure 2. (A) Pedigree of family. **(B)** Results of homozygosity mapping showing regions of overlapping homozygous variants (Coloured region containing the mutation). (**C**) Result of exome sequencing seen in Integrative Genomics Viewer (IGV) showing the single base deletion in *GJC2* gene. (**D**) Sanger sequencing chromatograms along with the sequences showing no deletion in the control and homozygous deletion in the patient and heterozygous deletion in mother.

1. Array Comparative Genomic Hybridization analysis

Array Comparative Genomic Hybridization (CytoScan750K_SNP Array (Affymetrix, Santa Clara, CA, USA)) in the patient and affected sibling did not reveal any significant genomic deletion/ duplication. However there were many regions of loss of heterozygosity (homozygous alleles) which was helpful to narrow down the region of interest in variant identification (Figure 2B).

2. Exome sequencing analysis

Exome capture was performed on genomic DNA samples from patient using TargetSeq Exome Capture kit and sequencing was done on SOLiD 5500xL platform. The reads obtained were analysed using Lifescope™ software by mapping against Human Genome Build 19, followed by detection of single nucleotide variants and indels. The variants identified were compared with those in NCBI dbSNP database (GRCh37/hg19). Variant annotation was done using SeattleSeq for location and predicted function.

After filtering of variants, none of the SNP variants were found to be present in overlapping homozygous regions detected by homozygosity mapping. At the same time five potential Indel variants were identified to lie in overlapping homozygous region. Of these, only one variant; a single base pair (G) deletion in *GJC2* gene, was found to be matching with the clinical phenotype (Figure 2C). This deletion at base number 228345527 on chromosome 1, causes a frameshift at the 23rd amino acid creating a stop codon (TGA) at codon number 38 which is likely to result in a truncated protein. Further analysis for functional significance of this variant is in process.

3. Sanger sequencing analysis

The single base deletion identified in the patient by Exome sequencing was also confirmed by Sanger sequencing (Figure 2D) in both the affected siblings using ABI 3130 Genetic analyzer (Life Technologies, CA, USA). Both parents were found to be heterozygous for the variation.

Publications

1. Aneja A, Sharma A, Dalal A and Sondhi V (2012). R542X mutation in SMPD1 gene: genetically novel mutation with phenotypic features intermediate between type A and type B Niemann-Pick disease. ***BMJ Case Reports*** doi:10.1136/bcr-2012-006959.
2. Angalena R, Aggarwal S, Phadke SR and Dalal A (2012). Compound heterozygote condition in beta thalassemia major due to a novel single nucleotide deletion (-T) at codon 69 in association with IVS 1-5 (G>C) mutation. ***International Journal of Laboratory Hematology*** 34: e7-e9.
3. Bashyam MD, Chaudhary AK, Reddy EC, Reddy V, Acharya V, Nagarajaram HA, Devi ARR, Bashyam L, Dalal AB, Gupta N, Kabra M, Agarwal M, Phadke SR, Tainwala R, Kumar R and Hariharan SV (2012). A founder ectodysplasin A receptor *(EDAR)* mutation results in a high frequency of the autosomal recessive form of hypohidrotic ectodermal dysplasia in India. ***British Journal of Dermatology*** 166: 819-829.
4. Bashyam MD, Chaudhary AK, Sinha M, Nagarajaram HA, Devi ARR, Bashyam L, Reddy EC and Dalal A (2012). Molecular genetic analysis of MSUD from India reveals mutations causing altered protein truncation affecting the C-termini of E1α and E1β. ***Journal of Cellular Biochemistry*** 113: 3122-3132.
5. Dalal A, Bhavani GSL, Togarrati PP, Bierhals T, Nandineni MR, Danda S, Danda D, Shah H, Vijayan S, Gowrishankar K, Phadke SR, Bidchol AM, Rao AP, Nampoothiri S, Kutsche K and Girisha KM (2012). Analysis of the *WISP3* gene in Indian families with progressive pseudorheumatoid dysplasia. ***American Journal of Medical Genetics A*** 158A: 2820-2828.
6. Dutta UR, Pidugu VK and Dalal A (2012). Molecular cytogenetic characterization of a non-robertsonian dicentric chromosome 14;19 identified in a girl with short stature and amenorrhea. ***Case Reports in Genetics*** 2012: Article ID 212065, doi:10.1155/2012/212065.
7. Dutta UR, Pidugu VK and Dalal AB (2012). Molecular and cytogenetic characterization of two patients with recurrent miscarriages and X-autosome translocation. ***Journal of Research in Medical Sciences*** 17: 572-574.
8. Dutta UR, Pidugu VK, Goud V and Dalal AB (2012). Mosaic Down syndrome with a marker: molecular cytogenetic characterization of the marker chromosome. ***Gene*** 495: 199-204.
9. Kumar R, Panigrahi I, Dalal A and Agarwal S (2012). Sickle cell anemia-Molecular diagnosis and prenatal counseling: SGPGI experience. ***Indian Journal of Pediatrics*** 79: 68-74.

10. Padma Priya T and Dalal AB (2012). Tuberous sclerosis: diagnosis and prenatal diagnosis by MLPA. ***Indian Journal of Pediatrics*** 79: 1366-1369.

11. Patil SJ, Bhat V, Dalal A and Santosh JS (2012). Confirmation of the Zechi-Ceide syndrome. ***American Journal of Medical Genetics A*** 158A: 1467-1471.

12. Patil SJ, Ponnala R, Shah S and Dalal A (2012). Mosaic Trisomy 9 presenting with congenital heart disease, facial dysmorphism and pigmentary skin lesions: intricate issues of genetic counseling. ***Indian Journal of Pediatrics*** 79: 806-809.

13. Pidugu VK and Dutta UR (2012). Fluorescence *in situ* hybridization: technology and its illustrated application in molecular medicine. ***Journal of Cytology and Genetics*** 13: 1-8.

14. Ponnala R, Ranganath P, Dutta UR, Pidugu VK and Dalal AB (2012). Phenotypic and molecular characterization of partial trisomy 2q resulting from insertion-duplication in chromosome 18q: a case report and review of literature. ***Cytogenetic and Genome Research*** 136: 229-234.

15. Ranganath P and Pradhan M (2012). Complete Pentalogy of Cantrell with craniorachischisis: a case report. ***Journal of Prenatal Medicine*** 6: 10-12.

16. Ranganath P, Sharma V, Danda S, Nandineni MR and Dalal A (2012). Novel mutations in the neuraminidase-1 *(NEU1)* gene in two patients of sialidosis in India. ***Indian Journal of Medical Research*** 136: 1048-1050.

17. Verma PK, Dalal A, Mittal B and Phadke SR (2012). Utility of MLPA in mutation analysis and carrier detection for Duchenne muscular dystrophy. ***Indian Journal of Human Genetics*** 18: 91-94.

18. Verma PK, Ranganath P, Dalal AB and Phadke SR (2012). Spectrum of lysosomal storage disorders at a medical genetics center in Northern India. ***Indian Pediatrics*** 49: 799-804.

19. Vineeth VS, Malini SS, Sreenivasa G and Dutta UR (2012). High incidence of sperm dysfunction in a varicocele infertile man: case report. ***Asian Pacific Journal of Reproduction*** 1: 63-66.

20. Dutta UR, Pidugu VK, Goud ChV, Hoefers C, Hagemann M and Dalal A. Identification and molecular cytogenetic characterization of a novel complex Y chromosome rearrangement in a boy with disorder of sexual development. ***Gene*** (In press).

21. Dutta UR, Ponnala R, Pidugu VK and Dalal AB. Chromosomal abnormalities in Amenorrhea: a retrospective study and review of 637 patients in South India. ***Archives of Iranian Medicine*** (In press).

22. Dutta UR, Pidugu VK and Dalal AB. Partial proximal trisomy 14: identification and molecular characterization in a girl with global developmental delay. ***Genetic Counseling*** (In press).

23. Love JM, Prosser D, Love DR, Chintakindi KP, Dalal AB and Aggarwal S. A novel glycine decarboxylase gene mutation in an Indian family with nonketotic hyperglycinemia. ***Journal of Child Neurology*** (In press).

24. Ranganath P and Dalal AB. Congenital metacarpal pseudoarthrosis, cleft palate, short stature, advanced bone age, and genu valgum: a new syndrome or a variant of Devriendt syndrome? ***Clinical Dysmorphology*** (In press).

शोध
Research

LABORATORY OF MOLECULAR GENETICS

Centre of Excellence (CoE) for Genetics and Genomics of Silkmoths

Faculty	*J Nagaraju	Khorana Chair
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	Chandrapal Singh	Senior Research Fellow
	S Suresh Kumar	Senior Research Fellow
	Deepa Badrinarayan	Senior Research Fellow
	G Gopinath	Senior Research Fellow
	TR Sitalakshmi	Senior Research Fellow
	Vandana	Senior Research Fellow
	K Akanksha	Senior Research Fellow
	Parveen Kumar	Junior Research Fellow
Other Members	Varsha	Staff Scientist
	VV Satyavathi	Technical Officer
	A Sobhan Babu	Technical Officer
	M Muthulakshmi	Technical Officer
	S Annapurna Bhavani	Technical Officer
	Archana Tomar	Bioinformatician
	MJ Reddy	Technical Assistant
	R Lakshmi Vaishna	Technical Assistant
	Shantanu Shukla	Research Associate (Since Jul. 2012)
	Nagaraj Sambrani	Project Associate(Since Sep. 2012)
	Saikat Chakraborty	Project-Junior Research Fellow
	S Srividya	Project-Junior Research Fellow (Since Oct. 2012)
	Adarsh K Gupta	Project Assistant
	K Shree Rohit Raj	Project Assistant
	Shweta Anjan	Project Assistant (Since May 2012)
	S Babu	CDFD-IKP Fellow

* deceased 31 Dec. 2012

Objectives

1. Introduction of anti-baculoviral property from transgenic silkworms to commercial silkworm strains followed by field trials;
2. Characterization and maintenance of *Bombyx mori* nucleopolyhedrosis virus (BmNPV) resistant transgenic silkworm strains;
3. Studies on host–pathogen interaction as mediated by microRNAs (miRNAs);
4. Development of baculoviral resistant strains using marker assisted selection;
5. Translation of genetic and genomic knowledge of *Bombyx mori* to Indian wild silkmoths;
6. Functional characterization of sex-determination genes in *B. mori*;
7. Sequencing of *B. mori* W chromosome to identify upstream regulator(s) of sex determination; and
8. Understanding the evolutionary dynamics of *B. mori* Z chromosome in relation to autosomes and sex chromosomes of other species.

The progress made in the projects related to transgenic silkworms, miRNAs and genetic diversity of wild silkmoths is reported here.

Summary of work done until the beginning of this reporting year (Upto March 31, 2012)

- We have successfully developed transgenic silkworms resistant to baculovirus and also transferred the resistance property to a commercial high yielding baculovirus susceptible, diapausing silkworm strain through recurrent backcross strategy.
- We have discovered several BmNPV-encoded miRNAs in *B. mori* and found that BmNPV suppresses the small RNA-mediated host defence to successfully proliferate in the host cells by employing bmnpv-miR-1.

- We have characterized partial sequences of silk genes namely Fibroin and Sericins in muga silkworm, *Antheraea assama*.
- We isolated microsatellite markers with a view to understand the phylogeography of ecoraces of tropical tasar silkworm, *A. mylitta* and muga silkworm, *A. assama*.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

Objective 1: Introduction of RNAi-based transgene to high yielding silkworm strains to construct baculovirus resistant strains followed by field trials and maintenance of transgenic silkworm strains.

The anti-baculoviral property in the Nistari genetic background was transferred to a high yielding, baculovirus susceptible bivoltine commercial silkworm strain, CSR2 through transgene (dsRed marker phenotype) selection coupled with microsatellite marker-assisted screening and repeated backcrossing. The various steps involved in the transfer of transgene from Nistari to CSR2 lines are pictorially represented in Figure 1. The recurrent backcrossed lines, which were at BC_4F_{13} were further advanced to BC_4F_{22} generation by rigorous selection for various traits such as fecundity, cocoon shape, cocoon weight, cocoon shell weight, cocoon shell ratio and silk filament length. Also, the introgressed lines were subjected to baculoviral infection to ascertain their resistance level *vis-a-vis* control lines. The CSR2 line incorporated with the transgene has commercial silk and cocoon traits (~1.4 g cocoon weight; >800 m filament length) similar to the nontransgenic CSR2 line. The transgenic silkworm lines, the introgressed transgenic lines, other productive recipient silkworm lines and various genetic stocks are being monitored for the transgene stability, viral resistance and unique traits of the strains under laboratory conditions at the collaborating institutes namely Central Silk Board (CSB), Bangalore and Andhra Pradesh State Sericulture Research and Development Institute (APSSRDI), Hindupur. CDFD in coordination with Biotech Consortium India Limited (BCIL) approached the Review Committee on Genetic Manipulation (RCGM) by providing a road map for field trials of silkworms. As per the recommendations of RCGM, three transgenic lines will be tested in selected R&D institutes of CSB and APSSRDI.

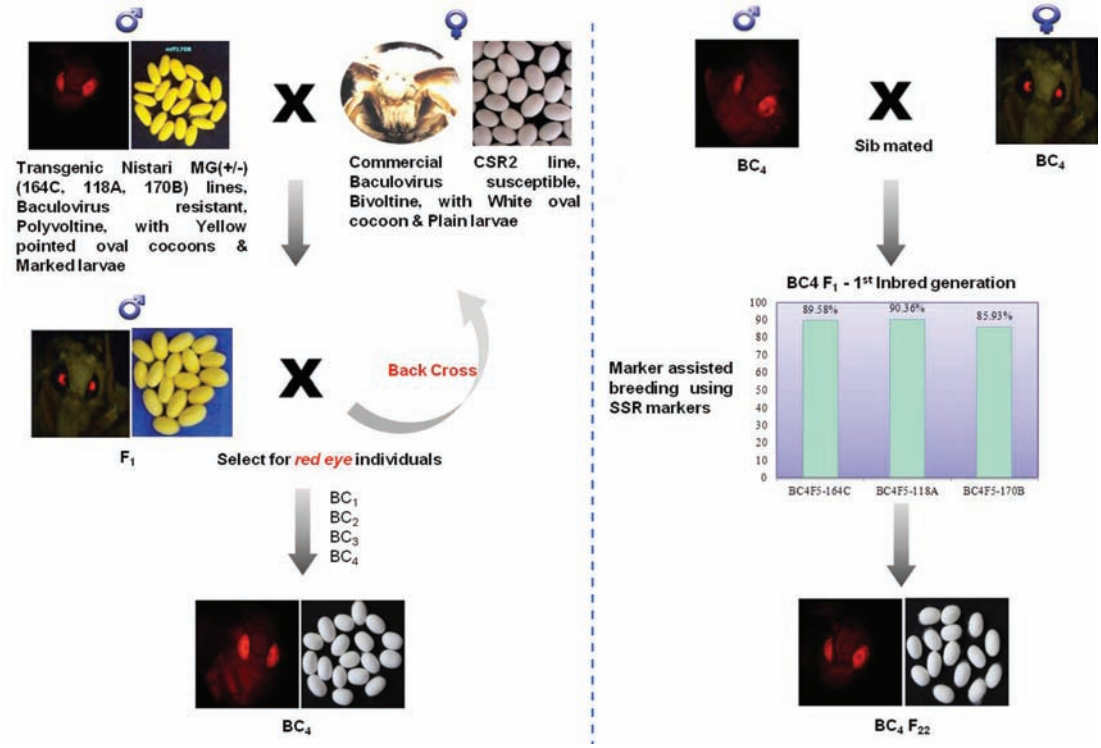

Figure 1. Schematic diagram showing introduction of transgene (dsRNA for multiple essential baculoviral genes) from the transgenic Nistari lines to high yielding CSR2 strain through recurrent backcross strategy. The recurrent backcrossed lines were further advanced to BC4F22 generation.

Objective 2: Studies on host-pathogen interaction as mediated by miRNAs

In recent years, the role of miRNAs in different biological processes including host-pathogen interaction is a topic of intensive research. Many of the recent studies have indicated the key role of virus-encoded miRNAs in regulating various host defense responses. In the present study, we have reported a BmNPV encoded miRNA, bmnpv-miR-3, that regulates the expression of its own late genes (*cis* targets) including the basic DNA binding protein (P6.9), which is important for the late replication of virus in the host, B. mori (Figure 2A-C). We have performed both cell culture and in vivo experiments to demonstrate the role of bmnpv-miR-3 in the infection cycle of BmNPV in the host. Our results showed that bmnpv-miR-3 expresses during early stage of infection and negatively regulates the expression of P6.9 and other late genes, which are crucial for the virus in the later stage of infection. We noticed a remarkable increase in BmNPV load, when bmnpv-miR-3 was blocked by Locked Nucleic Acid (LNA) – modified oligonucleotides, implying the involvement of its target genes in BmNPV proliferation. Besides, knockdown of the viral RNA polymerase subunit resulted in a decrease in the expression of cis targets, but an increase in the expression of bmnpv-miR-3, suggesting that bmnpv-miR-3 is likely to be transcribed by host RNA polymerase (Figure 3A-C). Our results suggest that bmnpv-miR-3 mediated controlled regulation of BmNPV P6.9 and other late genes in the early stage of infection provides suitable environment for BmNPV to escape the early immune responses of the host.

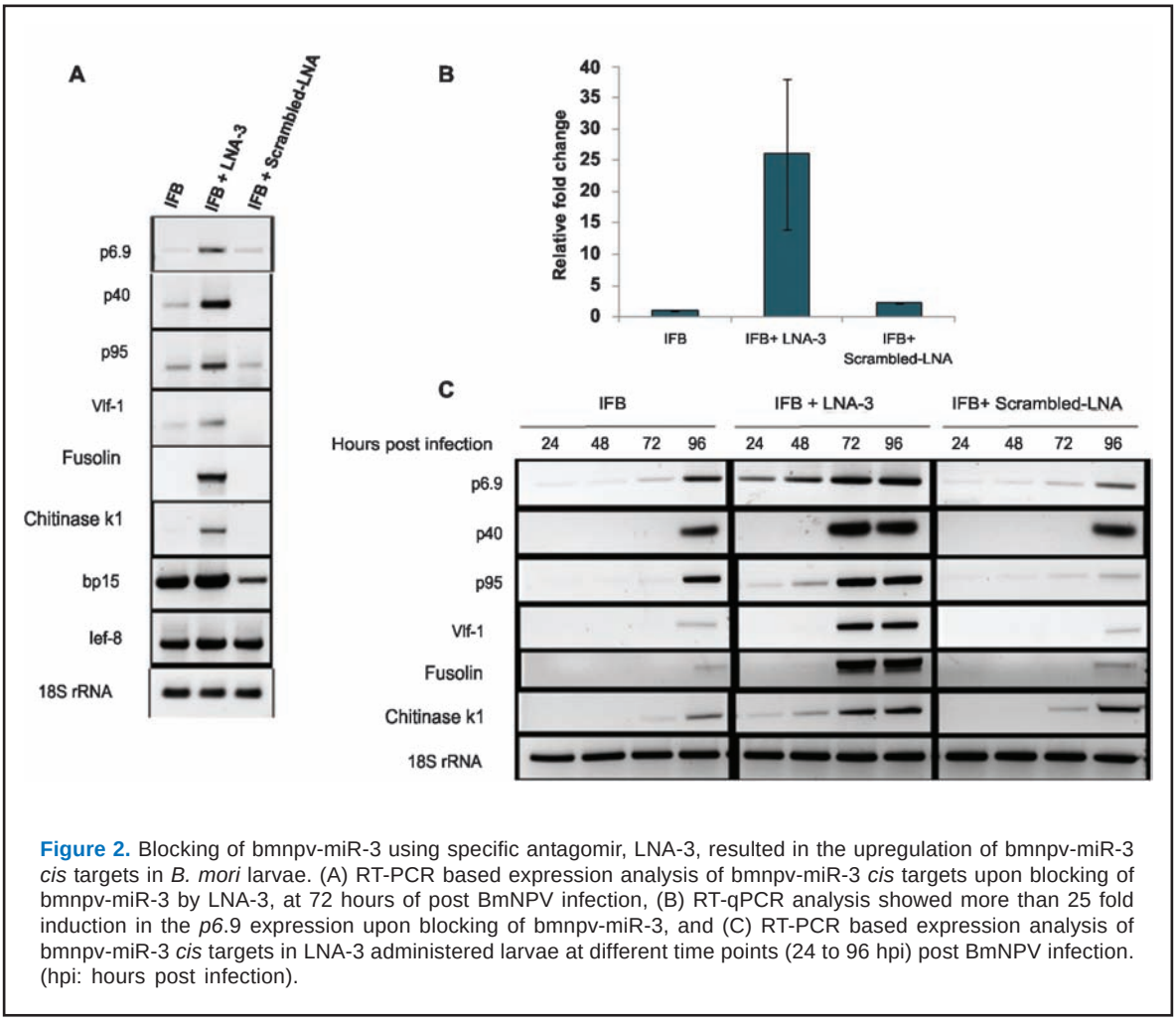

Figure 2. Blocking of bmnpv-miR-3 using specific antagomir, LNA-3, resulted in the upregulation of bmnpv-miR-3 *cis* targets in *B. mori* larvae. (A) RT-PCR based expression analysis of bmnpv-miR-3 *cis* targets upon blocking of bmnpv-miR-3 by LNA-3, at 72 hours of post BmNPV infection, (B) RT-qPCR analysis showed more than 25 fold induction in the *p6*.9 expression upon blocking of bmnpv-miR-3, and (C) RT-PCR based expression analysis of bmnpv-miR-3 *cis* targets in LNA-3 administered larvae at different time points (24 to 96 hpi) post BmNPV infection. (hpi: hours post infection).

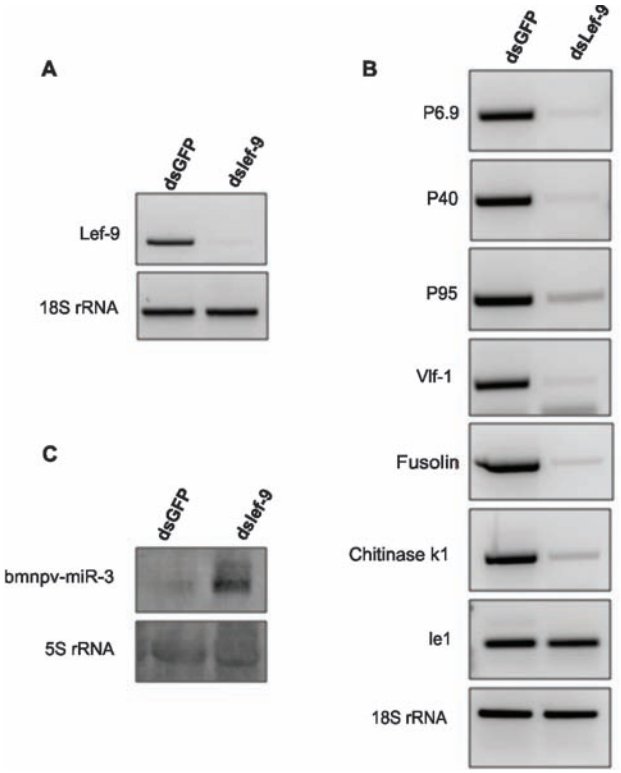

Figure 3. Knockdown of the RNA polymerase subunit gene, *lef*-9 of BmNPV, negatively affects expression of bmnpv-miR-3 *cis*-targets. (A) RT-PCR analysis showing knockdown of *lef*-9 in *B. mori* larvae, (B) Expression analysis of bmnpv-miR-3 *cis*-targets upon *lef*-9 knockdown, determined by RT-PCR, and (C) Enhanced bmnpv-miR-3 expression observed upon knockdown of *lef*-9, examined by Northern blot.

Objective 3: Characterization of silk genes in Indian golden silkmoth (*A. assama*)

The Indian golden silkmoth, popularly known as muga silkmoth, is a semi-domesticated silk producing insect confined to a narrow habitat range of the Northeastern region of India. The beautiful muga silk with golden luster is one of the most sought-after biomaterials for its indispensible properties like tensile strength, elasticity and luster. The characterization of the silk genes of *A. assama* is hampered by the unavailability of its genomic data. So we carried out transcriptome sequencing of posterior and middle silkgland tissues and filtered for Fibroin specific sequences based on the conserved 5' and 3' termini of other reported Fibroin sequences. The resulting Fibroin specific contigs were used to design primers specific to the 5' and 3' termini. Long PCR on genomic DNA resulted in the full length (9 kb) amplification of Fibroin gene, which was cloned in to pWKS30, a low-copy plasmid. The full length Fibroin gene is inclusive of a short and highly conserved 5' non-repetitious terminus of 407 bp and a shorter 3' non-repetitious terminus of 252 bp. The gene has one small intron of 131 bp in its 5' non-repetitious region and the rest 90% of the gene codes for the Alanine-Glycine rich highly repetitious crystalline portion of Fibroin protein. This repetitious nature deprecates the possibility of conventional primer-walking for progressive sequencing. Therefore, the full length sequencing was accomplished through a series of restriction digestions followed by sub-cloning and re-sequencing. As part of this full-length sequencing, the Fibroin insert was released and digested separately with specific restriction enzymes. The subclones, which were less than 1kb, were sequenced directly; while the longer ones were digested again for further sequencing. The restriction map based on the overlapping sequences of the sub-clones was confirmed by the poly-Alanine and non poly-Alanine repeat motifs that resulted in the complete sequence of Fibroin transcript. Northern hybridization revealed the expression of Fibroin exclusively in the posterior silkgland (PSG).

Objective 4: Genetic diversity and population structure of *A. assama*

Owing to the prevailing socio-political problems, the muga silkworm habitats in the Northeastern region have not been accessible, hampering the phylogeography studies of this rare silkmoth. Recently, we have been successful in our attempt to collect muga cocoon samples, although to a limited extent, from their natural habitats (Figure 4). Out of 87 microsatellite markers developed previously for *A. assama*, 13 informative markers were employed to genotype 97 individuals from six populations to analyze their population structure and genetic variation. We observed highly significant genetic diversity in one of the populations (WWS-1, a population derived from West Garo Hills region of Meghalaya state). Further analysis with and without WWS-1 population revealed that dramatic genetic differentiation (global FST = 0.301) was due to high genetic diversity contributed by WWS-1 population. Analysis of the remaining five populations (excluding WWS-1) showed a marked reduction in the number of alleles at all the employed loci. Structure analysis showed the presence of only two clusters: one formed by WWS-1 population and the other included the remaining five populations, inferring that there is no significant genetic diversity within and between these five populations, and suggesting that these five populations are probably derived from a single population (Figure 4). Patterns of recent population bottlenecks were not evident in any of the six populations studied. *A. assama* inhabiting the WWS-1 region revealed very high genetic diversity, and was genetically divergent from the other five populations studied. These efforts should be continued to identify such populations from this region as well as other muga silkworm habitats. The information generated will be very useful in conservation of the dwindling muga culture in Northeast India.

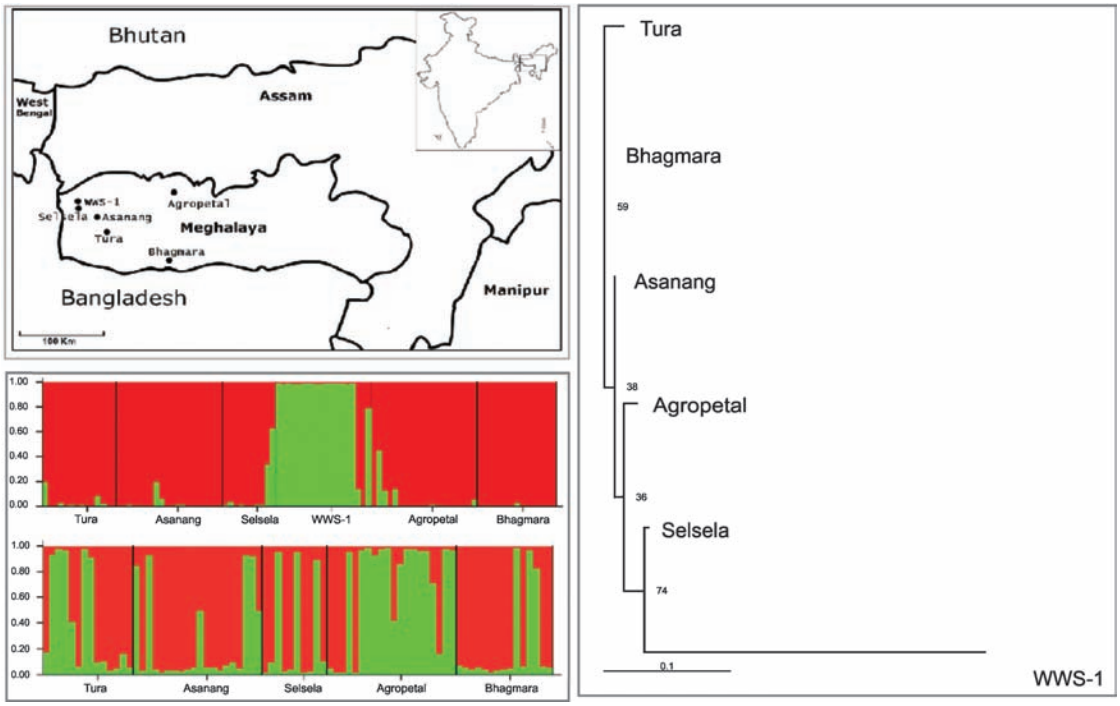

Figure 4. Population structure of six *A. assama* populations.

APEDA-CDFD CENTRE FOR BASMATI DNA ANALYSIS

Faculty	*J Nagaraju	Khorana Chair
Other Members	Sabahat Noor	Technical Officer
	Manju Shukla	Project Assistant

* deceased 31 Dec. 2012

Objectives

1. Testing the purity of Basmati samples received from Export Inspection Council (EIC), Ministry of Commerce, Govt. of India, Basmati rice exporters from India and other countries; and
2. Fine mapping and characterization of the candidate genes governing grain appearance traits of Basmati rice.

Basmati samples analyzed at APEDA-CDFD Centre in the current reporting year (April 1, 2012 – March 31, 2013)

During the period under report, a total of 200 (EIC samples 194, Private samples 6) Basmati samples were analyzed and the number of samples indicating the percentage of adulteration with non-basmati rice is shown in figure below.

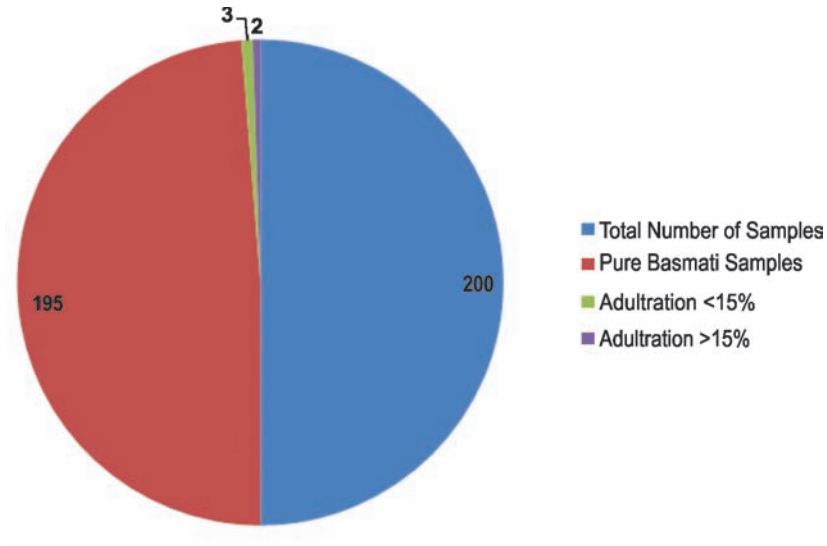

Figure 5. Basmati samples analyzed at APEDA-CDFD centre in the current reporting year (2012–2013).

Project 1: Fine mapping and association study of candidate genes in a region on chromosome 5 possibly controlling grain appearance traits of Basmati rice.

Summary of work done until the beginning of this reporting year (Upto March 31, 2012)

Previously, 47 Quantitative Trait Loci (QTLs) governing 18 economically important traits of Basmati rice have been identified in a mapping population of 189 F_2 individuals of a cross between Basmati370 and Jaya by screening 134 polymorphic microsatellite markers. As F_2 is a primary mapping population wherein phenotypic data was recorded on a single plant without any replications, it was decided to confirm the same QTLs in a permanent population like Recombinant Inbred Lines (RILs). Accordingly, the F_2 material has been advanced to F_7 generation comprising 155 RILs where phenotyping of 18 traits was carried out.

Details of progress made in the current reporting year (April 1, 2012 – March 31, 2013)

During the period under report, the DNA was isolated from 155 RILs and is being screened with the same polymorphic SSR markers which have been used in our previous F_2 study. Out of 74 SSR markers screened so far, 52 microsatellites and 1 indel marker present in the region harbouring grain size QTLs, already identified in F_2 population between the markers RM289 and RM18600 on chromosome 5, were selected for marker analysis in the RILs. One microsatellite marker i.e., RM18582 was found to show close association with the grain size QTLs. This marker has the potential to be used in marker-assisted improvement of the grain size in Basmati rice.

The QTL qGL5.1 was identified for grain length by interval mapping in the marker interval of RM6024 and RM1237 with phenotypic variation explained (PVE) of 3.7%, which may be a minor QTL or harboring a modifier gene. A major effect QTL, qGB5.1 was identified on chromosome 5 in the marker interval of RM1237 - RM18582 with PVE of 3.58% by composite interval mapping (CIM) and 4.51% by interval mapping (IM) but located far away from the consistent QTL qGW offering room for further dissecting into a gene. A single QTL qLB5.1 for length and breadth (LB) ratio in the marker interval of RM1237 and RM18582 was identified with PVE of 10.7% in the vicinity of the QTLs controlling grain length and grain breadth as LB ratio is a derived trait from the grain length and grain breadth. The genetic distance of the flanking markers harbouring QTL cluster in the previous study was 26.5 cM whereas in the present study it was possible to narrow it down to 15.7 cM. The physical distance also has come down from 11,128 kb to 685 kb.

Screening the mapping population of 155 RILs with the remaining 60 microsatellites is in progress for confirmation and fine mapping of the grain size QTL. Future work plan includes:

1. Further narrowing down of targeted QTL region through:

a. Association mapping;

b. Development of advanced backcross population and near isogenic lines (NILs);

c. Prediction of candidate genes and their structural and functional analysis.

2. Use of SoLiD data to align genomic sequence of the identified QTL region with rice reference genome sequences to check for the variations at genomic level.

Publications

1. Arunkumar KP, Sahu AK, Mohanty AR, Awasthi AK, Pradeep AR, Urs SR and Nagaraju J (2012). Genetic diversity and population structure of Indian golden silkmoth (*Antheraea assama*). ***PLoS One*** 7: e43716.

2. Begum H, Reddy TM, Malathi S, Reddy BP, Arcahk S, Nagaraju J and Siddiq EA (2012). Molecular analysis for genetic distinctiveness and relationships of indigenous landraces with popular cultivars of mango (*Mangifera indica* L.) in Andhra Pradesh, India. ***The Asian and Australasian Journal of Plant Science and Biotechnology*** 6: 24-37.

3. Narra D and Srivatsava V (2012). Quantitative competitive PCR for the detection and quantification of genetically modified cotton event MON-531. ***International Journal of Basic and Applied Sciences*** 1: 92-102.

4. Pidugu VK, Pothula RKS, Narra D and Srivatsava V (2012). Development of a multiplex polymerase chain reaction method for specific detection of genetically modified cotton events MON 531 and MON 15985. ***International Journal of Basic and Applied Sciences*** 1: 45-53.

5. Siddiq EA, Vemireddy LR and Nagaraju J (2012). Basmati rices: genetics, breeding and trade. ***Agricultural Research*** 1: 25-36.

6. Singh CP, Singh J and Nagaraju J (2012). A baculovirus-encoded microRNA (miRNA) suppresses its host miRNAs biogenesis by regulating the exportin-5 co-factor Ran. ***Journal of Virology*** 86: 7867-7879.

7. Singh YT, Mazumdar-Leighton S, Saikia M, Pant P, Kashung S, Neog K, Chakravorty R, Nair S, Nagaraju J and Babu CR (2012). Genetic variation within native populations of endemic silkmoth *Antheraea assamensis* (Helfer) from Northeast India indicates need for *in situ* conservation. ***PLoS One*** 7: e49972.

8. Sinha DK, Nagaraju J, Tomar A, Bentur JS and Nair S (2012). Pyrosequencing-based transcriptome analysis of the Asian rice gall midge reveals differential response during compatible and incompatible interaction. ***International Journal of Molecular Sciences*** 13: 13079-13103.

9. Yonemura N, Tamura T, Uchino K, Kobayashi I, Tatematsu K, Iizuka T, Sezutsu H, Muthulakshmi M, Nagaraju J and Kusakabe T (2012). PhiC31 integrase-mediated cassette

exchange in silkworm embryos. ***Molecular Genetics and Genomics*** 287: 731-739.

10. Subbaiah EV, Royer C, Kanginakudru S, Satyavathi VV, Babu AS, Sivaprasad V, Chavancy G, DaRocha M, Jalabert A, Mauchamp B, Basha I, Couble P and Nagaraju J (2013). Engineering silkworms for resistance to baculovirus through multigene RNA interference. ***Genetics*** 193: 63-75.

11. Surapaneni M, Vemireddy L, Begum H, Reddy P, Neetasri C, Nagaraju J, Anwar SY and Siddiq EA. Population structure and genetic analysis of different utility types of mango (*Mangifera indica* L.) germplasm of Andhra Pradesh state of India using microsatellite markers. ***Plant Systematics and Evolution*** (In press).

Other publications

1. Arunkumar KP (2012). Review of: Annual Review of Genetics, 2011. Bonnie L. Bassler *et al.* (eds). ***Current Science*** 103: 947-949.

Patents

1. J Nagaraju *et al.* Single tube multiplex assay for detection of adulterants in Basmati rice samples.

Indian Patent Application No.: 662/CHE/2006
Indian Patent No.: 251825
Date of grant: April 10, 2012

LABORATORY OF GENOMICS AND PROFILING APPLICATIONS

Faculty	Madhusudan Reddy Nandineni	Staff Scientist
PhD Students	Anujit Sarkar	Senior Research Fellow
	Soumya Rao	Junior Research Fellow
	Mugdha Singh	Junior Research Fellow (Since Aug. 2012)
Other Members	G Sreeja Reddy	Project Assistant
	Srujana Nagireddy	Project Assistant (Till Aug. 2012)
	Yamini Sharma	Project-Junior Research Fellow (Since Sep. 2012)

Objectives

1. Development of novel strategies/methodologies for enrichment of human DNA from mixtures containing human and non-human DNAs for DNA profiling-based human identification; and
2. To study the human genetic diversity among various population groups in India.

Project 1: Development of novel strategies/ methodologies for enrichment of human DNA from mixtures containing human and non human DNAs for DNA profiling based human identification

Summary of work done until the beginning of this reporting year (Upto March 31, 2012)

Devising novel strategies for forensic human DNA identification is critical to circumvent the problems associated with the recalcitrant and challenging forensic samples such as those contaminated with non-human DNAs and PCR inhibitors. Enrichment of forensically relevant short tandem repeats (STRs), which showed promising results in our preliminary studies had been adapted and standardized for this purpose. In an effort to develop an STR-enrichment protocol for human identification (HID) purposes, three different methods of STR enrichment namely, primer extension capture (PEC), short hybridization and long hybridization were evaluated to test their efficiency to enrich STR regions from simulated forensic samples. Initial experiments with these simulated samples demonstrated that all the three methods were proficient in enriching the target loci in the presence of high amounts of non-human DNA contamination, whereas further experiments with PCR inhibitors revealed that PEC and short hybridization techniques were efficient (as compared to long hybridization protocol) in overcoming the effects of PCR inhibitors in DNA profiling. As described in the previous report, the enrichment strategy demonstrated an increased tolerance to various potent PCR inhibitors such as hematin, humic acid and tannic acid up to 5-fold when as little as 5 ng of initial template DNA was used to generate the STR profiles by employing the commercial multiplex STR kit (Amp*Fl* STR® Identifiler® Plus, Life Technologies, Inc.).

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

Since the challenging forensic samples usually contain limiting amounts of human DNA admixed with various PCR contaminants, sensitivity is an important factor for any enrichment technique. Hence, the experiments with simulated samples contaminated with PCR inhibitors were also carried out with as scant as 2 ng of input DNA. Calcium, which is a component found abundantly in bone and teeth samples and considered as a potent PCR inhibitor was also included for the evaluation of enrichment method. It was observed that both PEC and short hybridization were able to generate the STR profiles from 2 ng of initial template DNA when mixed with up to 1 mM of hematin, 0.4 µg/µl of humic acid, 1 µg/µl of tannic acid and 4 mM of calcium, which was ~3-4 fold increase in tolerance as compared to the STR profiles generated with the same commercial multiplex STR kit without enrichment (controls). Though, these two methods (PEC and short hybridization) have proved to be successful with comparable enrichment efficiencies, PEC method, where the primers got extended after hybridization with target templates, was assumed to be more stable in withstanding stringent washing conditions than partial double stranded molecules obtained after hybridization. Hence, further STR enrichment experiments with simulated samples were carried out employing PEC method.

To simulate the conditions of forensic samples as close as to their natural context, various concentrations of humic acid, tannic acid and calcium were mixed simultaneously with the human DNA along with bacterial DNA since the possibility of occurrence of all these inhibitors together with non-human DNAs in buried human remains such as skeletal bones is very high under normal circumstances. These simulated DNA samples, heavily infested with all possible PCR inhibitors were subjected to enrichment by PEC method for the recovery of respective STR loci, followed by multiplex PCR amplification of these loci employing Amp*Fl*STR® Identifiler® plus PCR amplification kit. Analysis of the results revealed that DNA profiles could be successfully obtained from as little as 2 ng of template human DNA contaminated with 15% of the maximum independent tolerance limits of each of the inhibitors (mentioned above) coupled with contamination of non-human DNA at 1:10000 ratio (human to bacterial DNA by weight).

Validation of the enrichment method on forensic samples

As the above-mentioned PEC enrichment technique proved to be successful in sequence-specific capture of STR regions in simulated samples, the strategy was tested with real life forensic samples for validation studies. DNA samples obtained from skeletal bones, teeth, fabric, etc. which generated either partial STR profile or no profile were subjected to enrichment by PEC method.

As observed from the STR profiles obtained from few of the highly contaminated forensic samples, multiplex STR PCR kits were unable to generate larger amplicons (as they are more vulnerable to inhibition), even though sufficient quantities of intact human DNA was detected. However, enrichment of STR loci by PEC method prior to STR amplification facilitated in minimizing the effect of the inhibitors and generating the complete STR profile (as represented in Figure 1).

In sample 2, qPCR assay was unable to detect any human DNA and even the commercial STR kit failed to generate any STR profile, but the same sample upon enrichment with PEC method prior to multiplex PCR showed the amplification of maximum number of STR loci, demonstrating the robustness and reliability of hybrid-capture method in enhancing the quality of template DNA during HID testing. This strategy was further used to successfully generate STR profiles from various challenging forensic exhibits. Thus the application of sequence-specific STR capture and enrichment strategy for challenging and recalcitrant forensic samples would be of tremendous help to the forensic DNA profiling community in increasing the success rate of DNA profiling of these exhibits.

Project 2: To study human genetic diversity in various population groups in India.

Summary of work done until beginning of this reporting year (Upto March 31, 2012)

The second area of interest of the laboratory is to assess the genetic diversity among different population groups in India and to examine the phenotypic effects of genetic variation(s) within and between population groups. As part of the genotype-phenotype correlation studies, SNPs implicated in skin pigmentation were tested for association in different Indian populations. Further, as a step towards designing a SNP-based forensic panel for HID in Indian populations, Genplex panel (a 48-plex SNP-based genotyping system for HID proposed elsewhere for various global populations) was tested for its applicability in the Indian populations and was found to be less informative in these populations as only a subset of the panel (15-20 SNPs) was found to possess the desired characteristics (high heterozygosity and low F_{st}) for forensic HID purposes. A preliminary approach to shortlist additional SNPs for HID testing in Indian populations was described in the previous report.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

1. Evaluation of Kidd SNP panel in Indian populations.

Dr. Kenneth Kidd proposed a SNP-based panel comprising of 92 SNPs for HID testing. The panel had met the desired criteria for HID testing in various continental populations, but was not tested in Indian populations. Hence, it was decided to test its applicability in Indian population groups. In this study, the Illumina *GoldenGate*® Genotyping Assay system (96-plex) was employed to genotype more than 150 samples belonging to unrelated individuals residing in different geographical locations of India, like Andhra Pradesh, Assam, Jharkhand, Jammu, Tamil Nadu and West Bengal. The genotyping assay was carried out as per manufacturer's protocol. Statistical analyses revealed that the mean call rate of the assay was 97.65%. Three of the 92

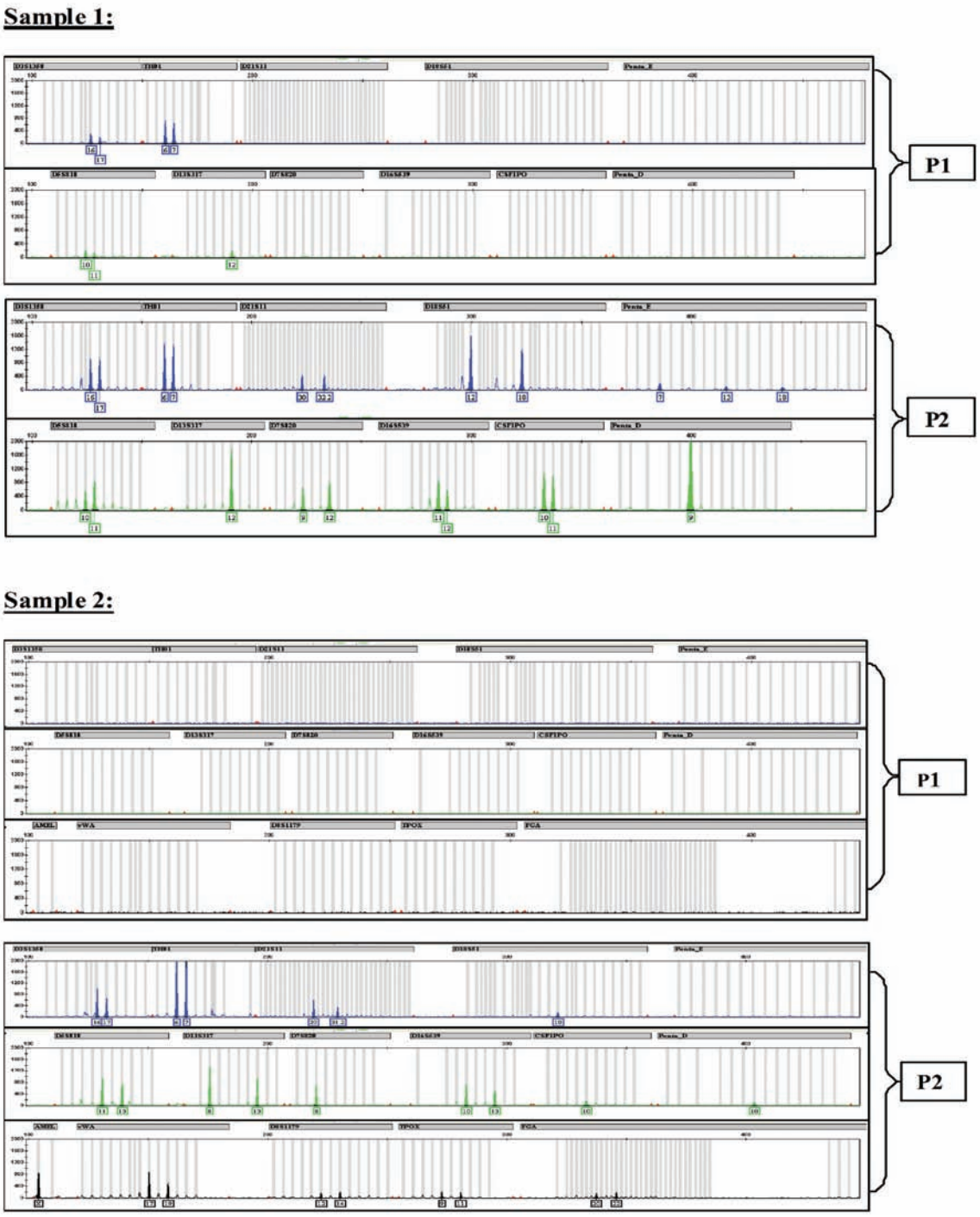

Figure 1. Samples 1 and 2 represent the electropherograms of forensic samples obtained after amplification using multiplex STR PCR amplification kit. Panels P1 and P2 represent STR profiles, without and with STR enrichment by PEC method, respectively.

SNPs tested, which had less than 90% call rate, were discarded from further analysis. The genetic variation/ allele distribution studies were carried out at two levels, *viz.*, within population and between populations.

(a) Within population studies

The within population study was carried out separately for each of the populations to determine the genetic variation and applicability of the Kidd panel. The summary of the within population study is shown in Table 1. As can be gleaned from the table, the mean minor allele frequency (MAF) of the whole panel was within the acceptable limits for HID testing in accordance to similar studies reported elsewhere, however, for many of these loci when genotyped in Indian populations, the MAF was found to be low, which tended to decrease the overall discriminating power of the HID SNP panel in these populations and hence were discarded from the proposed SNP panel.

Parameter	AP	Assam	Jharkhand	Jammu	Tamil Nadu	West Bengal
Average MAF	0.3854	0.3555	0.3846	0.3963	0.3709	0.3437
Average Heterozygosity	0.4436	0.4905	0.4962	0.4792	0.4585	0.465
LD pairs	5	2	4	5	4	2

Table 1. Summary statistics of each population. AP: Andhra Pradesh. MAF: Minor allele frequency. LD pairs: SNP pairs found to be in linkage disequilibrium

Further, many SNP pairs were also found to be in linkage disequilibrium (LD), perhaps owing to their physical linkage or other evolutionary factors, which has further reduced the number of informative SNPs for HID testing (due to absence of independent assortment of these loci).

(b) Between population studies

The F_{st} studies were mainly carried out across the six populations mentioned above. When SNPs satisfying the desired criteria *i.e.*, heterozygosity > 0.4 and F_{st} < 0.02, were sought to be identified, it was found that only 30 of the 96 SNPs tested satisfied these conditions; a number which is not sufficient to give high power of discrimination desirous for a HID SNP panel. In order to devise a SNP panel for HID testing for Indian populations (consisting of 60-80 SNPs), we wished to screen and incorporate additional SNPs appropriate for these populations. Hence additional SNPs were screened from public databases which could potentially form the identity-testing SNPs in Indian populations.

2. Screening SNPs from databases to obtain desired SNPs to be tested for Indian populations

The screening strategy reported in the previous report was modified slightly for SNP screening, wherein, instead of obtaining the SNPs using filters available through the SPSmart database alone, all the genotypes for the listed SNPs (Illumina_Human660Quad chip containing 592652 SNPs) typed in all the major SNP databases (HapMap data, Release # 28 dated August 2010, 1000 Genome Project data, Phase I, May 2011, CEPH U. Stanford HGDP (Human Genome Diversity Project) dataset and CEPH NIH-U, Michigan HGDP dataset) were downloaded and classified according to their chromosomal locations. Only unique unrelated samples (N=2744) were analyzed using Powermarker software. The samples were divided according to major geographical regions as mentioned in SPSmart and each region was considered as a single population for further analysis.

The allele distribution data available from the databases was downloaded and used to calculate the statistical parameters like heterozygosity and F_{st} and the SNPs which successfully passed the desired filters were shortlisted and various statistical tools were employed to screen the SNPs with desired characteristics. A summary of the various filters utilized for this purpose is shown in Figure 2. At the end of this screening exercise, ~ 270 SNPs have been shortlisted and in future these would be genotyped in Indian populations employing the Illumina *GoldenGate*® Genotyping Assay system to test for their suitability for HID testing.

3. Studies on human salivary microbiome in Indian populations and its implications on human genetic diversity studies (New project)

Metagenomics aims at studying uncultured organisms to understand the true diversity of microbes, their functions, cooperation and evolution, in environments such as soil, water, ancient remains of animals and in sites on living organisms. In the context of human beings, the commensal microbial symbionts (microbiome) are estimated to be highly diverse and provide traits

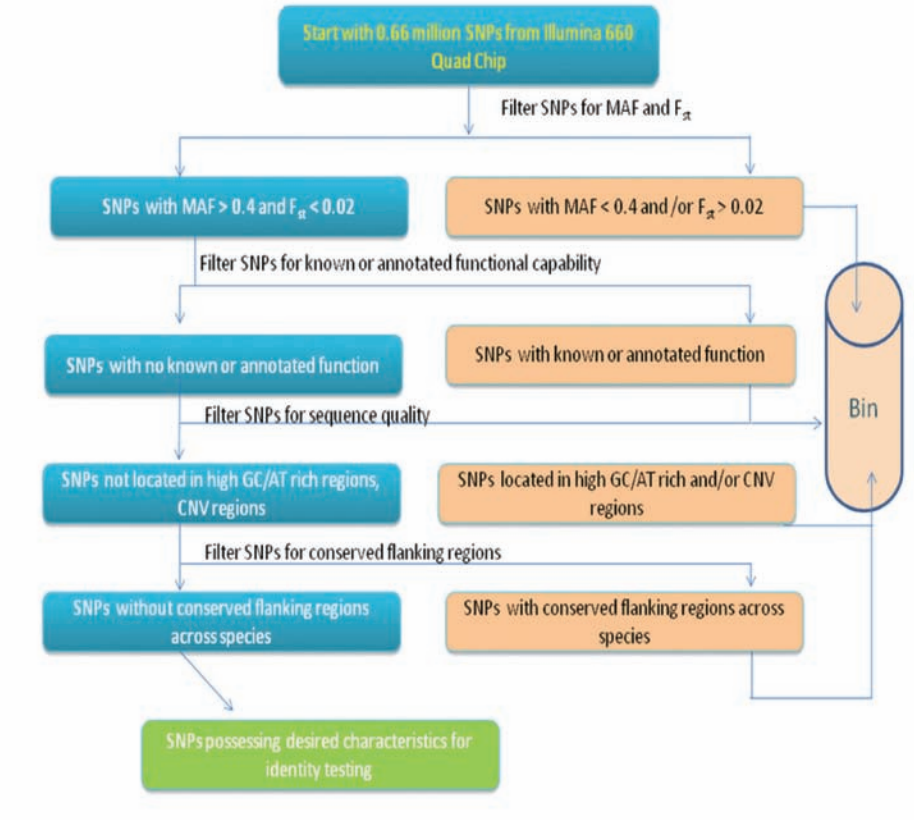

Figure 2. Outline of the strategy for short listing SNPs for human identification in Indian populations.

that humans did not need to evolve on their own. Though there are several microbial habitats in the human body, but the oral cavity is unique as it provides immense possibilities for a diverse range of microbiota in the intraoral niches including dental surfaces, cheek, hard palate, tongue and saliva. The primary objective of the project is to study the human salivary microbiome to identify the various bacterial taxa in saliva that may be able to provide insights into human population structure and migrations.

The microbial diversity would be studied on the basis of the occurrence and prevalence of various bacterial genera in the saliva of the samples. It is planned to study the microbiome diversity in saliva samples sourced from various geographical locations (States) in India. The genera will be identified by amplification and sequencing of the 16S rRNA gene sequences and comparing them with the sequence entries in the ribosomal database project (RDP-II). A study of the variation in the occurrence and prevalence of various bacterial genera would provide the microbial diversity of the salivary microbiome in Indian populations and will provide new insights into the population structure of various Indian populations.

Publications

1. Dalal A, Bhavani GSL, Togarrati PP, Bierhals T, Nandineni MR, Danda S, Danda D, Shah H, Vijayan S, Gowrishankar K, Phadke SR, Bidchol AM, Rao AP, Nampoothiri S, Kutsche K and Girisha KM (2012). Analysis of the *WISP3* gene in Indian families with progressive pseudorheumatoid dysplasia. ***American Journal of Medical Genetics A*** 158A: 2820-2828.

2. Ranganath P, Sharma V, Danda S, Nandineni MR and Dalal A (2012). Novel mutations in the neuraminidase-1 *(NEU1)* gene in two patients of sialidosis in India. ***Indian Journal of Medical Research*** 136: 1048-1050.

LABORATORY OF FUNGAL PATHOGENESIS

Understanding the Pathobiology of an Opportunistic Human Fungal Pathogen *Candida glabrata*

Faculty	Rupinder Kaur	Staff Scientist
PhD Students	Gaurav Bairwa	Senior Research Fellow
	Maruti Nandan Rai	Senior Research Fellow
	Sapan Borah	Senior Research Fellow
	Vivek Kumar Srivastava	Senior Research Fellow
	Vandana Sharma	Senior Research Fellow
	Mubashshir Rasheed	Junior Research Fellow
Other Members	Suneetha KJ	Technical Officer
	Shivarathri Raju	Project Assistant
	Ritu Taigwal	Project Assistant (Since Sep. 2012)
	Gujjula Rahul	Project Assistant (Since Nov. 2012)

Candida *spp.* are the leading cause of disseminated fungal infections and rank fourth among the most common nosocomial pathogens. *C. glabrata*, a regular commensal of human oral cavity and gastrointestinal tract, accounts for 12-20% of total Candida blood stream infections. *C. glabrata* infections, which range from mild mucosal to severe life-threatening systemic infections in immunocompromised individuals, are difficult to treat, in part, owing to intrinsic low susceptibility of *C. glabrata* towards widely used azole antifungals. *C. glabrata* is a haploid budding yeast which exists in the blastoconidial form in both commensal and pathogenic states. Research in our laboratory is aimed at a better understanding of the interaction of *C. glabrata* with host immune cells, antifungal drug resistance mechanisms and iron uptake and homeostasis mechanisms operational in *C. glabrata*.

Project 1: Functional genomic analysis of *C. glabrata*-macrophage interaction.

Objectives

1. Analysis of intracellular behavior;
2. Screening of a *C. glabrata* mutant library for altered survival profiles; and
3. Identification and analysis of genes required for survival *in vitro*.

Summary of work done until the beginning of this reporting year (upto March 31, 2012)

Using an *in vitro* system comprised of human monocytic cell line THP-1, we demonstrated that wild-type *C. glabrata* cells were able to inhibit maturation of phagolysosome, counteract/survive the reactive oxygen species (ROS) generated and replicate in THP-1 macrophages. We further showed that *C. glabrata* cells, upon phagocytosis by THP-1 macrophages, modify their chromatin architecture to a closed, condensed form and mutants defective in chromatin remodeling and/or DNA damage repair are attenuated for virulence in the murine model of disseminated candidiasis. Based on global transcriptional profiling, biochemical and microscopy data, we proposed that *C. glabrata* response to THP-1 macrophage internal milieu is composed of three distinct phases: an Early-, a Mid- and a Late-phase. While the Early-phase (0-2 h) is defined by activated DNA damage repair signaling, shut-down of translational machinery and remodeled carbon metabolism, the Mid-phase (3-12 h) represents the adaptive response of *C. glabrata* to macrophage environment and is characterized by hetero-chromatinization of the *C. glabrata* genome. Late-phase *C. glabrata* cells symbolize proliferating cells with active transcriptional machinery. Additionally, by screening of a library of 18,350 *C. glabrata* Tn*7* insertion mutants for altered survival profiles in THP-1 macrophages, via signature-tagged mutagenesis (STM) approach, we identified a set of 56 genes that are required to survive and/or replicate in the intracellular milieu of THP-1 cells. Identified genes were implicated in diverse biological processes including chromatin and cell wall organization, signal transduction and golgi vesicle transport.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

Reconfigured carbon metabolism, epitomized by decreased glycolysis and increased

gluconeogenesis, glyoxylate cycle and fatty acid degradation is a characteristic signature of several macrophage-internalized fungal pathogens including *Cryptococcus neoformans*, *C. albicans* and *C. glabrata*. Thus, to investigate the possibility whether glucose limitation and presence of alternative carbon sources in the macrophage internal milieu act as cues for remodelling of chromatin, we performed three experiments. First, we checked the ability of mutants defective in chromatin organization to utilize different compounds as sole carbon sources and found *Cgrsc3-aΔ*, *Cgrsc3-bΔ*, *Cgchz1* and *Cghfi1* mutants to be growth-attenuated in medium containing oleic acid, sodium acetate, citric acid and lactic acid as sole carbon sources (Figure 1A). CgRsc3-A and B are orthologs of *S. cerevisiae* Rsc3 which is a component of a 17-subunit RSC (remodel the structure of chromatin) complex. *CgCHZ1* and *CgHFI1* code for histone chaperone for Htz1/H2A-H2B dimer and an adaptor protein required for structural integrity of the SAGA (Spt-Ada-Gcn5-Acetyltransferase) complex, respectively.

Second, we examined acetylation of histone H3 on lysine 56 in *C. glabrata* cells grown in medium containing sodium acetate as the sole carbon source and found it to be diminished compared to dextrose-grown cells (Figure 1B). This is in accord with the reduced H3K56 acetylation observed in macrophage-internalized *C. glabrata* cells. Importantly, chromatin extracted from both mid-phase macrophage-ingested *C. glabrata* cells and sodium acetate-grown cells was resistant to micrococcal nuclease digestion indicating that cellular response to macrophage internalization and alternative carbon source utilization may involve similar chromatin modifications.

Third, we measured total cellular lysine deacetylase (KDAC) activity in macrophage-internalized and sodium acetate-grown cells as reversible protein lysine acetylation is pivotal to the regulation of cellular metabolism. We observed a 2- to 3-fold increase in KDAC activity when *C. glabrata* cells

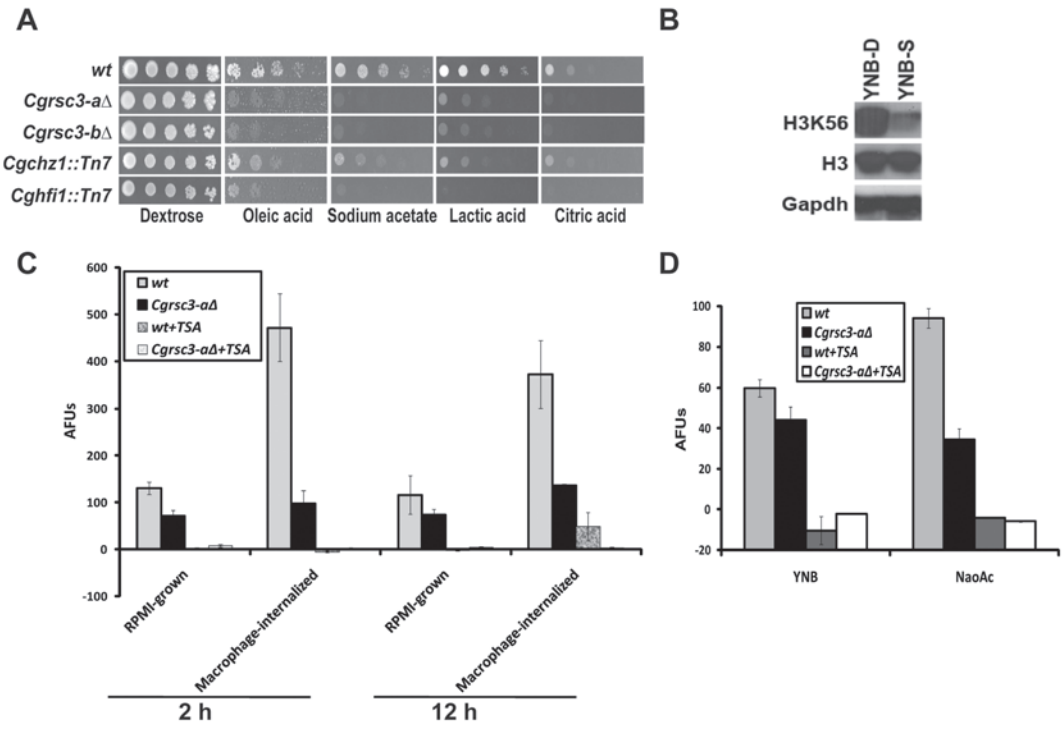

Figure 1. Macrophage-internalized and sodium acetate-grown *C. glabrata* cells display elevated lysine deacetylase activity. **(A)** Serial dilution-spotting assay to assess the growth of *C. glabrata* strains in indicated medium. **(B)** Immunoblot analysis on whole-cell extracts of wild-type cells, grown for 6 h in YNB medium containing either 2% dextrose (YNB-D) or 2% sodium acetate (YNB-S) as the sole carbon source, with antibodies against indicated proteins/modifications. **(C)** Measurement of cellular lysine deacetylase activity in RPMI-grown and macrophage-internalized *C. glabrata* cells using trifluoroacetyl-lysine as a substrate. Trichostatin A (TSA, 10 nM) treatment was used as the assay specificity control. Data represent the mean of three independent analyses (± SEM). **(D)** Measurement of cellular lysine deacetylase activity in *C. glabrata* cells grown either in dextrose- (YNB) or sodium acetate (NaoAc)-supplemented medium. Data represent the mean of three independent analyses (± SEM).

were either ingested by macrophages or grown in medium containing sodium acetate as the sole carbon source (Figure 1C and D).

Intriguingly, *Cgrsc3-aΔ* mutant did not show elevated KDAC activity under these conditions (Figure 1C and D) indicating an impaired metabolic regulation. Collectively, these data suggest that response of *C. glabrata* cells to macrophage environment could be a mimic of the cellular carbon starvation response and chromatin architecture reconfiguration plays an important role in the metabolic adaptation of macrophage-ingested *C. glabrata* cells.

Additionally, we screened *C. glabrata* mutants, identified through the STM screen for reduced survival in THP-1 macrophages, for their ability to prevent maturation of phagolysosome and identified three mutants which co-localized with acidified phagosomes. Experiments are currently underway to characterize these mutants and better understand the mechanisms that *C. glabrata* employs to modulate phagolysosomal acidification in macrophages.

Project 2: Innate resistance of *C. glabrata* to fluconazole

Objectives

1. Understanding the molecular basis of low inherent susceptibility of *C. glabrata* towards fluconazole; and
2. Identification of targets for combinatorial therapy with azole antifungals.

Summary of work done until the beginning of this reporting year (upto March 31, 2012)

We have previously reported two components of RNA polymerase II mediator complex (CgMed2 and CgPgd1) and three players of Rho GTPase-mediated signaling cascade (CgBem2, CgSlt2 and CgBnr1) to be essential for survival of stress imposed by the azole antifungal, fluconazole. Fluconazole targets an essential enzyme of the ergosterol biosynthesis pathway, lanosterol 14α-demethylase (CgErg11). CgBem2, CgSlt2 and CgBnr1 encode a RhoGAP (GTPase activating protein) domain-containing protein, a terminal MAP kinase of Protein kinase C (PKC)-mediated cell wall integrity (CWI) pathway and a formin protein, respectively. PKC signaling is known to be regulated by a small guanosine triphosphatase, Rho1. Further, we demonstrated that disruption of CgBem2 resulted in bud-emergence defects, azole susceptibility, constitutive activation of PKC-mediated CWI signaling and defective regulation of multidrug transporters upon fluconazole exposure. We also showed that genetic abrogation of CgSlt2 rendered *C. glabrata* cells unable to survive fluconazole stress and defects in the transcriptional up-regulation of multidrug efflux pumps partially accounted for the viability loss of *Cgslt2Δ* mutant.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

In the current study, we have focussed on *CgMED2* which codes for a fungal-specific, tail-subunit of the multiprotein mediator complex. Mediator complex is composed of 3 modules, the head, the middle and the tail wherein the tail region interacts with gene-specific activators/repressors and the head and the middle modules interact with core RNA polymerase subunits to form the RNA polymerase II holoenzyme. Mediator complex is essential for activator-dependent transcription in eukaryotic cells. To investigate the molecular basis underlying increased sensitivity of *Cgmed2::Tn7* mutant to fluconazole, we first created a clean knock-out strain by deleting the CgMed2-encoding ORF, *CAGL0C04477g*, *via* homologous recombination-based strategy, using nourseothricin acetyltransferease (confers resistance to nourseothricin) as a selection marker. Serial dilution spotting assays verified the enhanced susceptibility of *Cgmed2Δ* deletion strain to fluconazole and this elevated sensitivity was complemented by expressing *CgMED2* ectopically from a plasmid (Figure 2A).

To examine whether CgMed2 is involved in the transcriptional activation of multidrug transporters upon fluconazole exposure, we checked the expression of the *CgCDR1* gene which codes for the major multidrug efflux pump in *C. glabrata*, via quantitative real-time PCR. Compared to 5-fold elevated transcription of *CgCDR1* in wild-type cells, *Cgmed2Δ* could upregulate *CgCDR1* only by 1.5-fold in response to fluconazole treatment. Consistent with diminished *CgCDR1* transcript levels, *Cgmed2Δ* mutant also exhibited significantly reduced ATP-dependent efflux of rhodamine 6G (R6G) dye, a CgCdr1 substrate. Importantly, both wild-type and *Cgmed2Δ* mutant displayed ~ 5-fold increase in *CgERG11* transcript levels upon fluconazole exposure. Together, these data

indicate a specific role for CgMed2 in the transcriptional regulation of multidrug efflux pumps.

Expression of genes encoding multidrug transporters in *C. glabrata* is regulated by a Zn_2Cys_6 zinc cluster-containing transcription factor, CgPdr1, which is known to interact with the Med15 tail-subunit of the mediator complex. To examine if CgMed2-mediated transcriptional activation of *CgCDR1* is *via* its interaction with CgPdr1, we tagged CgMed2 with the *myc* epitope at both N- and C-terminal. Functionality of N- and C-terminally-*myc*-tagged CgMed2 was verified by their ability to complement the fluconazole sensitivity of *Cgmed2Δ* mutant (Figure 2A). Western blot and immuno-

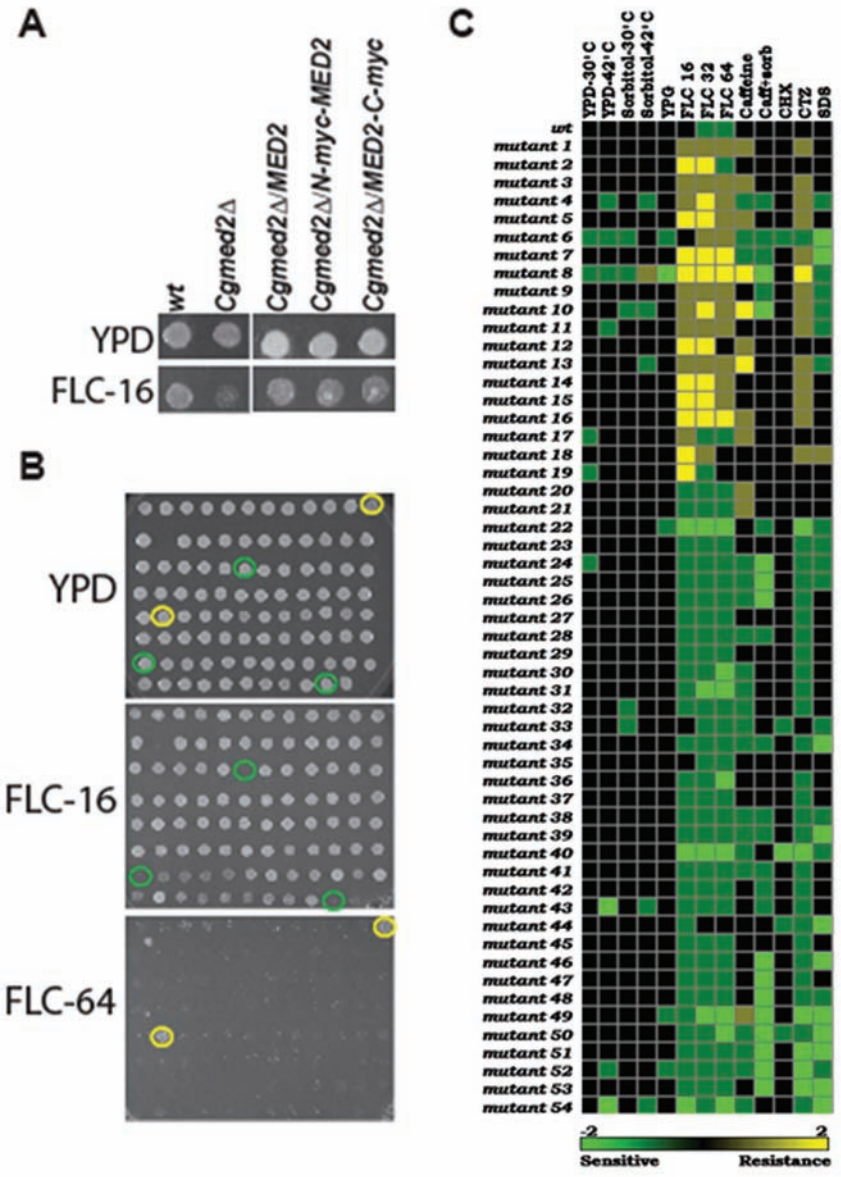

Figure 2. Growth profiles of *C. glabrata* mutants with altered fluconazole susceptibility profiles. **(A)** Spot assay to assess the growth of indicated *C. glabrata* strains in YPD and YPD medium containing 16 μg/ml fluconazole (FLC-16). **(B)** Representative plate images from the altered fluconazole susceptibility mutant screen. Green and yellow circles denote mutants which displayed sensitivity to 16 μg/ml (FLC-16) and resistance to 64 μg/ml (FLC-64) fluconazole, respectively. **(C)** Heat map illustrating the growth of fluconazole-resistant and fluconazole-sensitive mutants in the presence of diverse stresses. Growth conditions tested were rich medium (YPD), thermal stress (42° C), sorbitol (1 M), glycerol-containing medium (YPG, 3%), cell wall stress (caffeine, 10 mM), membrane stress (SDS, 0.05%), antifungal stress (fluconazole (FLC, 16, 32 and 64 μg/ml) and clotrimazole (CTZ, 30 μg/ml)) and cycloheximide (CHX, 1 μg/ml). Scaled growth scores are color-coded according to the legend at the bottom.

precipitation experiments are currently ongoing to examine the interaction between CgMed2 and CgPdr1 upon fluconazole exposure.

Additionally, we screened 9,134 *C. glabrata* Tn*7* insertional mutants for altered fluconazole susceptibility profiles using plate growth assays (Figure 2B) and identified a total of 200 and 231 mutants which displayed sensitivity and resistance to fluconazole, respectively. After three rounds of retesting, we selected a set of 54 mutants, which are likely to carry Tn*7* insertions in unique genes, for further analysis. Of these, 19 mutants were resistant to fluconazole while 35 mutants exhibited sensitivity to fluconazole (Figure 2C). Phenotypic profiling of these mutants revealed varied levels of susceptibility to azole antifungals (fluconazole and clotrimazole), CgCdr1 substrate (cycloheximide) and thermal and cell wall stress (Figure 2C). Mutants also differed in their ability to utilize glycerol as carbon source and sorbitol to rescue thermal and cell wall stress-related growth defects (Figure 2C). Notably, mutants with dysfunctional mitochondria have been reported to be growth-attenuated in glycerol-supplemented medium and highly resistant to azole antifungals. Mapping of the Tn*7* insertions in this select set of 54 mutants is currently underway to deduce the identities of the genes disrupted.

Publications

1. Rai MN, Balusu S, Gorityala N, Dandu L and Kaur R (2012). Functional genomic analysis of *Candida glabrata*-macrophage interaction: role of chromatin remodeling in virulence. ***PLoS Pathogens*** 8: e1002863.

2. Bairwa G, Balusu S and Kaur R. Aspartyl proteases in human pathogenic fungi: roles in physiology and virulence. ***The Fungal Cell Wall***. Editor: Héctor M Mora-Montes. Nova Science Publishers (In press).

LABORATORY OF IMMUNOLOGY

Role of advanced glycation end products (AGE) in inducing various cellular activities related to diabetic responses and its regulation

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Objectives

1. Understanding the biological effects of advanced glycation endproducts (AGE)-mediated lipogenesis;
2. Understanding the molecular mechanism of autophagy; and
3. Studies on regulation of cytokine receptors to regulate tumorigenesis and inflammatory responses.

Summary of work done until the beginning of this reporting year (Upto March 31, 2012)

Several protein tyrosine kinase (PTK) inhibitors predominantly isoflavones, such as genistein, erbstatin, quercetin, daidzein, present in red clover, cabbage and alfalfa, show apoptotic effects against cancer cells. In this study, we found that biochanin, a methoxy form of genistein, inhibited IL-8-mediated activation of nuclear transcription factor kappaB (NF-κB), activator protein 1 (AP-1), and its dependent genes more potently than genistein. Both biochanin and genistein potently inhibited activity of Lck and Syk, but biochanin specifically inhibited activity of IKK. Genistein was unable to inhibit IL-8-induced IKK activity, but it blocked PV-induced IKK activity. The data showed that both biochanin and genistein are potent inhibitors of PTK, but biochanin is a potent inhibitor of serine/threonine kinase too. Biochanin inhibited NF-κB activation not only by blocking the upstream IKK, but also PTK that phosphorylate tyrosine residues of IκBα Thus, the double-edged sword effect of inhibition of NF-κB via inhibition of both serine/threonine kinase and PTK by biochanin might show useful therapeutic value against activities of cells that lead to tumorigenesis and inflammation (Manna SK, Biochem. Pharmacol., 83: 1383-1392, 2012). Thus, the double-edged sword effect of biochanin to inhibit cellular kinases may be useful to regulate several biological responses that are deleterious to cells, and use this molecule as a therapeutic.

Advanced glycation end products (AGE) accumulate in diabetic patients due to high blood glucose levels and cause multiple deleterious effects. In this report we provided evidence that the AGE increased cell death, one such deleterious effect. Methyl glyoxal coupled human serum albumin (AGE-HSA) induced transcription factors like NF-κB, NF-AT, and AP-1. AGE acts through its cell surface receptor, RAGE and degranulates vesicular contents, including interleukin-8 (IL-8). Degranulated IL-8 acts through its receptors, IL-8Rs and induces sequential events in cells – increase in intracellular Ca^{2+}, activation of calcineurin, dephosphorylation of cytoplasmic NF-AT, nuclear translocation of NF-AT, and expression of FasL. Expressed FasL increases activity of caspases and induces cell death (Mahali *et al.* J. Biol. Chem., 286: 34903-34913, 2011). Thus, this study may be important in several age-related neuronal diseases where AGE-induced apoptosis is observed because of high amounts of AGE.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

1. Beta-D-glucoside protects against advanced glycation end products (AGEs)-mediated diabetic responses by suppressing ERK and inducing PPAR gamma DNA binding

Advanced glycation end products (AGE) that accumulate, due to high amounts of 3- or 4-carbon sugars derived from glucose, cause multiple consequences in diabetic patients and aged persons. The transcription factor, peroxisome proliferator-activated receptor gamma (PPARγ), is often downregulated in the diabetic condition. Drugs targeting PPARγ for diabetes therapy were developed. We found that AGE inhibited PPARγ activity induced by PPARγ activators, like troglitazone (Figure 1A), rosiglitazone, oleamide, and anandamide. AGE induced translocation of PPARγ from nucleus to cytoplasm (Figure1B), which was increased on activation of ERK in cells. Antioxidants that inhibit AGE-induced NF-κB activation via ROI generation were unable to protect AGE-mediated decrease in PPARγ activity. Only mangiferin, a β-D-glucoside, prevented AGE-mediated decrease in PPARγ activity, and inhibited phosphorylation of ERK (Figure 1C) and cytoplasmic translocation of PPARγ. Mangiferin interacts with PPARγ and enhanced its DNA binding activity as predicted by *in silico* studies (Figure 1D) and shown by *in vitro* DNA-binding activity (Figure 1E). Overall, our data suggest that (i) mangiferin inhibited AGE-induced ERK activation thereby inhibited PPARγ phosphorylation and cytoplasmic translocation; (ii) mangiferin interacts with PPARγ and enhances its DNA-binding ability. With these dual effects, mangiferin can be a potential candidate for developing therapeutic drug against diabetes.

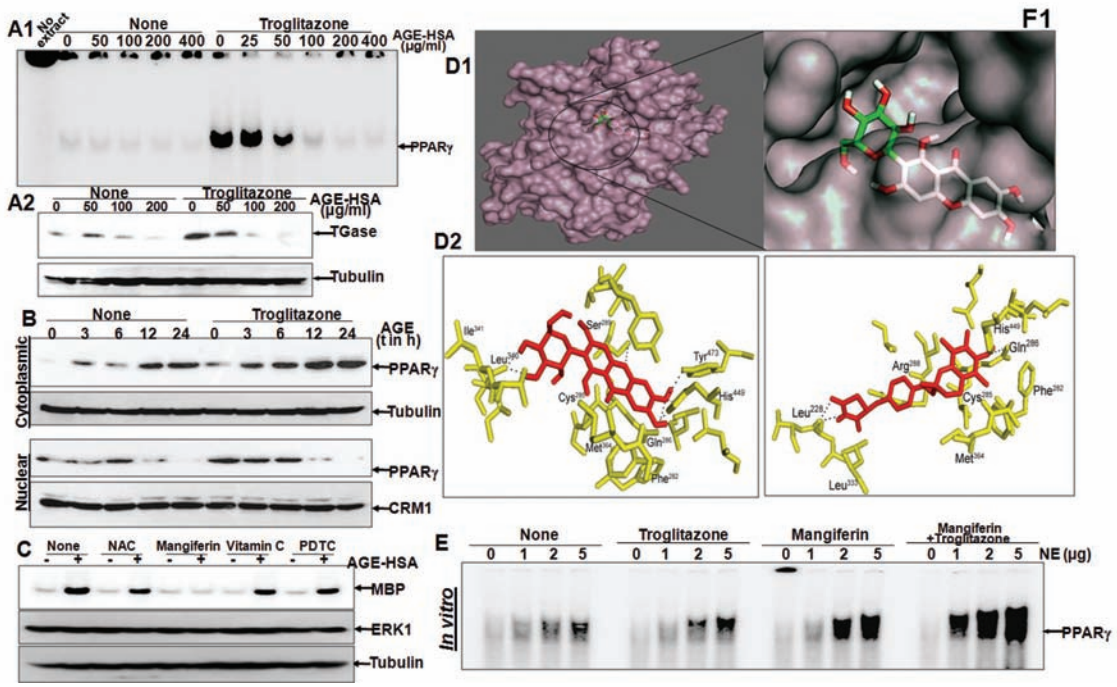

Figure 1. Advanced glycation endproducts (AGE)-mediated downregulation of PPARγ activity induced by troglitazone is protected by mangiferin. Jurkat cells, stimulated without or with 10 μM troglitazone for 6h were treated with different concentrations of AGE-HSA for 12h. Nuclear extracts (NE) were prepared and PPARγ DNA binding was assayed by gel shift assay **(A1)**. Cells, stimulated without or with 10 μM troglitazone for 6h were treated with different concentrations of AGE-HSA for 12h. Whole cell extracts were prepared and amount of TGase was determined by Western blot from 100 ìg of extract **(A2)**. Jurkat cells, stimulated with troglitazone for 6h were treated with 100 μg/ml AGE-HSA for different times. Amount of PPARγ was determined from CE (100 μg) and NE (50 μg) as detected by Western blot **(B)**. Jurkat cells were treated with NAC (5 mM), mangiferin (10 μM), vitamin C (2 mM), and PDTC (100 μM) for 2h and then stimulated with 100 μg/ml AGE-HSA for 12h. Whole cell extracts were used to assay the activity of ERK using MBP as substrate **(C)**. 50 μg of whole cell extracts were used to detect ERK1 by Western blot and the same blot was reprobed for tubulin. Docking interaction of mangiferin with PPARγ (PDB ID: 2PRG) **(D1)**. Mangiferin (PUBCHEM ID: 5281647) and Troglitazone (PUBCHEM ID: 5591) form strong H bond interaction with amino acids of PPARγ **(D2)**. Different concentrations of NE proteins were incubated with mangiferin (10 μM), troglitazone (5 μM), or both for 2h and then assayed for PPARγ DNA binding **(E)**.

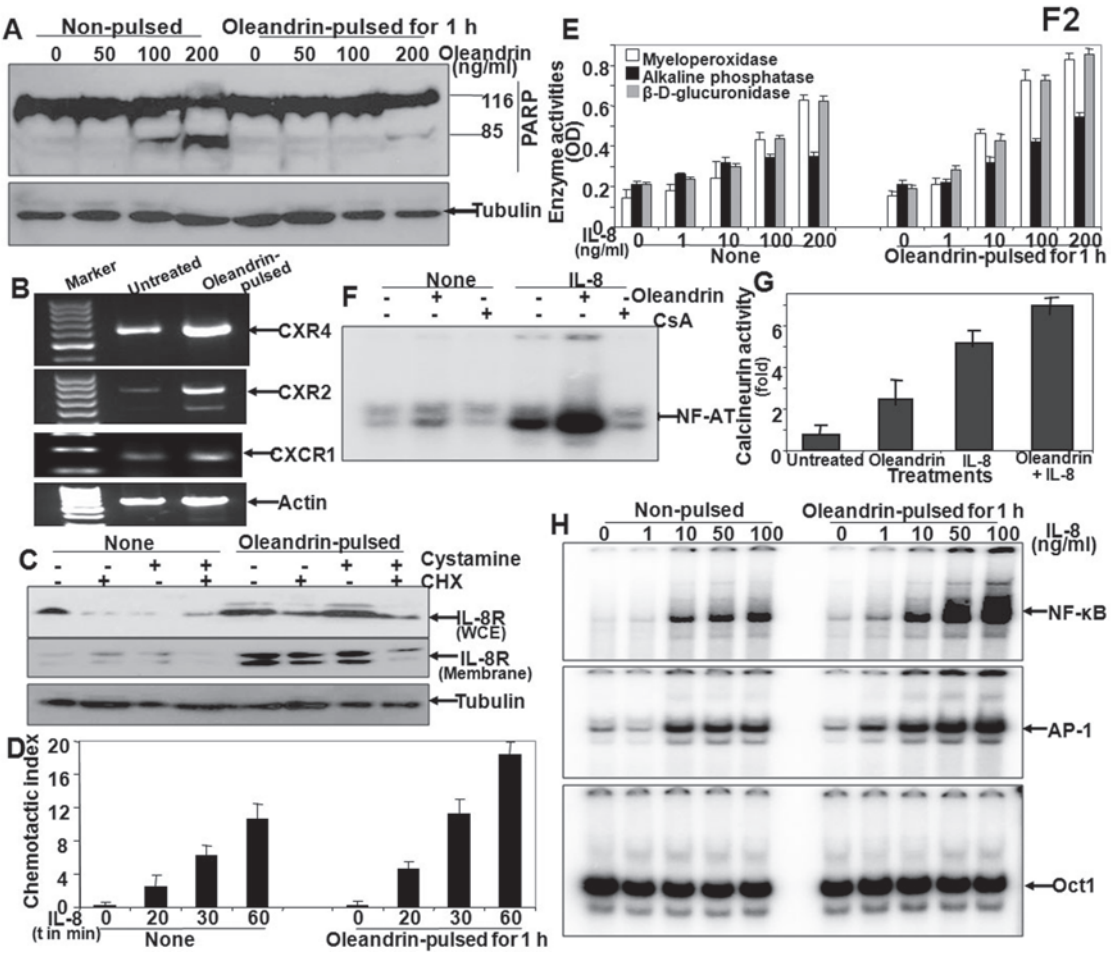

Figure 2. Pulse treatment of oleandrin increases IL-8-mediated biological responses and suppresses cell death. U-937 cells were treated with different concentrations of oleandrin for 1h and then cells were washed and cultured for 24 h. Cells were then treated with different concentrations of oleandrin for 24h. Cell death was determined by PARP cleavage. The PARP (pro- and cleaved fragment) fragmentation was detected from whole cell extract (WCE) of cells with similar treatments and detected by Western blot **(A)**. Total RNA was isolated from cells pulsed with oleandrin followed by cultured for 24h. The amounts of CXCR4, CXCR2, IL-8, and actin were measured by RT-PCR **(B)**. U-937 cells were pulsed with 100 ng/ml oleandrin for 1h, then washed and treated with 1 μM cycloheximide or 10 μM cystamine for 1h and then cultured for 24h. The amount of IL-8Rs were determined from 100 μg of WCE and 50 μg of membrane extract by Western blot **(C)**. The U-937 cells' migration was determined in Boyden chemotactic chamber and chemotactic index (cells number of induced migration/un-induced migration) is indicated in the figure as determined from oleandrin-pulsed and non-pulsed cells against different concentrations of IL-8 **(D)**. Oleandrin-pulsed and non-pulsed cells were suspended in phenol-free DMEM and stimulated with different concentrations of IL-8 for 4h. Activities of myeloperoxidase, β-D-glucuronidase and alkaline phosphatase were measured from the culture supernatant and absorbances were indicated in the figure **(E)**. U-937 cells were pulsed with oleandrin and incubated with CsA (2.5 μM) for 2h and then stimulated with IL-8. The amount of NF-AT DNA binding was measured by gel shift assay **(F)**.Oleandrin-pulsed cells were stimulated with IL-8 (100 ng/ml) for 2h and the calcineurin activity was determined by measuring inorganic phosphate released from phospho-peptide (RII peptide) **(G)**. Oleandrin-pulsed and non-pulsed cells were stimulated with different concentrations of IL-8 for 4h. NE were prepared and NF-κB, AP-1, and Oct1 DNA binding was determined by gel shift assay **(H)**.

2. Cardiac glycoside-pulse enhances IL-8-mediated biological responses by increasing cell surface IL-8 receptors

Cardiac glycosides are potent inducers of cell death, but very toxic to cells. Use of these molecules as therapeutics after reducing toxicity would be viable strategy. In this report we provide evidence that oleandrin alone induced cell death, but pulse treatment of it did not show any induction of cell death (Figure 2A). Pulse exposure of oleandrin, but not by azadirachtin, resveratrol,

thiadiazolidine, or benzofuran enhanced IL-8-, but not TNF-, IL-1-, EGF-, or LPS-mediated induction of NF-κB. This enhancement of NF-κB activation is not restricted in specific cell types. Increase in IL-8-mediated biological responses further proved in the oleandrin-pulsed cells upon overexpression of TRAF6. Oleandrin-pulsed cells did not show increase in NF-κB activation mediated by other ligands for G-protein-coupled receptors, except IL-8. Oleandrin-pulse increased expression of IL-8Rs (CXCR1 and CXCR2) (Figure 2B & 2C) thereby increased IL-8-induced biological responses like chemotaxis (Figure 2D), proteolytic enzymes release (Figure 2E), and activation of NF-κB and AP-1 (Figure 2H). Increase in IL-8Rs further enhanced IL-8-mediated intracellular Ca^{2+} release, calcineurin activation (Figure 2G), NF-AT activation (Figure 2F), and wound healing. Oleandrin pulse treatment decreased cell surface IL-8Rs by changing the microviscosity and further culturing compensated IL-8Rs by degranulation and expression of NF-AT-dependent transcription. Overall, for the first time we are providing data that the pulse exposure of toxic cardiac glycoside enhances biological activity in a typical manner by activating IL-8-mediated biologic responses. This study might be helpful to design oleandrin for therapy against those diseases where cell migration is required to improve the conditions of patients.

Publications

1. Fialho AM, Salunkhe P, Manna S, Mahali S and Chakrabarty AM (2012). Glioblastoma multiforme: novel therapeutic approaches. ***ISRN Neurology*** 2012: Article ID 642345, doi:10.5402/2012/642345.
2. Mahali SK and Manna SK (2012). Beta-D-glucoside protects against advanced glycation end products (AGEs)-mediated diabetic responses by suppressing ERK and inducing PPAR gamma DNA binding. ***Biochemical Pharmacology*** 84: 1681-1690.
3. Manna SK (2012). Double-edged sword effect of biochanin to inhibit nuclear factor kappaB: suppression of serine/threonine and tyrosine kinases. ***Biochemical Pharmacology*** 83: 1383-1392.
4. Mulakayala C, Babajan B, Madhusudana P, Anuradha CM, Rao RM, Nune RP, Manna SK, Mulakayala N and Kumar CS. Synthesis and evaluation of resveratrol derivatives as new chemical entities for cancer. ***Journal of Molecular Graphics and Modelling*** (In press).

LABORATORY OF BACTERIAL GENETICS

Studies on Gene Regulation, Transcription Termination, and Amino Acid and Ion-Transport in *Escherichia coli*

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	Vimala Allada	Project Associate
	P Hima Bindu	Project Associate
	Vijay Gunasekaran	CDFD-IKP Fellow
	Noor Md Shaik	CDFD-IKP Fellow

The work undertaken by the group in this reporting year is described below under the following objectives:

Objectives

1. To understand the role of Rho-dependent transcription termination in avoidance of R-loops in *Escherichia coli*;
2. To characterize a novel pathway for potassium translocation in *E. coli*;
3. To determine mechanisms of export of basic amino acids in *E. coli*;
4. To examine the interplay between (p)ppGpp metabolism and tmRNA;
5. To test the role of (p)ppGpp in transcription elongation;
6. To delineate the role of transketolases in *E. coli* physiology; and
7. To develop new processes for dehairing of animal skins and hides during leather manufacture.

Summary of work done until the beginning of this reporting year (Upto March 31, 2012)

The work undertaken in earlier years on each of the objectives has been summarized in the first parts of the corresponding descriptions below.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

1. Role of Rho-dependent transcription termination in avoidance of R-loops in *E. coli*

It is well established that transcription and translation are coupled in all bacteria including *E. coli*. When transcription proceeds in the absence of translation, for example beyond the end of an open-reading frame, it is terminated by a process called Rho-dependent transcription termination (RDTT) in which the Rho protein binds the nascent untranslated transcript and mediates the release of RNA polymerase from DNA. Another protein that participates in RDTT is NusG, and both Rho and NusG are individually essential for viability in

E. coli. Compromised RDTT function, arising from missense mutations in *rho* or *nusG*, is associated with a phenotype of "polarity relief", that is, absence of premature transcription termination immediately downstream of a nonsense mutation in the promoter-proximal gene of an operon.

In last year's Annual Report, two lines of evidence emanating from the work of this laboratory were described to support the hypothesis that RDTT is essential for prevention of excessive occurrence of RNA-DNA hybrids or R-loops across the genome. One of the assays for detection of R-looped regions exploits the sensitivity to sodium bisulphite of the displaced non-template DNA strand that results in C-to-T changes in nucleotide sequence of the latter. With the aid of this assay, we could show that R-loops occur genome-wide at a basal level of around 5% in wild-type *E. coli*, and that the frequency of their occurrence is elevated in a *nusG* missense mutant deficient for RDTT. The second line of evidence was that the lethality associated with complete absence of Rho or NusG in wild-type *E. coli* could be rescued (on defined medium but not rich medium) by ectopic expression of UvsW, an R-loop helicase from phage T4, thereby establishing that it is indeed excessive R-loops that are probably responsible for inviability of these mutants.

In the current year, additional experiments were undertaken with the UvsW-expressing strains to exclude alternative explanations for the finding that such strains retain viability on defined medium even in absence of Rho and NusG proteins. For example, it has been shown earlier that UvsW is able not only to unwind R-loops but also to catalyze the regression of blocked replication forks. We therefore considered the possibility that suppression by UvsW of lethality associated with compromised RDTT is because of an enhanced ability to restart replication following double-strand breaks at blocked forks in these mutants. We found, however, that UvsW-mediated rescue of Δ*rho* lethality occurs even in strains that are deficient for RecA, RecB, or PriA, which are some of the other proteins that are crucially involved in fork restoration and restart. Thus, it appears that UvsW is acting more to prevent fork blockage by R-loop unwinding than to resolve the blocked forks through its fork regression activity.

The additional results that were obtained in the current year in this regard were the following: (i) The rich-medium sensitivity of Δ*rho* mutants expressing UvsW was elicited not only on LB medium but also on nutrient agar and on defined medium supplemented with 5% (but not 0.5%) (wt/vol) Casamino acids, indicating that it is the growth rate and not any specific component of the growth medium that modulates UvsW's ability to rescue Δ*rho* lethality. (ii) UvsW expression did not alter the nonsense polarity-relief phenotype conferred by a *rho* missense mutation at two different loci that were tested, and even the Δ*rho* strain expressing UvsW was polarity-relieved; these data indicate that UvsW was not merely substituting for Rho's termination function while mediating the rescue of Δ*rho* lethality. (iii) The *E. coli* enzymes RNases HI and HII catalyze degradation of RNA in RNA-DNA hybrids, and we found that the Ts growth phenotype of a mutant doubly defective for these enzymes can be partially rescued by UvsW; this observation supports the notion that UvsW acts *in vivo* to reduce toxicity associated with excessive RNA-DNA hybids. (iv)We also found that the Ts phenotype of a mutant deficient for both RNases HI and HII is manifested only in rich medium, suggesting that R-loops act to impede replication fork movement. (v) We have previously shown that *rho* or *nusG* missense mutations can suppress lethality associated with defective RNase E function, and in the present year it was demonstrated that such suppression can also be achieved with Δ*rho* mutation in presence of UvsW. (vi) Finally, UvsW expression could also suppress inviability arising from exposure of a wild-type strain to either of two Rho inhibitors, namely the antibiotic bicyclomycin or the protein Psu from phage P4.

Future work in the laboratory on this project is being directed towards (i) employment of additional assays for R-loop demonstration in RDTT-defective mutants; (ii) deriving the relationships between RDTT and DNA supercoiling in R-loop avoidance and generation; (iii) identifying the determinants of R-loop formation in particular regions of the genome, such as antisense transcription, nucleotide sequence preferences, and so on; and (iv) delineating the mechanisms of R-loop toxicity, for example, whether it is through transcription-replication conflicts.

2. Evidence for a novel cryptic pathway for potassium translocation in *E. coli*

In earlier studies, we have found that the commonly used *E.coli* strain MC4100, lacking the nucleoid protein H-NS in combination with either a deficiency for thioredoxin 1 or thioredoxin reductase (collectively designated Trx) is rendered sensitive

to an extracellular K^+ concentration ($[K^+]_e$) $\geq$ 20 mM, a phenotype that has also been reported for a strain deleted for *ptsN*. PtsN is the terminal phospho-acceptor protein of a paralogous phospho-transferase pathway comprising PtsP-PtsO-PtsN and the phosphorylation substrate of PtsN is unknown. The K^+ sensitive (K^S) phenotype of the *trx hns* (TH) and *ptsN* mutants persisted in the absence of known K^+ uptake systems, indicating that the K^S phenotype may result due to the activity of an as yet uncharacterized K^+ transport system. To delineate the mechanistic basis of the K^S phenotype we have earlier isolated and characterized genetic suppressors of the K^S phenotype. We have found that the K^S phenotype of the *trx hns* (TH) and the *ptsN* mutants was dependent upon elevated ppGpp pools contributed by the *spoT1* allele of MC4100. Accordingly presence of the *spoT*$^+$ allele suppressed the K^S phenotype of the TH and the *ptsN* mutants and did so by mediating a reduction in cellular ppGpp level. In addition the K^S phenotype of the TH and *ptsN* mutants was also suppressed by expression of the K^+ carrier proteins TetA, and a truncated version of the KdpA (KdpA') K^+ translocator subunit or by a null mutation in *ycgO*, that encodes an inner membrane protein of unknown function. The K^S phenotype of the TH but not of the *ptsN* mutant was suppressed by null mutations in *ptsP* and *ptsO*, indicating that the absence of dephospho-PtsN is the common feature of the K^+ sensitivity displayed by the TH and *ptsN* mutants. In addition, barring the effect of *spoT*$^+$, all genetic suppressors of K^+ sensitivity exerted their effects without causing significant alterations of cellular ppGpp level.

In this year we assessed the effects of heterologous overexpression of *ycgO* on the growth of the parent in media of varying $[K^+]_e$ and found that overproduction of YcgO led to a K^+ sensitive phenotype in the parent and in a strain that lacked known K^+ uptake systems, that was suppressed by expression of *tetA* and by the presence of *spoT*$^+$, but not by other suppressors of the K^S of the TH and *ptsN* mutants, indicating that the activity of YcgO may be causal to their K^S phenotypes and that ppGpp may modulate the activity of YcgO. Overall our studies indicate that the perturbations caused by the *trx hns* and the *ptsN* mutations may act in distinct ways to limit the amount of dephospho-PtsN leading to unfettering of a novel ppGpp modulated K^+ translocation pathway in a medium of high $[K^+]_e$ specified by the activity of YcgO. Based on the genetic suppressor studies, we propose that the *trx*, *hns* mutations may exert their effects at a step(s) upstream of PtsN and influence its phosphorylation status, to limit the amount of dephospho-PtsN and that dephospho-PtsN may fetter the activity of YcgO, rendering its activity cryptic in the parent. The genetic relationship between the *trx hns* and the *ptsN* mutations can also be explained if one considers that TrxA/B and H-NS stimulate (directly or indirectly) expression of *ptsN*. We have discounted this possibility because expression of a chromosomal *ptsN-lac* transcriptional fusion (located in *ptsN*) was not affected in strains lacking H-NS or TrxA. Our current studies are directed towards examining the effect of overexpression of *ycgO* on cellular K^+ levels and testing the notion that dephospho- PtsN may directly interact with YcgO and fetter its activity.

Recently it has been reported by other workers that besides displaying a K^S phenotype, growth of a strain lacking PtsN is impaired in a medium of intermediate (22 mM) $[K^+]_e$ containing 5 mM L-leucine (Leu), leading to a Leu sensitive (Leu^S) phenotype that is suppressed by isoleucine and valine (ILV) supplementation. This phenotype is thought to arise due to a combination of altered intracellular K^+ levels and L-leucine in the *ptsN* mutant that perturbs cellular AHAS (acetohydroxyacid synthase) activity synergistically in a medium of intermediate $[K^+]_e$, giving rise to a state of isoleucine pseudo-auxotrophy. In *E. coli* K-12 the activities of the isoenzymes AHASI and AHASIII constitute the first committed step in the biosynthesis of branched chain amino acids leucine, isoleucine and valine. The activity of a third AHAS namely the valine insensitive AHASII encoded by *ilvGM* is absent in *E. coli* K-12 owing to the presence of a naturally occurring frameshift mutation in *ilvG*. In addition based on a recent report it appears that in a certain genetic background the pathology of the K^+ sensitivity of the *ptsN* mutant in *E. coli* K-12 may be solely related to K^+ mediated perturbations of cellular AHAS activity based on the observation that both the Leu^S and the K^S phenotypes associated with a *ptsN* mutant are reversed in a strain that is *ilvG*$^+$, thought to encode with *ilvM* an AHAS that may be insensitive to K^+. Consistent with recent reports we found that a deficiency of PtsN in MC4100 led to a Leu^S phenotype in medium of a $[K^+]_e$ of 22 mM supplemented with 5 mM Leu, which was suppressed by exogenous ILV at a concentration of 5 mM. However the presence of

ilvG^{+} (or exogenous ILV) suppressed the Leu^{S} but not the K^{S} phenotype of the *ptsN* mutant. Our studies thus indicate that K^{+} mediated perturbation of ILV biosynthesis constitutes one but not the only casualty of the K^{+} mediated physiological perturbation in the *ptsN* mutant and that a strain specific variation(s) is perhaps responsible for the *ilvG*$^{+}$ mediated suppression of K^{S} of the *ptsN* mutant.

3. Studies on basic amino acid export and exploiting ArgP-ArgO regulation to obtain L-arginine overproduction in *E. coli*

Earlier work from this laboratory had identified an anonymous ORF *yggA* (subsequently re-designated as *argO*) to encode a novel arginine (Arg) exporter ArgO in *E.coli*. These studies had also shown that *argO* expression is regulated by a transcription factor ArgP, and that certain gain-of-function variants of ArgP (designated ArgP^{d}) conferred high and constitutive expression of ArgO leading to increased excretion of Arg into the culture medium. These findings have been circumscribed as an inventive process for microbial production of Arg, and patented by CDFD in several countries.

Towards understanding the mechanism of Arg export mediated by ArgO we have earlier reported the identification of amino acid residues in ArgO, critical for mediating canavanine (Can) export and its topology in the inner membrane using alkaline phosphatase fusions to ArgO. Furthermore we obtained evidence for functional inter/intrahelical interactions in ArgO based on the isolation of second site suppressor mutations of primary mutations that were critical for mediating export of Can. The canavanine sensitive (Can^{S}) phenotype of the ArgO V118E substitution variant was suppressed by the V132A and A60P amino acid substitutions individually whereas that of the S156F substitution was suppressed by the I51T substitution. Overall these studies are indicative of existence of putative functional interactions between transmembrane (TM) segments TM2-TM4 and TM2-TM5 of ArgO. The V118E/V132A suppressor pair may represent an intrahelical interaction. We have extended these studies by constructing combinations of the second site suppressor substitutions A60P, I51T and V132A with other primary substitutions in ArgO that impaired ArgO activity and our results suggest that the suppressive effects of the second site amino acid substitutions in ArgO are specific to a given primary ArgO substitution, namely the V118E and the S156F substitutions. We are currently exploring alternate approaches to validate the indicated TM interactions in ArgO.

So far in *E. coli*, ArgO represents the only example of a solute exporter involved in the export of a basic amino acid. In order to identify novel genes whose products may promote export of Arg or L-lysine (Lys) we have earlier reported the isolation of a plasmid from a multicopy *E. coli* genomic library, whose presence in a strain lacking ArgO suppresses its Can^{S} phenotype. Our studies have shown that canavanine resistance is mediated by the presence on the plasmid of a novel ORF *ybjE*, predicted to encode an inner membrane protein. Elimination of YbjE exacerbated the Can^{S} phenotype of an *argO* null mutant but its deficiency on its own did not lead to a Can^{S} phenotype in the parent. On the other hand a *ybjE* but not an *argO* null mutant was rendered hypersensitive to the toxic analogue of Lys, thialysine. Furthermore, the *ybjE* mutant was impaired for growth in a medium containing Lys-Ala but not in media containing Arg-Ala or His-Ala dipeptides indicating that growth inhibition may result to due toxic intracellular build up of Lys. A strain lacking ArgO grew in all the above mentioned media and the *argO* mutation did not exacerbate the impaired growth of a *ybjE* null mutant in Lys-Ala medium. Accordingly *ybjE* has been renamed as *lysO*, encoding a putative novel Lys exporter. Our results therefore suggest that *E. coli* appears to employ distinct exporters for the export of the two basic amino acids Arg and Lys.

In continued studies on LysO, we have obtained evidence that growth inhibition of a *lysO* null mutant in a medium containing the Lys-Ala dipeptide correlated with increased cellular Lys content. In studies directed towards understanding the regulation of *lysO*, we examined the *lysO* promoter region and located two binding sites for the ArgR repressor, positioned 102 bp and 123 bp upstream of the translational initiation codon of *lysO* and a 32 bp inverted repeat located 248 bp upstream of the first ARG box. A deletion of the inverted repeat did not alter the expression of a *lysO-lac* transcriptional fusion whereas *lysO-lac* expression was impaired in Arg supplemented minimal media in an ArgR dependent manner. By primer extension the transcription start site of *lysO* was found to be located 36 bases upstream of the translation initiation codon of *lysO*. Currently we are examining the binding of purified ArgR to the *lysO* regulatory region, to understand its repressive effect on *lysO* expression.

As mentioned above, an *argO* mutant was not impaired for growth in a medium containing the Arg-Ala dipeptide and to understand the basis of its resistance to Arg-Ala, we have isolated transposon generated mutants, bearing secondary lesions in an *argO* background that are rendered hypersensitive to Arg-Ala and have found that null mutations in another ORF *ydhE* encoding an inner membrane protein orthologous to the multidrug efflux protein NorM of *V. parahaemolyticus* render an *argO* mutant hypersensitive to Arg-Ala. An *argO ydhE* double mutant was also hypersensitive to other arginine containing dipeptides such as Arg-Val, Arg-Leu and Arg-Ile. Loss of YdhE in the parent led to a modest impairment of its growth in Arg-Ala medium but a strain lacking YdhE was not rendered sensitive to the toxic Arg analogue Can. Our studies indicate that YdhE may function as a dedicated Arg exporter whereas ArgO activity serves mainly to export Can and coincidentally exports Arg.

Finally, in work completed this year under a program of co-operation with the IKP Knowledge Park, Hyderabad, improvements were undertaken on the patented process to achieve Arg excretion in shake flask culture supernatants, up to values of 420 mg per litre. The CDFD-IKP Fellow who had performed this work has registered a start-up company to which the technology has been licensed by CDFD for further development and commercialization, and the company has been successful in securing funding from the Small Business Innovation Research Initiative (SBIRI) for this task.

4. Understanding the genetic interaction between (p)ppGpp and tmRNA(*ssrA*)/*smpB* system

In work described in earlier reports, the lethal phenotype arising from the combined deficiency of (p)ppGpp and tmRNA (synthetic lethality) was genetically characterized and the following were inferred:

a) Absence of (p)ppGpp – mediated modulation of transcription contributes to synthetic lethality.

b) Genetic suppression studies using biochemically characterized RNA polymerase (RNAP) mutants defective for elongation properties indicated that the synthetic lethal phenotype could be a consequence of elongation defect and implied a possible role for (p)ppGpp in the modulation of transcription elongation *in vivo*.

c) Studies done using various mutant alleles of *ssrA* indicated that its ribosome rescue function but not that of peptide-tag addition is necessary for supporting cell survival in a (p)ppGpp deficient strain.

ssrA codes for small stable RNA that functions like an alanyl-tRNA and a messenger RNA in order to rescue stalled ribosomes. It is generally believed that SsrA-mediated rescue occurs on ribosomes that contain a 3'-mRNA end at or very near a vacant A site (non-stop mRNA). The alanyl-tRNA like activity of SsrA results in the incorporation of an alanine residue to the growing polypeptide chain and this is followed by the addition of a 10-aminoacid tag and the termination of translation due its mRNA like activity. Our earlier studies had shown that slow and fast moving RNAP mutants suppressed and accentuated respectively the ppGpp^0 *ssrA* synthetic lethality. Based on this finding we reasoned that the faster movement of RNAP in the ppGpp^0 strain could result in lesions that require the ribosome rescue function of *ssrA* for survival. Generation of non-stop mRNA-ribosome complex *in vivo* can be mediated by the action of certain mRNA endoribonucleases that make up the toxin component of the toxin-antitoxin systems. We obtained a strain lacking five toxin-antitoxin (AT) loci and tested for ppGpp^0 *ssrA* synthetic lethality in this genetic background. We expected not to observe synthetic lethality in this background assuming that one or more of the toxins (mRNA endoribonucleases) would be responsible for mRNA cleavage necessitating SsrA–mediated ribosome rescue in the ppGpp^0 strain. Contrary to our expectation the strain continued to exhibit synthetic lethality, indicating that atleast the 5-AT loci tested were not important for the generation of mRNA truncations and *SsrA*-mediated rescue of ribosomes.

The functionality of the *ssrA* mediated ribosome rescue system can also be tested through an artificial generation of non-stop mRNA (3'- end without a stop codon) and studying the effect on growth. Using an IPTG inducible non-stop mRNA generating plasmid (kind gift from Prof. Sue Lin Chao) it was observed that the ppGpp^0 strain was 100-fold more sensitive to the presence of IPTG than a wild-type strain and this increased sensitivity was not observed when the plasmid also carried

the *ssrA* gene. We interpret this as an indication of the SsrA-ribosome rescue machinery working close to saturation in strains lacking (p)ppGpp.

Using an *E. coli* genomic library generated in the medium-copy number plasmid pACYC184 we identified gene(s) capable of conferring multi-copy suppression of the *ssrA*-ppGpp^0 synthetic lethality. A clone carrying the complete *ydaW* and *rzpR* genes and 5' truncated *ydaV* and 3' truncated *trkG* genes conferred suppression. By a series of sub-cloning and recombineering experiments we have identified that the deletion of the *ydaW* open reading frame is required to observe suppression. The function of this gene and the mechanism of suppression need investigation.

We also made a serendipitous observation that the *ssrA* ppGpp^0 synthetic lethality is not observed during growth in minimal A media containing glucose and casaminoacids or only casaminoacids as carbon source. This brings up the question if specific component(s) in LB media or the physiology of the strain during growth in rich media such as LB is responsible for eliciting the synthetic lethal phenotype.

It has been reported that *ssrA*/*smpB* genes aid in cell survival when stable DNA-protein complexes are artificially induced and possibly also during the formation of stalled RNAP elongation complexes. The protein factors that help in the clearance of stalled RNAP elongation compelex are Mfd, Rho, GreA and GreB. We find suppression of *ssrA* ppGpp^0 synthetic lethality when the wild type allele of *rho* is replaced with the *rho-4* allele which encodes a hypomorphic Rho protein that exhibits termination defect. In *E. coli*, the Rho protein causes termination of transcription especially under conditions when the nascent RNA is not translated. The Rho protein binds nascent RNA and the RNAP to cause termination of transcription. We are currently trying to develop a model to explain our findings.

5. (p)ppGpp – a role in transcription elongation?

E. coli has two well studied elongation factors called GreA and GreB. When RNAP encounters a block during elongation and backtracks, the transcription factors GreA and GreB suppress pausing by stimulating the intrinsic nucleolytic activity of RNAP. These factors exhibit structural homology to DksA that can positively or negatively modulate the effect of (p)ppGpp on transcription initiation at the promoters of amino acid biosynthetic genes and ribosomal RNA respectively. However studies have not been performed to study the relationship between (p)ppGpp and the Gre factors. Our preliminary genetic data indicate that a phenotype seen in the *greA greB* double mutant can be altered through the modulation of intracellular (p)ppGpp pool. The *greA greB* mutant exhibits temperature sensitive growth phenotype in LB, presumably because prolonged RNAP pausing prevents replication and/or transcription and this is suppressed in genetic backgrounds carrying mutant alleles of *relA* and *spoT* consistent with an idea that the elevation of intracellular (p)ppGpp content can suppress the temperature sensitivity.

6. Role of transketolases in *E. coli* physiology

Two isoforms of transketolase enzyme, namely, TktA and TktB have been identified in *E. coli*. Expression of *tktB* is regulated by (p)ppGpp/Rpos and comes up during stationary phase while TktA is the major transketolase during exponential growth. Transketolases are required for the transfer of two carbon units between sugar molecules, and are part of the non-oxidative pentose phosphate pathway that connects glycolysis and the pentose phosphate pathway.

Genetic studies carried out in transketolase deficient strain i.e., a *tktA tktB* double mutant and previously reported, revealed that:

1. Transketolase activity is essential to sustain the growth of *E. coli* in LB media and that the growth defect can be partially compensated by: a) elimination of the purine/pyrimidine salvage pathways through inactivation of DeoB (phosphopentomutase) resulting in reduced ribose-5-phosphate pool; b) activation of *glpK*, coding for glycerol-3-phospate kinase; c) presence of the *pntAB* genes, coding for the subunits of the membrane bound pyridine nucleotide trans-hydrogenase on multi-copy plasmid and presumed to increase its intracellular activity and d) glucose supplementation to LB media.
2. The suppression of growth defect observed in all the suppressor strains excepting that of multi-copy *pntAB* is contingent on the presence of the wild-type chromosomal copy of *pntA* gene. We interpret this result to indicate that restoration of growth in the various suppressor backgrounds is through the

modulation of intracellular pyridine co-factor levels. It needs to be studied if the suppressor mutations modulate directly the expression of the *pntAB* genes or that the PntAB activity independently contributes to the net cellular pyridine cofactor pool.

We measured the pyridine cofactor levels in various strain backgrounds and the results are presented in Table 1. Since the *tktA tktB* double mutant is inviable we constructed a strain wherein growth is sustained by the expression of TktB from a conditional Amp^R plasmid whose replication is IPTG-dependent. The cultures were grown in permissive conditions (LB amp IPTG) overnight and sub-cultured (1:1500) and growth continued under permissive or non-permissive (LB) growth conditions to mid-log phase. Cells were harvested and normalized (using A_{600}) and the extraction performed for pyridine cofactor analyses. The results clearly indicate that with the exception of $NADP^+$ the intracellular levels of the other cofactors are dramatically lowered in the transketolase deficient strain and the presence of the suppressor mutations largely restore the cofactor levels to that observed under permissive growth condition in the *tktA tktB* double mutant.

Relevant genotype (growth condition)	NAD^+	NADH	$NADP^+$	NADPH
Wild type	189.5 ± 2.69	37.05± 15.49	15.78± 0.68	22.96 ± 11.29
tktA tktB (LB)	7.8 ± 1.36	0.31 ± 0.62	10.34± 1.34	Not detectable
tktA tktB (LB amp IPTG)	151.01± 14.14	14.08 ± 5.58	21.82± 2.37	14.89 ± 1.13
tktA tktB (LB glucose)	67.3 ± 13.93	6.71 ± 2.32	8.59 ± 1.04	0.27 ± 0.29
tktA tktB deoB (LB)	142.97± 13.56	17.82 ± 2.76	15.61± 1.19	6.72 ± 3.79
tktA tktB deoB (LB amp IPTG)	148.36 ± 12.2	14.48 ± 7.35	12.82± 1.68	7.29 ± 2.81
tkt tktB deoB (0.2% ribose in LB)	9.03	5.22	8.03	2.27
tktA tktB deoB sup8 (LB)	206.56 ± 6.14	22.54± 12.83	33.01± 2.04	4.45 ± 0.26
tktA tktB deoB sup8 (LB amp IPTG)	201 ± 40.49	28.83± 10.23	24.43± 7.41	5.99 ± 2.27
tktA tktB/pACYC184 (LB)	7.26 ± 2.17	1.88 ± 0.32	9.33 ± 0.92	0.22 ± 0.38
tktA tktB/pACYC184 (LB amp IPTG)	93.33	30.36	17.06	3.41
tktA tktB/pACYC184-*pntAB* (LB)	37.9 ± 3.44	8.69 ± 1.35	7.29 ± 1.54	1.06 ± 0.27
tktA tktB/pACYC184-pntAB (LB amp IPTG)	158.19± 27.47	24.65 ± 2.11	7.88 ± 4.69	13.13 ± 8.07

Table 1. Pyridine cofactor levels.

7. Studies on biological approaches to the dehairing of animal skins and hides during leather manufacture

For leather manufacture, skins and hides from animal carcasses are commonly preserved from putrefaction during storage and transport by the application of salt (salting); and their subsequent dehairing is achieved (after removal of salt by extensive washing) by the application either of chemicals such as lime and sulphide (chemical process) or of enzyme preparations from any of a variety of sources (biological or enzymatic process), or by a suitable combination of chemical and enzymatic processes (enzyme-assisted dehairing). Both salting and the chemical dehairing processes contribute substantially to environmental pollution. Accordingly, the efforts to use enzymes to substitute, either partially or completely, for chemicals in the dehairing process has gained considerable importance.

Commercially available enzyme preparations (proteases, lipases, etc., usually from bacterial or fungal sources) of varying degrees of purity are used in dehairing. The two surfaces of a skin or hide are referred to as the grain side and the flesh side, respectively, and the enzyme preparations are commonly applied to the flesh side during the dehairing process. Two important considerations are (i) an absolute need to preserve the integrity of collagen in the skin or hide, and (ii) the desirability to retain also the integrity of the hairs (hair-saving), since the latter represent a commercially valuable by-product of the dehairing process.

In work undertaken a few years ago in collaboration with the Central Leather Research Institute, Chennai, we had shown that live cultures of the yoghurt bacterium *Lactobacillus plantarum* grown in milk are doubly effective, first as a substitute to salting in the protection of skins and hides of goat, sheep and buffalo from putrefaction (for up to several months), and also to achieve their satisfactory dehairing in a hair-saving process. It appears that the quality of soft leather obtained using this process may be suitable for the manufacture of products such as gloves or chamois leathers.

The time taken to achieve dehairing by the chemical or enzymatic processes is typically of the order of several hours to a day, and is around two to three days with the use of live *Lactobacillus* culture preparations. Any reduction in the time taken for dehairing will be of value to industry since it would result in, among other features, faster turnaround times, less inventory costs, and less likelihood of undesirable events such as skin putrefaction. Furthermore, in the enzymatic or enzyme-assisted methods for dehairing, it would be advantageous in terms of input costs if satisfactory dehairing can be achieved with smaller amounts of enzyme preparation to be applied.

In work completed during the present year, we have developed a process by which the dehairing of animal skins and hides is achieved within a matter of two to ten minutes, that is, much faster than that obtained by any of the methods in current practice. In this simple yet novel process, a suitable source of enzyme is placed on the flesh side of a skin or hide and direct electric current of appropriate polarity is then applied across the thickness of the skin for a few minutes; this is achieved by placing the skin between a pair of metal surfaces that are then connected to a source of electric current such as a set of dry cells, a lead-acid battery, or an electrophoresis power pack. After this treatment, the skin is gently scraped to result in a hair-saving mode of dehairing (Figure 1).

An important consideration is the polarity of voltage applied and the consequent direction of electric current flow through the skin (that is, whether it is from the flesh side to grain side or the reverse) that is suitable for the dehairing process; our experiments indicate that this is determined by the nature of the enzyme source as well as by the pH, and that for any particular combination the dehairing is achieved only with one polarity and not the other. These observations provide strong support to the notion that it is electrophoretic enzyme delivery to the hair follicles which is responsible for the extreme rapidity of the dehairing process. An additional advantage with this method is that the quantity of enzyme needed for dehairing is substantially less than that in the absence of any applied voltage.

Figure 1. Example of dehairing of goat skin following application of enzyme and direct electric current for 10 minutes. Images shown at left and right are, respectively, of skin before and after treatment; in the latter, one part of the skin has been gently scraped to depict the ease of hair removal.

We have shown that this method is effective for dehairing of skins or hides from a variety of animals, as well as with different commercial enzyme preparations. Dehairing could also be achieved with a sonicated extract of cells of *L. plantarum*, which is classified as a GRAS (Generally Regarded as Safe) microorganism in industry. The method has also successfully been applied to achieve dehairing of a stack of several skins, in which enzyme has been applied to the flesh side of each skin, the skins are stacked one above the other in the same orientation, and electric current is then passed across the entire stack.

It is expected that the electrophoretic process may also be useful in other steps of leather manufacture that employ enzymes, such as soaking, liming, bating, and degreasing. We are at present trying to engage with suitable industries to undertake further testing and development of applications of the enzyme electrophoretic process in leather processing and manufacture.

Publications

1. Marbaniang CN and Gowrishankar J (2012). Transcriptional cross-regulation between gram-negative and gram-positive bacteria, demonstrated using ArgP-*argO* of *Escherichia coli* and LysG-*lysE* of *Corynebacterium glutamicum*. ***Journal of Bacteriology*** 194: 5657-5666.
2. Leela JK, Syeda AH, Anupama K and Gowrishankar J (2013). Rho-dependent transcription termination is essential to prevent excessive genome-wide R-loops in *Escherichia coli*. ***Proceedings of the National Academy of Sciences of the USA*** 110: 258-263.

Other Publications

1. Gowrishankar J (2012). Public funding for research projects: roles of experts and finance officials in decision-making. ***Current Science*** 102: 1499.

LABORATORY OF COMPUTATIONAL BIOLOGY

Computational Studies on Protein Structure, Function and Interactions

Faculty	HA Nagarajaram	Staff Scientist
PhD Students	Anupam Sinha	Senior Research Fellow
	H Rachita	Senior Research Fellow
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	Suryanarayana Seera	Junior Research Fellow
	VA Ramesh	Junior Research Fellow (Since Jul. 2012)

Objectives

Studies on protein-protein interaction networks (PPIN):

1. Structural and functional characterization of hubs in human PPIN;
2. Studies on spatio-temporal dynamics of human PPIN; and
3. Analysis of Human-Virus PPI (HU-Vir PPI) network.

Summary of work done until beginning of this reporting year (Upto March 31, 2012)

1. Studies on hubs in human PPIN

Studies were carried out to examine the relationship between the extent of splice variation and the average unstructuredness of protein products. The nodes with top 5% of the splice variant count showed a considerably higher propensity for disorderedness than the rest of the nodes. Similar studies were performed for nodes with top 10% and 15% of the splice variant count. We had also analyzed the combined effect of splice variation, domain composition and disorderedness on the degree of the nodes. The nodes with high structural disorderedness showed high degree difference as compared to the nodes with low disorderedness suggesting that the propensity of a node for large number of interactions arises substantially from its structurally disordered splice variants.

2. Studies on tissue-specific human PPINs

We first curated a dataset of human PPIs using BIOGRID, DIP, HPRD, IntAct and MINT. This dataset comprises of 78356 unique undirected interactions for 12142 human proteins. To get tissue-specific PPI network we integrated the PPI physical interaction data with the gene expression data available from microarray (for 70 normal tissues). The construction of tissue-specific network relies on the very fact that protein products of two genes can only interact when both the genes are expressed in the same concerned tissue.

3. Studies on human-virus PPIs

We studied the role of intrinsically disordered proteins (IDPs) in human-viral PPI networks. We found that about 70% of the human proteins interacting with viral proteins are disordered. We also found that these IDPs are involved in vital cellular processes such as cell cycle regulation, apoptosis, DNA and RNA binding, transcription, translation, protein trafficking, protein degradation pathway and signaling. We merged Human-Virus PPI (Hu-Vir PPI) with Human PPI (Hu-PPI) network and generated a network referred to as Bridged Human Virus PPI network (BHVN). Analyses on BHVN showed that viral proteins act as articulation points i.e. they connect previously unconnected components in the Hu-PPI network. 12 viruses belonging to ssRNA and dsDNA classes formed articulation points. Preliminary studies on viral articulation points indicated that there is similarity between viral articulation points from related viruses.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

Project 1:Structural and functional characterization of hubs in human PPI network

1. As stated in the previous report we examined the relation between the degree of genes/nodes in human protein-protein interaction network with respect to the number of splice variants. We found that on average, hubs in HPRD PPI network have greater number of splice variants than the non-hubs. This observation was confirmed across multiple PPI databases like IntAct, Reactome etc.
2. We further extended our studies to other eukaryotic organisms such as *Caenorhabditis elegans, Drosophila melanogaster, Mus musculus* and *Rattus norvegicus.* We found that in all the organisms (Figure 1) except *C. elegans* hubs have higher number of splice variants.

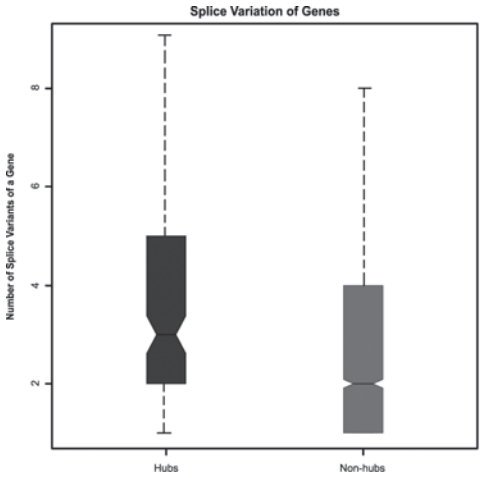

Figure 1. Splice Variant count in hubs and non-hubs of the Mouse (*Mus musculus*) PPI Network. Hubs are characterized by the presence of large number of isofroms as compared to non-hubs (Wilcox ranksum test P=2.509e-05).

3. The existence of a large number of proteins (splice variants) contained in the ENSEMBL database (release 62) has been verified experimentally at the level of the transcripts (mRNA sequences) but not at the level of amino acid sequences. Hence, we repeated our studies with a list of proteins (splice variants) whose existence has been experimentally verified. Figure 2 shows the splice variant count distribution for Hubs and Non-hubs in the HPRD PPI network. As can be seen Hubs have significantly higher number of splice variants than Non-Hubs (Wilcoxon ranksum test P=1.612e-10). Similar trends were observed for the BioGrid, Intact, HOMOMINT and Reactome databases.

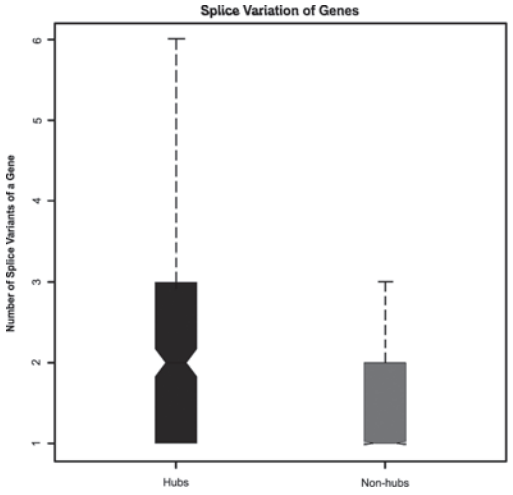

Figure 2. Splice Variant count in hubs and non-hubs of the HPRD PPI Network. Only those Splice Variants (proteins) were used for calculation whose existence was experimentally validated. Presence of the proteins in the PRIDE database was considered as a proxy for experimental validation. Hubs are characterized by the presence of large number of isoforms as compared to Non-hubs (Wilcoxon ranksum test P=1.612e-10

Project 2: Studies on spatio-temporal dynamics of human PPI networks

1. Mapping of tissue-wise expression data pertaining to 70 tissues onto human global PPI resulted in 70 tissue-specific networks. Proteins in the tissue-specific networks were grouped into five distinct classes on the basis of their degree and expression breadth (EB; the number of tissues they are expressed) (Figure 3). They are: 1) *House-keeping hubs (HKH):* Proteins expressed in at least 60 tissues and also form hubs in all the tissues they are expressed 2) *Tissue-preferred hubs (TPH):* Proteins expressed in at least 60 tissues but are hubs in at most 10 tissues; 3) *Tissue-specific hubs (TSH)*: Proteins expressed in <10 tissues and hubs in all those tissues 4) *Housekeeping non-hubs* (HKNH): Proteins expressed in >60 tissues and non-hubs in all of them and 5) *Tissue-specific non-hubs* (TSNH) Proteins expressed in <10 tissues and are non-hubs in those tissues. Of the total of 1979 hubs 908 were HKH, 220 were TSH and only 138 were TPH. Among 7610 non hubs 1903 were TSNH and the 3663 were HKNH. Comparative analysis of TSH, TPH and HKH revealed that TSH and HKH exhibit distinct properties as discussed below while, TPH exhibit properties similar to HKH.
2. In-depth analysis of TSH and HKH revealed significant differences between these two groups at sequence, structural and functional levels. TSHs are longer proteins enriched with more disordered regions as compared to HKHs. TSHs are also evolving at faster rates than HKHs. We found that HKHs contain more number of charged and more exposed residues than TSHs. We also looked into the % of residues in the loop regions and found that TSHs have higher fraction of residues in loop regions as compared to HKHs. We found HKHs have higher fraction of residues in LCRs as compared to TSHs. Despite having similar number of binding surfaces TSHs and HKHs distinctly differ in the number of interactions

they make with other proteins; TSHs are associated with lower degree centrality as compared to HKHs suggesting that TSH are "unsaturated" with regard to their binding capability and are perhaps evolving with regard to their interactions. TSHs are less expressed both at transcript and protein level and also enriched with PEST motifs indicating their easy degradation and tight regulation. TSHs are mostly secreted, transporters, signaling proteins in contrast to HKHs which are involved in transcription, translation and complex formation. Moreover, HKHs are subjected to more number of protein translational modifications than TSHs which can affect protein conformational or functional specificity facilitating its multi-specificity with partners.

we rebuilt our dataset by including them. We further noted some redundancies and duplicate entries in the dataset and hence the entire dataset was subjected to rigorous filtering process to remove obsolete entries, duplicate entries etc. The resultant data comprise of 3392 unique interactions between 270 viral proteins from 74 different viruses and 1736 human proteins. This dataset was used for all our further studies.

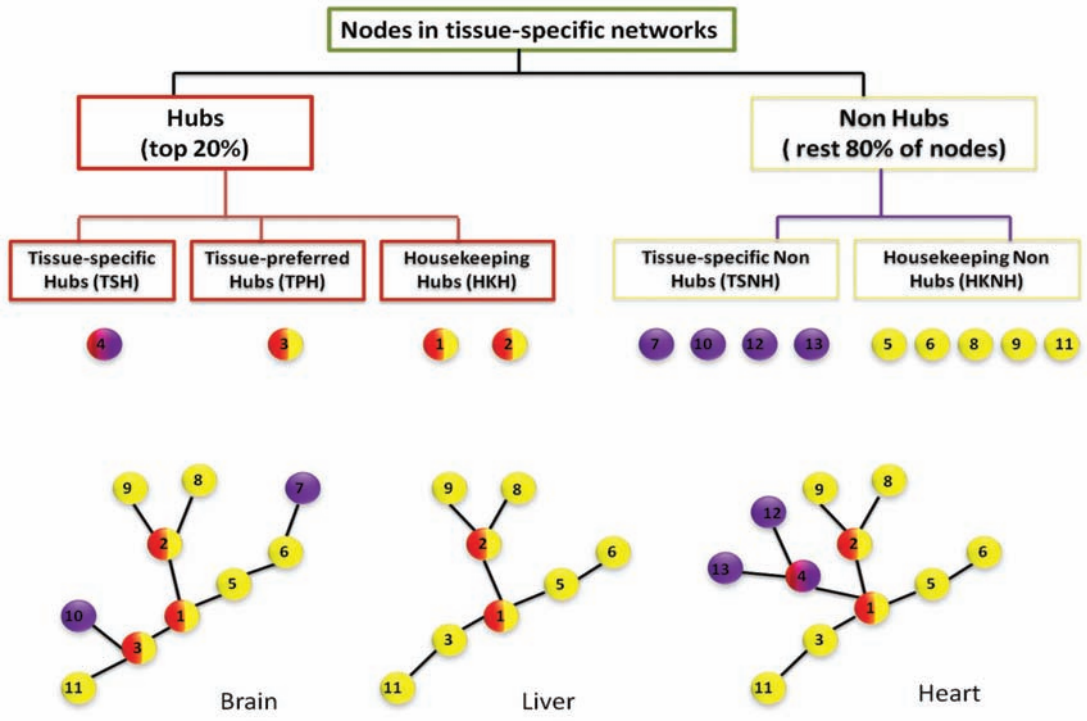

Figure 3. Schematic representation of tissue-specific networks and various kind of hubs and non hubs. Hubs are shaded with red colour. Tissue-specific proteins are colored in violet and housekeeping proteins in yellow colour.

Project 3: Analysis of human and virus protein-protein interaction (Hu-Vir PPI) networks.

1. As mentioned in the previous report we had identified viral articulation points in Bridged Hu-Vir PPI Network (BHVN) for different viruses. As the protein-protein interaction data became available for Dengue virus, HTLV1 and HTLV2

2. Global survey was conducted on Hu-PPI and Hu-Vir PPIs. 176 human proteins interacting with viral proteins did not have any known human interaction partners in Hu-PPI (Figure 4). This prompted us to look into functions of those 176 peripheral proteins and compare them with functions of peripheral proteins in Hu-PPI network using Gene Ontology (GO). We observed that peripheral components of Hu-PPI network are actually involved in metabolic processes where as those interacting with viral proteins were enriched in functions related to chromatin remodeling, ion binding, stress related pathways and transcription (p-value <0.05).

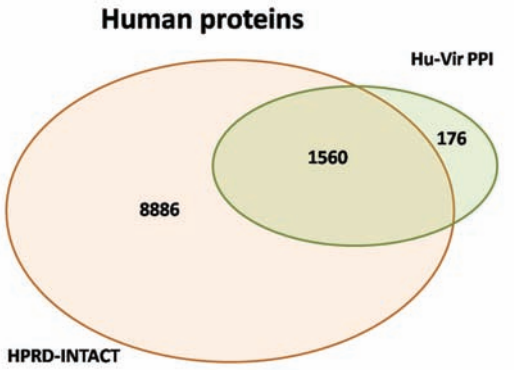

Figure 4. Venn diagram showing distribution of human proteins in Hu-PPI and Hu-Vir PPI data.

3. The BHVN constructured using the new revised dataset was used for identifying viral articulation points. Articulation points are the nodes whose removal results in an increase in the number of components in the network. They act as bridging elements between two components and add to the complexity of the network. These articulation points are conserved *i.e.,* similar proteins from related viruses form articulation points when mapped on to Hu-PPI network. Functional domain analysis of such similar proteins suggested that they have same functional domains. Functional annotation studies showed that viruses connect metabolic pathways to PPI network and hence seem to take over the regulation of metabolic pathways.

4. HIV1 was found to be connecting highest number (101 proteins) of peripheral nodes to the Hu-PPI network hence further analysis was carried out on HIV1. For any functional connection to occur between two proteins, they should be in close proximity with each other and this is achieved by their co-expression in the same sub-cellular localization. In order to study functional relevance of bridged connections via viral articulation points, gene expression data was downloaded from NCBI Gene Expression Omnibus (GEO). The median of all the expression values was used as the cut off for determing expression or no expression of various genes. All possible pairs of proteins bridged by HIV1 articulation points were made between bi-connected nodes which are part of giant component and articulation point connected peripheral nodes. Then each pair was given score 1 if the proteins in the pair are co-expressed in a tissue. All the co-expressed protein pairs were were taken and their subcellular localization was predicted using LOCATE (http://locate.imb.uq.edu.au/). Further studies are underway.

Future plans and directions

1. Integration and analysis of human nsSNP data on protein-protein interaction networks.

2. Further analysis of viral-human bridge PPI network.

3. Studies on tissue-wise PPI networks integrated with drug-protein interaction data.

4. Further studies on structural and functional characterization of hubs in HPPIN.

Publications

1. Acharya V and Nagarajaram HA (2012). Hansa: an automated method for discriminating disease and neutral human nsSNPs. ***Human Mutation*** 33: 332-337.

2. Bashyam MD, Chaudhary AK, Reddy EC, Reddy V, Acharya V, Nagarajaram HA, Devi ARR, Bashyam L, Dalal AB, Gupta N, Kabra M, Agarwal M, Phadke SR, Tainwala R, Kumar R and Hariharan SV (2012). A founder ectodysplasin A receptor *(EDAR)* mutation results in a high frequency of the autosomal recessive form of hypohidrotic ectodermal dysplasia in India. ***British Journal of Dermatology*** 166: 819-829.

3. Bashyam MD, Chaudhary AK, Sinha M, Nagarajaram HA, Devi ARR, Bashyam L, Reddy EC and Dalal A (2012). Molecular genetic analysis of MSUD from India reveals mutations causing altered protein truncation affecting the C-termini of E1α and E1β. ***Journal of Cellular Biochemistry*** 113: 3122-3132.

4. Bashyam MD, Purushotham G, Chaudhary AK, Rao KM, Acharya V, Mohammad TA, Nagarajaram HA, Hariram V and Narasimhan C (2012). A low prevalence of *MYH7/MYBPC3* mutations among familial hypertrophic cardiomyopathy patients in India. ***Molecular and Cellular Biochemistry*** 360: 373-382.

5. Kumar P and Nagarajaram HA (2012). A study on mutational dynamics of simple sequence repeats in relation to mismatch repair system in prokaryotic genomes. ***Journal of Molecular Evolution*** 74: 127-139.

6. Sinha A and Nagarajaram HA (2013). Effect of alternative splicing on the degree centrality of nodes in protein-protein interaction networks of *Homo sapiens*. ***Journal of Proteome Research*** 12: 1980-1988.

Other publications

1. Acharya V and Nagarajaram HA (2013). Response to: Statistical analysis of missense mutation classifiers. ***Human Mutation*** 34: 407.

LABORATORY OF MOLECULAR CELL BIOLOGY

Signal Transduction Pathways in Macrophages and Host-Pathogen Interaction in Tuberculosis

Faculty	Sangita Mukhopadhyay	Staff Scientist
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	Nazia Parveen	Senior Research Fellow
	Atul Udgata	Senior Research Fellow
	Arghya Das	Senior Research Fellow
	Gourango Pradhan	Senior Research Fellow
	Parul Singh	Senior Research Fellow
	Vishwanath Jha	Junior Research Fellow
	Komal Dolasia	Junior Research Fellow
Other Members	R Nagender Rao	Scientist
	Niteen R Pathak	Senior Technical Officer
	Philip Raj Abraham	Research Associate
	Asma Ahmed	Research Associate
	Khalid Hussain Bhat	Research Associate
	Rahila Qureshi	Project-Junior Research Fellow (Since Aug. 2012)
	Susiharan GS	Project Assistant (Since May 2012)
Collaborators	Shekar C Mande	NCCS, Pune
	Sudip Ghosh	NIN, Hyderabad
	V Valluri and S Aparna	Mahavir Hospital, Hyderabad & BPRC, Hyderabad
	Seyed E Hasnain	IIT, Delhi

Objectives

1. Signal transduction pathways in macrophages regulating its innate-effector immune responses; and
2. Studying how various candidate proteins of *Mycobacterium tuberculosis* interfere with macrophage signaling cascades to modulate host's protective responses against the bacilli.

Project I: Role of PPE18 protein in intracellular survival and pathogenicity of *M. tuberculosis*

Summary of work done until the beginning of this reporting year (upto March 31, 2012)

PPE18 (Rv1196), also known as Mtb39a, a member of the PPE family, is expressed more in *Mycobacterium tuberculosis* (Mtb) as compared to *M. bovis.* Also, comparative genome analyses of the avirulent H37Ra strain vs virulent H37Rv strain revealed presence of 53 insertions and 21 deletions in H37Ra relative to H37Rv. Interestingly, PPE18 harbored one of those deletions in H37Ra, indicating that this gene may be pathophysiologically important. Previous work by us (Nair *et al.* [2009] J. Immunol. 183: 6269; Nair *et al.* [2011] J. Immunol. 186: 5413-5424) documented that PPE18 binds to toll like receptor (TLR) 2 on macrophages and upregulates IL-10 cytokine production which favors a Th2-type response. Also, its interaction with TLR2 leads to phosphorylation of the SOCS3 protein which then physically interacts with the IκBα-NF-κB/c-rel complex preventing nuclear translocation of p50 and p65 NF-κB and c-rel transcription factors. As a consequence, there is a downregulation of transcription of NF-κB-regulated genes like IL-12 and TNF-α. We now aim to understand whether PPE18 plays any role in the survival and multiplication of Mtb bacilli during infection.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

PPE18 confers a growth advantage to Mtb *in vivo* in mouse model

To understand the role of PPE18 in Mtb virulence *in vivo*, C57Bl/6 mice were infected with either wild-type (WT) or *ppe18* knock-out (KO) strains of Mtb *via* the aerosol route and the bacterial burden was

estimated in lung, liver and spleen of infected animals at 3 different time points (3 weeks, 6 weeks and 9 weeks) after infection. The aerosol infection deposited 80~130 colony forming units (CFUs) per lung (as assessed by counting CFUs in two infected mice per Mtb strain at day 1 post-infection). Infection through aerosol deposits Mtb directly into the lungs and hence is considered to be closest to the physiological mode of infection. Lungs being the primary site of infection showed maximum CFUs at all the time points examined (Figure 1A). In mouse model upon infection, bacteria are known to disseminate from lungs to liver and spleen. We observed a steady rise in the bacterial load in all the organs at 3 week after aerosol infection and then a decrease at 6 week and 9 week post-infection. Interestingly, the number of *ppe18* KO bacteria remained significantly less in all the organs at almost all the time points investigated (Figure 1A). In the lungs of *ppe18* KO-infected mice, the mean bacterial counts (± SEM) were significantly lower at 3 weeks post-infection as compared to those of infected with WT Mtb strain and this trend continued to later time points also (6 weeks and 9 weeks) (Figure 1A). Similar observations were made in liver as well as in spleen (Figure 1A). PPE18 has previously been reported to be non essential for bacterial growth *in vitro*. Our results indicate that PPE18 probably plays a role in replication and survival of Mtb *in vivo* and thus, may be a candidate virulent factor**.**

Mice infected with *ppe18* KO strain show a reduced degree of inflammation and tissue damage and tuberculosis induced fatality as compared to mice infected with WT strain

We next examined the tissue damage in lung, liver and spleen in mice infected with WT and *ppe18* KO Mtb strains *in vivo* by histopathological analyses. The extent of inflammation and tissue damage due to infection as seen in the hematoxylin and eosin (H&E) stained sections of lung and liver from mice infected with WT Mtb was found to be markedly pronounced than that observed in mice infected with the *ppe18* KO Mtb (Figure 1, B-D). Mice infected with *ppe18* KO had more intact alveolar spaces while mice infected with WT Mtb almost had none, especially at 21 and 60 weeks post-infection (Figure 1B). The lesions and tissue damage observed in the WT Mtb-infected animals were graded 4 (marked with 51-75% tissue affected) and 5 (severe with 76-100% tissue affected) and those in the *ppe18* KO-infected animals were graded 3 (moderate with 26-50% tissue affected), 60 weeks post-infection (Figure 1B). A similar trend was observed in the liver (Figure 1C). Effect of infection was not observed in spleen of both WT- and *ppe18* KO Mtb-infected mice sacrificed at 3 weeks. Histiocytosis or accumulation of macrophages in spleen was observed only at 21 and 60 weeks post-infection in mice infected with WT Mtb strain, however, the spleen tissue structure of *ppe18* KO strain-infected mice appeared to be normal (Figure 1D).

Our observations thus indicated that in comparison to the WT, the *ppe18* KO strain elicited a reduced and delayed inflammatory response in lung, liver and spleen of the infected mice. To understand the total effect of *in vivo* growth and inflammation, survival of mice infected with WT and *ppe18* KO strains of Mtb was monitored over a prolonged period of time. No deaths were registered in the group of mice infected with the *ppe18* KO strain during the entire study period of 60 weeks, however, in the group of mice infected with the WT Mtb, survival rate had dropped to 25%, 60 weeks post-infection (Figure 1E). Also, mice infected with *ppe18* KO strain visibly appeared healthier. The percentage increase in the weight of mice infected with *ppe18* KO strain 9 weeks after infection was 55 ± 2% compared to the 31.9 ± 5% increase in the weight of mice infected with the WT strain. We are presently characterizing PPE18-induced modulation of the immune responses that contribute to Mtb virulence in mice.

Project II: Understanding the role of *M. tuberculosis* hsp60 as Th1/Th2 immuno-modulator

Summary of work done until the beginning of this reporting year (upto March 31, 2012)

Macrophage is known to regulate T-cell effector responses as Th1 or Th2. While Th1 is protective, Th2 favors Mtb survival. We have earlier demonstrated a novel role of the *M. tuberculosis* heat shock protein 60 (Mtbhsp60, Cpn60.1) protein to favor Th2-environment by modulating the surface TLR2 population in macrophages (Khan *et al.* [2008] Cell Microbiol. 10: 1711). To understand in detail how Mtb proteins influence the TLR-signaling to modulate macrophage effector-APC functions and the Th balance, we have demonstrated that Mtbhsp60 interacts with both TLR2 and TLR4, but its interaction with TLR2 leads to clathrin-dependent endocytosis resulting in an increased activation of p38 MAPK and IL-10 cytokine that favors Th2. In contrast, upon interaction with TLR4, Mtbhsp60

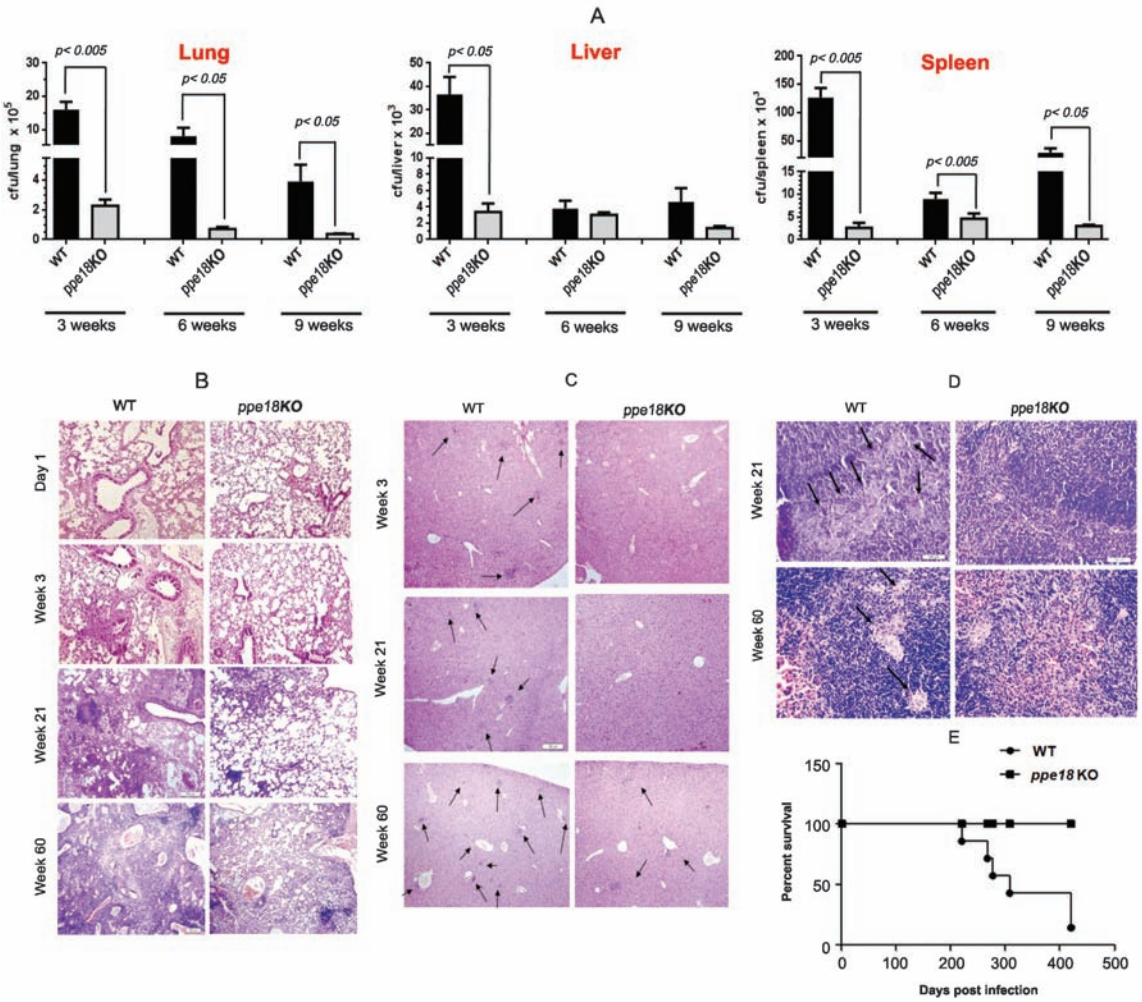

Figure 1. PPE18 protein plays an important role in intracellular survival and pathogenicity of *Mycobacterium tuberculosis* in mice. C57BL/6 mice were infected aerogenically with a low dose of either WT or *ppe18* KO strains of Mtb. At different time points post infection, mice were sacrificed and CFU counts were measured in lung, liver and spleen **(A)**. Data are mean ± SEM of results for five mice per group for each time point. Liver **(B)**, Lung **(C)** and Spleen **(D)** sections from mice infected with either WT (left panel) or *ppe18* KO (right panels) strains of Mtb were stained with Hematoxylin and eosin (H&E) at different time points post infection. Photographs of representative sections from 2 mice visualized at 40X magnification are shown. Arrows indicate the sites of lymphocytic infiltration. In another set of experiment, survival of C57BL/6 mice (n = 8) following a low-dose aerosol infection with either WT or *ppe18* KO strains of Mtb was monitored for 420 days post infection **(E)**.

remains predominantly localized on the cell-surface due to reduced endocytosis of the protein, that leads to p38 MAPK activation and poorer IL-10 production but triggers ERK ½ and TNF-α production. These results were further confirmed using macrophages from TLR2 and TLR4 knock-out mice. Inhibition of endocytosis by MDC increased cell surface accumulation of Mtbhsp60 and compromised its ability to induce IL-10. In such situation, we observed an increase in the TNF-α production.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

The *E. coli* heat shock protein 60 (Ecolihsp60) is retained mainly on the macrophage surface upon interaction with either TLR2 or TLR4 and triggers induction of TNF-α

Although the protein sequence of Ecolihsp60 is significantly similar to that of Mtbhsp60, the biochemical features of Mtbhsp60 deviate significantly from the characteristic properties of

the Ecolihsp60. The Mtbhsp60 exists in a lower oligomeric state as compared to its *E. coli* counterpart due to substitutions in some crucial interface residues required to stabilize its inter-subunit interactions and also lacks ATPase activity. Also at the structural level, Mtbhsp60 significantly deviates from Ecolihsp60 (Figure 2A). Thus, in the next experiment we investigated whether Ecolihsp60 modulates TNF-α/IL-10 cytokines post TLR interaction in a different fashion. We observed that although Ecolihsp60 interacted with both TLR2 and TLR4 (Figure 2B), but unlike Mtbhsp60, it failed to undergo endocytosis through TLR2 (Figure 2C) and preferentially induced TNF-α through both TLR2 and TLR4 (Figure 2D) but very little IL-10. In the presence of isotype-matched antibodies, the level of TNF-a was significantly higher as compared to that of TLR2 or TLR4 alone and almost summed up the levels of TNF-α produced together by these receptors (Figure 2D). These observations led us to speculate that the cellular localization of Mtbhsp60 post-binding to TLRs activates different signaling cascades that finally dictate the type of inflammatory response to be produced in macrophages. In the near future we will focus on identifying how the Mtbhsp60 protein targets the TLR-signaling to influence macrophage APC functions and T-cell immune responses.

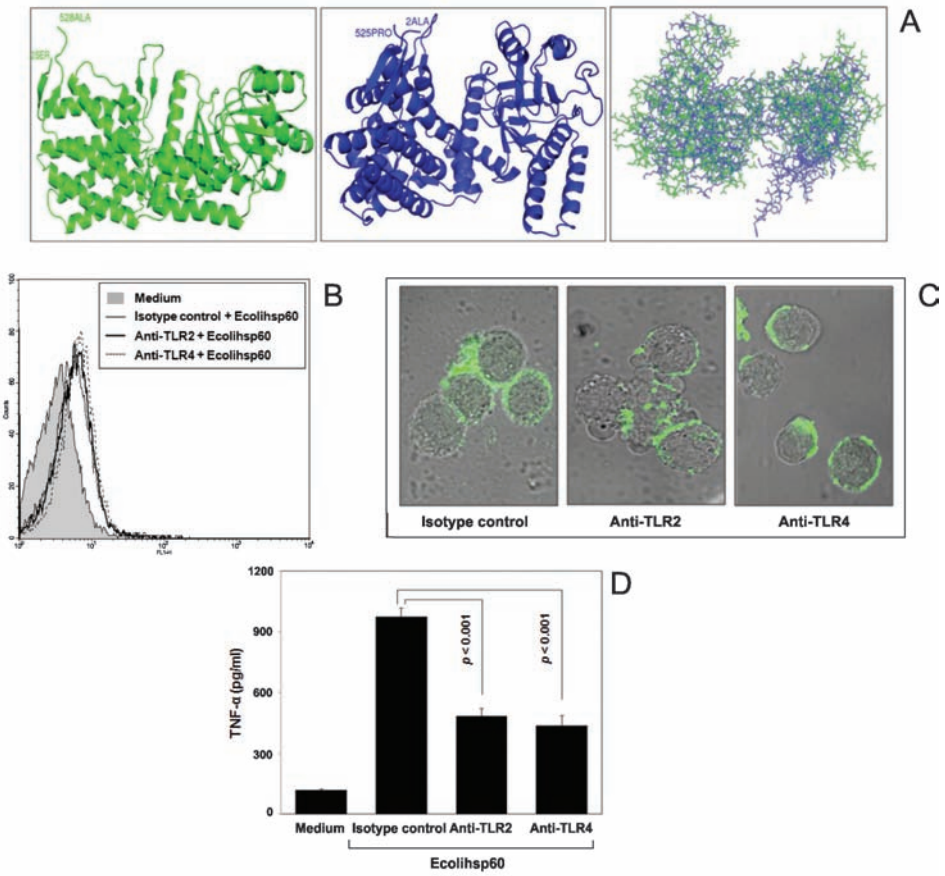

Figure 2. Interaction of Ecolihsp60 either with TLR2 or TLR4 results in induction of TNF-α. The secondary structure of the Mtbhsp60 protein model, predicted based on homology modeling with Modeller software is shown (Green) after its energy minimization, the solved crystal structure of Ecolihsp60 obtained from Protein Data bank (chain-A of PDB-code:2EU1) is displayed (Blue) and the superimposed structures of Mtbhsp60 and Ecolihsp60 is shown **(A)**. In the next experiment, PMA-differentiated THP-1 macrophages were pre-treated with anti-TLR2 mAb or anti-TLR4 mAb or isotype-matched control Ab and then incubated with 10 mg/ml of FITC labeled Ecolihsp60 at 4°C for 30 min. The cells were fixed and the fluorescence was measured by flow cytometry **(B)**. In another experiment, PMA-differentiated THP-1 macrophages were pre-treated with anti-TLR2 mAb or anti-TLR4 mAb or isotype-matched control antibody for 1 h, followed by incubation with Ecolihsp60-FITC (10 mg/ml) at 37°C for 15 min. The cells were fixed and endocytosis of the protein was assessed by confocal laser-scanner microscopy **(C)**. Also, PMA-differentiated THP-1 macrophages were pre-treated with 10 µg/ml of anti-TLR2 mAb or anti-TLR4 mAb or isotype-matched control antibody for 1 h and then incubated with 3 µg/ml Ecolihsp60. TNF-α levels were quantified after 48 h in different culture supernatants by EIA **(D)**. Data are representative of Mean ± SD of three different experiments.

Publications

1. Akhter Y, Ehebauer MT, Mukhopadhyay S and Hasnain SE (2012). The PE/PPE multigene family codes for virulence factors and is a possible source of mycobacterial antigenic variation: perhaps more? ***Biochimie*** *94: 110-116.*

2. *Bhat KH, Ahmed A, Kumar S, Sharma P and Mukhopadhyay S (2012). Role of PPE18 protein in intracellular survival and pathogenicity of Mycobacterium tuberculosis in* mice. ***PLoS One*** *7: e52601.*

3. Bhat KH, Chaitanya CK, Parveen N, Varman R, Ghosh S and Mukhopadhyay S (2012). Proline-Proline-Glutamic Acid (PPE) protein Rv1168c of Mycobacterium tuberculosis augments transcription from HIV-1 Long Terminal Repeat promoter. ***Journal of Biological Chemistry*** *287: 16930-16946.*

4. Mukhopadhyay S, Nair S and Ghosh S (2012). Pathogenesis in tuberculosis: transcriptomic approaches to unraveling virulence mechanisms and finding new drug targets. ***FEMS Microbiology Reviews*** *36: 463-485.*

5. Bhat KH, Das A, Srikantam A and Mukhopadhyay S. PPE2 protein of Mycobacterium tuberculosis may inhibit nitric oxide in activated macrophages. ***Annals of the New York Academy of Sciences*** *(In press).*

LABORATORY OF NEUROSPORA GENETICS

What keeps the Neurospora genome repeat-free?

Faculty	DP Kasbekar	Haldane Chair (Since Jul. 2012)
Other Members	A Sheeba	Technical Officer
	K Sreethi Reddy	Technical Assistant (Since Oct. 2012)

Objectives

Meiotic silencing by unpaired DNA (MSUD) is a presumed RNAi-mediated elimination of the transcripts of any *Neurospora crassa* gene that is not properly paired with a homolog in meiosis. Recent results from our laboratory, obtained in the course of constructing a recombinant inbred line (RIL), have suggested that inbreeding can affect MSUD in a genotype-independent manner. The major objective of the research in the past year was to verify this result, and to complete making the RIL.

In crosses of the standard laboratory Oak Ridge (OR) wild type strains with the *::Bml*^{r} and *::mei-3* tester strains, MSUD of the *bml* (*β-tubulin*) and *mei-3* genes causes dramatic ascus-development abnormalities. MSUD does not occur in homozygous *tester A* x *tester a* crosses, nor in crosses of the testers with the semi-dominant suppressors of MSUD (*e.g.*, *Sad-1, Sad-2*), and the asci develop normally. Presumably, the suppressor alleles prevent the proper pairing of their wild-type homologues, and thus induce them to autogenously silence themselves. Wild-isolated *N. crassa* strains were classified into three types based on the phenotype of their crosses with the testers. In crosses with "OR" and "Sad" type strains the *Bml*^{r} and *mei-3* genes are, or are not, silenced. Whereas in crosses with "Esm" type, *bml* was silenced but not *mei-3*$^{+}$. We proposed that *bml* is more sensitive to silencing than *mei-3*, and that sequence polymorphisms between the OR-derived tester and Sad and Esm genomes might cause one or more genes essential for meiotic silencing to become unpaired and silence itself, thus shortening the duration of silencing. Thus, MSUD could become very fleeting in the cross with Sad type, of intermediate duration in the cross with Esm type, and persist throughout the cross only with OR type (Figure 1). In which case, if a new tester is made in the genetic background of a Sad type strain, and a cross is performed that is heterozygous for the tester allele but isogenic for the rest of the genome, then we would expect to see MSUD. To test this prediction we decided to construct an isogenic recombinant inbred line from the Sad type wild strains Bichpuri-1 *a* and Spurger-3 *A*.

The Sad type wild strains, Bichpuri-1 *a* (B) and Spurger-3 *A* (S), were crossed with each other to produce generation f1. In the f1, and in each successive generation, pairs of sibling strains of opposite mating type were crossed to produce the next generation. We confirmed that in a line the later generations are more isogenic than the earlier generations, and that different lines become isogenic for different genomic segments from the B and S strains. After 10 generations of sibling crosses we generated a pair of isogenic *mat A* and *mat a* strains that is now ready to be used to make the tester strain. Although Bichpuri-1 *a* and Spurger-3 *A*, and most of their f1 progeny were consistently and reproducibly Sad type in crosses with the *::Bml*^{r} and *::mei-3* testers, the later generation strains of each line showed Sad, Esm, or Sad / Esm types with variable expressivity. Since all later generation genotypes are, in principle, obtainable in the f1, the observed transition from an apparently stable Sad phenotype to an apparently unstable Sad/Esm phenotype is probably not due to genotype differences between the generations. Therefore, it appears that the Sad versus Esm difference can have a genotype-independent basis.

Summary of work done (prior to the faculty member joining CDFD i.e., before July 2012)

Only one exceptional *Neurospora crassa* strain contains transposons. This strain, isolated from Adiopodoume in West Africa, contains the retrotransposon *Tad*, whereas all the other (>1000) Neurospora strains examined (by J. A. Kinsey and colleagues) contained only relics of *Tad* inactivated by RIP. No other transposon is known in Neurospora. RIP is a mutational process that acts during a sexual cross and targets G:C to A:T

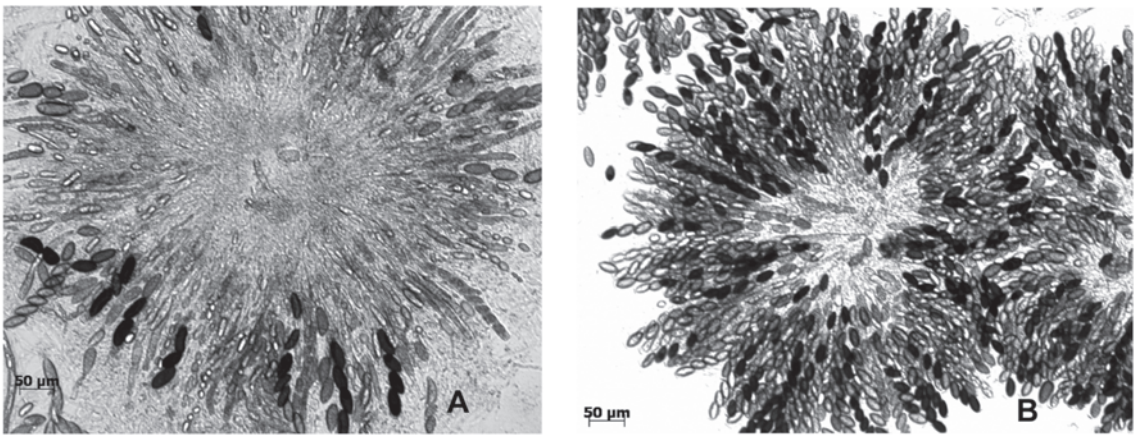

Figure 1. Two wild-isolated *N. crassa* strains induce different phenotypes in their crosses with the ascus-dominant *Dip-1* mutant. A rosette of asci from the cross of the *Dip-1 a* strain (FGSC 9536) with the Roanoke-1m *A* (FGSC 2227) strain (A) shows the *Dip-1* mutant phenotype, namely, several asci with two to four large ascospores instead of the normal eight, but in the rosette from the cross of the *Dip-1 a* strain with the wild-isolated Klong Rangsit (FGSC 6488) strain (B) almost all asci are eight-spored.

hypermutation to repeated DNA sequences. We developed an assay for RIP, and using it we showed (1) the RIP machinery is titrable by chromosome segment duplications (*Dp*) > 300 kbp; and (2) the Adiopodoume strain is one of seven wild-isolated Neurospora strains identified to exert a dominant RIP suppressor phenotype. The Adiopodoume strain contains ~40 copies of *Tad*, each ~7 kb, therefore this ~280 kbp of duplicated DNA might contribute to titration of the RIP machinery, whereas *Tad* would remain vulnerable to RIP in low copy strains. The studies leading to 1 also defined the breakpoints of several *Dp*-generating chromosome rearrangements onto the genome sequence. We pioneered transformation of a closely related pseudohomothallic species, *N. tetrasperma*, to initiate the genetic analysis of diplophase-specific processes such as RIP and MSUD. In related work, we identified Fmf-1p as a master regulator of sexual differentiation and mapped the *dow* mutation.

In other studies, we found that LBR (a vertebrate nuclear membrane protein that tethers chromatin to nuclear lamina) has sterol biosynthetic activity, and we identified its essential amino acid residues by site-directed mutagenesis. Our laboratory is unique in having studied the response of dictyostelids (free-living soil amoebae that feed on bacteria) to antimicrobial isoflavonoids made by leguminous plants. Based on these studies we proposed a novel plant-microbe interaction wherein leguminous plants use isoflavonoids to recruit dictyostelids to clear bacteria from the vicinity of root lesions.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

The fraction of Esm type progeny increases with inbreeding: Both the B and S strains consistently and reproducibly displayed the Sad phenotype. Seventy-six progeny strains in the f1, and 10-20 progeny strains in each succeeding generation were crossed with the testers. Only two (2.6%) of the f1 strains tested were Esm type, and the rest were Sad type. In contrast, a larger fraction of progeny were Esm type in the later generations. Esm types represented 14.5% of the f2+f3+f4 (N= 191), and 57.5% in the f5+f6+f7+f8 (N= 94). None of the 357 strains examined was OR type. To rule out the possibility that the observed variation in phenotype is due to a failure to control for variations in temperature, age of the crosses at analysis, variation in media formulation, and clerical errors; we performed a blind experiment in which 48 f1 strains and 49 f5 strains were examined afresh in parallel. The frequency of Esm types was 4/48 in the f1 and 10/49 in the f5. These results allow us to reject the null hypothesis that the f1 and f5 have the same Esm frequencies ($p < 0.045$, one-tailed z-test).

Later generation strains also show an apparently unstable Sad/Esm phenotype: Twenty-five Sad type f1 progeny were re-examined by re-crossing them with the testers and all re-scored as Sad type. However, re-examination of progeny from the later generations showed that a subset that had scored as Sad type, could subsequently retest as Esm type, and others that scored as Esm type, could retest as Sad type. These results suggested that although the B and S wild strains and most of their f1 progeny were stably Sad type, the later generations have a more variable phenotype and upon re-assay at least a subset of strains can switch between the Sad or Esm types.

Significance of our results: The change from an apparently stable Sad phenotype in the f1 to an apparently unstable Sad/Esm phenotype in later generations is not easily attributed to genetic differences between the strains of the different generations. First, the f1 and later generations (f2, f3, etc.) are all genetically equivalent, in that, they contain about equal contributions of the B and S genomes, and any genotype obtained in a later generation is, in principle, obtainable in the f1. Second, the later generations are more isogenic than the earlier ones (*e.g.*, f1 siblings differ in 50% of their genomes, whereas f8 siblings differ in <0.5%), therefore one would expect a more uniform phenotype among the f8, yet they appeared more variable.

Near-isogenic crosses are likely to be an exception in *N. crassa* since it is an out-crossing heterothallic species. Therefore when such a cross is made in the laboratory, it might experience exceptionally little (or no) meiotic unpairing, and could trigger positive feedback mechanisms to enhance the detection of unpairing and induce silencing. For instance, assembly of the Sad-2 –containing perinuclear complex, in which aberrant RNA molecules derived from unpaired genes are converted into dsRNA may be made more efficient by having the proto-structures for assembling such complexes become long-lived and remain associated with the zygote nuclei and their descendents. That is, the proto-complex might undergo perdurance along with the progeny nuclei. During vegetative growth of the progeny, a subset of mitotic nuclei might retain these proto-structures all the way through to the next cross, whereas they might be lost from other nuclei. Consequently, crosses involving nuclei that retain such structures would show an increase in meiotic silencing strength, and those involving nuclei that lost these structures would show a relative decrease in meiotic silencing strength. Thus the variable perdurance might account for the variable expressivity in meiotic silencing strength in crosses with the testers. An alternative model to account for the apparently genotype-independent change from a stable Sad phenotype to an unstable Sad/Esm phenotype is that *bml* expression levels (or stability levels, turnover rates, etc.) might decrease with inbreeding, independent of effects of meiotic silencing, thereby making the *bml* meiotic silencing test more sensitive in crosses with these strains (since the inbred strains have lower *bml* levels, silencing of *bml* is easier). As for the unstable Esm/Sad phenotype, it could be that *bml* expression levels have decreased to near a key threshold in the inbred strains. Below this threshold, one would observe the phenotype as Esm, above this threshold; one would observe the Sad phenotype. Because any one of these '*bml* near threshold' strains may have slightly different *bml* expression levels from cross to cross, these strains could be observed to switch from Esm to Sad (or *vice versa*) from cross to cross. The latter model raises the question of why expression of *bml* is depressed by inbreeding.

Publications

1. Kasbekar DP (2013). Neurospora duplications and genome defense by RIP and meiotic silencing. ***Neurospora: Genomics and Molecular Biology.*** Editors: DP Kasbekar and K McCluskey, Caister Academic Press, Norfolk, UK. Pages 109-127.

Other Publications

1. * Kasbekar DP (2012). Lymphohematopoietic licence: sterol C-14 reductase activity of lamin B receptor (Lbr) is essential for neutrophil differentiation. ***Journal of Biosciences*** 37: 199-201.
2. Kasbekar DP (2012). Green-carding the referee and Haldane's spell. ***Journal of Biosciences*** 37: 579.
3. Kasbekar DP (2012). The Sad paradox: mutations with dominant *and* recessive phenotypes. ***Journal of Biosciences*** 37: 933-936.
4. Kasbekar DP (2013). Myth versus mutant: story of *o*. ***Journal of Biosciences*** 38: 1.

* Work done elsewhere

LABORATORY OF MAMMALIAN GENETICS

Epigenetic Mechanisms Underlying Developmental Pathways

Faculty	Sanjeev Khosla	Staff Scientist
PhD Students	Garima Sharma	Senior Research Fellow
	Amitava Basu	Senior Research Fellow
	Rachana Roshan Dev	Senior Research Fellow
	Imtiyaz Yaseen	Senior Research Fellow
	Thushara Thamban	Junior Research Fellow
Other Members	M Sri Lalitha	Technical Officer
	Vaishnavo Pai	Project Associate
	Prachi Joshi	Project-Junior Research Fellow
	Srinivas Animireddy	Project-Junior Research Fellow (Till Jan. 2013)
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	Shekhar Mande	NCCS, Pune
	Rakesh Mishra	CCMB, Hyderabad
	Vinay K Nandicoori	NII, New Delhi

Project 1: *DNMT3L*: Role in development

Summary of work done until the beginning of this reporting year (upto March 31, 2012)

We had previously reported analysis of the regulatory mechanisms underlying the transcription of *DNMT3L* in Drosophila. Transgene reporter assay in Drosophila was performed wherein the promoter region flanked by *loxP* sites, was inserted upstream of the *hsp70* promoter driven *mini-white* reporter gene containing P-element vector pCaSpeR. The analysis of the reporter gene transcription showed that the presence of DNMT3L promoter/Exon1 region in the reporter construct causes repression of the GFP expression.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

Role of *DNMT3L* promoter in regulation of its transcription

For functional analysis of the *DNMT3L* promoter-Exon 1 CpG island that had previously been shown to be hypomethylated in cervical and ocular cancer samples, we performed transient transfection assay in mammalian HeK cell line with two overlapping fragments from this region. Approximately 70% decrease in expression of the GFP reporter gene in the mammalian cells was observed for both the versions of the DNMT3L Promoter-Exon 1 CpG island and in both orientations. The extent of the inhibition of GFP expression in presence of this region was similar to that observed for H19 ICR, a known transcriptional repressor (Figure 1). The inhibitory nature of this CpG island was found to be due to its interaction with Polycomb proteins that are known to inhibit transcription. Concordant with the observation of its interaction with Polycomb proteins, our results also showed that this region adopts an inactive chromatin conformation in both the Drosophila transgene reporter gene assay and the mammalian transient transfection assay.

Project 2: Host epigenetic response to infection

Summary of work done until the beginning of this reporting year (upto March 31, 2012)

During the interaction with *Mycobacterium tuberculosis*, not only does the host cell reprogram its epigenetic markings at several loci in the genome so that the affected gene may be appropriately modulated but also the mycobacterium can produce molecules that interact or influence the effectors of host epigenetic modifications. We have previously initiated studies to identify (i) putative DNA methyltransferases in *M. tuberculosis* and (ii) DNA methylation changes in the host genome.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

To influence the host epigenetic circuitry, the mycobacterial factor could be (i) a DNA methyltransferase; (ii) a histone modifier (histone methyltransferase, acetyltransferase, etc.); (iii) a protein that interacts with DNA; (iv) a protein that

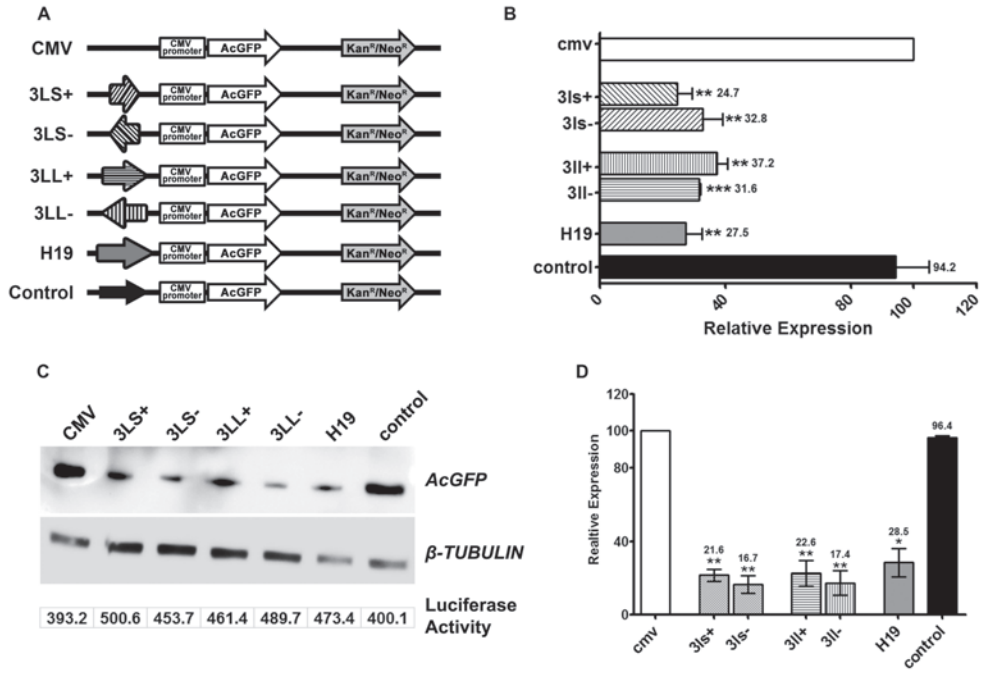

Figure 1. Functional analysis of the DNMT3L promoter-Exon 1 CpG island by reporter gene assay in transiently transfected mammalian cells. A. Graphical representation of the various constructs transfected into HEK293 cells. Shown for each construct is the reporter AcGFP gene, its CMV promoter, the selection *Kan*^{R}/*Neo*^{R} marker, the various DNMT3L promoter-Exon 1 CpG island fragments and the control Chr1 fragment and the H19 ICR inserted upstream of the CMV promoter. **B.** Relative transcriptional level analysis of the reporter AcGFP gene in the various constructs by Real-Time PCR. **C.** A representative Western Blot analysis showing AcGFP protein expression for HEK293 cells transfected with the various constructs mentioned in A. Luciferase activity for the pG5luc vector co-trasfected with the above mentioned constructs is shown below the â-TUBULIN panel. **D.** Relative AcGFP protein expression levels for the cells transfected with the various constructs. Error bars represent standard error of mean. Asterisks indicate significant difference (Student's t test, * - $p < 0.05$, ** - $p < 0.01$, *** - $p < 0.001$).

interacts with histones, or (v) a protein that interacts with chromatin modifiers. Based on a combination of bioinformatic analysis and Co-Immuno-precipitation assay we have identified a few mycobacterial genes that could be putative DNA demethylase or Histone methyltransferases. Further experiments are being carried out to characterize their role in modulating the host epigenetic circuitry.

We had previously reported identification of mycobacterial proteins that can methylate DNA. One of these proteins was found to be secreted out of BCG and our transient transfection assay showed that it can localize to the Thp1 nucleus. By performing deletion experiments a nuclear localization signal has been identified in the C-terminus of this protein (Figure 2). Site-directed mutagenesis experiments are underway to pin point the NLS sequence motif. We plan to identify the role of this protein during infection and its correlation with the host epigenetic circuitry.

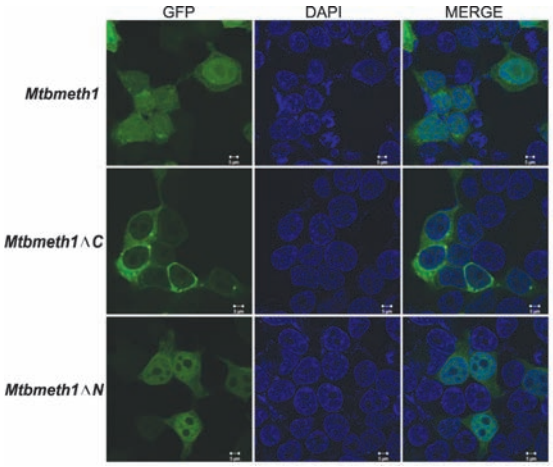

Figure 2. Subcellular localization of the putative DNA methyltransferase *Mtbmeth1* in mammalian cells after transient transfection. Constructs of *Mtbmeth1* and its deletion mutant in fusion with GFP were transiently transfected in HeK cells and the subcellular localization was examined under a confocal microscope. *Mtbmeth1ΔC* and *Mtbmeth1ΔN* denote the C-and N-terminal deletion of *Mtbmeth1* respectively. Bar is ~5 μM.

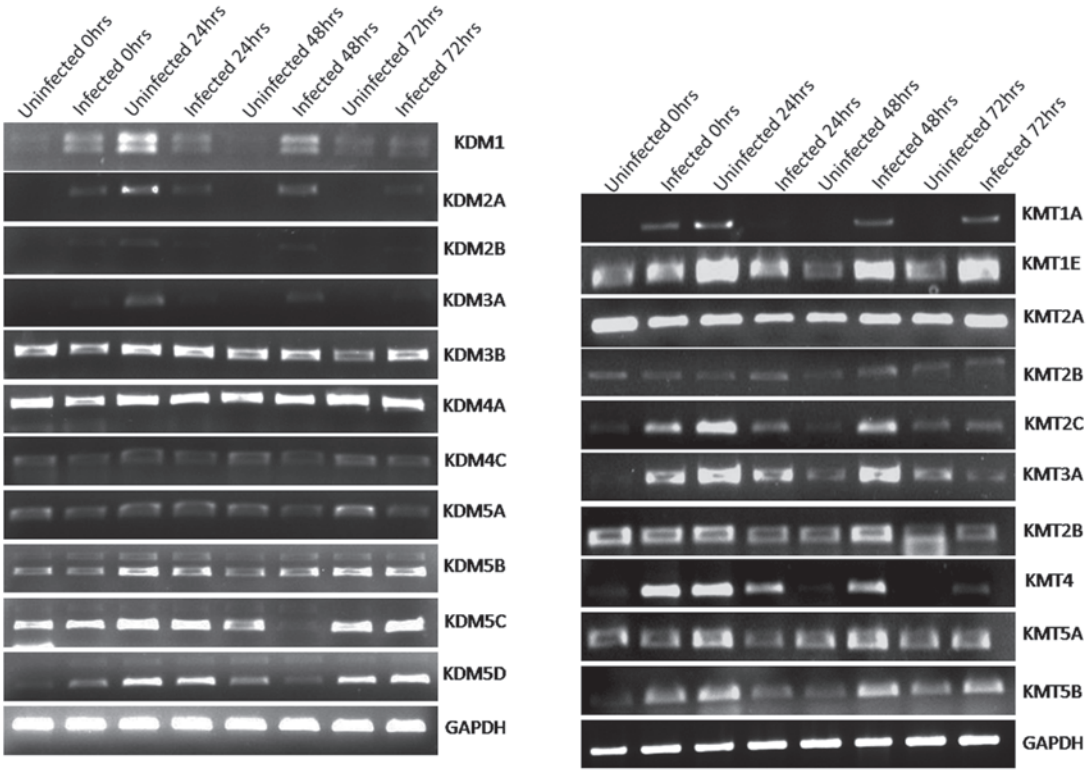

Figure 3. Expression analysis of the various mammalian Histone methyltransferases and demethylases upon infection with *BCG*. Semi-quantitative RT-PCR for the various Histone methyltransferases (KMTs) and demethylases (KDMs) was performed on uninfected and *BCG*-infected Thp1 cells. Time points mentioned in the labels on the top refer to the number of hours the cells were left in culture after the *BCG* infection. As a control Thp1 cells were also maintained in culture without infection for the same time.

In order to respond to the infection by *M. tuberculosis*, the host cells would have to reprogram the epigenetic markings at several loci in the genome so that the affected gene may be appropriately modulated. It has been our endeavor to examine these epigenetic changes and identify the genetic loci where these changes are brought about. This, we believe, will provide us important evidence about the genes in the host that might be participating in a response to mycobacterial infection. Previously, we had performed examination of the DNA methylation changes upon infection in the treated macrophage cell line, Thp1. The loci that showed changes in DNA methylation upon infection are being validated at present. We are also in process of examining the expression level of several Histone methyltransferases (KMTs) and Histone Demethylases (KDMs) by RT-PCR and Western in BCG infected Thp1 cells. As can be seen from Figure 2, a few histone methyltransferases and demethylases do show changed expression in *BCG* infected Thp1 cells. The validation of the changed expression level and its correlation with mycobacterial infection is being studied at present.

Publications

1. Gokul G and Khosla S (2012). DNA methylation and cancer. ***Subcellular Biochemistry*** 61: 597-625.

LABORATORY OF MOLECULAR ONCOLOGY

Genomics and Molecular Genetics of Cancer and Genetic Disorders

Faculty	Murali D Bashyam	Staff Scientist
PhD Students	Ratheesh Raman	Senior Research Fellow
	Md Khursheed	Senior Research Fellow
	P Ramaswamy	Senior Research Fellow
	Sita Rama Raju	Senior Research Fellow
	Raju Kumar	Junior Research Fellow (Since Jul. 2012)
	A Srinivas	Junior Research Fellow (Since Feb. 2013)
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	Vasantha K Bhaskara	Research Associate (Since Oct. 2012)
	Ajay K Chaudhary	Technical Assistant
	K Viswakalyan	Research Assistant
	Sandeep N Madana	Research Assistant (Since Jun. 2012)
	Neha Gupta	Project-Junior Research Fellow
	Kamtam Ramesh	Project-Junior Research Fellow (Since Jul. 2012)
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	C Sundaram	NIMS, Hyderabad
	S Uppin	NIMS, Hyderabad
	M Srinivasulu	MNJ Hospital, Hyderabad
	Subramanyeshwar Rao	IACHRC, Hyderabad
	KVVN Raju	IACHRC, Hyderabad
	Sujit C Patnaik	IACHRC, Hyderabad
	Mohana Vamsy	Omega Hospitals, Hyderabad
	AR Ramadevi	Sandor Proteomics, Hyderabad
	Neerja Gupta	AIIMS, New Delhi
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	Ishwar C Verma	SGRH, New Delhi
	Mamta Muranjan	KEM Hospital, Mumbai
	Sheela Nampoothiri	AIMS, Cochin
	Jayarama S Kadandale	CHG, Bengaluru
	Ramana Davuluri	Wistar Institute, USA
	Jonathan Pollack	Stanford University, USA

Objectives

1. Identification and characterization of important deregulated genes/pathways in cancers prevalent in India; and
2. Identification and characterization of disease causing mutations in genetic disorders.

Summary of work done until the beginning of this reporting year (Upto March 31, 2012)

Colorectal Cancer (CRC): 50% of early onset rectal (but not colon) cancer samples did not harbour deregulated canonical Wnt signalling or mismatch repair (MMR) inactivation. Interestingly, despite the absence of canonical Wnt activation, the early-onset sporadic rectal cancer (EOSRC) samples exhibited significant chromosomal aberrations. One such aberration at 5p11.2 (including *hTERT*) presented as a gain in Wnt- and loss in Wnt+ samples.

Pancreatic Cancer (PaCa): We characterized a possible tumour suppressor function for *ARID1B* encoding a member of the SWI/SNF chromatin

remodelling complex, which was found to be deleted in several PaCa cell lines and xenografts. Permanent transfectancts generated using *ARID1B* cDNA in MiaPaCa2 PaCa cell line (harbouring *ARID1B* homozygous deletion) exhibited reduced colony formation ability in liquid media and soft agar, though there was no difference in conventional growth, apoptosis and cell cycle analyses. In addition, preliminary analysis revealed hypermethylation of *ARID1B* promoter CpG island in PaCa cell lines. ARID1B exhibited significantly reduced expression in tumour when compared to matched normal tissue, as determined by immunohistochemistry (IHC) on a PaCa tissue microarray (TMA).

Phenylketonuria (PKU): Molecular genetic analysis of PKU in seven Indian patients revealed complete absence of *Phenylalanine hydroxylase* (*PAH*) missense mutations; four novel *PAH* mutations were identified.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

CRC: We performed genome-wide DNA copy number and transcript profiling on additional microsatellite stable (MSS) EOSRC samples, stratified for Wnt status. Interestingly, several distinct copy number alterations, validated by quantitative PCR (Q-PCR), were identified in the Wnt- *vis-à-vis* Wnt+ samples. Analysis of array transcript profiles generated for 36 Wnt- and 16 Wnt+ EOSRC samples using Significance Analysis of Microarrays and Gene Set Enrichment Analysis (GSEA) validated enrichment of the Wnt/β-Catenin gene set in Wnt+ samples. Surprisingly, non-canonical Wnt pathway genes were enriched in a subset of Wnt- samples (Figure 1A); this observation was validated using quantitative-reverse transcription PCR (Q-RT-PCR) (Figure 1B). This is the first report of possible presence of non-canonical Wnt driven tumours in rectal cancer.

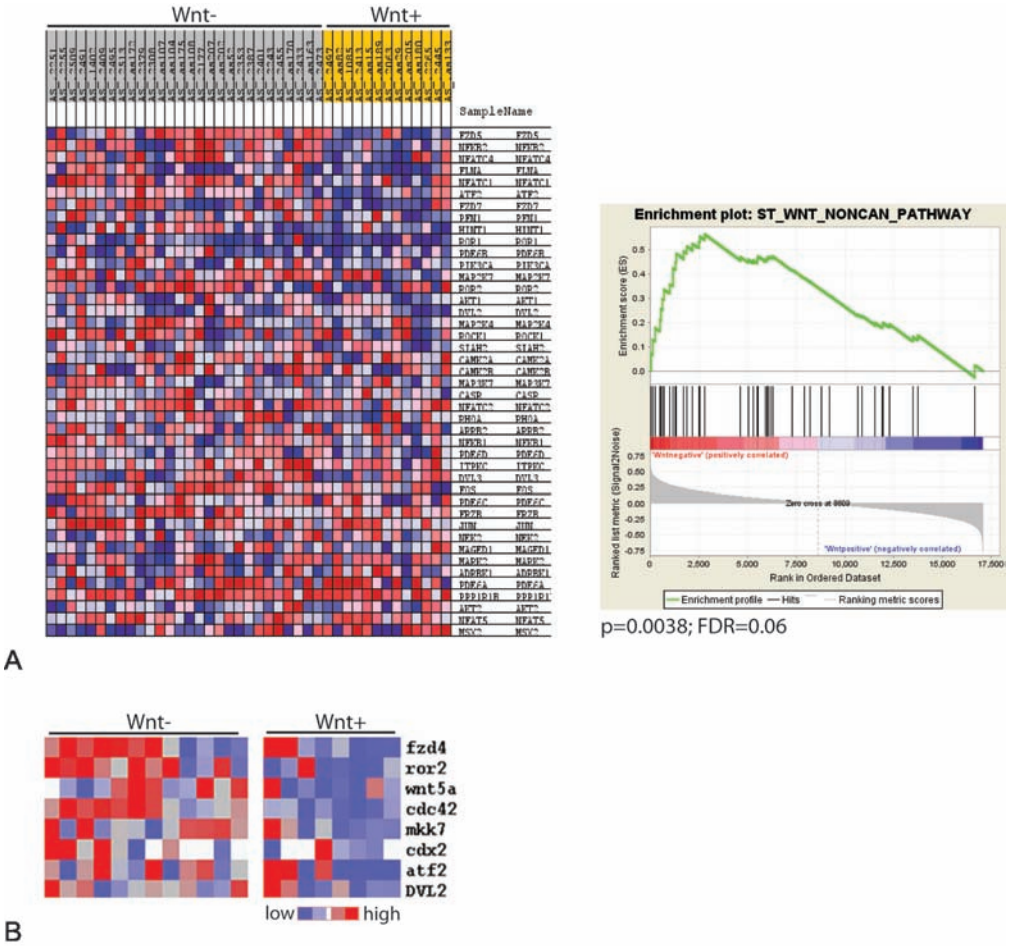

Figure 1. Gene set enrichment analysis identifies significant upregulation of non-canonical Wnt pathway genes specifically in Wnt- EOSRC (Panel A). The differential expression of non-canonical Wnt pathway genes is validated using Q-RT-PCR (Panel B).

PaCa: Azacytidine and TSA treatment resulted in significant elevation in *ARID1B* transcript levels only in PaCa cell lines that exhibited reduced expression, corroborated by identification of extensive methylation of promoter CpG island using bisulphite sequencing (Figure 2A). *ARID1B* expressing PaCa cells exhibited significantly increased senescence-associated â-galactosidase activity (Figure 2B). A pool of several *ARID1B* permanent MiaPaCa2 clones exhibited significantly reduced colony formation ability in liquid culture when compared to pooled vector clones, a difference not observed with clones generated in Panc1 (a PaCa cell line harboring elevated *ARID1B* levels); thus validating results obtained with individual MiaPaCa2 clones. The loss of *ARID1B* expression in PaCa (determined by IHC on a TMA) was associated significantly with advanced tumour stage (p=0.0185, Fisher's exact test) indicating perhaps it could be a late event (Figure 2C). The results therefore strongly support a tumour suppressor role for *ARID1B* in PaCa akin to a similar role of other SWI/SNF components in many cancers.

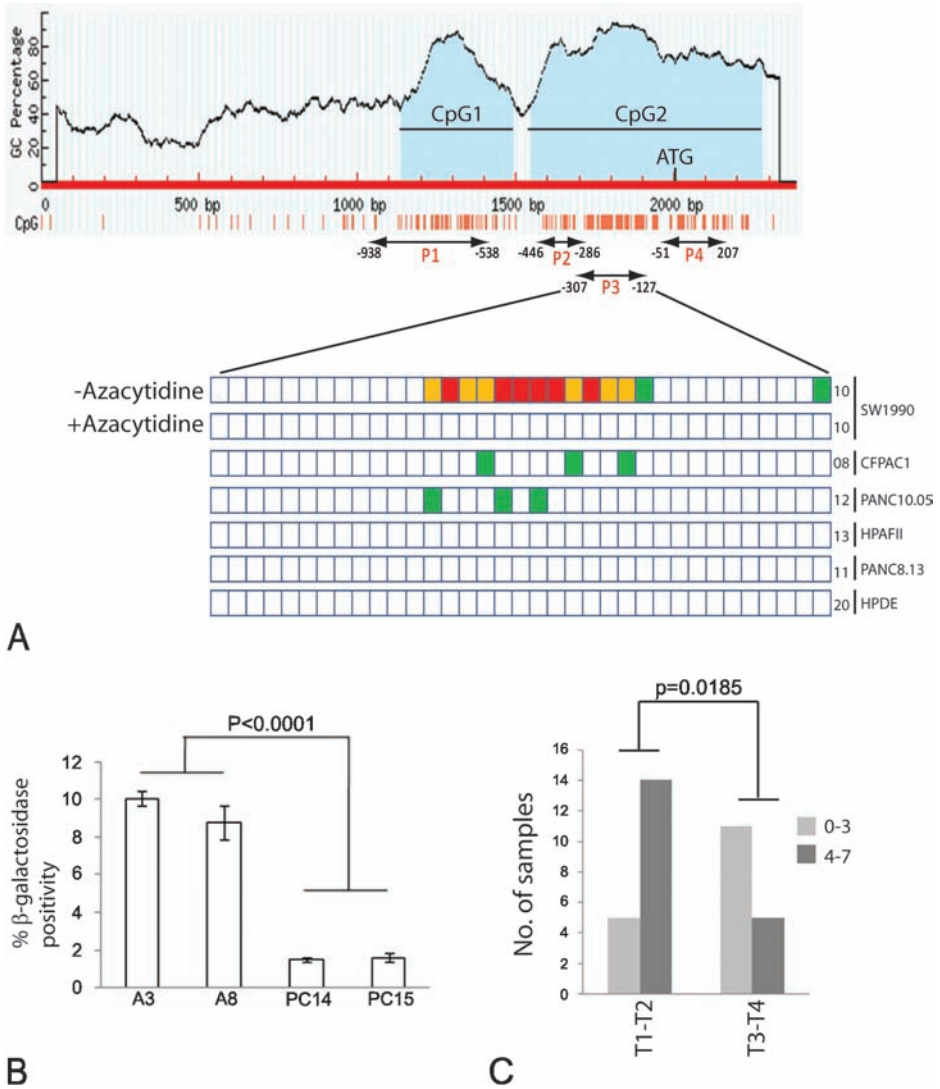

Figure 2. *ARID1B* CpG island (Panel A, top) methylation profile (Panel A, bottom) in PaCa cell lines harbouring low (SW1990, CFPAC1 and PANC10.05) or high (HPAFII and PANC8.13) *ARID1B* transcript levels and in primary human pancreatic ductal epithelial line (HPDE) also harbouring high *ARID1B* levels. Each horizontal row of squares (Panel A, bottom) represents result for one cell line; each square represents one CpG dinucleotide and percent Cytosine methylation is denoted by a colour code (white, <10%; green, 10-33%; orange, 34-66%; red, >66%). The total number of clones analyzed for each cell line is given at the end of each row. Methylation status following Azacytidine (8µM) treatment was evaluated only in SW1990. Panel B depicts results for senescence-associated β-galactosidase staining in permanent *ARID1B* or vector MiaPaCa2 clones. Panel C shows result of IHC-based detection of ARID1B in pancreatic tumour samples stratified for tumour stage.

PKU: We extended *PAH* mutation analysis to twenty six suspected Indian PKU families; disease causing mutations were detected in twenty four. A total of twenty different mutations were identified of which eight 'unique' India-specific mutations accounted for fourteen of twenty four mutation positive families (Figure 3A). Interestingly, only five were missense mutations while five were splice and four were nonsense mutations, respectively (Figure 3A). Two nonsense mutations were characterized to confirm significant reduction in mutant transcript levels possibly through activation of nonsense mediated decay (Figure 3B). All missense mutations affected conserved amino acid residues and sequence and structure analyses suggested significant perturbations in enzyme activity of respective mutant proteins. This is the first report of identification of a significantly low proportion of missense *PAH* mutations in PKU families and together with the presence of a high proportion of splice and nonsense mutations, points to a unique *PAH* mutation profile in Indian PKU patients.

Future plans

1. Identification of genes/pathways that drive oncogenesis in Wnt- MSS EOSRC.
2. Characterization of *ARID1B* transcriptional targets with respect to PaCa.
3. Characterization of selected mutations affecting transcript stability/processing identified through screening of various genetic disorders.

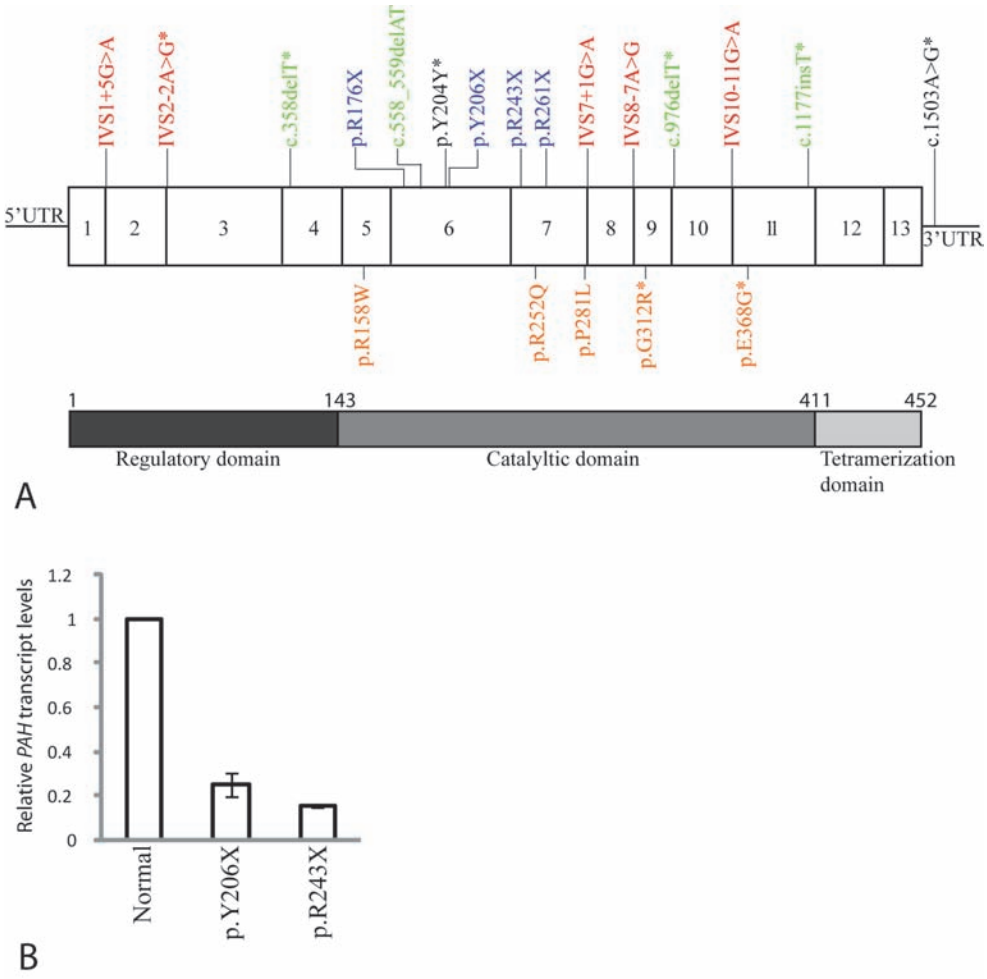

Figure 3. Analyses of *PAH* mutations identified from Indian PKU patients. Panel A (top) shows the location of mutations in the *PAH* gene. Red, splice; blue, nonsense; green, in/del; orange, missense; black, silent and 3'UTR. India-specific mutations are denoted by '*'. A bar diagram (bottom) depicts three important PAH domains. Panel B shows the result of quantitative reverse transcription PCR carried out on RNA isolated from proband lymphoblasts (for mutation p.Y206X and p.R243X) and from a normal lymphoblast sample.

Publications

1. Bashyam MD, Chaudhary AK and Bhat V (2012). The IVS2+837T>G appears to be a relatively common 'rare' β-globin gene mutation among β-Thalassemia patients in the South Indian state of Karnataka. ***Hemoglobin*** 36: 497-503.

2. Bashyam MD, Chaudhary AK, Reddy EC, Reddy V, Acharya V, Nagarajaram HA, Devi ARR, Bashyam L, Dalal AB, Gupta N, Kabra M, Agarwal M, Phadke SR, Tainwala R, Kumar R and Hariharan SV (2012). A founder ectodysplasin A receptor *(EDAR)* mutation results in a high frequency of the autosomal recessive form of hypohidrotic ectodermal dysplasia in India. ***British Journal of Dermatology*** 166: 819-829.

3. Bashyam MD, Chaudhary AK, Sinha M, Nagarajaram HA, Devi ARR, Bashyam L, Reddy EC and Dalal A (2012). Molecular genetic analysis of MSUD from India reveals mutations causing altered protein truncation affecting the C-termini of E1α and E1β. ***Journal of Cellular Biochemistry*** 113: 3122-3132.

4. Bashyam MD, Purushotham G, Chaudhary AK, Rao KM, Acharya V, Mohammad TA, Nagarajaram HA, Hariram V and Narasimhan C (2012). A low prevalence of *MYH7/MYBPC3* mutations among familial hypertrophic cardiomyopathy patients in India. ***Molecular and Cellular Biochemistry*** 360: 373-382.

5. Muranjan M, Agarwal S, Lahiri K and Bashyam M (2012). Novel biochemical abnormalities and genotype in Farber disease. ***Indian Pediatrics*** 49: 320-322.

6. *Shain AH, Giacomini CP, Matsukuma K, Karikari CA, Bashyam MD, Hidalgo M, Maitra A and Pollack JR (2012). Convergent structural alterations define SWItch/Sucrose Non-Fermentable (SWI/SNF) chromatin remodeler as a central tumor suppressive complex in pancreatic cancer. ***Proceedings of the National Academy of Sciences of the USA*** 109: E252-E259.

7. Kavela S, Shinde SR, Ratheesh R, Viswakalyan K, Bashyam MD, Gowrishankar S, Vamsy M, Pattnaik S, Rao S, Sastry RA, Srinivasulu M, Chen J and Maddika S (2013). PNUTS functions as a proto-oncogene by sequestering PTEN. ***Cancer Research*** 73: 205-214.

8. Raman R, Kotapalli V, Adduri R, Gowrishankar S, Bashyam L, Chaudhary A, Vamsy M, Patnaik S, Srinivasulu M, Sastry R, Rao S, Vasala A, Kalidindi N, Pollack J, Murthy S and Bashyam M. Evidence for possible non-canonical pathway(s) driven early-onset colorectal cancer in India. ***Molecular Carcinogenesis*** (In press).

* Work done elsewhere

LABORATORY OF CANCER BIOLOGY

Cellular Senescence and Sirtuin Biology, and Cancer Cervix Progression

Faculty	Gayatri Ramakrishna	Staff Scientist (Till Sep. 2012)
PhD Students	Shashi Kiran	Senior Research Fellow
	Babul Moni Ram	Senior Research Fellow
	Tariq Anwar	Senior Research Fellow
	Rajendra Angara	Junior Research Fellow
Other Members	Nirupama Chatterjee	Technical Officer
	Sapna Singh	Research Associate
	Vineesha	Project-Junior Research Fellow
	Praveen	Project-Junior Research Fellow (Till Jan. 2013)
	Juby Mathew	Project-Junior Research Fellow (Since Sep. 2012)
Collaborators	Nashreen Islam	Tejpur University, Assam
	Renu Wadhwa	AIST, Japan
	P Uday Kumar	NIN, Hyderabad

Objectives

The major focus of our research includes:

1. Understanding the process of cellular senescence; and
2. Role of serine threonine phosphatase, calcineurin, during cervix progression.

Project 1: Understanding the mechanism of cellular senescence

Telomere attrition is a well known cause for cellular senescence. However, oxidative damage can accelerate ageing leading to premature senescence. In this context we had earlier proposed a role for wild type Ras in growth arrest (Singh *et al.,* FASEB 2005, and Bose *et al*., 2011). In fact, senescence is now considered an important growth arrest mechanism in context of neoplastic transformation. We are currently focusing on two main aspects (a) Role of sirtuins in cellular senescence, and (b) effect of peroxovanadates as redox modulators in accelerating the process of senescence.

Summary of work done until beginning of this reporting year (Upto March 31, 2012)

We had earlier reported that expression of nucleolar SIRT7 in young fibroblast was very prominent, decreased during late passages and became undetectable in the senescent cells. We had also evaluated the role of SIRT1 in cervical neoplasia and reported its overexpression in cervical intraepithelial lesions. In addition, we reported the use of catalase resistant peroxovanadate compound, as an alternate tool to induce premature cellular senescence.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

1a. Understanding the biology of Sirtuins in context of senescence

Besides the genetic makeup of the cell, the epigenome plays a crucial role in gene regulation. The epigenome in turn is maintained by acetylation and methylation of the chromatin and its associated proteins. Chromatin modifications are brought about by DNA methyl transferases (DNMTs) and Histone deacetylases (HDACs). Amongst the various histonedeacetylases known, members of the silent information regulator 2 (Sir2) family are conserved from yeast to humans and regulate lifespan in various organisms. Some of the recent reports point to role of Sirtuins as critical regulators at the crossroads between cancer and aging. However, the exact function of the various isoforms in the context of cell proliferation and ageing is still unclear in higher organisms. In the previous report, using fibroblast cultures we had shown that SIRT7 levels decline following replicative senescence. Intriguingly, we also found the loss of nucleolar SIRT7 during replicative senescence

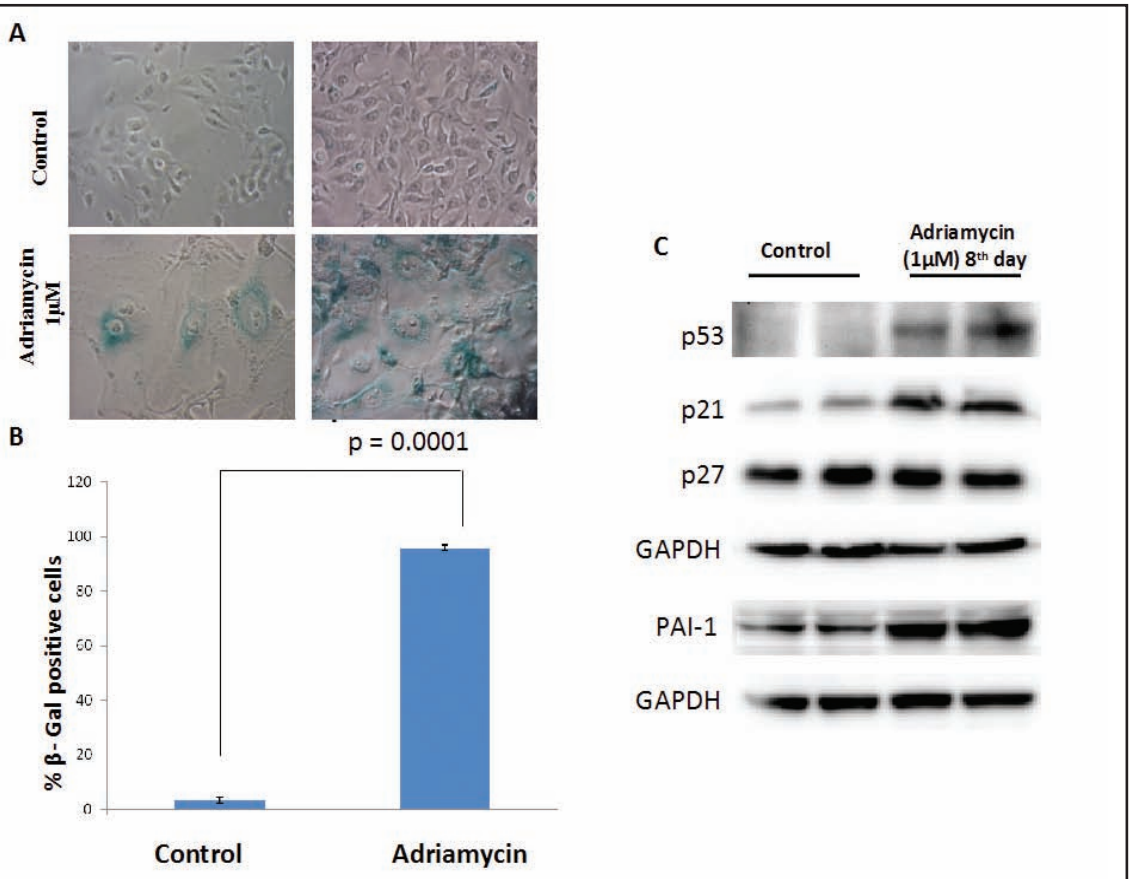

Figure 1. Induction of senescence in adrimaycin treated cells. **(A)** Senescence associated β-galactosidase (SA β-Gal) staining in U2OS cells treated with adriamycin (1μM) **(B)** Percentage SA β- Gal positive cells **(C)** Immunoblot analysis of growth arrest markers in control and adriamycin treated U2OS cells.

in primary fibroblasts (TIG, WI38). In the present reporting year we undertook a detailed study on standardizing conditions for stress induced premature senescence by the DNA-damage agent adriamycin a widely used anticancer agent that acts by stabilizing "cleavable complexes" of DNA with topoisomerase II. Premature cellular senescence was induced in osteosarcoma cells, U2OS, by treating with low dose of adriamycin / doxorubicin.

The adriamycin treated cells showed enlarged morphology starting at 3rd day and by 8th day more than 90% of the cells exhibited enlarged and flattened morphology indicative of accelerated senescence. Most of the enlarged cells stained positive for senescence associated β-galactosidase activity (SA-beta Gal), as detected by 5-bromo-4-chloro-3-indolyl β-D-galactoside (X-gal) staining at pH 6.0 (Figure 1A, B). We also checked for the general growth arrest markers like p53, p21/WAF1 and p27/Kip1 in the adriamycin treated cells (8th day). We found upregulation of p53 and p21/WAF1 in the senescent cells but there was no change in the expression of p27/Kip1 in the senescent cells as compared to control cells. Senescent cells also exhibited higher expression of Plasminogen Activator Inhibitor 1 or PAI-1, which is considered to be a marker for senescence (Figure 1C). The expression level of all the different isoforms of Sirtuins (SIRT1-7) was checked by quantitative Real Time-PCR in proliferating (control) and senescent U2OS cells. A significant increase in the expression of SIRT4 (3 fold) and SIRT6 in the senescent cells was noted (Figure 2). Additionally we also performed the subcellular localization of various Sirtuin isoforms. Intriguingly, SIRT2 which is mostly cytoplasmic showed a nuclear expression in senescent cells. Unlike the replicative senescence where a loss of nucleoloar SIRT7 was observed, no alterations in its localization pattern was seen in adriamycin induced premature senescence. In brief, we found that a low dose of adrimaycin

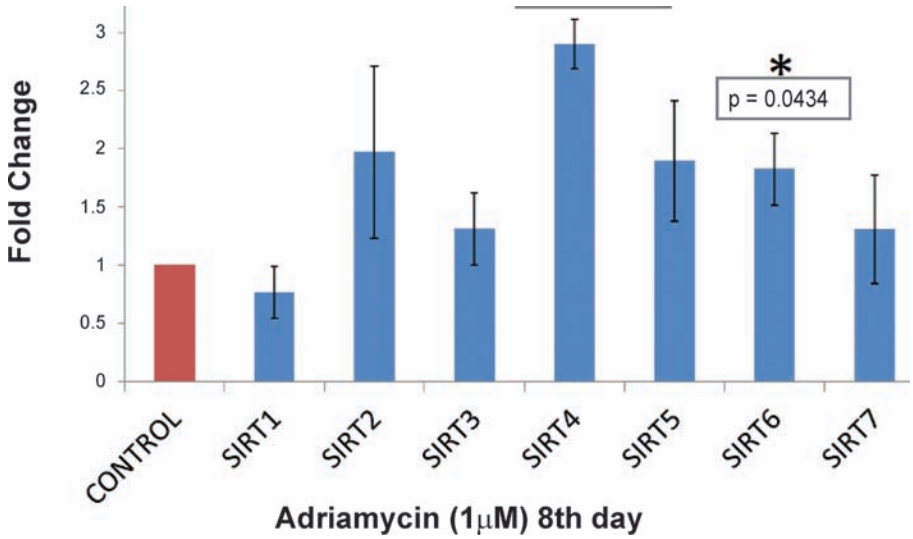

Figure 2. Expression of various Sirtuin isoforms in senescent U2OS cells normalized to control cells.

induces characteristic features of senescence in U2OS cells and this is accompanied with increased levels of SIRT4, SIRT6 and shuttling of cytoplasmic SIRT2 to nucleus.

1b. Role of Sirtuins in cervical neoplasia

Recent studies point to a close connection between cancer and ageing with Sirtuins at the crossroads. However, the role of human Sirtuin isoforms in malignancies is still controversial. We therefore designed a study to evaluate the correlation of SIRT1 expression with proliferation marker Ki-67, and growth arrest/senescence marker p27, during cervical cancer progression. The expression was evaluated by immunohistochemistry in formalin fixed archival human cervical samples: normal/ ASCUS, preneoplastic squamous intraepithelial lesions (SIL) and invasive squamous cell carcinoma (SCC). Expression of SIRT2 and SIRT7 was found to be higher in progressive grades of cancer in the following order: Normal<SIL<SCC and correlated well with the proliferative index of Ki-67. Intriguingly, SIRT1 levels were higher only in the benign stages of squamous intraepithelial lesions and correlated with the growth arrest marker p27 (Figure 3).

1c. Chemical tools which change the cellular redox states to study premature senescence

In continuation with the previous studies on Sirtuins and ageing, we are also trying to evaluate the role of peroxovanadate compounds to induce stress induced premature senescence (SIPS). Hydrogen peroxide is the most preferred oxidative agent to study SIPS. However, a very high dose of peroxide (100-500μM) is needed to induce SIPS *in vitro*, as the cells are abundantly equipped with catalase which effectively destroys the peroxides. The present study was designed to evaluate the role of peroxovanadium compounds in inducing SIPS as they are resistant to catalase activity. Our results indicated that diperoxovanadate (DPV) can induce features of senescence *viz.* flattened morphology, upregulation of p21, PAI-1 and HMGA2 in mouse fibroblasts (NIH3T3) at much less dose (25μM) compared to H_2O_2 (150μM). In addition, we report altered localization of cyclin-D1 to cytoplasm in the senescent cells. However, our attempt to induce senescence in lung carcinoma cell line A549 using the similar doses of DPV was not successful. Hence, another peroxovanadium compound polyacrylic acid sodium salt peroxovanadate (PAAV), which is more catalase resistant and a stronger oxidant than DPV was tried. PAAV treatment resulted in growth arrest of A549 with features of premature senescence and SA-betagalactosidase positivity. Cytomorphological changes including cytoskeletal reorganization was a marked feature of DPV and PAAV treated cells. We surmise a role of an early activation of Rac1-GTPase as a necessary event triggering the peroxovanadium mediated premature senescence.

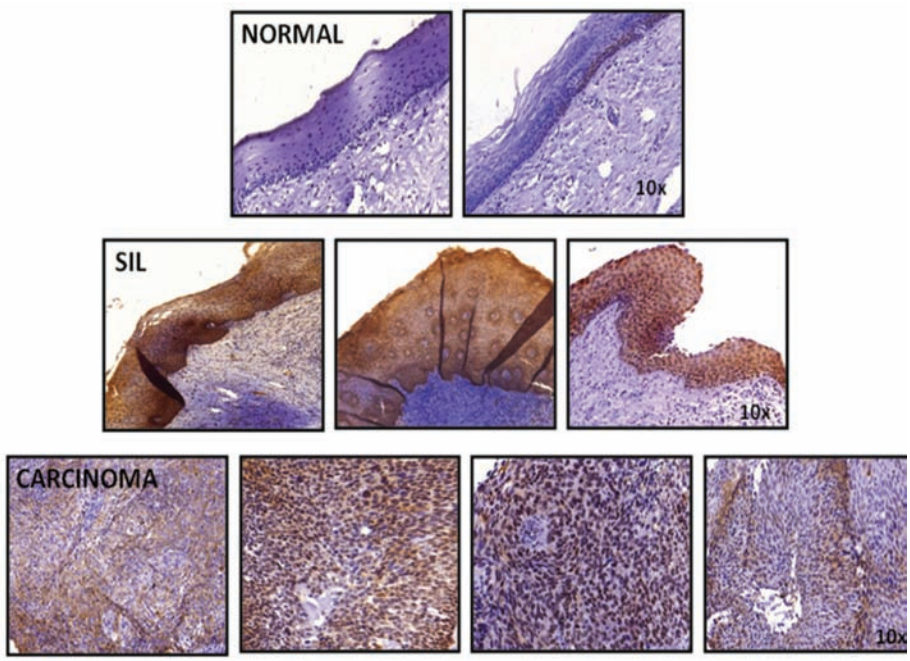

Figure 3. Expression pattern of SIRT1 in normal, dysplastic (SIL) and squamous cell carcinoma of cervix.

Project 2: Pathways in cancer cervix progression

Cervical cancer is a leading cause of mortality among women especially in rural India. Our research group's current focus is on: cancer cervix prevention strategies in rural population and role of candidate biochemical pathways and genetic/ epigenetic changes during cancer cervix progression.

Summary of work done until beginning of this reporting year (Upto March 31, 2012)

We had earlier reported that activity of calcineurin, a serine theroine phosphatase, is higher in cervical cancer cell lines (SiHa, Hela, C33A) compared to their normal immortalized counterpart (HaCaT). Cyclosporine A inhibited the growth and foci formation in SiHa cells and serendipitously we made an unusual observation that cyclosporine-A treatment leads to massive cellular vacuolation.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

Immunosuppressant, cyclosporine A, results in non-apoptotic cell death in cervical cancer cells

Calcium (Ca^{2+}) has been known for long as an almost universal intracellular messenger, controlling a diverse range of cellular processes, such as gene transcription, cell proliferation and cell death. Calcium signaling is mediated through many signal transduction cascades involving calcium interacting proteins and one such important signaling event is activation of protein phosphatase calcineurin and its downstream effector NFAT (Nuclear Factor Activated in T cells). The role of calcineurin signaling is well established in immune cells, cardiac cells and certain neuronal cells. However, there is still a lacuna in understanding of calcineurin mediated pathways with regard to other epithelial cell types. Earlier we reported a significant increase in calcineurin activity in cervical cancer cell lines. To test if calcineurin inhibition also results in growth alterations in cervical cancer cell lines, we used cyclosporine A (CsA) a well known immuno-suppressant and pharmacological inhibitor of calcineurin. CsA not only inhibited the growth of cancer cervix cells but also induced massive dilation in the endoplasmic reticulum (ER). An increase in ER-Unfolded protein response (UPR) pathway was noted in CsA treated cells, which culminated in a caspase independent cell death.

Publications

1. Ramakrishna G, Anwar T, Angara RK, Chatterjee N, Kiran S and Singh S (2012). Role of cellular senescence in hepatic wound healing and carcinogenesis. ***European Journal of Cell Biology*** 91: 739-747.

LABORATORY OF COMPUTATIONAL AND FUNCTIONAL GENOMICS

Faculty	Akash Ranjan	Staff Scientist
PhD Students	Rohan Misra	Senior Research Fellow
	Bhavik Sawhney	Senior Research Fellow
	Ajit Roy	Senior Research Fellow
	Suhail Yousuf	Senior Research Fellow
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	Debasish Kumar Ghosh	Junior Research Fellow (Since Feb. 2013)
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	Jamshaid Ali	Project-Junior Research Fellow
	G Srujana	Project-Junior Research Fellow
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	Lothar H Wieler	Freie University, Germany
	Astrid Lewin	Robert Koch Institute, Germany
	M Sritharan	University of Hyderabad, India

Project I: Genome analysis and functional characterization of the genomes of microbial organisms

Characterization of the promoter and transcription factor binding sites in *Mycobacterium tuberculosis*

Adaptation to the various conditions encountered by the pathogen during the establishment of an infection is thought to require strict gene expression control. In prokaryotes, much of this control is at the level of transcription. There are thirteen sigma factors encoded in the genome of *M. tuberculosis*. Although some of these have been characterized, many remain to be characterized in terms of the promoter recognition specificities and their physiological roles. Furthermore, over 140 putative transcriptional regulators are presumably involved in gene expression modulation in this pathogen.

Objectives

1. To study gene expression and regulation in mycobacteria, with special emphasis to pathogenesis, using the non-pathogenic and relatively fast growing *Mycobacterium smegmatis* as a model organism; and
2. To study the promoter context of mycobacterial transcription factors in order to further understand and expand their regulons.

Summary of work done until the beginning of this reporting year (upto March 31, 2012)

A Machine Learning (ML) approach was applied to the problem of promoter prediction in *M. tuberculosis.* Different ML algorithms were evaluated and Naive Bayesian was determined to best suit the available data.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

Promoter probability densities were calculated on the basis of the Naive Bayesian model. It is believed that DNA characteristics such as GC content, Tm, DNA bending, etc., may play a role in RNA Polymerase binding beyond the canonical sequence information. Therefore, these DNA features were incorporated into the promoter prediction model. Figure 1 shows the promoter probabilities within the intergenic region of Rv0040 and Rv0041, which are situated on opposite strands. Regions of higher promoter probabilities around 43.5 kb indicate greater likelihood of RNA Polymerase binding sites, which are currently unannotated for this genomic region.

Project II: Genome analysis and functional characterization of *Plasmodium falciparum*

1. A machine learning approach for the classification and prediction of exons and introns in *Plasmodium falciparum* 3D7

Plasmodium falciparum is the causative organism of the most deadly form of malaria, which led to a high morbidity and mortality in the last few decades. It belongs to the phylum of Apicomplexa, which includes parasites of many tropical diseases. *P. falciparum* 3D7 has been a genome of interest for

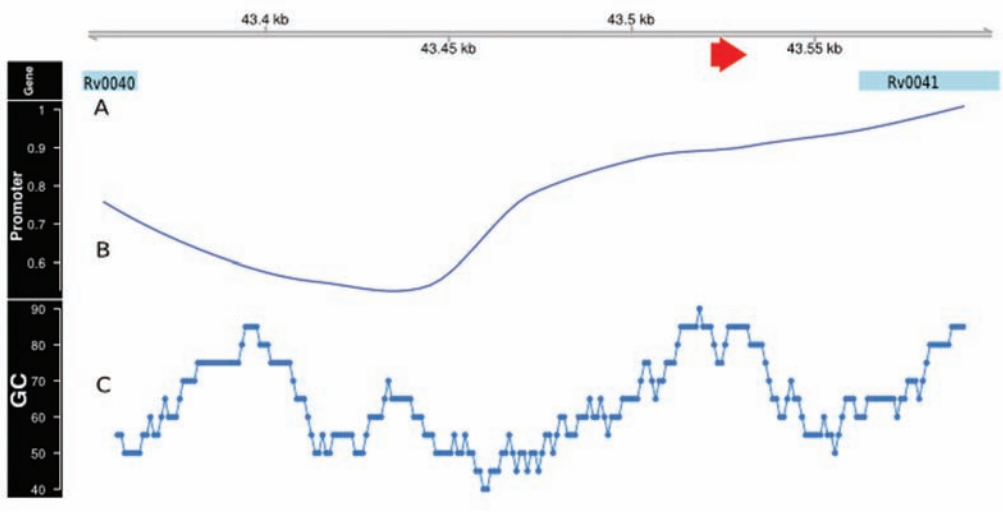

Figure 1. Graph of promoter probability in the integenic region between Rv0040 & Rv0041. **(A)** Genic organization. **(B)** Promoter probabilities obtained from Machine Learning. **(C)** GC content. Higher probability scores around 43.5 kb may represent a possible RNA Polymerase binding region, which is indicated by the red arrow.

its AT- biasness, which is ~80% in the exons and ~90% in the introns and intergenic regions. Since a large percentage of its genome is unannotated, the gene models generated are predictive and incomplete. Work based on the full length cDNA analysis for the genomes of apicomplexa, revealed that there exist many inconsistencies in the gene models reported for this organism and suggested a scope for improvement of the same. The present work addresses the problem of classification and prediction of exons and introns of *P. falciparum* 3D7 using the machine learning classifiers of the WEKA software (http://www.cs.waikato.ac.nz/ml/weka), and develop an efficient method of classification and prediction for the same.

Objective

1. To develop an improved method of classification and prediction of the intron and exon sequences in *P. falciparum 3D7.*

Summary of work done until the beginning of this reporting year (upto March 31, 2012)

We have shown that the numeric data transformation by correlation method has performed better as a feature for the classification and prediction of the exon and intron sequences in *P. falciparum.* We also showed that a window size of 60, which can accommodate an average exon and intron in any gene, has worked best for the model.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

In the present study, we have considered the experimentally validated datasets of *P. falciparum* 3D7 for generating a gold standard dataset, which was divided into training (80% of the gold standard data) test (10% of the data) and validation set (10% of the data). We have divided the sequences in each of the dataset of different window sizes starting from 9–300 in size which were numerically transformed using their dinucleotide frequency and correlation. Models were generated on the training set applying the RandomForest (RF), machine learning classifier (MLC) of the WEKA software for the dinucleotide frequency and correlation data. The performance accuracy of the model generated was evaluated on the independent test set, which showed high precision (0.82 for exons and 0.84 for introns), recall values (0.86 for exons and 0.80 for introns) and Receiver Operating Characteristic (ROC) (0.88 for both exons and introns) for the window size 60 (Figure 2) for the dinucleotide correlation data. The sensitivity (86.70), specificity (80.37), accuracy (83.67) and Matthews Correlation Coefficient (MCC) (0.67) values calculated for the same, were also reasonably high. The ROC curves for each of the window sizes were plotted as the threshold curves of exons and introns for the frequency and correlation data, which showed that the window size 60, showed better ROC for the

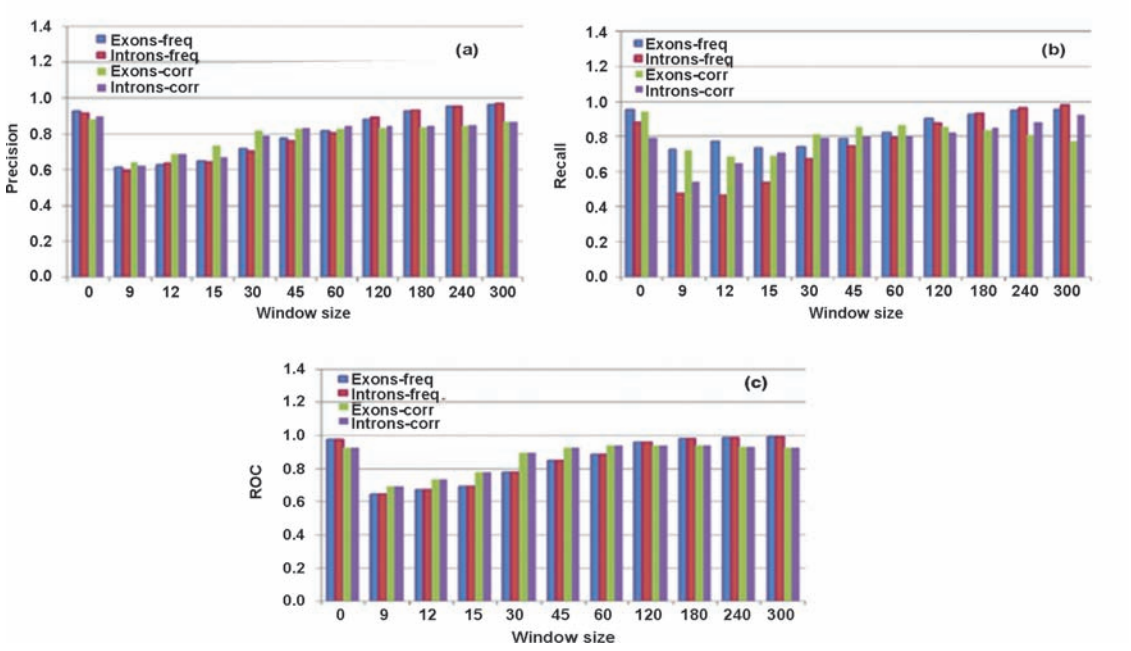

Figure 2. Performance of the training model generated by RandomForest (RF) classifier on the test sets of different window sizes. The precision **(a)** recall **(b)** and ROC-AUC **(c)** values were obtained for the exon and intron sequences, which shows that the values increase with increase in the window size for the frequency data and the values increase till window size 60 and then either decrease or remain stable for the correlation data.

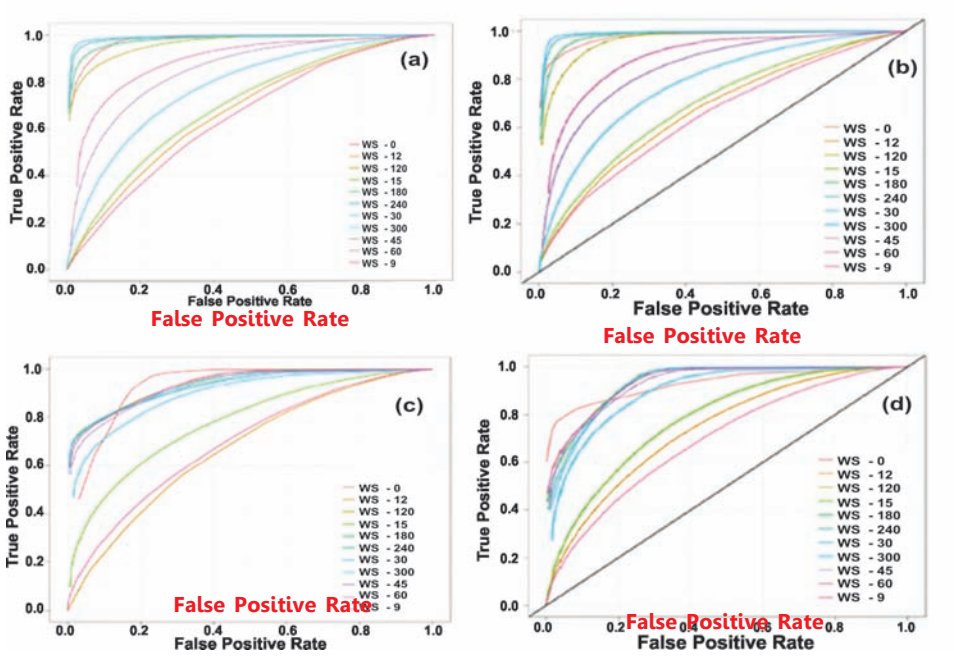

Figure 3. ROC curves obtained by evaluating the test set applying the model generated by Random Forest classifier for different window sizes. The ROC curves for each of the window sizes were plotted as the threshold curves of exons and introns for the frequency **(a and b)** and correlation **(c and d)** data. We can observe that the ROC curves are better for the larger window size for the frequency data whereas they are better for window size 60 for the correlation data.

dinucleotide correlation data (Figure 3). We have observed that all the values calculated increased with an increase in the window size for the frequency data, whereas the values increased and were highest for window size 60 for the correlation data. The models generated were used for the prediction of exons and introns in an independent validation set of *P. falciparum* 3D7.

2. Analytical study of *Plasmodium falciparum* Acyl CoA binding protein.

Acyl-CoA Binding Protein (ACBP) is a low to medium molecular weight protein (MW: 10-55 KDa) which is relatively well conserved in eukaryotic organisms. This protein functions in fatty acid biosynthesis pathway and play an important role in regulation of intracellular acyl-CoA pool size modulation, transport of acyl-CoA for beta-oxidation, vesicular trafficking, complex lipid biosynthesis, and gene regulation. Though fatty acids are essential bio-macromolecules, their entry into metabolic pathways are restricted unless they are activated by thioesterification with Coenzyme-A (Co-A) to form Acyl-CoA esters. Activated fatty acids undergo metabolic utilization, or storage mediated by ACBPs. Among the four isoforms of *P. falciparum* ACBP, structure of one isoform is solved by X-ray crystallography but we are yet to understand complete functional relevance of ACBPs in lower eukaryotic organisms like plasmodia. ACBP have been shown to be essential proteins for *Trypanosoma brucei* in its host cell dependent blood-stream stage, it would thus be interesting to study its role in biology of *P. falciparum*.

Objective

1. Comparative analysis of Pf ACBPs and Human ACBPs.

Summary of work done until the beginning of this reporting year (upto March 31, 2012)

We have done comparative analysis of Pf ACBPs and human ACBPs. We have expressed all the four ACBPs as histidine-tagged recombinant proteins.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

The maximum expression of ACBPs occurs at merozoite stage in which the lipid changes are observed. In order to know whether expression of PfACBP has anything to do with lipid changes in merozoite stage or not, we started *Plasmodium falciparum* culture and are in the process of further standardization.

Further, our studies show that one of PfACBP, PfACBP15 (PF3D7_1001100.1), significantly differs from other ACBPs (Figure 4). A hydropathy index plot for ACBP 15 (PF3D7_1001100.1) using Prot Scale analysis is shown in Figure 5. In some organisms, like *Arabidopsis thaliana* and *Cryptosporidium parvum*, ACBPs have been reported with additional membrane bound Ankyrin repeats.

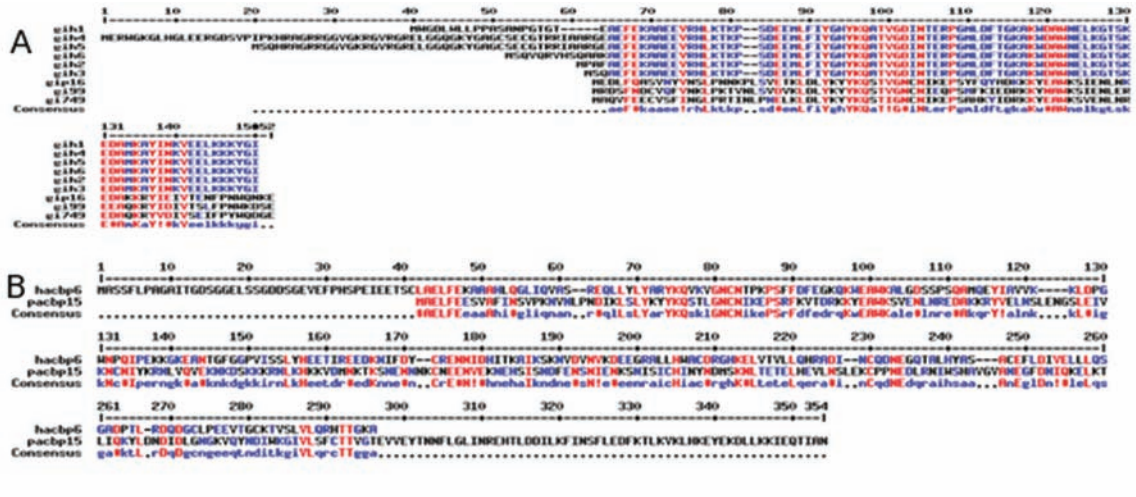

Figure 4. Sequence alignment of different ACBPs. **(A)** *Plasmodium falciparum* ACBPs, and (**B)** Pf ACBP15 with human ACBP.

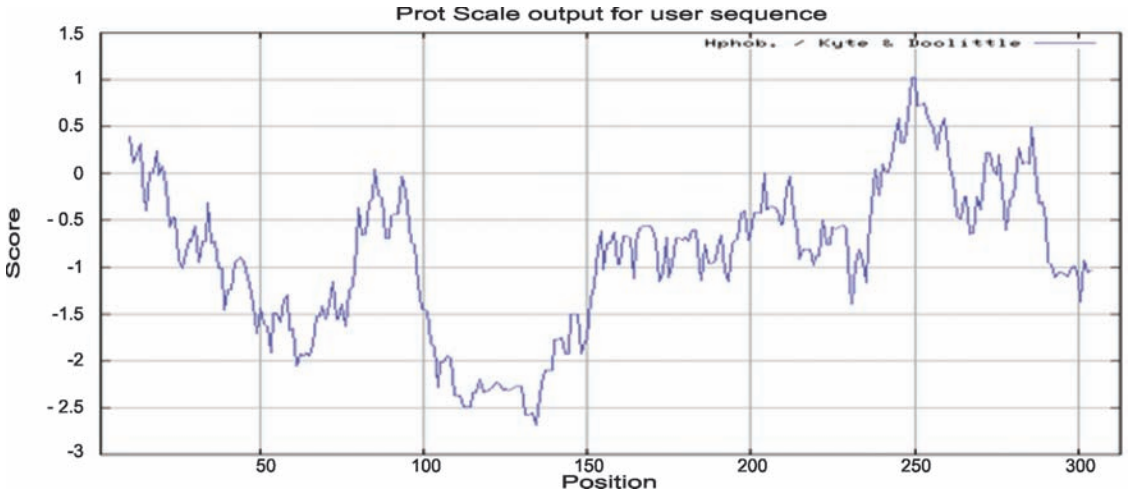

Figure 5. Hydropathy index of ACBP-15 (PF3D7_1001100.1) using Prot Scale analysis.

Publications

1. Ali J, Thummala SR and Ranjan A (2012). The parasite specific substitution matrices improve the annotation of apicomplexan proteins. ***BMC Genomics*** 13 (Suppl. 7): S19.
2. Muley VY and Ranjan A (2012). Effect of reference genome selection on the performance of computational methods for genome-wide protein-protein interaction prediction. ***PLoS One*** 7: e42057.
3. Muley VY and Ranjan A (2013). Evaluation of physical and functional protein-protein interaction prediction methods for detecting biological pathways. ***PLoS One*** 8: e54325.

LABORATORY OF TRANSCRIPTION

Mechanism of Transcription Termination and Antitermination in *Escherichia coli*

Faculty	Ranjan Sen	Staff Scientist
PhD Students	Amitabh Ranjan	Senior Research Fellow
	Rajesh Kumar	Senior Research Fellow
	Saurabh Mishra	Senior Research Fellow
	V Vishalini	Senior Research Fellow
	Mohd Zuhaib Qayyum	Junior Research Fellow
	Gairika Ghosh	Junior Research Fellow (Since Feb. 2013)
Other Members	Debashis Dey	Research Associate
	Rajeswari	Research Associate
	Savita Sharma	Research Associate
	Suprava Nayak	Research Associate (Since Jun. 2012)
	Sudha Kalyani	Research Associate (Since Oct. 2012)
	Sapna Godavarthi	Technical Officer
	Radhika Kunamneni	Project Assistant (Till Sep. 2012)
	M Pallavi	Project Assistant
	Ragini Mishra	Project Assistant (Since Dec. 2012)
Collaborator	Udayaditya Sen	SINP, Kolkata

Objectives

Mechanisms of bacterial transcription termination and antitermination processes are still not very clear and offer an exciting subject for study. In our laboratory, studies in the following areas are in progress:

1. Mechanism of action of transcription termination factor, Rho;
2. Molecular basis of Rho-NusG interaction;
3. Mechanism of conversion of NusA into an antiterminator by N;
4. Mechanism of action of transcription antitermination of Rho-dependent termination by an anti-rho factor, Psu;
5. Physiological significance of Rho dependent termination; and
6. Designing transcription modulators using synthetic biology approaches.

Summary of work done until the beginning of this reporting year (Upto March 31, 2012)

1. We established the existence of *in vivo* kinetic coupling between the two molecular motors, Rho and RNA polymerase using suppression of the defects of different Rho, NusG and RNAP mutants (Microbiology, 2012).
2. We proposed a multi-pronged strategy employed by the transcription antiterminator, N, to overcome the factor-dependent transcription termination (Nucl. Acids Res., 2012).
3. In collaboration with a crystallography group, we have solved the structure of the Rho-inhibitor, Psu (J. Biol. Chem, 2012).

Details of the progress made in the current reporting year (April 1, 2012- March 31, 2013)

1. The interaction surface of a bacterial transcription elongation factor required for complex formation with an antiterminator during transcription antitermination

The bacterial transcription elongation factor, NusA, functions as an antiterminator when it is bound to the antiterminator protein, N. Mode of the N-NusA interaction is unknown, knowledge of which is essential to understand the antitermination process. It was reported earlier that, outside the elongation complex (EC), N interacts with the C-terminal, AR1 domain of NusA. However, the functional significance of this interaction is obscure. We identified mutations in NusA-N-terminal domain (NTD), specifically defective for N-mediated antitermination. These are located at a convex

surface of the NusA-NTD, opposite to its concave RNA polymerase (RNAP)-binding surface. These NusA mutants disrupted the N-*nut* site interactions on the nascent RNA, emerging out of a stalled EC. In the N/NusA-modified EC, a Cys-53(S53C) from this convex surface of the NusA-NTD formed a specific disulfide bridge with a Cys-39 (S39C) of the NusA-binding region of the N protein. We concluded that, when bound to the EC, the N-interaction surface of NusA shifts from the AR1 domain to its NTD domain. This occurred due to a massive away-movement of the adjacent AR2 domain of NusA upon binding to the EC. We propose that, the close proximity of this altered N-interaction site of NusA to its RNAP-binding surface, enables N to influence the NusA-RNAP interaction during transcription antitermination that facilitates the conversion of NusA into an antiterminator (Figure 1).

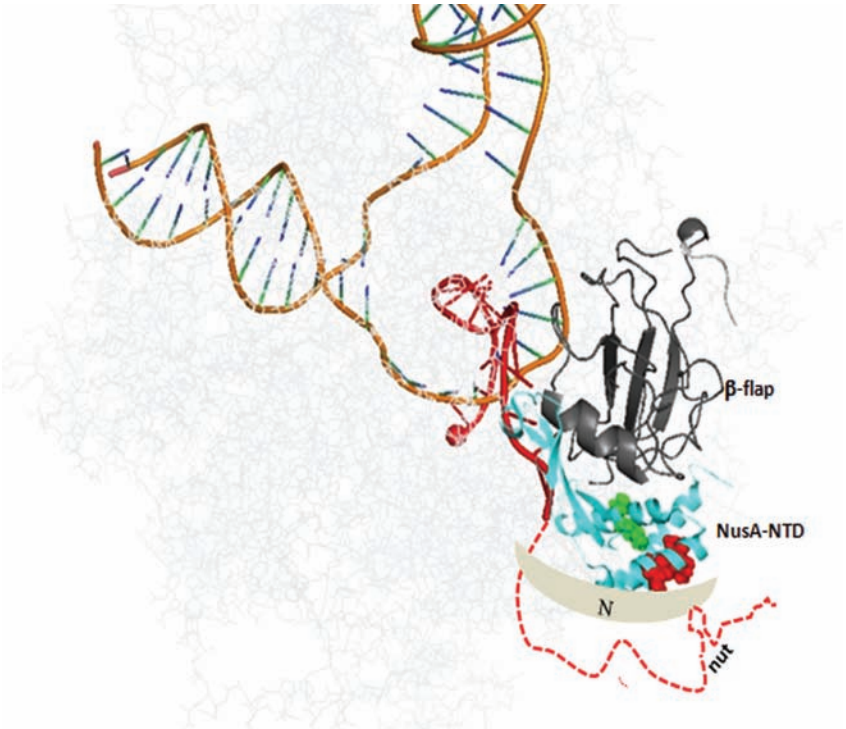

Figure 1. A possible model of the N-NusA NTD-EC ternary complex. Exiting RNA (red), b-flap (dark grey), NusA-NTD (cyan) are highlighted. Rest of the β/β' are shown in the light grey. N is shown as a cartoon. N-and RNAP-binding residues of the NusA-NTD are shown in red and green spheres, respectively. The RNA outside the EC is shown as dotted line.

2. Structural and mechanistic basis of antitermination of Rho-dependent transcription termination by a bacterio-phage capsid protein.

The conserved bacterial transcription terminator, Rho, is a potent target for bactericidal agents. Psu, a bacteriophage P4 capsid protein, is capable of inducing antitermination to the Rho-dependent transcription termination. Knowledge of structural and mechanistic basis of this antitermination is required to design peptide-inhibitor(s) of Rho derived from Psu. Using suppressor genetics, cross-linking, protein foot-printing, and FRET analyses, we describe a conserved disordered structure, encompassing 139-153 amino acids of Rho, as the primary docking site for Psu. Also a neighbouring helical structure, comprised of 347-354 amino acids, lining its central channel, plays a supportive role in the Rho-Psu complex formation. Based on the crystal structure of Psu, its conformation in the capsid of the P4 phage, and its interacting regions on Rho, we have built an energy-minimized structural model of the Rho:Psu complex. In this model, a V-shaped dimer of Psu interacts with the two diagonally opposite subunits of a hexameric Rho, enabling Psu to form a “lid” on the central channel of the latter (Figure 2). We show that, this configuration of Psu makes the central channel of Rho inaccessible, and causes a mechanical impediment to its translocase activity (Figure 2).

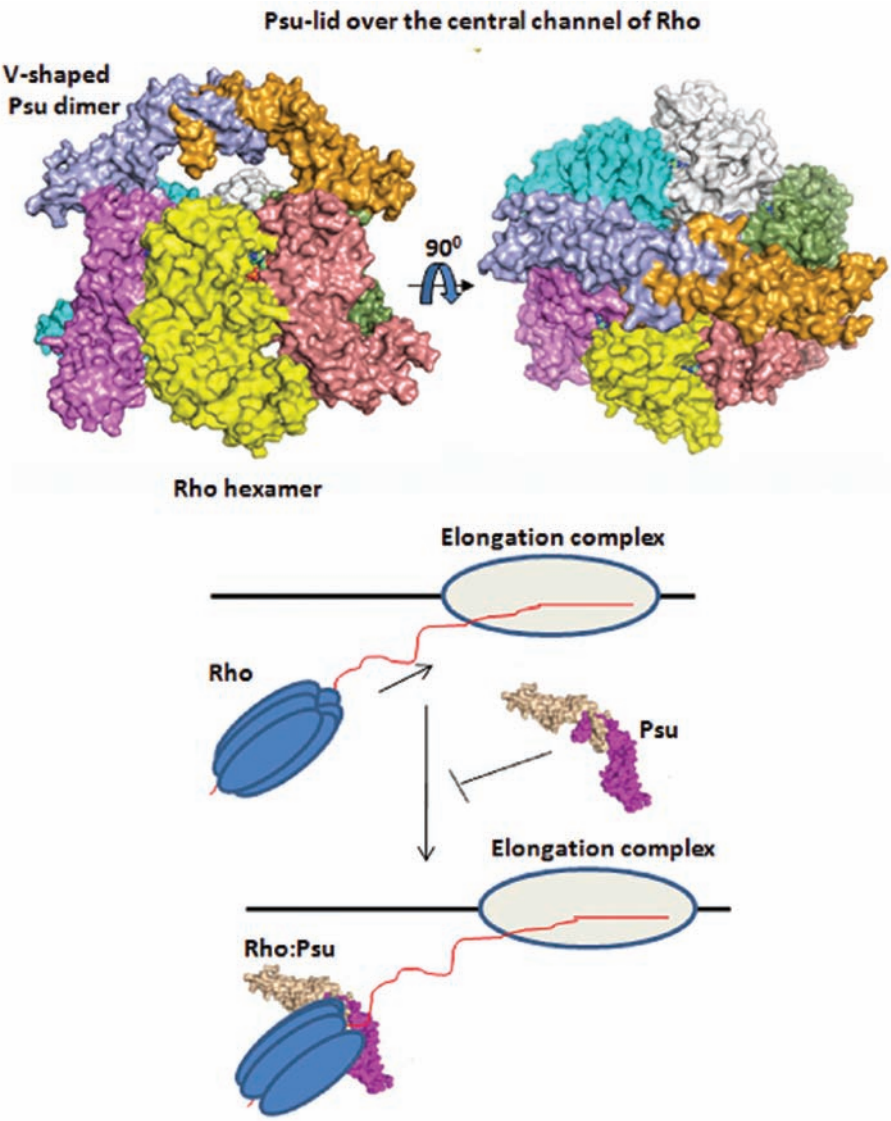

Figure 2. Structural model of a Rho:Psu complex. Proposed mechanism of Psu-induced mechanical impediment to the translocase activity of Rho.

Future plans/directions

The following projects, being pursued in our laboratory, are in different stages of completion: (i) Role of NusA in Rho-dependent termination (ii) Importance of Rho-nascent RNA interactions *in vivo* (iii) Mechanism of NusG mediated stimulation of Rho, and (iv) Characterization of predicted Rho-binding proteins.

Publications

1. Banerjee R, Nath S, Ranjan A, Khamrui S, Pani B, Sen R and Sen U (2012). The first structure of polarity suppression protein, Psu from Enterobacteria phage P4, reveals a novel fold and a knotted dimer. ***Journal of Biological Chemistry*** 287: 44667-44675.

2. Muteeb G, Dey D, Mishra S and Sen R (2012). A multipronged strategy of an anti-terminator protein to overcome Rho-dependent transcription termination. ***Nucleic Acids Research*** 40: 11213-11228.

3. Shashni R, Mishra S, Kalayani BS and Sen R (2012). Suppression of *in vivo* Rho-dependent transcription termination defects: evidence for kinetically controlled steps. ***Microbiology*** 158: 1468-1481.

LABORATORY OF CELL SIGNALLING

Investigating the Role of Inositol Pyrophosphates in Eukaryotic Cell Physiology

Faculty	Rashna Bhandari	Staff Scientist & WT-DBT India Alliance Senior Fellow
PhD Students	Swarna Gowri Thota	Senior Research Fellow
	Jadav Rathan Singh	Senior Research Fellow
	Manasa VL Chanduri	Senior Research Fellow
	Aushaq Bashir Malla	Senior Research Fellow
	Sitalakshmi Thampatty R	Senior Research Fellow (Since Mar. 2013)
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	Ruth Manorama Ravoori	Technical Assistant
	Dharmika Kumar	Project-Senior Research Fellow
	Somadri Ghosh	Project-Senior Research Fellow
	CP Unnikannan	Project-Senior Research Fellow
Collaborators	Satish Kumar	CCMB, Hyderabad
	Sagar Sengupta	NII, Delhi
	Nagaraj Balasubramanian	IISER, Pune

Objectives

Inositol pyrophosphates are derivatives of inositol that contain pyrophosphate or diphosphate moieties in addition to monophosphates. They include diphosphoinositol pentakisphosphate (PP-IP_5, or IP_7) and bis-diphosphoinositol tetrakisphosphate ($[PP]_2$-IP_4 or IP_8), which participate in diverse biological functions, including DNA recombination, vesicular trafficking, apoptosis and osmotic regulation. The beta phosphate group of inositol pyrophosphates can be transferred to pre-phosphorylated serine residues on proteins to form pyrophosphoserine. Pyrophosphorylation occurs on several proteins within the cell, including proteins involved in ribosome biogenesis, vesicular trafficking and glycolysis. 5PP-IP_5 (IP_7) is synthesised from inositol hexakisphosphate (IP_6) and ATP by IP_6 kinases. Mammals have three isoforms of IP_6 kinase, IP6K1, IP6K2 and IP6K3, whereas *Saccharomyces cerevisiae* have a single IP_6 kinase, KCS1.

Our aim is to understand the biochemical link between protein pyrophosphorylation and cellular phenomena regulated by inositol pyrophosphates. We utilise *S. cerevisiae,* mammalian cell lines, and knockout mouse strains as model systems to investigate the signalling and metabolic pathways that are altered when inositol pyrophosphate levels are perturbed. In particular, we focus on the following objectives:

1. Examine the role of inositol pyrophosphates in yeast physiology;
2. Understand the cellular functions of mammalian inositol hexakisphosphate kinase 1 (IP6K1);
3. Study the role of inositol pyrophosphates in whole animal physiology.

Summary of work done until the beginning of this reporting year (Upto March 31, 2012)

We observed that *S. cerevisiae* strains lacking KCS1 display slow growth, reduced ribosome levels, and lower rates of protein synthesis. Steady state levels of 35S precursor rRNA, and the rate of rRNA transcription were reduced. These data suggested that inositol pyrophosphates regulate ribosome biogenesis in yeast by participating in RNA polymerase I mediated transcription of rRNA. To determine whether IP_7 regulates rRNA transcription via protein pyrophosphorylation, we tested RNA polymerase I components in an *in vitro* pyrophosphorylation assay using radiolabelled IP_7, and determined that RPA34, RPA43 and RPA190, subunits of the RNA polymerase I elongation complex, are pyrophosphorylated by IP_7.

To understand the cellular functions of IP_7 in mammals, we use mouse embryonic fibroblasts (MEFs) derived from IP6K1 knockout (*Ip6k1*$^{-/-}$) embryos, which have 70% reduced levels of IP_7 compared with wild type (WT) MEFs. These cells provide an excellent model to study specific cellular functions of inositol pyrophosphates that may be

biochemically linked with protein pyrophosphorylation. We monitored WT and *Ip6k1*$^{-/-}$ MEFs for their response to hydroxyurea (HU), a DNA damage agent which causes replication stress, inducing double strand DNA breaks and triggering repair by homologous recombination (HR). HU treated *Ip6k1*$^{-/-}$ MEFs arrested at the G1/S boundary, indicating that checkpoint activation following DNA damage is intact in the absence of IP6K1, but displayed decreased viability and reduced recovery compared with WT cells. Markers associated with DNA repair, including the RecQ family helicase BLM, were recruited to DNA damage sites, indicating that HR repair is initiated in *Ip6k1*$^{-/-}$ MEFs. However, nuclear BLM foci persisted long after drug removal, suggesting that repair did not proceed to completion. Expression of catalytically active but not inactive IP6K1 could restore the repair process in knockout MEFs, implying that inositol pyrophosphates are required for HR mediated DNA repair.

To study the role of inositol pyrophosphates in whole animals, we have established a colony of *Ip6k1*$^{+/-}$ heterozygous mice and are breeding them to obtain wild type and knockout litter-mates. Our preliminary phenotypic characterisation of these mice revealed that *Ip6k1*$^{-/-}$ male mice are infertile. We determined that testes of *Ip6k1*$^{-/-}$ mice have reduced number of elongated spermatids, which

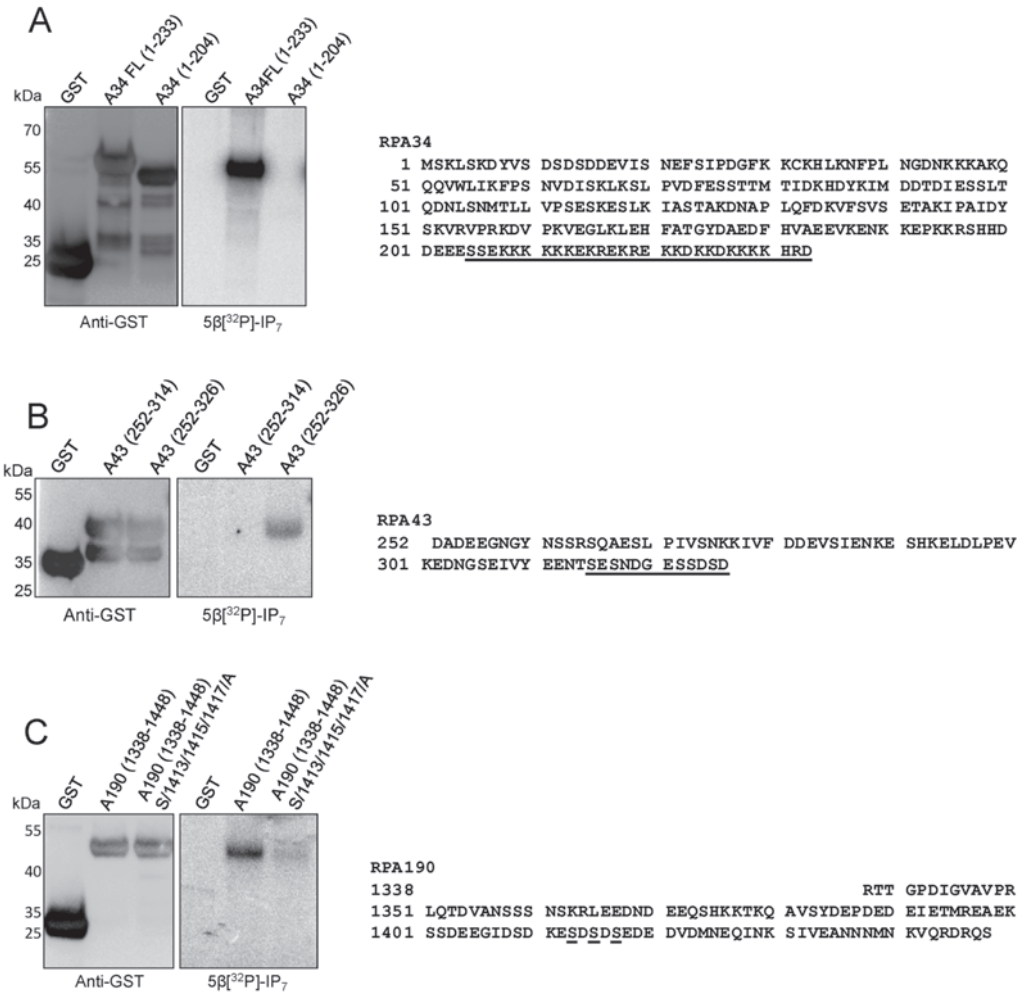

Figure 1. Yeast RNA polymerase I subunits are pyrophosphorylated by IP_7. GST or GST-tagged RNA polymerase I subunits RPA34 **(A)**, RPA43 **(B)** and RPA190 **(C)** were expressed in *S. cerevisiae*, immobilized on glutathione beads, incubated with radiolabelled IP_7, resolved by NuPAGE, and transferred to PVDF membranes. Blots were subjected to autoradiography to monitor pyrophosphorylation, followed by immunoblotting with a tag-specific antibody. The protein sequence used in each case is indicated on the right, and deletions or point mutations introduced in each protein are underlined.

display misshapen heads and bent tails. This may explain the absence of spermiation in *Ip6k1*$^{-/-}$ testes, which is reflected in the absence of mature spermatozoa in the epididymides.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

Project 1: Regulation of yeast ribosome biogenesis by IP_7

Having identified three RNA polymerase I subunits as targets for IP_7-mediated pyrophosphorylation, we conducted site-directed mutagenesis to map the serine residues targeted by IP_7. The C-terminal lysine-rich unstructured domain of RPA34, which contains two serine residues interspersed with glutamates (S205 and S206), was mapped as the site pyrophosphorylated by IP_7 (Figure 1A). Interestingly, we ruled out reported phosphorylated serines, S10, S12 and S14, as the sites for IP_7 pyrophosphorylation on RPA34 (data not shown). On RPA43 we identified the C-terminal tail, which contains five serine residues, as the site for pyrophosphorylation (Figure 1B). Here again, we did not identify any of the five reported phosphorylated serines as targets for IP_7. RPA190 is the largest component of RNA polymerase I, making up the active site of the enzyme. We mapped IP_7 phosphorylation sites to S1413, S1415 and S1417, which lie in the unstructured part of the Jaw domain of RPA190, close to the active site (Figure 1C).

It is possible that IP_7-mediated pyrophosphorylation of one or more serine residues that we have identified is required for optimal transcription activity of RNA polymerase I. We are currently conducting assays to monitor rRNA transcription and protein synthesis in cells expressing these mutant RNA polymerase subunits that cannot be pyrophosphorylated.

Project 2: Cellular functions of mammalian inositol hexakisphosphate kinase 1 (IP6K1): Role of inositol pyrophosphates in homologous DNA recombination

Following up on our observation that MEFs lacking IP6K1 display incomplete HR mediated DNA repair, we wondered whether repair is delayed, but eventually complete. We therefore monitored DNA repair subsequent to HU removal by conducting a TUNEL assay to measure DNA damage. While the level of TUNEL staining fell to baseline 12 h after drug removal in WT MEFs, DNA damage continued to persist in *Ip6k1*$^{-/-}$ MEFs (Figure 2A). To determine whether *Ip6k1*$^{-/-}$ MEFs enter mitosis despite the persistence of damaged DNA, we stained cells for histone H3 phosphorylation at Ser10, a marker for the initiation of mitosis. An increase in the mitotic population in WT MEFs followed the timeline of DNA repair (Figure 2B and C). *Ip6k1*$^{-/-}$ MEFs displayed delayed entry into mitosis 10 h after HU removal (Figure 2C), despite the persistence of DNA damage (Figure 2A). When proliferation of MEFs was monitored up to 4 days after HU removal, there was an eventual increase in viable *Ip6k1*$^{-/-}$ MEFs, although it was still lower than WT MEFs (Figure 2D). Proliferation of cells by continuing DNA replication without repairing damage can result in the accumulation of chromosomal lesions. Defects in HR can lead to increased sensitivity to mitomycin C, a drug that induces DNA interstrand crosslinks, blocking DNA replication. Analysis of metaphase spreads following mitomycin C treatment may therefore be used to probe defects in DNA repair. When treated with mitomycin C, *Ip6k1*$^{-/-}$ MEFs show more chromosomal abnormalities such as triradial and quadriradial chromosomes, and chromatid breaks, compared to WT MEFs (Figure 2E and F).

In summary, our data reveal a role for inositol pyrophosphates synthesised by IP6K1 in HR-mediated repair of DNA double strand breaks in mammalian cells. A research paper describing this work has recently been published (Jadav *et al*., Journal of Biological Chemistry, 2013). At a mechanistic level, inositol pyrophosphates may act by binding or pyrophosphorylating one or more proteins involved in HR. In the near future we will focus on identifying molecular targets that mediate the involvement of IP6K1 in HR**.** Our observation that *Ip6k1*$^{-/-}$ MEFs accumulate chromosomal aberrations raises the possibility that these cells possess a higher tumourigenic potential compared with their wild type counterparts. We will therefore conduct studies to determine the effects of altered IP6K1 activity on tumourigenesis and cancer chemotherapy.

Project 3: Physiological role of IP_7 in mice: Regulation of platelet function by IP6K1

This is a new activity. This project explores the link between inositol pyrophosphates and inorganic polyphosphate (polyP), a linear polymer of orthophosphate moieties linked by phosphoanhydride bonds. PolyP of chain length 60-100 phosphate units is present in dense granules of mammalian platelets, and regulates the blood clotting cascade at multiple stages. Budding yeast lacking the IP_6 kinase KCS1 display

substantially lowered levels of polyP, prompting us examine whether *Ip6k1*$^{-/-}$ mice, which have 70% reduced levels of IP_7, have any defects in polyP accumulation and platelet function.

Western blot analysis confirmed that extracts from WT mouse platelets contain IP6K1, but there is no detectable band in *Ip6k1*$^{-/-}$ platelets (Figure 3A). Earlier studies have shown that the DNA binding fluorophore DAPI stains polyP present in human platelets. DAPI staining of platelets isolated from WT mice revealed polyP accumulation, whereas very low polyP levels were observed in isolated *Ip6k1*$^{-/-}$ platelets (Figure 3B, C). The fluorescent lipophilic dye DiOC6 which stains platelet membranes was used to detect isolated platelets, and showed no difference in staining intensity between WT and *Ip6k1*$^{-/-}$ platelets.

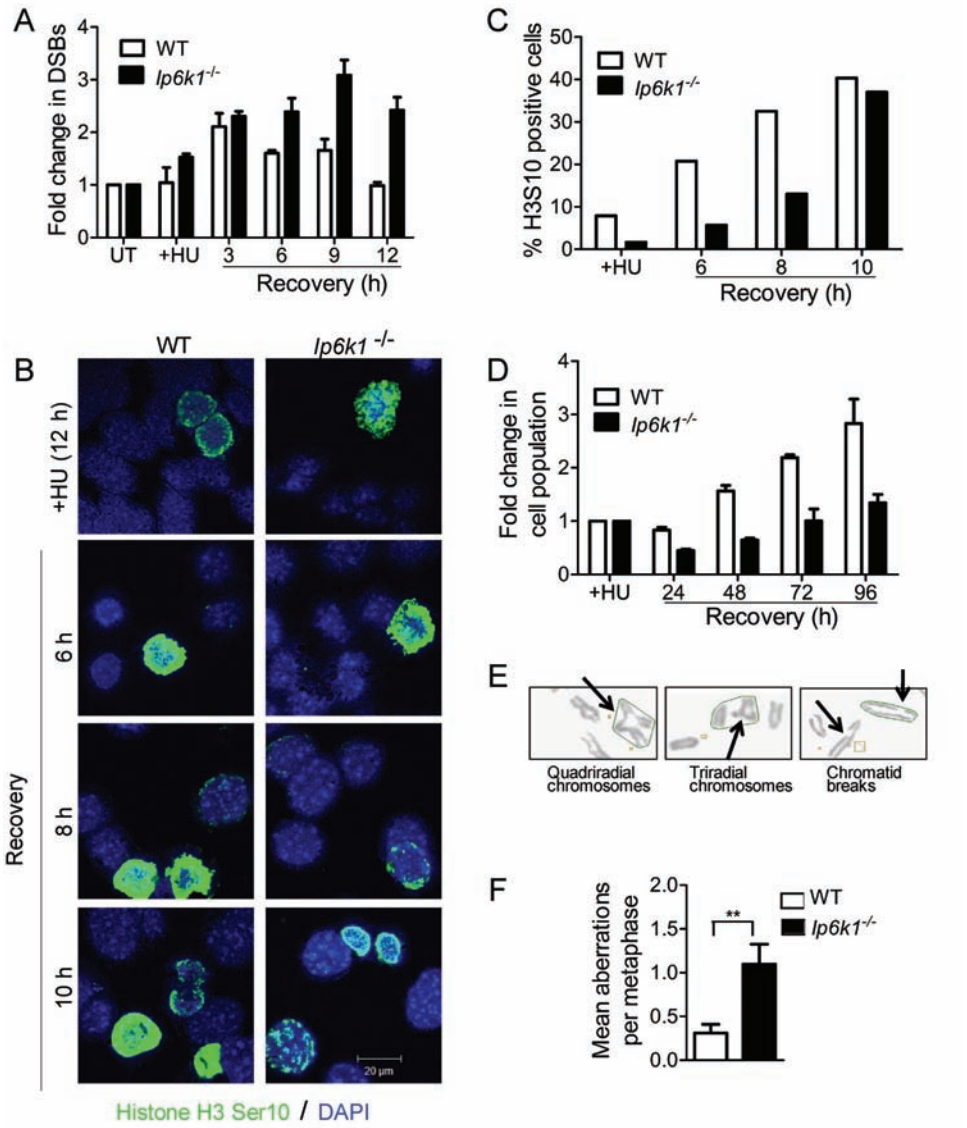

Figure 2. Persistence of DNA damage in *Ip6k1*$^{-/-}$ MEFs. (A) Detection of DNA double strand breaks (DSBs) by TUNEL staining and flow cytometry analysis after HU (12 h, 0.5 mM) treatment of MEFs and recovery for the indicated time; bars represent mean±range of two independent experiments. **(B)** Representative immunofluorescence images of histone H3 Ser10 phosphorylation in MEFs after HU (12 h, 0.5 mM) treatment and recovery for the indicated time. **(C)** Quantitation of (B); bars indicate the percentage of histone H3 Ser10 positive cells (n=140; representative of two experiments). **(D)** Cell viability measurement by MTT assay following treatment with HU (12 h, 0.5 mM), and recovery for the indicated time; bars represent mean±range of two independent experiments. **(E)** Representative images showing chromosomal lesions (marked by arrows) found in metaphase spreads from MEFs treated with mitomycin C (12 h, 300 nM). **(F)** Quantitation of (G); data (mean±s.e.m. n=41) are representative of two experiments. P values are from a two-tailed Student's *t*-test (**pd≤0.01).

Analysis of haematologic parameters in WT and *Ip6k1*$^{-/-}$ mice revealed no difference in platelet count, platelet size or other blood parameters between these groups (data not shown). To monitor platelet activation by thrombin we measured the levels of surface P-selectin, a cell adhesion molecule released from platelet α-granules (Figure 3D). No alteration in P-selectin surface expression in *Ip6k1*$^{-/-}$ platelets implies that IP6K1 does not influence platelet α-granule content or its thrombin

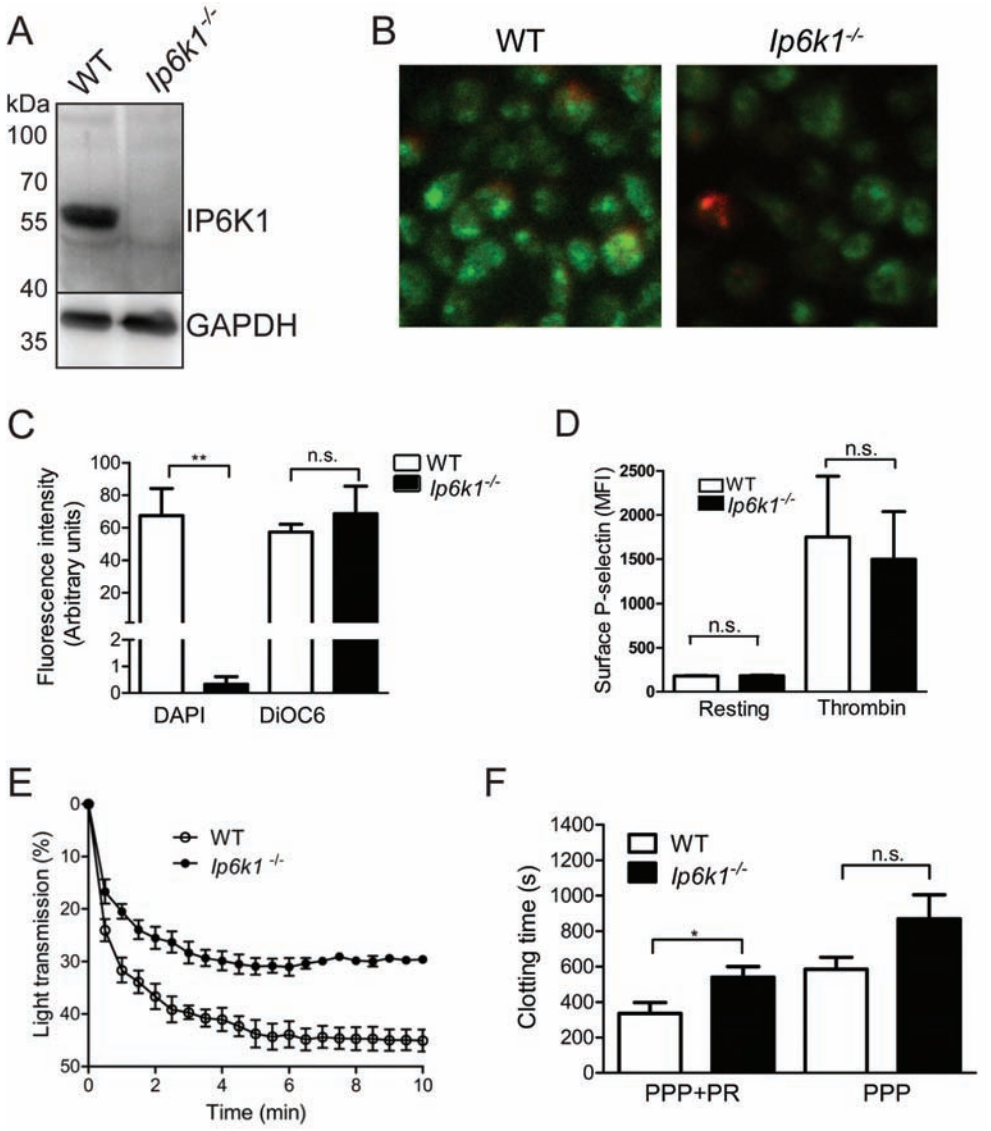

Figure 3. Altered platelet function in *Ip6k1*$^{-/-}$ mice. **(A)** Western blot analysis of lysates prepared from WT and *Ip6k1*$^{-/-}$ platelets pooled from 3 mice of each genotype, using an antibody against IP6K1. GAPDH was used as a loading control. The blot is representative of 3 independent experiments. **(B)** Representative confocal fluorescence micrographs of platelets isolated from WT and *Ip6k1*$^{-/-}$ mice, stained with DAPI (red) to detect polyP and DiOC6 (green) to visualize platelets. **(C)** Quantification of images in (B), using ImageJ software. Data are mean±s.e.m. (n=8 mice of each genotype, with 20 platelets analyzed per mouse). **(D)** Surface P-selectin expression in resting and thrombin stimulated WT and *Ip6k1*$^{-/-}$ platelets analysed by flow cytometry. Data are median fluorescence intensity (MFI), mean±s.e.m. (n=3). **(E)** Thrombin stimulated aggregation of washed platelets from WT and *Ip6k1*$^{-/-}$ mice measured spectrophotometrically as a decrease in percent light transmission over a period of 10 min. Samples were pooled from 3 mice of each genotype for the analysis. Data are mean±s.e.m. from 3 independent experiments. **(F)** Change in turbidity as a function of time was monitored spectrophotometrically at 405 nm in recalcified platelet releasates (PR) mixed with platelet poor plasma (PPP). Clotting time, the time taken to reach maximum absorbance, was measured in WT and *Ip6k1*$^{-/-}$ samples of PPP+PR or PPP alone. Data are mean±s.e.m. (n=8). *p* values are from a two-tailed Student's t test (**p* d≤0.05; ** *p* d"0.01; n.s., not significant, *p*> 0.05).

stimulated release. Following activation by different agonists, platelets adhere and aggregate to form a plug at the site of injury, leading to primary haemostasis. Platelet aggregation upon thrombin stimulation was measured in washed platelets isolated from WT or *Ip6k1*$^{-/-}$ mice. We observe a significant decrease in the extent of aggregation of *Ip6k1*$^{-/-}$ platelets (Figure 3E). This could be attributed to compromised von Willebrand factor function, which is regulated by polyP present in α-granules. To examine the effect of polyP reduction on plasma clotting time, we added platelet releasates from WT and *Ip6k1*$^{-/-}$ mice to their autologous citrated platelet poor plasma (PPP), prior to recalcification and clot turbidity measurement. Total clotting time, the time taken to reach maximum turbidity following recalcification, is significantly lengthened in *Ip6k1*$^{-/-}$ samples (Figure 3F). On the other hand, clotting time of recalcified PPP alone was unaltered in *Ip6k1*$^{-/-}$ compared with WT. This clarifies that changes in platelet derived factor(s), and not plasma components, are responsible for the prolonged clotting time observed in *Ip6k1*$^{-/-}$ samples.

Our data so far reveal that the metabolic link between inositol pyrophosphates and polyP is conserved between yeast and mammals. Reduction in platelet polyP in *Ip6k1*$^{-/-}$ mice leads to compromised platelet aggregation and lengthened clotting time. We are currently examining whether these changes lead to haemostasis defects in *Ip6k1*$^{-/-}$ mice. Our finding that IP6K1 is a novel player in platelet aggregation and blood clotting assumes clinical significance in the context of thrombotic and bleeding disorders.

Publications

1. Jadav RS, Chanduri MVL, Sengupta S and Bhandari R (2013). Inositol pyrophosphate synthesis by inositol hexakisphosphate kinase 1 is required for homologous recombination repair. ***Journal of Biological Chemistry*** 288: 3312-3321.

LABORATORY OF PLANT MICROBE INTERACTIONS

Understanding Virulence Mechanisms of *Xanthomonas* Plant Pathogens and Interaction with Host Plants

Faculty	Subhadeep Chatterjee	Staff Scientist
PhD Students	Rikky Rai	Senior Research Fellow
	Sheo Shankar Pandey	Senior Research Fellow
	Akanksha Kakkar	Senior Research Fellow
	Raj Kumar Verma	Junior Research Fellow
	Biswajit Samal	Junior Research Fellow (Since Jul. 2012)
Other Members	Binod Bihari Pradhan	Technical Officer
	Anil Kondreddy	Research Associate
	Sree Gowrinadh Javvadi	Project-Junior Research Fellow
	L Santhosh Kumar	Project-Junior Research Fellow

Objectives

1. Identification and characterization of virulence factors of *Xanthomonas*;
2. Role of cell-cell communication in *Xanthomonas* colonization and virulence;
3. Function of protein secretion system in *Xanthomonas* and its role in virulence; and
4. Role of PAMP in pathogen recognition and plant defense response.

Summary of work done until beginning of this reporting year (Upto March 31, 2012)

We are trying to understand the virulence mechanisms of important *Xanthomonas* pathogens like, *Xanthomonas campestris* pv. *campestris* (Xcc; a pathogen of crucifers), *Xanthomonas oryzae* pv. *oryzae*, *Xanthomonas oryzae* pv. *oryzicola* (Xoo, Xola; pathogens of rice) and *Xanthomonas axonopodis* pv. *citri* (Xac; pathogen of citrus). In *Xanthomonas oryzae* pv. *oryzae* (Xoo), a pathogen of rice, we have previously identified several virulence associated functions which are regulated by Diffusible Signal Factor (DSF). Xoo exhibits atypical regulation of virulence associated functions, in contrast to closely related *Xanthomonas*. We have also proposed a model for the role of Xoo DSF in coordinating the switch between the planktonic and biofilm lifestyle of this bacterium. We are presently studying the role of chemotaxis, motility and components of cell-cell signaling in virulence of Xoo. We have also initiated studies to understand the role of DSF in regulating virulence associated function in *Xanthomonas oryzae* pv. *oryzicola* (Xcola) which causes a serious disease of rice known as Bacterial Leaf Streak (BLS).

Previously we have isolated a novel adhesin of Xoo, XadM, which is required for virulence. In this study we have further characterize the role of XadM in entry, attachment and colonization of Xoo.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

Project 1: Role of DSF in virulence of *Xanthomonas oryzae* pv. *oryzicola* (Xcola)

Since DSF exhibits atypical regulation of virulence associated functions in closely related *Xanthomonas*, we wanted to understand the role of DSF in *Xanthomonas oryzae* pv. *oryzicola* (Xcola). Xcola has an atypical lifestyle as compare to Xoo (a xylem dwelling pathogen), as it infects the rice plant by gaining entry through stomata and grows in the parenchyma tissue. Xcola exhibits streak like symptoms as opposed to long lesions exhibited by Xoo on the mid vein of rice leaves. We have made deletion mutants of *rpfF* and components of DSF mediated cell-cell signalling in Xcola. Phenotypic characterization of Δ*rpfF* mutant of Xcola indicated that DSF is required for virulence and *in planta* growth of Xoo (Figure 1). To understand why DSF mutants of Xcola exhibits *in planta* growth deficiency, we have performed microarray analysis of transcriptional changes between wild type, DSF deficient mutants with or without exogenous supplementation of DSF of Xcola along with phenotypic characterization of DSF regulated traits. Transcriptional studies indicated that several genes involved in iron metabolism are altered in the DSF deficient Δ*rpfF* mutant. Growth assay under low iron conditions, biochemical analysis of iron content, iron uptake assay and *in planta* iron supplementation

experiments indicated that the *in planta* growth deficiency of the *"rpfF* mutant of Xcola is due to deficiency in ferric (Fe^{+3}) uptake. Along with iron, we have also identified several other virulence associated functions that are regulated by DSF such as Type III secretion system and its effectors, attach and form biofilms. Furthermore, we show that XadM is exposed on the cell surface and its expression is regulated by growth conditions and plays an important role in the early attachment and entry inside rice leaves (Figure 2). We have also proposed a model for the role of XadM in the

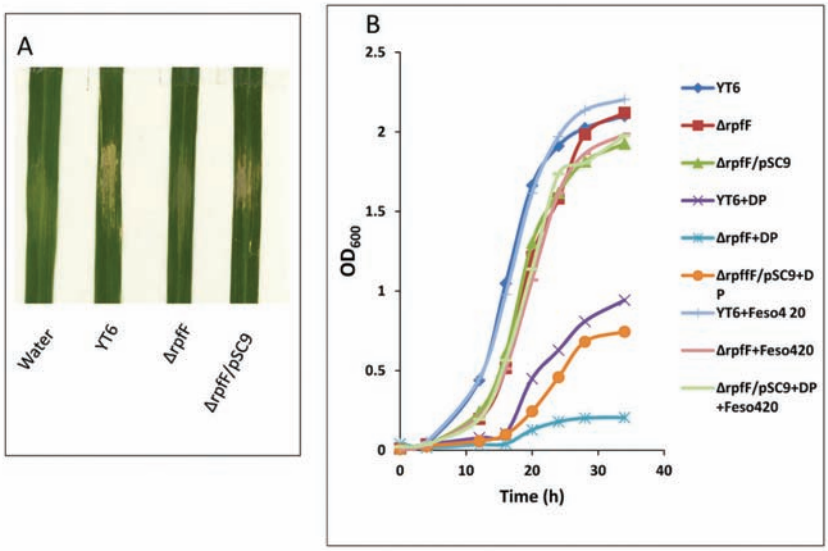

Figure 1. DSF deficient mutant of *Xanthomonas oryzae* pv. *oryzicola* exhibits virulence deficiency on rice. Rice leaves were inoculated with the YT6 (wild type), *"rpfF* (DSF^-) and *"rpfF*/pSC9 (*rpfF* mutant harboring the complementing plasmid). Typical symptoms of Bacterial Leaf Streak (BLS) are seen after 14 days post inoculation. (B) DSF is required for growth under low iron conditions. Different strains of Xcola were grown in rich media (Peptone sucrose; PS), PS + 2,2'-dipyridyl (Dp; iron chelator) with or without exogenous iron ($FeSO_4$) supplementation.

components involved in biofilm formation and motility. In future, we want to do detail study to understand the role of DSF in regulating these virulence associated function.

Project 2: Understanding the mechanism of attachment and biofilm formation in *Xanthomonas*

By screening a transposon induced mutant library of *Xanthomonas oryzae* pv. *oryzae*, the bacterial blight pathogen of rice, we have identified a novel 5.241 kb open reading frame (ORF) named *xadM* that is required for optimum virulence and colonization. This ORF encodes a protein, XadM, of 1746 amino-acids that exhibits significant similarity to Rhs family proteins. The XadM protein contains several repeat domains similar to a Wall-Associated Surface Protein (WASP) of *Bacillus subtilis*, which has been proposed to be involved in carbohydrate binding**.** The role of XadM in *X. oryzae* pv. *oryzae* adhesion was demonstrated by the impaired ability of a *xadM* mutant strain to cell-cell and cell-host attachment. In our proposed model, XadM plays an important role in the first step of colonization, the early attachment of Xoo at the hydathodal entry points on the rice leaf. XadM then promotes attachment of Xoo cells with the host cell-wall and with secreted extracellular polysaccharide, promoting stable biofilm formation (Figure 3). Interestingly, XadM (an Rhs family protein) homologs are present in several diverse bacteria including many *Xanthomonas* and animal pathogenic bacteria belonging to *Burkholderia* spp. The *rhs* genes are a family of enigmatic genes present in diverse bacteria and have been implicated to play a role of a rearrangement hot spot. Despite their ubiquity, *rhs* genes have not been assigned a definitive function. This is the first report of a role for XadM, an Rhs family protein, in adhesion and virulence of any pathogenic bacteria. We are doing further molecular genetics and gain of function studies to understand the contribution of *rhs* family of adhesins in *Xanthomonas* virulence.

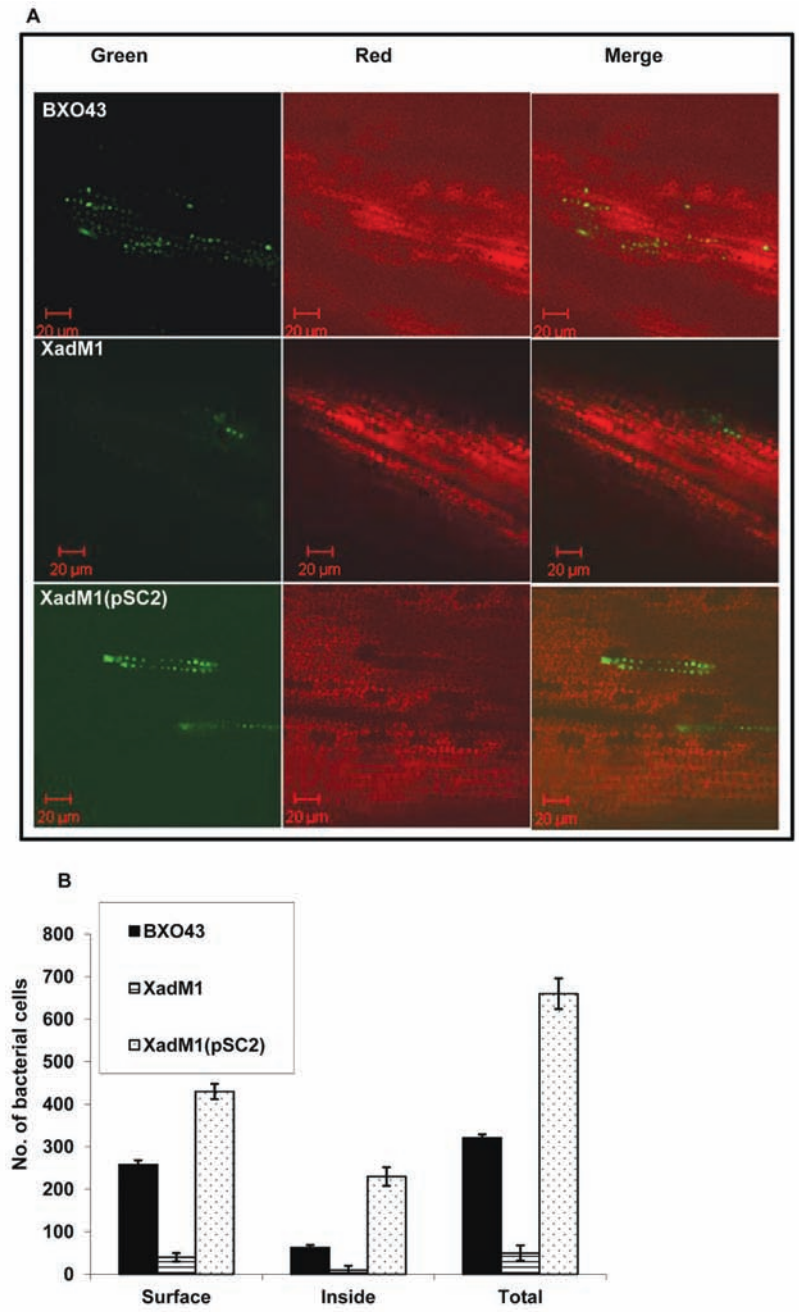

Figure 2. XadM is required for early attachment and entry of *X*. *oryzae* pv. *oryzae* into rice leaves. **(A)** Inoculation of rice leaves with enhanced green fluorescent protein-tagged *X*. *oryzae* pv. *oryzae* strains were done and confocal microscopy based assay were conducted 1h after inoculation. The panels depict confocal microscope based projection images (200 by 200 by 60µm^3 in the X, Y and Z axis beginning from the dorsal surface) of rice leaves inoculated with wild type (BXO43), XadM1 (*xadM*1 mutant) and XadM1(pSC2). Scale bar: 20 µm. **(B)** Reduction of leaf attachment and entry is associated with *xadM* mutation of *X*. *oryzae* pv. *oryzae*. The number of enhanced green fluorescent protein-expressing cells of different strains of *X*. *oryzae* pv. *oryzae* on the surface as well as inside rice leaves after 1h of infection as determined using confocal microscopy. Data were collected up to approximately 600 µm in length from the tip of the leaf and a distance of approximately 80 µm in depth from the dorsal surface of each leaf. Each bar shows mean and standard deviation of values obtained from three leaves. The values obtained for the XadM1 mutant were found to be significantly different ($p < 0.05$) compared with either the wild type strain or the XadMI mutant harboring the complementing plasmid, XadM1(pSC1), in a student's two tailed t test for independent means. Similar results were obtained in independent experiments.

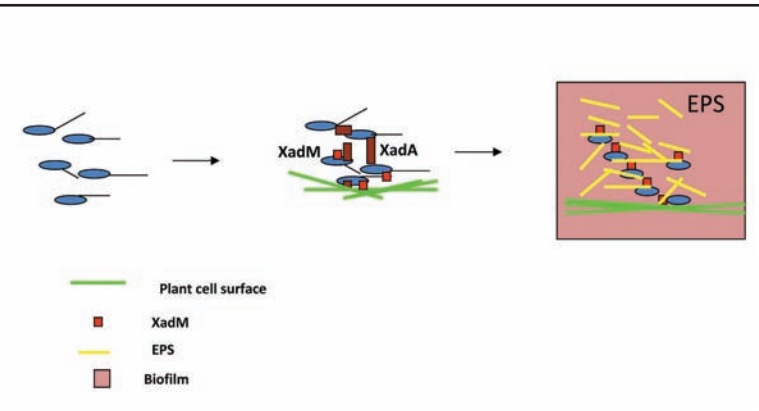

Figure 3. A proposed model for the role of XadM in attachment and biofilm formation of *X*. *oryzae* pv. *oryzae*. XadM along with XadA is required for the initial attachment of Xoo on hydathodal entry points present on the leaf surface. Inside the hydathode, XadM is required for the tight attachment with the plant cell-wall and also contributes to the attachment of Xoo cells with secreted extracellular polysaccharide. XadA promotes cell-cell attachment and XadM is involved in attachment of Xoo on host cell-wall and extracellular polysaccharide, which promotes stable biofilm formation inside rice leaves.

Publications

1. Almeida RPP, Killiny N, Newman KL, Chatterjee S, Ionescu M and Lindow SE (2012). Contribution of *rpfB* to cell-to-cell signal synthesis, virulence, and vector transmission of *Xylella fastidiosa*. ***Molecular Plant-Microbe Interactions*** 25: 453-462.
2. Pradhan BB, Ranjan M and Chatterjee S (2012). XadM, a novel adhesin of *Xanthomonas oryzae* pv. *oryzae*, exhibits similarity to Rhs family proteins and is required for optimum attachment, biofilm formation and virulence. ***Molecular Plant-Microbe Interactions*** 25: 1157-1170.
3. Rai R, Ranjan M, Pradhan BB and Chatterjee S (2012). Atypical regulation of virulence-associated functions by a diffusible signal factor in *Xanthomonas oryzae* pv. *oryzae*. ***Molecular Plant-Microbe Interactions*** 25: 789-801.
4. Beaulieu ED, Ionescu M, Chatterjee S, Yokota K, Trauner D and Lindow S (2013). Characterization of a Diffusible Signaling Factor (DSF) from *Xylella fastidiosa*. ***mBio*** 4: e00539-12.
5. Pandey A and Chaterjee S (2013). Signaling in plant-microbe interactions. ***Plant Stress*** 7: 52-59.

Other Publications

1. Chatterjee S (2013). Review of: Annual Review of Microbiology, 2011. Susan Gottesman and Caroline S Harwood (eds). ***Current Science*** 104: 653-654.

LABORATORY OF CELL DEATH & CELL SURVIVAL

Molecular Mechanisms Controlling Cell Life and Death

Faculty	Maddika V Subba Reddy	Scientist & WT-DBT India Alliance Intermediate Fellow
PhD Students	Neelam Rani	Senior Research Fellow
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	G Narmadha Reddy	Senior Research Fellow
	Swapnil R Shinde	Junior Research Fellow
	Parveen Kumar	Junior Research Fellow
	Varun J Shah	Junior Research Fellow (Since Jul. 2012)
Other Members	Tabasum Sidiq	Research Associate (Since Oct. 2012)
	J Kiranmai	Project-Junior Research Fellow
	Murali Mohan Maddu	Project-Junior Research Fellow (Since Sep. 2012)
	Ranita De	Project-Junior Research Fellow (Since Sep. 2012)
	Nanci Rani K	Technical Assistant

Objectives

1. To dissect the functional network of phosphatases regulating cell life and death;
2. To identify and characterize novel protein complexes in maintaining genomic stability; and
3. To understand the cellular functions of canonical and non-canonical ubiquitination.

Summary of work done until the beginning of this reporting year (Upto March 31, 2012)

Phosphatases are a group of ubiquitously expressing enzymes, which are responsible for the removal of a phosphate group of various substrates in a cell. Several studies have suggested an intricate involvement of phosphatases in controlling cellular life and death, but systematic studies to dissect the complex network of phosphatases and functional role of their interactions in these processes are lacking. We initiated our studies on functional phosphatase network with the identification of interacting partners of every phosphatase in the cell. In this work we have previously identified and characterized WWP2 as a novel functional E3 ubiquitin ligase for PTEN (Maddika *et al*., Nature Cell Biol. 2011). In addition to WWP2, we identified the protein phosphatase-1 nuclear targeting subunit PNUTS (PPP1R10) as a potential PTEN-associated protein. We have shown that PNUTS directly interacted with the lipid-binding domain (C2 domain) of PTEN and sequestered it in the nucleus. Depletion of PNUTS leads to increased apoptosis and reduced cellular proliferation in a PTEN-dependent manner. PNUTS expression was elevated in certain cancers compared with matched normal tissues. Overall, our studies revealed PNUTS as a novel PTEN regulator and a likely oncogene. (Kavela *et al.*, Cancer Res. 2013).

Details of progress in the current reporting year (April 1, 2012 - March 31, 2013)

Project 1: Functional studies on phosphatase networks

We are continuing our studies on identification of new components in the cellular phosphatase networks. PHLPP1 (PH domain leucine rich repeat protein phosphatase 1) is a Serine/Thronine protein phosphatase and has recently been characterized as a potential tumor suppressor. The loss of PHLPP1 is reported in various cancers such as colon, lung, breast, ovarian and prostate cancers. Functionally, PHLPP1 is shown to directly dephosphorylate Akt and antagonizes the cellular phosphotidylinositol-3 kinase (PI3K)/Akt signalling pathway thus triggers apoptosis and suppresses tumor growth. By utilizing tandem affinity purification approach we have identified WDR48 and USP12 as novel PHLPP1 associated proteins (Figure 1A). WDR48-USP12 complex deubiquitinates PHLPP1 (Figure 1B) and thereby enhances its protein stability. Similar to PHLPP1 function, WDR48 and USP12 negatively regulate Akt activation and thus promote cellular apoptosis.

Functionally, we show that WDR48 and USP12 suppress proliferation and migration of tumor cells (Figure 1C & 1D). Collectively, our results reveal WDR48 and USP12 as novel PHLPP1 regulators and potential suppressors of tumor cell survival. Our further studies are focused on mapping the functional networks of other phosphatases in cells such as lipid phosphatases, dual specificity

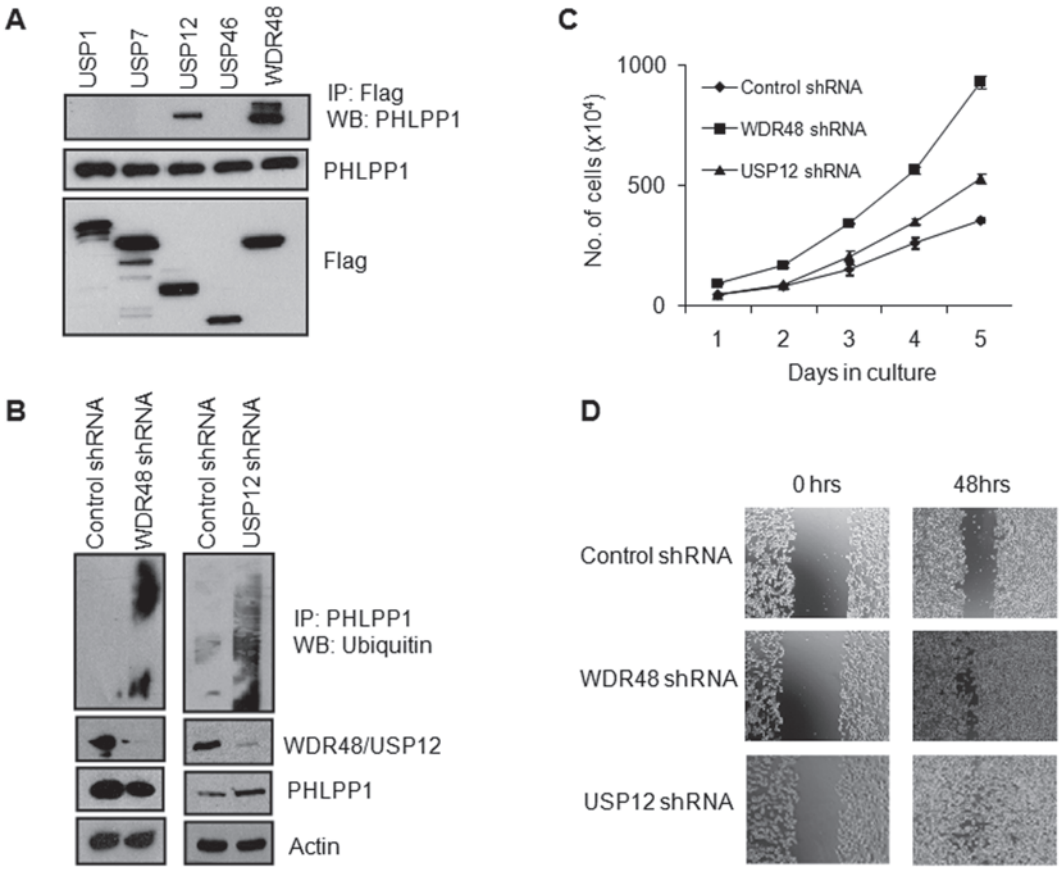

Figure 1. WDR48-USP12 complex controls cell proliferation by regulating PHLPP1. (A) 293T cells were transfected with the indicated Flag tagged plasmids and the interaction of endogenous PHLPP with WDR48 and USP12 was evaluated by immunoprecipitation with Flag antibody followed by immunoblotting with PHLPP1 antibody. **(B)** HCT116 cells were transfected with either control shRNA or shRNA against WDR48 and USP12. Cell lysates prepared after 6 hour MG132 (10 μM) treatment were subjected to immunoprecipitation and the ubiquitinated PHLPP1 was detected with anti-ubiquitin antibody. **(C)** HCT116 cells transfected with different shRNAs were seeded and their proliferation was measured by Tryphan blue exclusion for 5 days. **(D)** HCT116 cells expressing control shRNA or WDR48 shRNA were allowed to grow to confluence, and their ability to migrate was analyzed by using scratch assay.

phosphatases, non-receptor protein tyrosine phosphatases and receptor protein tyrosine phosphatases.

Project 2: Roles of canonical and non-canonical ubiquitination in cells

Ubiquitination is an ATP-dependent, highly ordered multistep enzymatic process which results in covalent attachment of ubiquitin to the substrate. Ubiquitin linked to the substrates serves as a molecular tag that marks proteins for either degradation by proteasome dependent pathway or to function in wide variety of processes in a proteasome independent manner. In this project we are interested in studying both the canonical and non-canonical functions of ubiquitination in cells. During our studies on canonical ubiquitination, we are interested in identifying proteosomal substrates of various E3 ligases. WWP2 is an E3 ubiquitin ligase that belongs to NEDD-4 like family HECT-type E3 ligases. It plays an important role in different cellular functions such as transcription, embryonic

stem cell fate, cellular transport, T-cell activation and Apoptosis. In this study we identified p73 as a novel substrate of WWP2 that might be functionally important in WWP2 pro-oncogenic function.

p73 is a p53 related transcription factor that exists in full length and N-terminal truncated ΔNp73 isoforms. Due to their opposing functions in controlling cell survival it is critical to maintain the balance between these two proteins but the precise mechanism that regulate their levels are not clear. In our study, we identified WWP2, an E3 ligase as a novel p73 associated protein that ubiquitinates and degrades p73. In contrast, WWP2 also promotes degradation of ΔNp73 but independent of its catalytic function. We showed that WWP2 heterodimerizes with another HECT E3 ligase WWP1, which specifically ubiquitinates and degrades ΔNp73. During cellular stress WWP2 is inactivated that leads to upregulation of p73 whereas WWP2-WWP1 complex is intact to degrade ΔNp73 thus playing an important role in shifting the balance between p73 and ΔNp73. Collectively, our results reveal a new functional E3 ligase complex that differentially regulates cellular p73 and δNp73 (Figure 2). Our future studies in this project are further focused on characterizing the non-canonical functions of ubiquitination.

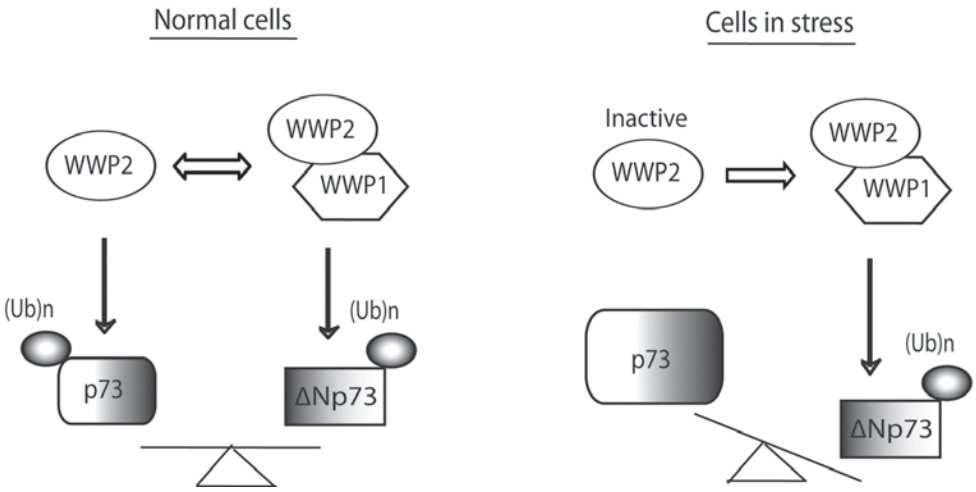

Figure 2. A proposed model to show the role of WWP2 and WWP2-WWP1 heterodimeric complex in regulating p73 and ΔNp73 levels in normal and stress conditions.

Publications

1. Jain MV, Paczulla AM, Klonisch T, Dimgba FN, Rao SB, Roberg K, Schweizer F, Lengerke C, Davoodpour P, Palicharla VR, Maddika S and Los M (2013). Interconnections between apoptotic, autophagic and necrotic pathways: implications for cancer therapy development. ***Journal of Cellular and Molecular Medicine*** 17: 12-29.
2. Kavela S, Shinde SR, Ratheesh R, Viswakalyan K, Bashyam MD, Gowrishankar S, Vamsy M, Pattnaik S, Rao S, Sastry RA, Srinivasulu M, Chen J and Maddika S (2013). PNUTS functions as a proto-oncogene by sequestering PTEN. ***Cancer Research*** 73: 205-214.
3. Dulla B, Kirla KT, Rathore V, Deora GS, Kavela S, Maddika S, Chatti K, Reiser O, Iqbal J and Pal M. Synthesis and evaluation of 3-amino/guanidine substituted phenyl oxazoles as a novel class of LSD1 inhibitors with anti-proliferative properties. ***Organic & Biomolecular Chemistry*** (In press).

LABORATORY OF DROSOPHILA NEURAL DEVELOPMENT

Understanding Patterning and Development of Central Nervous System using *Drosophila melanogaster*

Faculty	Rohit Joshi	WT-DBT India Alliance Intermediate Fellow
PhD Students	Risha Khandelwal	Senior Research Fellow
	Neha Ghosh	Junior Research Fellow
	Ravi Ranjan	Junior Research Fellow (Since Jul. 2012)
	Rashmi Sipani	Junior Research Fellow (Since Feb. 2013)
Other Members	P Kalyani	Technical Officer
	Sruthakeerthi V	Project Assistant (Till Aug. 2012)
	Ankush Auradkar	Project Assistant (Till Dec. 2012)
	Karnika Tripathi	Project Assistant (Since Sep. 2012)

Objective

The key objective of the laboratory is to understand how neural progenitor cells attain their positional identity in developing Central Nervous System (CNS) of an organism and how does this translate into generation of a variety of cell types found in CNS (as represented in the Figure 1). Hox family of transcription factors are known to play an important role in giving the positional identity to the cells and generation of a variety of cell types along the AP axis of the CNS during development. The molecular basis of this phenomenon is not well investigated. We are interested in understanding the molecular basis of Hox function in patterning CNS using *Drosophila melanogaster* as our model organism, focusing mainly on early embryonic and late larval stages of development. To this end, the specific aims of our laboratory are as follows:

1. Understanding the molecular function of Hox gene *Abdominal-A (Abd-A)* in larval CNS patterning

Abdominal region of the *Drosophila* larval CNS has lesser number of neurons compared to its thoracic counterpart. Hox gene *Abd-A* is known to cause programmed cell death (apoptosis) of neural progenitor cells (also called Neuroblasts-Nbs) and therefore limit the number of neurons in abdominal region of CNS. The precise molecular details of how *Abd-A* causes Nb apoptosis are unknown. Genetic evidence suggests a role for a helix-loop-helix transcription factor Grainyhead (Grh) along with Abd-A in control of this apoptosis. Characterization of the molecular basis of this link is the primary goal of this project. Moreover, since Grh is involved in Nb apoptosis and is not expressed in neuronal progeny refractory to this apoptosis, it is of interest to define *grh* regulation in these cells which keeps *grh* "on" in the Nbs and "off" in the neuronal progeny of Nbs.

2. Understanding the role of Hox gene *Deformed* (*Dfd*) in patterning of embryonic subesophageal ganglia

Hox genes express in CNS (in neural progenitor cells) in embryonic stages of development (as represented in Figure 1) but how does their expression patterns the embryonic nervous system is not well understood. *Deformed (Dfd)* is known to express in the cells of subesophageal ganglion of embryonic CNS, and this project focuses on understanding auto-regulation of *Dfd* in this region and to find out how this helps in giving cells their specific positional identity. This is being done by using a 630bp long auto-regulatory CNS specific enhancer for *Dfd* which recapitulates the expression of *Dfd* gene in developing embryonic CNS.

3. Investigating the role of *Abdominal-B (Abd-B)* and *Double-sex (Dsx)* in terminal CNS patterning.

The set of Nbs in the terminal region of CNS show sex specific proliferation and survival. Although the role of the sex determining hierarchy and Hox gene Abd-B, in growth and differentiation of *Drosophila* genital discs, is well worked out, little is known about how sex determination hierarchy and Abd-B intersects with cell proliferation and survival behavior of terminal Nbs (tNbs) in the larval VNC. Double-sex (Dsx) is the most downstream transcription factor of the sex-specification hierarchy. I intend to test the interaction between Abd-B and Dsx in gender specific proliferation of these cells.

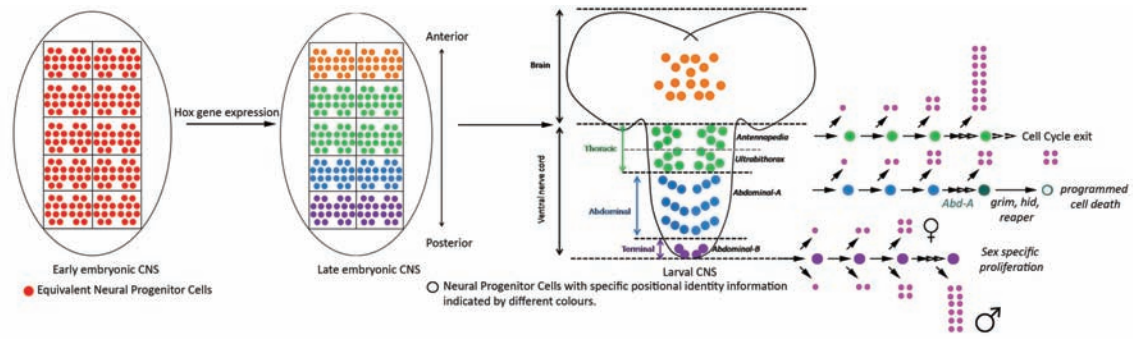

Figure 1. Early embryonic CNS comprises of an equivalent population of neural progenitor cells (shown in red circles) which start to express specific Hox genes and therefore acquire specific positional identity (represented by different colored circles). These cells generate a variety of different cell types in both embryonic and larval CNS. In larval stages thoracic and abdominal Nbs differ in their number and proliferation profile as shown. Thoracic Nbs stop proliferation by cell cycle exit, while abdominal Nbs (in both sexes) and terminal Nbs (tNb in females) die as a result of apoptosis, the tNbs in males continue dividing and give rise to more neurons as shown.

Summary of work done until the beginning of this reporting year (Upto March 31, 2012)

1. Understanding the molecular function of Hox gene *Abd-A* in larval CNS patterning

It is known that *grim* gene plays primary role in this apoptosis and relevant enhancer for the *grim* gene in Nbs lies in 23kb genomic region referred to as NBRR-Neuroblast Regulatory Region. The region has been divided into 4 overlapping genomic fragments (of 8kb, 10kb, 8 kb and 8kb each) that are to be cloned into *pCasPer-lacZ* reporter construct to generate *enhancer-lacZ* transgenic lines for screening. These 4 fragments have been amplified by PCR from genomic DNA using region specific primers. The first 8kb fragment has been already cloned into *pCasPer-nls-lacZ* shuttle vector and microinjections are being done for the same. To study the Nbs specific regulation of *grh,* a 4kb enhancer of *grh* responsible for its expression in Nb was divided into three fragments to identify the minimal enhancer which will recapitulate its expression in Nbs. The three genomic fragments have been cloned into shuttle vectors and made into transgenic lines.

2. Role of Hox gene *Deformed (Dfd)* in patterning of embryonic subesophageal ganglia

The CNS specific 630bp autoregulatory enhancer of *Dfd* was cloned into shuttle vector and transgenic lines were being made to check its expression in specific cell types (especially Nbs) in subesophageal region of the embryonic brain. Simultaneously, a protein expression was standardized for Dfd, Exd and Hth. The 630bp *Dfd* autoregulatory element was scanned for Hox-Exd binding sites and two putative compound binding sites were identified for these two transcription factors. *In vitro* binding studies were done on these binding sites using EMSA and both of the binding sites showed binding to Dfd-Exd hetrodimer. In order to investigate the *in vivo* relevance of these binding sites, these sites were mutagenized in 630bp DNA element and these various mutagenized forms of the enhancers have been subcloned into the *pCasPer-nls-lacZ* shuttle vector and the transgenic lines are being made for the same. These transgenic lines will be tested for their capacity to activate the reporter β-galactosidase to test the relevance of the binding site and its direct role in autoregulation of *Dfd* gene.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

1. Understanding the molecular basis of Hox gene Abdominal-A (Abd-A) in larval CNS patterning

A systematic screening of the 23kb NBRR is ongoing to identify Nb specific *grim* enhancer responsible for *grim* activation and Nb apoptosis. The 23kb region has been divided into 4 overlapping genomic fragments (of 8kb, 10kb, 8 kb and 8kb each) which are being screened for their ability to drive Nb specific expression of *lacZ* reporter in late third instar larval (LL3) brain. These 4 fragments have been amplified by PCR using region specific primers from genomic DNA and all the four fragments have been cloned into *pCasPer-lacZ* shuttle vectors to make transgenic lines, and

transgenic line for two of the fragments have already been made and one of them has been analyzed which has helped us to narrow down the search for the relevant *grim* enhancer to an 8kb region. The 4kb enhancer of *grh* has been fragmented into three parts and the relevant enhancer for the expression of *grh* has been further narrowed to a 1.5kb region.

2. Role of Hox gene *Deformed* in patterning of embryonic subesophageal ganglia

The 630bp *Dfd* autoregulatory element was scanned for Hox-Exd binding sites and two putative compound binding sites were identified for these two transcription factors. *In vitro* binding studies were done on these binding sites using EMSA and both of the binding sites showed binding to Dfd-Exd hetrodimer. In order to investigate the in vivo relevance of these binding sites, these sites were mutagenized in 630bp DNA element and the mutagenized forms of the enhancers have been subcloned into the *pCasPer-nls-lacZ* shuttle vector and the transgenic lines have been made and are being analyzed for the same.

3. Investigating the role of *Abdominal-B (Abd-B)* and *Double-sex (Dsx)* in terminal CNS patterning

The standardizations for co-staining with BrDU and other antibodies for the larval nervous system has been done, this is important to monitor the dividing cells (Nbs and ganglion mother cells) in LL3 CNS. The co-staining procedure for BrDU and other epitopes will be used to monitor the tNbs division to test the role of Abd-B in this proliferation by making Abd-B null clones in larval CNS. This will be attempted in two genetic backgrounds, first wherein the dividing Nbs will be randomly marked by GFP using MARCM technique and in second case where GFP will be specifically driven in tNbs.

LABORATORY OF CELL CYCLE REGULATION

Elucidating the Role of Effector Proteins in G1 to S Phase Progression

Faculty	Shweta Tyagi	Ramalingswami Fellow
PhD Students	Aamir Ali	Senior Research Fellow
	Zaffer Ullah Zargar	Senior Research Fellow
	Swathi Chodisetty	Junior Research Fellow
	Amit Mahendra Karole	Junior Research Fellow (Since Jul. 2012)
Other Members	VN Sailaja	Technical Officer
	Jitendra Thakur	Research Associate (Since Jan. 2013)
	Manjari Mulukutla	Project-Junior Research Fellow
	Shravanti Kulkarni	Project-Junior Research Fellow
	Nidhi Kumari	Project Assistant (Since Oct. 2012)

Objectives

1. Identification of new effector proteins involved in regulation of E2F-responsive promoters; and
2. Study of chromatin modifying proteins in cell cycle regulation.

Project 1: Identification of new effector proteins involved in regulation of E2F-responsive promoters

One of the major roles of E2F proteins is to regulate the transition from G1 to S phase. However, how E2Fs affect passage into S phase is still poorly understood. In this project we aim to identify new effector proteins involved in regulation of E2F-responsive promoters and better understand how these effectors influence transcriptional regulation during G1 to S phase progression.

Summary of work done until beginning of this reporting year (Upto March 31, 2012)

We decided to take a candidate based approach to look for effector proteins. In order to harvest cells in a particular cell cycle phase, we synchronized HeLa cells using double thymidine block and determined the time points that we could use to harvest cells in G1/S, S, G2/M, early G1 and late G1 phase. We also standardized Chromatin immunoprecipitation (ChIP) for immunoprecipitation against E2F1 and E2F4 antibodies followed by qPCR.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

We are aiming to identify the effector proteins which modulate the expression of E2F responsive promoters. E2F family of proteins has both activating and repressive members. The repressive members include E2F3b, E2F4 and E2F5. We started our study with E2F4, wherein we aimed to probe for its interacting partners. E2F4 being a nuclear protein is present in very low amounts in cell. To circumvent this problem we cloned E2F4 into a bacterial expression vector pGex4t1 which leads to expression of a fusion protein GST-E2F4. Expression and purification of GST-E2F4 was standardized and eventually we could produce GST-E2F4 to homogeneity. GST-E2F4 bound to the glutathione agarose beads will be used in future for pulldown assays to probe for the interacting partners.

One major limitation of working with endogenous proteins is the low abundance of such proteins in the cell. Since we expect to use endogenous proteins in most our experiments, their scarce availability can prove to be a limiting factor for our future experiments. Therefore, we cultured HeLa Spinner cells which can be used for producing large amounts of cells in suspension cultures. HeLa cells were grown in Joklik's media and growth conditions were standardized.

Project 2: Study of chromatin modifying proteins in cell cycle regulation

Histone 3 lysine 4 trimethylation is linked to active gene expression, but its precise role in cell cycle regulation is now being uncovered. We have shown that MLL-family of H3K4 histone methyltransferases is linked to cell cycle regulation by interacting with E2F1. In this project, we are looking at other roles of this chromatin-modifying complex that may influence cell cycle regulation.

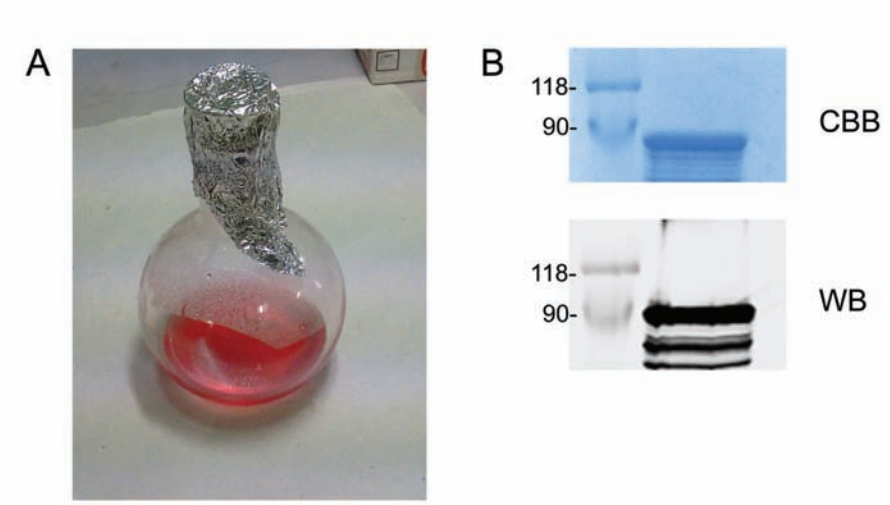

Figure 1. HeLa spinner cultures and GST-E2F4 expression. (A) HeLa spinner cells were grown in Joklik's media in a non CO_2 incubator. Up to $6x10^5$ cells/ml could be obtained. **(B)** GST-E2F4 was expressed and purified using GST beads. CBB, Coomassie Brilliant Blue staining; WB, Western blot using specific antibody against the E2F4 protein.

Summary of work done until beginning of this reporting year (Upto March 31, 2012)

To find out the role of MLL complex in cell cycle regulation, in our previous report we could establish the WDR5 siRNA transfection efficiency by techniques such as RT-PCR and Western-blot. Previous studies have shown that although all four core-components are essential for a functional MLL complex, the inactivation of WDR5 results in complete loss of activity of this complex. Therefore, depletion of WDR5 by siRNA should inactivate the whole MLL complex. We are now in the process of determining the cell cycle defects that may have appeared upon WDR5 knockdown.

Details of progress made in the current reporting year (April 1, 2012 – March 31, 2013)

To examine the cell cycle defects that may have appeared upon WDR5 knockdown, we decided to

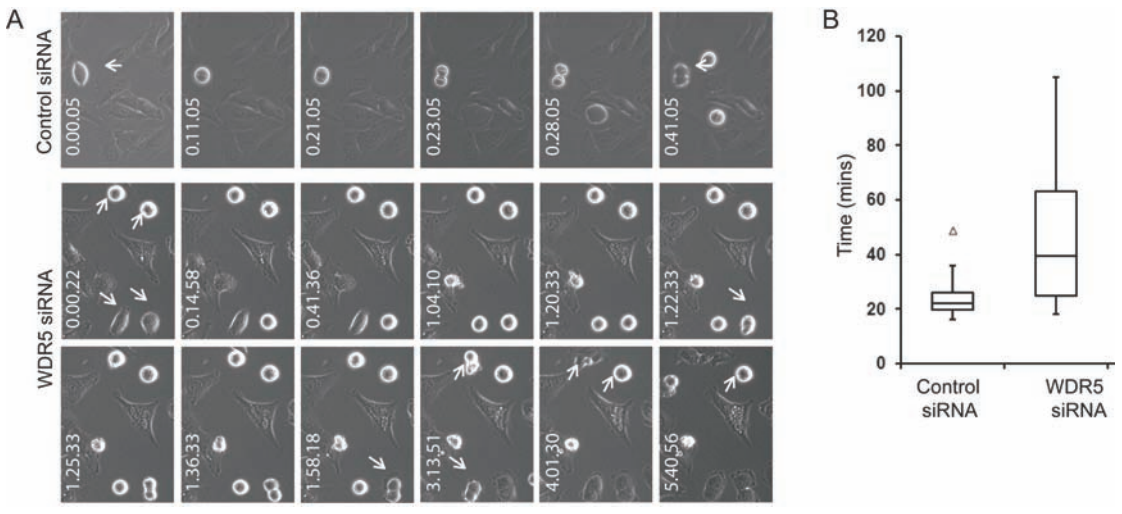

Figure 2. Loss of WDR5 results in delay in mitosis. (A) Series of phase contrast time-lapse images of U2OS cells captured at 1 min interval after treatment with Control or WDR5 siRNA. Selected images are shown. Arrows show cells of interest**. (B)** Quantification of total time taken in mitosis (prophase to telophase), in Control or WDR5 siRNA-treated U2OS cells (n=40). The start of mitosis was determined by rounding up of the cells.

monitor the siRNA treated cells using phase contrast time-lapse microscopy. Upon observation we found that WDR5 depleted cells displayed clear delay in progression through mitosis. On an average, the WDR5 depleted cell took twice as much time (mean time taken = 39.5 minutes) to complete mitosis compared to the control samples (mean time taken = 22 minutes). Some cells remained in mitosis for up to 6 hours after which they were no longer imaged. As the cells were imaged under phase contrast microscopy, we could roughly determine that WDR5-depleted cells spent more time in prophase than control cells. In order to establish a more direct reason as to why WDR5 knockdown cells are stalled in prophase, we will use high-magnification microscopy to image control and WDR5 siRNA-treated samples just before the nuclear envelope breakdown (NEB). We have initiated our imaging with control cells.

Publications

1. Zargar Z and Tyagi S (2012). Role of host cell factor-1 in cell cycle regulation. ***Transcription*** 3: 187-192.
2. * Michaud J, Praz V, Faresse NJ, Jnbaptiste CK, Tyagi S, Schutz F and Herr W. HCFC1 is a common component of active human CpG-island promoters and coincides with ZNF143, THAP11, YY1 and GABP transcription factor occupancy. ***Genome Research*** (In press).

* Work done elsewhere

अन्य वैज्ञानिक सेवाएँ / सुविधाएँ
Other Scientific Services / Facilities

LABORATORY ANIMAL FACILITY

Faculty Co-ordinators	Rashna Bhandari	Staff Scientist & WT-DBT India Alliance Senior Fellow
	Sanjeev Khosla	Staff Scientist
Other Members	Hole Jayant Pundalikrao	Officer-In-Charge
	Suman Komjeti	Technical Assistant

Objectives

1. To breed, maintain and supply laboratory animals to institutional scientists, while ensuring animal health and well being at all times;
2. Maintain inbred transgenic strains of mice in a controlled environment, as per CPCSEA guidelines. Breeding and experimentation of all strains of mice is undertaken in individually ventilated caging systems;
3. Assist users in procuring rodents for research, and conducting IAEC approved procedures;
4. Comply with regulatory government body requirements, in facilitating ethical research with animals, and streamlining operations to improve personnel performance and reduce operational costs.

Summary of work done until the beginning of this reporting year (Upto March 31, 2012)

The CDFD Laboratory Animal Facility (LAF) started its activities on July 1, 2011, within the premises of M/s Vimta Labs Limited, located at Genome Valley, Shameerpet, Hyderabad. Infrastructure was established to house mice in individually ventilated cages (IVCs), and conduct standard experimental procedures. All procedures conducted on animals housed in this facility are approved by the Institutional Animal Ethics Committee (IAEC) constituted by the Committee for the Purpose of Control and Supervision of Experiments on Animals (CPCSEA), Ministry of Environment and Forests, Govt. of India, at M/s Vimta Labs Ltd. Until March 2012, the facility housed approximately 100 mice of each transgenic strain, *Ip6k1* and *Nnat*.

Figure 1. Athymic nude mice bred at the CDFD Laboratory Animal Facility

Strains	Total (Male+Female)	Under Breeding (Male+Female)	Supplied during 2012-13
Ip6k1	130+100	0+7	133
Nnat	190+167	0+10	45
Balb/c	18+9	5+12	355
C57BL/6	74+81	0+3	26
Foxn1^{nu}	14+25	5+21	8

Table 1. Strain-wise break up of mouse strains housed at LAF as on March 31, 2013, and supplied to users during 2012-13.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

During this reporting year, CDFD LAF expanded substantially to house five inbred mouse strains including *Ip6k1, Nnat*, C57BL/6, *Foxn1*^{nu}, and Balb/c. These strains of mice were acquired from CPCSEA registered breeders. Mice were bred to expand the colonies and meet users' requirements. Currently this facility houses approximately 900 mice in 350 IVC cages (Table 1). During the year, 567 mice were supplied to users for IEAC approved experimentation.

Procedures conducted on these animals include blood sampling for measurement of biochemical parameters, embryo collection for the preparation of embryonic fibroblasts, tail biopsies for genotyping analysis, necropsy for histopathological analysis, antibody generation, tail vein injection, harvesting of peritoneal macrophages, and tumorigenesis studies. Several mice, especially those of the transgenic strains *Ip6k1* and *Nnat* are enrolled in long-term experimentation to monitor physiological

Figure 2. Nude mice are maintained in a separate room with an IVC system and air handling unit.

Sl. No.	Projects in progress
1.	Functional analysis of neuronatin's second intron by knock out strategy
2.	Protocol for establishment and histopathological characterization of *Ip6k1* knockout mice
3.	Signal transduction pathway in immune cells regulating their innate and effecter functions during oxidative stress
4.	Studies on the role of PNUTS in tumorigenesis in nude mice
5.	Protocol for comparative bio-burden study of fifteen strains of *Candida glabtrata* in Balb/c mice
6.	Immunization of Balb/c mice for generation of antibodies against few purified recombinant mycobacterial proteins
7.	Studying the effect of PPE 18(Rv1196) on LPS induced endotoxaemia in mice
8.	Protocol for the use of nude mice in the study of tumorigenesis
9.	Protocol for generation of mouse polyclonal antibodies
10.	Isolation of macrophages from Balb/c mice
11.	Cryopreservation of mouse embryos by vitrification
12.	Understanding the role of Rab711 in phagosome maturation and immune effector signalling
13.	Protocol for establishment and histopathological characterization of *Ip6k2* knockout mice
14.	Protocol for establishment of transgenic mouse model to study the role of *Ip6k1* in tumorigenesis

Table 2. IAEC approved projects proposed by various groups at CDFD, in progress during 2012-13.

and biochemical responses to age and diet. The IAEC approved projects in progress during this reporting year are mentioned in Table 2.

Future direction

In the near future, apart from continuing our current activities, our goal is to set up and establish a mouse embryo and sperm cryopreservation facility to archive and retrieve mouse strains important for our research. We are also looking into obtaining genetically modified transgenic and knockout mouse strains from various reputed international mouse laboratories to expand our colony and ensure animal supply for our researchers as and when required.

BIOINFORMATICS

Head	HA Nagarajaram	Staff Scientist
Other Members	R Chandra Mohan	Technical Officer
	K Prashanthi	Technical Assistant

Objectives

1. To maintain the CDFD website, to provide web based services and e-mail services;
2. To maintain various servers, workstations, PCs, printers and other peripheral devices;
3. To maintain Institute-wide LAN as well as the internet connectivity;
4. To coordinate the procurement process of workstations, PCs, laptops, printers, other peripheral devices and software required;
5. To secure the CDFD network from security threats; and
6. To integrate Institute's network into National and International grid computing networks.

Summary of work done until beginning of this reporting year (April 1, 2011 – March 31, 2012)

- Activities related to installation, administration and maintenance of servers which provide various services, databases and computational jobs were undertaken.
- Existing PC Annual Maintenance Contract was renewed. We have also renewed the agreement for remote monitoring and managed services for Sun servers in the Data Center set up.
- Migrated existing email server to Zimbra email server.
- Upgraded 4Mbps leased line from BSNL to 8Mbps.
- Proposal from DBT for the deployment of IPv6 has been initiated.

Details of progress made in the current reporting year (April 1, 2012 - March 31, 2013)

- Activities related to installation, administration and maintenance of servers which provide various services, databases and computational jobs were undertaken.
- Procured two high end servers with 4 processors, 512 GB RAM, 5TB internal storage.
- Internet, web, email-services were provided with enhanced functionalities.
- High-end PCs, workstations, laptops, scanners and printers were procured and installed.
- PC Annual Maintenance Contract was awarded to a new vendor M/s Bharat IT Services.
- Renewed the MoU with CDAC for availing GARUDA-grid facility.
- Upgraded the Firewall, procured additional antivirus licenses.
- Initiated the process of setting up a fail-safe server for the existing email server.

INSTRUMENTATION

Head	Raghavendrachar J	Staff Scientist
Other Members	RN Mishra	Senior Technical Officer
	SD Varalaxmi	Technical Officer
	M Laxman	Technical Officer
	RMK Satyanarayana	Technical Officer
	T Ramakrishna Reddy	Technical Assistant

Objective

To maintain repair and service all the equipments in laboratory. To provide pre-installation requirements for new instruments and to coordinate with the manufacturers/their agents in installation and warranty service of the new instruments. Also to provide the reports on the newly arrived instruments and to follow up with the suppliers for short shipped items.

Summary of work done until the beginning of this reporting year (April 1, 2011 – March 31, 2012)

During the year 2011-12, we installed 144 new equipments like Beckman High Speed Centrifuge, Hitachi Spectrofluorimeter, Robotic Protein Crystallization System, Accuri C6 Flowcytometer, Two Color IR Imaging System, Individually Ventilated Cages for Animal house, Microscopes, PCR Machines, Nanodrop Spectrophotometers, Refrigerated Centrifuges, Orbital Shakers, Electroporators, -80^{0}C Freezer, -20^{0}C Freezers, Cold cabinets etc. and had also completed 472 work orders for repair and maintenance of various laboratory equipments.

We had successfully set up the ID card printing system for issuing identity cards instantly to all our Staff, Research Scholars and Project Staff. In addition, we were involved in organizing the audio and visual requirements for presentations in various seminars, lectures and workshops, Foundation Day lecture series, distinguished Scientist lectures etc. held in CDFD. We were actively involved in conducting the Ramalingaswamy Fellows' Conclave and the DBT Silver Jubilee function at CDFD.

Details of progress made in the current reporting year (April 1, 2012 – March 31, 2013)

During the year 2012-13, we have installed 68 new equipments like Multi Mode Reader, Inverted Microscopes, Chemiluminescence Gel Documentation System, PCR Machines, Refrigerated Centrifuges, Shaking waterbaths, Electroporators, -80^{0}C Freezer, -20^{0}C Freezers, Cooled Incubator, Refrigerators etc. and have also completed 491 work orders for repair and maintenance of various laboratory equipments. We have successfully set up the Biometric Attendance System at both Tuljaguda and Gruhakalpa complexes registering the accurate attendance of all our employees and scholars.

In addition, we were involved in organizing the audio and visual requirements for presentations in various seminars, lectures and workshops, Foundation day lectures, distinguished Scientist lectures held in CDFD. We were actively involved in conducting the Seminar Workshop on Microbial Biology during 11th to 14th December 2012. We have maintained most of the equipment with maximum uptime in the laboratory. Most of the instruments are maintained by our Instrumentation staff, thereby saving on the expensive AMCs and with very little downtime of the equipment.

प्रकाशन
Publications

RESEARCH PAPERS

A. Publications during the year 2012

1 Acharya V and Nagarajaram HA (2012). Hansa: an automated method for discriminating disease and neutral human nsSNPs. ***Human Mutation*** 33: 332-337.

2. Akhter Y, Ehebauer MT, Mukhopadhyay S and Hasnain SE (2012). The *PE/PPE* multigene family codes for virulence factors and is a possible source of mycobacterial antigenic variation: perhaps more? ***Biochimie*** 94: 110-116.

3. Ali J, Thummala SR and Ranjan A (2012). The parasite specific substitution matrices improve the annotation of apicomplexan proteins. ***BMC Genomics*** 13 (Suppl. 7): S19.

4. Almeida RPP, Killiny N, Newman KL, Chatterjee S, Ionescu M and Lindow SE (2012). Contribution of *rpfB* to cell-to-cell signal synthesis, virulence, and vector transmission of *Xylella fastidiosa*. ***Molecular Plant-Microbe Interactions*** 25: 453-462.

5. Almeida RPP, Killiny N, Newman KL, Chatterjee S, Ionescu M and Lindow SE (2012). Contribution of *rpfB* to cell-to-cell signal synthesis, virulence, and vector transmission of *Xylella fastidiosa*. ***Molecular Plant-Microbe Interactions*** 25: 453-462.

6. Angalena R, Aggarwal S, Phadke SR and Dalal A (2012). Compound heterozygote condition in beta thalassemia major due to a novel single nucleotide deletion (-T) at codon 69 in association with IVS 1-5 (G>C) mutation. ***International Journal of Laboratory Hematology*** 34: e7-e9.

7. Arunkumar KP, Sahu AK, Mohanty AR, Awasthi AK, Pradeep AR, Urs SR and Nagaraju J (2012). Genetic diversity and population structure of Indian golden silkmoth (*Antheraea assama*). ***PLoS One*** 7: e43716.

8. Banerjee R, Nath S, Ranjan A, Khamrui S, Pani B, Sen R and Sen U (2012). The first structure of polarity suppression protein, Psu from Enterobacteria phage P4, reveals a novel fold and a knotted dimer. ***Journal of Biological Chemistry*** 287: 44667-44675.

9. Bashyam MD, Chaudhary AK and Bhat V (2012). The IVS2+837T>G appears to be a relatively common 'rare' β-globin gene mutation among β-Thalassemia patients in the South Indian state of Karnataka. ***Hemoglobin*** 36: 497-503.

10. Bashyam MD, Chaudhary AK, Reddy EC, Reddy V, Acharya V, Nagarajaram HA, Devi ARR, Bashyam L, Dalal AB, Gupta N, Kabra M, Agarwal M, Phadke SR, Tainwala R, Kumar R and Hariharan SV (2012). A founder ectodysplasin A receptor *(EDAR)* mutation results in a high frequency of the autosomal recessive form of hypohidrotic ectodermal dysplasia in India. ***British Journal of Dermatology*** 166: 819-829.

11. Bashyam MD, Chaudhary AK, Sinha M, Nagarajaram HA, Devi ARR, Bashyam L, Reddy EC and Dalal A (2012). Molecular genetic analysis of MSUD from India reveals mutations causing altered protein truncation affecting the C-termini of E1α and E1β. ***Journal of Cellular Biochemistry*** 113: 3122-3132.

12. Bashyam MD, Purushotham G, Chaudhary AK, Rao KM, Acharya V, Mohammad TA, Nagarajaram HA, Hariram V and Narasimhan C (2012). A low prevalence of *MYH7/MYBPC3* mutations among familial hypertrophic cardiomyopathy patients in India. ***Molecular and Cellular Biochemistry*** 360: 373-382.

13. Begum H, Reddy TM, Malathi S, Reddy BP, Arcahk S, Nagaraju J and Siddiq EA (2012). Molecular analysis for genetic distinctiveness and relationships of indigenous landraces with popular cultivars of mango (*Mangifera indica* L.) in Andhra Pradesh, India. ***The Asian and Australasian Journal of Plant Science and Biotechnology*** 6: 24-37.

14. Bhat KH, Ahmed A, Kumar S, Sharma P and Mukhopadhyay S (2012). Role of PPE18 protein in intracellular survival and pathogenicity of *Mycobacterium tuberculosis* in mice. ***PLoS One*** 7: e52601.

15. Bhat KH, Chaitanya CK, Parveen N, Varman R, Ghosh S and Mukhopadhyay S (2012). Proline-Proline-Glutamic Acid (PPE) protein

Rv1168c of *Mycobacterium tuberculosis* augments transcription from HIV-1 Long Terminal Repeat promoter. ***Journal of Biological Chemistry*** 287: 16930-16946.

16. Dalal A, Bhavani GSL, Togarrati PP, Bierhals T, Nandineni MR, Danda S, Danda D, Shah H, Vijayan S, Gowrishankar K, Phadke SR, Bidchol AM, Rao AP, Nampoothiri S, Kutsche K and Girisha KM (2012). Analysis of the *WISP3* gene in Indian families with progressive pseudorheumatoid dysplasia. ***American Journal of Medical Genetics A*** 158A: 2820-2828.
17. Dutta UR, Pidugu VK and Dalal A (2012). Molecular cytogenetic characterization of a non-robertsonian dicentric chromosome 14;19 identified in a girl with short stature and amenorrhea. ***Case Reports in Genetics*** 2012: Article ID 212065, doi:10.1155/2012/212065.
18. Dutta UR, Pidugu VK and Dalal AB (2012). Molecular and cytogenetic characterization of two patients with recurrent miscarriages and X-autosome translocation. ***Journal of Research in Medical Sciences*** 17: 572-574.
19. Dutta UR, Pidugu VK, Goud V and Dalal AB (2012). Mosaic Down syndrome with a marker: molecular cytogenetic characterization of the marker chromosome. ***Gene*** 495: 199-204.
20. Fialho AM, Salunkhe P, Manna S, Mahali S and Chakrabarty AM (2012). Glioblastoma multiforme: novel therapeutic approaches. ***ISRN Neurology*** 2012: Article ID 642345, doi:10.5402/2012/642345.
21. Gokul G and Khosla S (2012). DNA methylation and cancer. ***Subcellular Biochemistry*** 61: 597-625.
22. Hegde SR, Rajasingh H, Das C, Mande SS and Mande SC (2012). Understanding communication signals during mycobacterial latency through predicted genome-wide protein interactions and Boolean modeling. ***PLoS One*** 7: e33893.
23. Kumar P and Nagarajaram HA (2012). A study on mutational dynamics of simple sequence repeats in relation to mismatch repair system in prokaryotic genomes. ***Journal of Molecular Evolution*** 74: 127-139.
24. Kumar R, Panigrahi I, Dalal A and Agarwal S (2012). Sickle cell anemia-Molecular diagnosis and prenatal counseling: SGPGI experience. ***Indian Journal of Pediatrics*** 79: 68-74.
25. Mahali SK and Manna SK (2012). Beta-D-glucoside protects against advanced glycation end products (AGEs)-mediated diabetic responses by suppressing ERK and inducing PPAR gamma DNA binding. ***Biochemical Pharmacology*** 84: 1681-1690.
26. Manna SK (2012). Double-edged sword effect of biochanin to inhibit nuclear factor kappaB: suppression of serine/threonine and tyrosine kinases. ***Biochemical Pharmacology*** 83: 1383-1392.
27. Marbaniang CN and Gowrishankar J (2012). Transcriptional cross-regulation between gram-negative and gram-positive bacteria, demonstrated using ArgP-*argO* of *Escherichia coli* and LysG-*lysE* of *Corynebacterium glutamicum*. ***Journal of Bacteriology*** 194: 5657-5666.
28. Mukhopadhyay S, Nair S and Ghosh S (2012). Pathogenesis in tuberculosis: transcriptomic approaches to unraveling virulence mechanisms and finding new drug targets. ***FEMS Microbiology Reviews*** 36: 463-485.
29. Muley VY and Ranjan A (2012). Effect of reference genome selection on the performance of computational methods for genome-wide protein-protein interaction prediction. ***PLoS One*** 7: e42057.
30. Muranjan M, Agarwal S, Lahiri K and Bashyam M (2012). Novel biochemical abnormalities and genotype in Farber disease. ***Indian Pediatrics*** 49: 320-322.
31. Muteeb G, Dey D, Mishra S and Sen R (2012). A multipronged strategy of an anti-terminator protein to overcome Rho-dependent transcription termination. ***Nucleic Acids Research*** 40: 11213-11228.
32. Narra D and Srivatsava V (2012). Quantitative competitive PCR for the detection and quantification of genetically modified cotton event MON-531. ***International Journal of Basic and Applied Sciences*** 1: 92-102.
33. Padma Priya T and Dalal AB (2012). Tuberous sclerosis: diagnosis and prenatal diagnosis by MLPA. ***Indian Journal of Pediatrics*** 79: 1366-1369.

34. Patil SJ, Bhat V, Dalal A and Santosh JS (2012). Confirmation of the Zechi-Ceide syndrome. ***American Journal of Medical Genetics A*** 158A: 1467-1471.

35. Patil SJ, Ponnala R, Shah S and Dalal A (2012). Mosaic Trisomy 9 presenting with congenital heart disease, facial dysmorphism and pigmentary skin lesions: intricate issues of genetic counseling. ***Indian Journal of Pediatrics*** 79: 806-809.

36. Pidugu VK and Dutta UR (2012). Fluorescence *in situ* hybridization: technology and its illustrated application in molecular medicine. ***Journal of Cytology and Genetics*** 13: 1-8.

37. Pidugu VK, Pothula RKS, Narra D and Srivatsava V (2012). Development of a multiplex polymerase chain reaction method for specific detection of genetically modified cotton events MON 531 and MON 15985. ***International Journal of Basic and Applied Sciences*** 1: 45-53.

38. Ponnala R, Ranganath P, Dutta UR, Pidugu VK and Dalal AB (2012). Phenotypic and molecular characterization of partial trisomy 2q resulting from insertion-duplication in chromosome 18q: a case report and review of literature. ***Cytogenetic and Genome Research*** 136: 229-234.

39. Pradhan BB, Ranjan M and Chatterjee S (2012). XadM, a novel adhesin of *Xanthomonas oryzae* pv. *oryzae*, exhibits similarity to Rhs family proteins and is required for optimum attachment, biofilm formation and virulence. ***Molecular Plant-Microbe Interactions*** 25: 1157-1170.

40. Rai MN, Balusu S, Gorityala N, Dandu L and Kaur R (2012). Functional genomic analysis of *Candida glabrata*-macrophage interaction: role of chromatin remodeling in virulence. ***PLoS Pathogens*** 8: e1002863.

41. Rai R, Ranjan M, Pradhan BB and Chatterjee S (2012). Atypical regulation of virulence-associated functions by a diffusible signal factor in *Xanthomonas oryzae* pv. *oryzae*. ***Molecular Plant-Microbe Interactions*** 25: 789-801.

42. Ramakrishna G, Anwar T, Angara RK, Chatterjee N, Kiran S and Singh S (2012). Role of cellular senescence in hepatic wound healing and carcinogenesis. ***European Journal of Cell Biology*** 91: 739-747.

43. Ramasarma T (2012). A touch of history and a peep into the future of the lipid-quinone known as coenzyme Q and ubiquinone. ***Current Science*** 102: 1459-1471.

44. Ramasarma T (2012). Emergence of oxyl radicals as selective oxidants. ***Indian Journal of Biochemistry & Biophysics*** 49: 295-305.

45. Ramasarma T (2012). In praise of H_2O_2, the versatile ROS, and its vanadium complexes. ***Toxicology Mechanisms and Methods*** 22: 336-346.

46. Ranganath P and Pradhan M (2012). Complete Pentalogy of Cantrell with craniorachischisis: a case report. ***Journal of Prenatal Medicine*** 6: 10-12.

47. Ranganath P, Sharma V, Danda S, Nandineni MR and Dalal A (2012). Novel mutations in the neuraminidase-1 *(NEU1)* gene in two patients of sialidosis in India. ***Indian Journal of Medical Research*** 136: 1048-1050.

48. *Shain AH, Giacomini CP, Matsukuma K, Karikari CA, Bashyam MD, Hidalgo M, Maitra A and Pollack JR (2012). Convergent structural alterations define SWItch/Sucrose NonFermentable (SWI/SNF) chromatin remodeler as a central tumor suppressive complex in pancreatic cancer. ***Proceedings of the National Academy of Sciences of the USA*** 109: E252-E259.

49. Shashni R, Mishra S, Kalayani BS and Sen R (2012). Suppression of *in vivo* Rho-dependent transcription termination defects: evidence for kinetically controlled steps. ***Microbiology*** 158: 1468-1481.

50. Siddiq EA, Vemireddy LR and Nagaraju J (2012). Basmati rices: genetics, breeding and trade. ***Agricultural Research*** 1: 25-36.

51. Singh CP, Singh J and Nagaraju J (2012). A baculovirus-encoded microRNA (miRNA) suppresses its host miRNAs biogenesis by regulating the exportin-5 co-factor Ran. ***Journal of Virology*** 86: 7867-7879.

52. Singh YT, Mazumdar-Leighton S, Saikia M, Pant P, Kashung S, Neog K, Chakravorty R, Nair S, Nagaraju J and Babu CR (2012).

Genetic variation within native populations of endemic silkmoth *Antheraea assamensis* (Helfer) from Northeast India indicates need for *in situ* conservation. ***PLoS One*** 7: e49972.

53. Sinha DK, Nagaraju J, Tomar A, Bentur JS and Nair S (2012). Pyrosequencing-based transcriptome analysis of the Asian rice gall midge reveals differential response during compatible and incompatible interaction. ***International Journal of Molecular Sciences*** 13: 13079-13103.

54. Verma PK, Dalal A, Mittal B and Phadke SR (2012). Utility of MLPA in mutation analysis and carrier detection for Duchenne muscular dystrophy. ***Indian Journal of Human Genetics*** 18: 91-94.

55. Verma PK, Ranganath P, Dalal AB and Phadke SR (2012). Spectrum of lysosomal storage disorders at a medical genetics center in Northern India. ***Indian Pediatrics*** 49: 799-804.

56. Vineeth VS, Malini SS, Sreenivasa G and Dutta UR (2012). High incidence of sperm dysfunction in a varicocele infertile man: case report. ***Asian Pacific Journal of Reproduction*** 1: 63-66.

57. Yonemura N, Tamura T, Uchino K, Kobayashi I, Tatematsu K, Iizuka T, Sezutsu H, Muthulakshmi M, Nagaraju J and Kusakabe T (2012). PhiC31 integrase-mediated cassette exchange in silkworm embryos. ***Molecular Genetics and Genomics*** 287: 731-739.

58. Zargar Z and Tyagi S (2012). Role of host cell factor-1 in cell cycle regulation. ***Transcription*** 3: 187-192.

B. Publications in 2013 (Till March 31, 2013)

59. Beaulieu ED, Ionescu M, Chatterjee S, Yokota K, Trauner D and Lindow S (2013). Characterization of a Diffusible Signaling Factor (DSF) from *Xylella fastidiosa*. ***mBio*** 4: e00539-12.

60. Jadav RS, Chanduri MVL, Sengupta S and Bhandari R (2013). Inositol pyrophosphate synthesis by inositol hexakisphosphate kinase 1 is required for homologous recombination repair. ***Journal of Biological Chemistry*** 288: 3312-3321.

61. Jain MV, Paczulla AM, Klonisch T, Dimgba FN, Rao SB, Roberg K, Schweizer F, Lengerke C, Davoodpour P, Palicharla VR, Maddika S and Los M (2013). Interconnections between apoptotic, autophagic and necrotic pathways: implications for cancer therapy development. ***Journal of Cellular and Molecular Medicine*** 17: 12-29.

62. Kasbekar DP (2013). Neurospora duplications and genome defense by RIP and meiotic silencing. ***Neurospora: Genomics and Molecular Biology***. Editors: DP Kasbekar and K McCluskey, Caister Academic Press, Norfolk, UK. Pages 109-127.

63. Kavela S, Shinde SR, Ratheesh R, Viswakalyan K, Bashyam MD, Gowrishankar S, Vamsy M, Pattnaik S, Rao S, Sastry RA, Srinivasulu M, Chen J and Maddika S (2013). PNUTS functions as a proto-oncogene by sequestering PTEN. ***Cancer Research*** 73: 205-214.

64. Leela JK, Syeda AH, Anupama K and Gowrishankar J (2013). Rho-dependent transcription termination is essential to prevent excessive genome-wide R-loops in *Escherichia coli*. ***Proceedings of the National Academy of Sciences of the USA*** 110: 258-263.

65. Muley VY and Ranjan A (2013). Evaluation of physical and functional protein-protein interaction prediction methods for detecting biological pathways. ***PLoS One*** 8: e54325.

66. Pandey A and Chaterjee S (2013). Signaling in plant-microbe interactions. ***Plant Stress*** 7: 52-59.

67. Permina EA, Medvedeva YA, Baeck PM, Hegde SR, Mande SC and Makeev VJ (2013). Identification of self-consistent modulons from bacterial microarray expression data with the help of structured regulon gene sets. ***Journal of Biomolecular Structure and Dynamics*** 31: 115-124.

68. Sinha A and Nagarajaram HA (2013). Effect of alternative splicing on the degree centrality of nodes in protein-protein interaction networks of *Homo sapiens*. ***Journal of Proteome Research*** 12: 1980-1988.

69. Subbaiah EV, Royer C, Kanginakudru S, Satyavathi VV, Babu AS, Sivaprasad V, Chavancy G, DaRocha M, Jalabert A, Mauchamp B, Basha I, Couble P and Nagaraju J (2013). Engineering silkworms for resistance

to baculovirus through multigene RNA interference. ***Genetics*** 193: 63-75.

C. Publications in Press (as on March 31, 2013)

70. Bairwa G, Balusu S and Kaur R. Aspartyl proteases in human pathogenic fungi: roles in physiology and virulence. ***The Fungal Cell Wall***. Editor: Héctor M Mora-Montes. Nova Science Publishers.

71. Bhat KH, Das A, Srikantam A and Mukhopadhyay S. PPE2 protein of *Mycobacterium tuberculosis* may inhibit nitric oxide in activated macrophages. ***Annals of the New York Academy of Sciences***.

72. Dulla B, Kirla KT, Rathore V, Deora GS, Kavela S, Maddika S, Chatti K, Reiser O, Iqbal J and Pal M. Synthesis and evaluation of 3-amino/ guanidine substituted phenyl oxazoles as a novel class of LSD1 inhibitors with anti-proliferative properties. ***Organic & Biomolecular Chemistry***.

73. Dutta UR, Pidugu VK and Dalal AB. Partial proximal trisomy 14: identification and molecular characterization in a girl with global developmental delay. ***Genetic Counseling***.

74. Dutta UR, Pidugu VK, Goud ChV, Hoefers C, Hagemann M and Dalal A. Identification and molecular cytogenetic characterization of a novel complex Y chromosome rearrangement in a boy with disorder of sexual development. ***Gene***.

75. Dutta UR, Ponnala R, Pidugu VK and Dalal AB. Chromosomal abnormalities in amenorrhea: a retrospective study and review of 637 patients in South India. ***Archives of Iranian Medicine***.

76. Love JM, Prosser D, Love DR, Chintakindi KP, Dalal AB and Aggarwal S. A novel glycine decarboxylase gene mutation in an Indian family with nonketotic hyperglycinemia. ***Journal of Child Neurology***.

77. * Michaud J, Praz V, Faresse NJ, Jnbaptiste CK, Tyagi S, Schutz F and Herr W. HCFC1 is a common component of active human CpG-island promoters and coincides with ZNF143, THAP11, YY1 and GABP transcription factor occupancy. ***Genome Research***.

78. Mohareer K, Sahdev S and Hasnain SE. *Spodoptera frugiperda* FKBP-46 is a consensus p53 motif binding protein. ***Journal of Cellular Biochemistry***.

79. Mulakayala C, Babajan B, Madhusudana P, Anuradha CM, Rao RM, Nune RP, Manna SK, Mulakayala N and Kumar CS. Synthesis and evaluation of resveratrol derivatives as new chemical entities for cancer. ***Journal of Molecular Graphics and Modelling***.

80. Raman R, Kotapalli V, Adduri R, Gowrishankar S, Bashyam L, Chaudhary A, Vamsy M, Patnaik S, Srinivasulu M, Sastry R, Rao S, Vasala A, Kalidindi N, Pollack J, Murthy S and Bashyam M. Evidence for possible non-canonical pathway(s) driven early-onset colorectal cancer in India. ***Molecular Carcinogenesis***.

81. Ranganath P and Dalal AB. Congenital metacarpal pseudoarthrosis, cleft palate, short stature, advanced bone age, and genu valgum: a new syndrome or a variant of Devriendt syndrome? ***Clinical Dysmorphology***.

82. Surapaneni M, Vemireddy L, Begum H, Reddy P, Neetasri C, Nagaraju J, Anwar SY and Siddiq EA. Population structure and genetic analysis of different utility types of mango (*Mangifera indica* L.) germplasm of Andhra Pradesh state of India using microsatellite markers. ***Plant Systematics and Evolution***.

D. Other Publications

1. Arunkumar KP (2012). Review of: Annual Review of Genetics, 2011. Bonnie L. Bassler *et al.* (eds). ***Current Science*** 103: 947-949.

2. Gowrishankar J (2012). Public funding for research projects: roles of experts and finance officials in decision-making. ***Current Science*** 102: 1499.

3. Kasbekar DP (2012). Green-carding the referee and Haldane's spell. ***Journal of Biosciences*** 37: 579.

4. * Kasbekar DP (2012). Lymphohematopoietic licence: sterol C-14 reductase activity of lamin B receptor (Lbr) is essential for neutrophil differentiation. ***Journal of Biosciences*** 37: 199-201.

5. Kasbekar DP (2012). The Sad paradox: mutations with dominant *and* recessive phenotypes. ***Journal of Biosciences*** 37: 933-936.

6. Acharya V and Nagarajaram HA (2013). Response to: Statistical analysis of missense mutation classifiers. ***Human Mutation*** 34: 407.
7. Chatterjee S (2013). Review of: Annual Review of Microbiology, 2011. Susan Gottesman and Caroline S Harwood (eds). ***Current Science*** 104: 653-654.
8. Kasbekar DP (2013). Myth versus mutant: story of *o*. ***Journal of Biosciences*** 38: 1.

* Work done elsewhere

PATENTS

Patents Granted

1. J Nagaraju *et al.* Single tube multiplex assay for detection of adulterants in Basmati rice samples.
   Indian Patent Application No.: 662/CHE/2006
   Indian Patent No.: 251825
   Date of grant: April 10, 2012

RETRACTIONS

During this reporting period, the following papers that were published from CDFD in earlier years were retracted by the respective journals at the request of the authors:

1. *Journal of Clinical Immunology* (2006) 26: 308-322 .
2. *Apoptosis* (2007) 12: 307-318.
3. *Cell Death and Differentiation* (2007) 14: 158-170.
4. *Journal of Cellular Biochemistry* (2009) 107: 203-213.
5. *Journal of Medicinal Chemistry* (2009) 52: 3184-3190.
6. *Breast Cancer Research and Treatment* (2010) 120: 671-683.
7. *Journal of Biological Chemistry* (2010) 285: 5888-5895.
8. *Journal of Biological Chemistry* (2011) 286: 4690-4702.
9. *Journal of Biological Chemistry* (2011) 286: 7339-7347.

मानव संसाधन विकास
Human Resource Development

PhD Program

For the PhD program CDFD invites applications from highly motivated candidates willing to take up challenges in modern biology, usually in the month of March. Keeping in view the interdisciplinary nature of modern biology, the Centre especially encourages persons from different scientific disciplines to take up challenges in these areas. Those admitted as Junior Research Fellows (JRFs) are encouraged to take admission in the PhD program of Manipal University or University of Hyderabad.

The eligibility for the program is MBBS or Masters degree in any branch of Science, Technology or Agriculture from a recognized University or Institute. Candidates (other than MBBS graduates) must have cleared National Eligibility Test (NET) with valid CSIR-JRF or UGC-JRF or DBT-JRF or ICMR-JRF or ICAR-JRF or INSPIRE-PhD or JEST or GATE (All India top 50 ranks of all Chemistry, Life Sciences and Biotechnology streams). Those who have appeared for their final semester examination, but are awaiting results, are also eligible to apply. Those with independent Senior Research Fellowships (SRF) from CSIR can also apply. As the number of applicants outnumbers the seats available each year by a ratio of 1:40 or more, eligible candidates are invited for a written examination followed by interviews of short-listed candidates.

As of March 31, 2013 the Centre has 95 Research Scholars working for their doctorates in different areas of research. In the reporting year 5 of the Research Scholars have completed PhD and are pursuing careers in science elsewhere in India or abroad.

Postdoctoral Program

In addition to the JRF program, the Centre also carries out training at the post-doctoral level. The post-doctoral fellows are funded through the extramural grants that CDFD receives. Some post-doctoral fellows are also selected competitively by the DST fast track young scientist scheme, or the DBT post-doctoral fellowship program.

Summer Training Program

CDFD provides admissions to summer training program to those students who are supported either by the Indian Academy of Science, Bangalore or Jawaharlal Nehru Centre for Advanced Scientific Research, Bangalore or the Kishore Vigyanik Protsahan Yojna, New Delhi. In the reporting year 22 students received summer training at the Centre.

Training for students from BITS, Pilani

CDFD has an agreement with BITS, Pilani to provide project training to their M.Sc. students. Under this programme, the students spend 6 months to 1 year at CDFD and work on active projects being carried out here. The project work helps the students in gaining hands-on experience in modern biology. In the reporting year, 7 students were given the opportunity to avail training under this programme.

Research Scholars Conferred PhD Degree During the Reporting Period

Scholar	Supervisor	Date of *viva voce* examination	Title of thesis
Khalid Hussain Bhat	Sangita Mukhopadhyay	27.04.2012	Regulatory role of *Mycobacterium tuberculosis* PPE proteins on proinflammatory signaling pathway and activation of HIV-1 LTR
Muley Vijay Kumar	Akash Ranjan	26.09.2012	Improved computational prediction and analysis of protein-protein interaction networks
G Sreejit	Sangita Mukhopadhyay	11.10.2012	Functional characterization of *Mycobacterium tuberculosis* proteins involved in modulating macrophage functions
Ghazala Muteeb	Ranjan Sen	11.12.2012	Studies of mechanistic aspects of antitermination of Rho dependent transcription termination
Carmelita N Marbaniang	J Gowrishankar	26.02.2013	ArgP protein of *Escherichia coli*: roles in osmoregulation, gene regulation and inter-relationship with LysG of *Corynebacterium glutamicum*

पुरस्कार एवं सम्मान
Awards and Honours

AWARDS & HONOURS

FACULTY & STAFF	
Dr. M Subba Reddy	1. Senior Innovative Young Biotechnologist Award (2013) 2. Elected as Associate of the Indian Academy of Sciences, Bangalore (2012)
Dr. Sangita Mukhopadhyay	1. Fellowship of the Indian Academy of Sciences, Bangalore (2013) 2. ICMR Kshanika Oration Award (2009) - *announced in 2013*
Dr. J Gowrishankar	1. Padma Shri (2013) 2. Moselio Schaechter Distinguished Service Award of the American Society of Microbiology (2012)
Ms. R Angalena	First prize for poster presentation at the 6th International Conference on Genetic & Molecular Diagnosis in Modern Medicine, Hyderabad (2013)
Dr. Usha Dutta (with Mr. Vijay Kumar P)	First prize for poster presentation & Prof. Askell Love award for best paper presentation at XI All India Conference on Cytology and Genetics, Bangalore (2012)
PhD STUDENTS & PROJECT PERSONNEL	
Mr. Ratheesh Raman	Best poster prize at 2nd Global Cancer Genome Consortium Meeting at ACTREC, Mumbai (2012)
Mr. Vijay Gunasekaran	Second prize for poster presentation at Bangalore India Bio-2012
Mr. Arghya Das	Best poster award at the International Immunology FIMSA Conference, New Delhi (2012)
Mr. Khalid Hussain Bhat	Best oral presentation award at the International Immunology FIMSA Conference, New Delhi (2012)

व्याख्यान, बैठक, कार्यशाला व अन्य महत्वपूर्ण कार्यक्रम

Lectures, Meetings, Workshops and Important Events

DISTINGUISHED VISITORS AND LECTURES

Visitor	Title of Lecture	Date
Dr. Varsha Singh Duke University, USA	Innate immune responses to bacterial pathogens: control by stress response pathways and the nervous system	02.04.2012
Dr. Palani Murugan R University of Cologne, Germany	Sensing, shifting and degradation: regulation of polyamine biosynthesis by novel mechanisms	01.05.2012
Dr Sivakumar Vallabhapurapu University of Cincinnati, USA	Novel insights into the regulation of alternative NF-κB pathway: a promising step towards understanding lymphoid malignancies	02.05.2012
Dr. Vishy Aiyar The University of Texas at Austin, USA	Genomic views of transcriptional and post-transcriptional gene regulation	03.05.2012
Dr. Ravi S Muddashetty Emory University, USA	microRNAs-dynamic modulators of neuronal activity	04.05.2012
Dr. Akanksha Chaturvedi National Institute of Health, USA	Integrating adaptive and innate immune receptor signaling in B cells	07.05.2012
Dr. Atanu Maiti University of Maryland School of Medicine, USA	Mechanism of human TDG in maintaining genetic and epigenetic integrity	21.05.2012
Dr. Sailu Yellaboina C R Rao AIMSCS Hyderabad, India	Integrating genomic datasets: embryonic stem cells and cancer	13.06.2012
Dr. Kiran Kulkarni Institute of Cancer Research, UK	Mechanistic insights into the regulation of cell cycle and cell migration	13.07.2012
Dr. Rajeshwar Rao Tekmal University of Texas Health Science Centre, USA	Therapeutic use of selective estrogen receptor modulators in human malignancies	17.07.2012
Dr. Deepak Kaushal Tulane National Primate Research Centre, USA	Genetic requirements for the survival of tubercle bacilli in primate lungs	20.07.2012
Dr. Ramanujam Srinivasan University of Singapore, Singapore	Fission yeast: a cellular playground for bacterial cytoskeletal proteins	31.07.2012
Dr. Sandip Kar German Cancer Research Center, Germany	An insight to mathematical and computational modeling in biology	31.08.2012
Dr. Nita Sachan Indian School of Business, Hyderabad, India	Innovation and technology commercialization: what's in it for you?	05.09.2012

Visitor	Title of Lecture	Date
Ms. Amita Desai & **Dr. Monika Sharma** German Research Foundation, Hyderabad, India	Funding opportunities for Indo-German research co-operation	04.10.2012
Dr. B Ravindran Institute of Life Science, Bhubaneswar, India	Did malaria contribute to evolution of TLR mediated inflammation in primates?	15.10.2012
Dr. Abul Arif Lerner Research Institute Cleveland Clinic, USA	Noncanonical role of aminoacyl-tRNA synthetases in regulation of gene expression, inflammation and metabolism	08.11.2012
Prof. Adam J Bogdanove Cornell University, USA	TAL effectors of Xanthomonas: a plant pathogenic bacterium delivers powerful tools to manipulate the eukaryotic genome	01.12.2012
Dr. Nick Leslie University of Dundee, UK	PTEN and PI 3-kinase signaling in cancer	03.12.2012
Dr. Syed Raza Ali University of California, USA	Novel treatments against bacterial infections	05.12.2012
Dr. Ramana Davuluri The Wistar Institute, USA	Isoform-level gene regulation: implications in development and disease	10.12.2012
Dr. Devyani Haldar Dr. Reddy's Institute of Life Sciences, Hyderabad, India	Role of histone acetylation/deacetylation in DNA metabolism	19.12.2012
Prof. Rajendra Prasad Jawaharlal Nehru University, Delhi, India	A systemic study of a major multidrug ABC transporter CDR1 of Candida	11.01.2013
Prof. Ajit Varki University of California, USA	Uniquely human changes in sialic acid biology: implications for evolution, immunity and disease	05.02.2013
Dr. James Chelliah Scripps Research Institute, USA	Pathogenic SYNGAP1 mutations impair cognitive development by disrupting the maturation of dendritic spines	06.02.2013
Dr. Paras K Anand St. Jude Children's Research Hospital, USA	Nod-like receptors in pathogen recognition and host defense	18.02.2013
Dr. Amitabha Majumdar Stowers Institute for Medical Research, USA	The role of a self-sustaining amyloidogenic protein in persistence of memory	25.02.2013
Dr. Deepti Jain National Centre for Biological Sciences, Bangalore, India	Functional complexes of prokaryotic transcription modulators: structures and mechanisms	26.03.2013

IMPORTANT EVENTS

Event	Partnering Institutions	Date
Institutional Bioethics Committee Meeting		19.04.2012
Arrival of Prof Kazuei Mita as Distinguished Visiting Professor from NIAS, Japan		09.05.2012
Exposure visit for in-service Biology teachers of Kendriya Vidyalaya Sangathan		17.05.2012
Fire drill		30.05.2012 - 31.05.2012
Summer Trainee's Colloquium		22.06.2012
MoU with Government of Andhra Pradesh (Crime Investigation Department and Andhra Pradesh Forensic Science Laboratory) to provide DNA fingerprinting services and training to the state	APFSL, CID and CDFD	11.07.2012
Visit of IPS officers under the Vertical Interaction Course organized by ASCI, Hyderabad		01.08.2012
14th Meeting of CDFD Research Area Panels-Scientific Advisory Committee (RAP-SAC)		03.08.2012 - 04.08.2012
Independence Day celebrations		15.08.2012
Official Language Implementation Committee (OLIC) Meeting		22.08.2012
Hindi Pakhwada Celebrations		03.09.2012 - 14.09.2012
Education tour by B.Sc. students from Avinasilingam University for Women, Coimbatore		21.09.2012
Dinner hosted in honour of Prof. Jules A Hoffmann, Nobel Laureate in Physiology or Medicine (2011)	IFCPAR and CDFD	10.10.2012

Event	Partnering Institutions	Date
Video-shooting for a science popularization television serial titled 'Temples of Modern India'	Pulse Media Pvt. Ltd., Vigyan Prasar and CDFD	10.10.2012 - 11.10.2012
Education tour by students from Dr DY Patil University, Navi Mumbai		12.10.2012
Mini-Symposium	Wellcome Trust-DBT India Alliance and CDFD	13.10.2012
Exposure visit for students and faculty from KV Pendharkar College, Pune		29.10.2012
26th Meeting of CDFD Finance Committee		31.10.2012
20th Meeting of CDFD Building Committee		31.10.2012
32nd Meeting of CDFD Governing Council		31.10.2012
17th Meeting of CDFD Society		08.12.2012
Seminar Workshop on Microbial Biology	CCMB and CDFD	11.12.2012 - 14.12.2012
Republic Day celebrations		26.01.2013
CDFD Foundation Day celebrations		29.01.2013
Educational tour by students of M.Sc.(Nursing) from Nizam's Institute of Medical Sciences, Hyderabad		15.02.2013
Educational tour by scholars from the Department of Biotechnology, Kathmandu University, Nepal		25.02.2013
Exposure visit for post graduate students of Microbiology from Aurora's Degree and P.G. College, Hyderabad		25.03.2013

सी डी एफ डी कर्मचारियों की विदेशों में प्रतिनियुक्ति

Deputations Abroad of CDFD Personnel

DEPUTATIONS ABROAD - FACULTY & STAFF

Faculty/Staff	Period	Country of Visit and Purpose
J Gowrishankar	13.06.2012 to 21.06.2012	**USA:** (i) Visit to the University of Pittsburgh, Pittsburg as part of NIH-funded collaboration between the University and CDFD (ii) to attend the Annual General Meeting of the American Society for Microbiology (ASM) at San Francisco where he was conferred with the Moselio Schaechter Distinguished Service Award of the ASM (iii) to visit the University of California.
	16.08.2012 to 28.08.2012	**USA:** (i) Presentation of research work at the Cold Spring Harbor Laboratory (CSHL) meeting on "Bacteria, Archaea & Phages" (ii) to visit the University of Illinois College of Medicine at Chicago, The Baylor College of Medicine at Houston, and Columbia University Medical Center at New York.
	14.03.2013 to 21.03.2013	**Taiwan:** Visit to the laboratory of Prof. Sue Lin-Chao at the Institute of Molecular Biology, Academia Sinica, Taipei.
J Nagaraju	05.04.2012 to 09.04.2012	**China:** Asia-Pacific Congress of Sericulture and Insect Biotechnology (APSERI-2012) in Southwest University, Chongqing.
	17.08.2012 to 26.08.2012	**South Korea**: 24th International Congress of Entomology (ICE 2012) organized by the International Atomic Energy Agency (IAEA) at Daegu.
	29.09.2012 to 10.10.2012	**Austria and Czech Republic:** (i) Meeting on "Exploring mechanical, molecular, behavioral or genetic methods of sex separation in mosquitoes" in Vienna (ii) Visit to the Laboratory of Molecular Cytogenetics at the Institute of Entomology, Budejovice.
	07.11.2012 to 23.11.2012	**USA:** (i) Visit to the Department of Biological Sciences Columbia University, New York (ii) Annual Meeting organized by the Entomological Society of America at Knoxville, Tennessee (iii) Visit to the Department of Integrative Biology, Center for Theoretical Evolutionary Genomics, University of California, Berkeley (iv) Visit to the Prosetta Corporation, San Francisco.
Ranjan Sen	04.06.2012 to 10.06.2012	**South Korea:** 12th Asian Conference on Transcription at Jeju Island.

Faculty/Staff	Period	Country of Visit and Purpose
MD Bashyam	31.03.2012 to 12.04.2012	**USA:** (i) AACR annual meeting in Chicago (ii) to interact with Dr. Ramana Davuluri at the Wistar Institute at Philadelphia (iii) to meet Dr. YD Ramu at the University of Pennsylvania.
	From 04.01.2013 (for 5 months)	**USA:** Visit to the laboratory of Dr. Ramana Davuluri at Wistar Institute, Philadelphia to learn next generation sequencing under the ICMR International fellowship program.
HA Nagarajaram	08.09.2012 to 13.09.2012	**Switzerland:** European Conference on Computational Biology - 12 at Basel.
Rupinder Kaur	27.03.2012 to 04.04.2012	**USA:** 11th ASM Conference on Candida and Candidiasis in San Francisco, California.
	09.06.2012 to 17.06.2012	**Germany:** 18th Congress of the International Society for Human and Animal Mycology 2012 at Berlin.
N Madhusudan Reddy	23.04.2012 to 10.06.2012	**Germany:** Research work in the Department of Evolutionary Genetics, Max Plank Institute for Evolutionary Anthropology, Leipzig as part of the Max Plank Partner Group Programme.
	11.06.2012 to 13.06.2012	**Indonesia:** Second Asia-Pacific Meeting of Medico-Legal Institutes and Agencies at the Jakarta Centre for Law Enforcement Cooperation (JCLEC) Complex, Semarang.
	24.11.2012 to 30.11.2012	**Thailand:** (i) 4th Asian Forensic Science Network Annual Meeting and Symposium 2012 (ii) Multidisciplinary Forensic Identification Meeting (iii) The Asian Multidisciplinary Forensic Network Meeting and Symposium.
Subhadeep Chatterjee	28.07.2012 to 02.08.2012	**Japan:** XV International Congress on Molecular Plant-Microbe Interactions (IS-MPMI) at Kyoto.
K Anupama	23.06.2012 to 29.06.2012	**USA:** Conference on Post – Transcriptional Control of Gene Expression: Mechanisms of mRNA Decay at Steamboat Springs, Colorado.
	20.02.2013 to 01.03.2013	**Taiwan:** Visit to the laboratory of Prof. Sue Lin-Chao at the Institute of Molecular Biology, Academia Sinica, Taipei.
Rohit Joshi	03.11.2012 to 12.11.2012	**Netherlands:** Conference on Stem Cells, Development and Differentiation in Amsterdam.

Faculty/Staff	Period	Country of Visit and Purpose
Arun Kumar KP	21.07.2012 to 01.08.2012	**USA:** Workshop on "Molecular evolution" at the Marine Biological Laboratory, Woods Hole, Massachusetts.
	19.09.2012 to 20.10.2012	**Czech Republic:** Visit to the Institute of Entomology, Budejovice for collaborative research on the project entitled "Comparative genetic analysis of sex chromosomes and sex determining genes in silkmoths".
	13.02.2013 to 17.02.2013	**France:** Workshop on "Lepidoptera adaptation: biology and genome" followed by a meeting on *Spodoptera frugiperda*.
	03.03.2013 to 09.03.2013	**Japan:** Visit to the University of Tokyo, Tokyo and National Institute of Agro-biological Sciences, Tsukuba under Indo-Japan Cooperative Science Programme.
MV Subba Reddy	21.02.2013 to 04.03.2013	**USA:** Keystone Symposia on Molecular and Cellular Biology at Colorado.
Usha Rani Dutta	16.07.2012 to 12.10.2012	**Germany:** DAAD re-invitation programme for former scholarship holders at Berlin.
Hole Jayant Pundalikrao	26.11.2012 to 02.12.2012	**Italy:** Training course on "Facility planning logistics and technological solutions" at Fondazione Guido Bernardini (FGB) Foundation at Milan.
Nirupama Chatterjee	22.10.2012 to 27.10.2012	**Japan:** Poster presentation in Keystone Symposia on "Ageing and diseases of ageing" at Tokyo.

DEPUTATIONS ABROAD - STUDENTS

Name of the Scholar	Period	Country of Visit and Purpose
Jamshaid Ali	14.05.2012 to 18.05.2012	**Germany:** 8th Annual BioMalPar|EVIMalaR Conference on "Biology and Pathology of the Malaria Parasite".
Gaurav Bairwa	31.07.2012 to 05.08.2012	**USA:** GSA meeting on "Yeast Genetics and Molecular Biology".
Pandilla Ramaswamy	14.08.2012 to 18.08.2012	**USA:** Conference on "Mechanisms and Models of Cancer".
L Shanthy	21.08.2012 to 25.08.2012	**USA:** Conference on "Bacteria, Archaea & Phages".
Carmelita N Marbaniang	03.09.2012 to 05.09.2012	**United Kingdom:** SGM Autumn Conference 2012.
Anupam Sinha	08.09.2012 to 12.09.2012	**Switzerland:** 11th European Conference of Computational Biology.
Vandana	22.09.2012 to 24.10.2012	**Japan:** Visit to the National Institute for Basic Biology to carry out replications for constructing 3D-pool of silkworm BAC library for PCR screening of W chromosome.
Anujit Sarkar	25.11.2012 to 30.11.2012	**Thailand:** 4th Asian Forensic Sciences Network Annual Meeting and Symposium 2012.
Maruti Nandan Rai	13.01.2013 to 18.01.2013	**USA:** Gordon Research Conference-Immunology of Fungal Infections.
Sawanth S Kumar	03.03.2013 to 30.03.2013	**Japan:** Visit to the University of Tokyo and National Institute of Agrobiological Sciences under DST sponsored Indo-Japan Cooperative Science Programme.

सीडीएफडी के संकाय एवं अधिकारी
Faculty and Officers of CDFD

SCIENTIFIC GROUP LEADERS (FACULTY)

Dr. J Gowrishankar

Dr. J Nagaraju (deceased 31.12.2012)

Dr. DP Kasbekar

Dr. Ranjan Sen

Dr. Sunil Kumar Manna

Dr. Sangita Mukhopadhyay

Dr. MD Bashyam

Dr. HA Nagarajaram

Dr. Akash Ranjan

Dr. Sanjeev Khosla

Dr. Gayatri Ramakrishna (till 28.09.2012)

Dr. Rupinder Kaur

Dr. Ashwin B Dalal

Dr. Rashna Bhandari

Dr. Madhusudan R Nandineni

Dr. Subhadeep Chatterjee

Dr. Abhijit A Sardesai

Dr. R Harinarayanan

Dr. Shweta Tyagi

Dr. Rohit Joshi

Dr. MV Subba Reddy

Dr. Arun Kumar KP

ADJUNCT FACULTY

Prof. EA Siddiq

Prof. T Ramasarma

Prof. Anuradha Lohia

Dr. Renu Wadhwa

Dr. Prajnya Ranganath

Dr. Shagun Agarwal

OTHER GROUP LEADERS

Mr. Raghavendrachar J

Ms. M Kavita Rao

Dr. Ankkur Goel

SENIOR ADMINISTRATIVE STAFF

Mr. J Sanjeev Rao

Mr. B Jagannathacharyulu

केन्द्र की समितियाँ

(31.03.2013 तक)

Committees of the Centre

(As on 31.03.2013)

MEMBERS OF CDFD SOCIETY

Shri S Jaipal Reddy Hon'ble Minister for S&T and Earth Sciences	-	President
Prof K VijayRaghavan Secretary, DBT, New Delhi	-	Member
Prof Samir K Brahmachari Director General, CSIR, New Delhi	-	Member (Ex-officio)
Prof P Balaram Director, IISc, Bangalore	-	Member (Ex-officio)
Prof VS Chauhan Director, ICGEB, New Delhi	-	Member
Prof Dipankar Chatterji IISc, Bangalore	-	Member
Shri MK Sharma Addl. Secretary, Ministry of Law, New Delhi (Nominee of Joint Secretary & Legal Adviser, MoL)	-	Member (Ex-officio)
Shri Sanjay Goel Director (Finance), DBT, New Delhi (Nominee of Joint Secretary & Financial Advisor, DBT)	-	Member (Ex-officio)
Shri SP Sharma Principal Scientific Officer BPR&D, New Delhi (Nominee of DG, BPR&D)	-	Member (Ex-officio)
Joint Secretary (PM) Ministry of Home Affairs, New Delhi	-	Member (Ex-officio)
Dr Suman Govil Advisor, DBT, New Delhi	-	Member (Ex-officio)
Dr J Gowrishankar Director, CDFD, Hyderabad	-	Member Secretary

MEMBERS OF CDFD GOVERNING COUNCIL

Prof K VijayRaghavan Secretary, DBT, New Delhi	-	Chairperson
Prof Samir K Brahmachari Director General, CSIR, New Delhi	-	Member (Ex-officio)
Prof P Balaram Director, IISc, Bangalore	-	Member (Ex-officio)
Prof VS Chauhan Director, ICGEB, New Delhi	-	Member
Prof Dipankar Chatterji IISc, Bangalore	-	Member
Shri MK Sharma Addl. Secretary, Ministry of Law, New Delhi (Nominee of Joint Secretary & Legal Adviser)	-	Member (Ex-officio)
Dr CN Bhattacharya Ministry of Home Affairs, New Delhi (Nominee of Joint Secretary (PM))	-	Member (Ex-officio)
Ms Anuradha Mitra Joint Secretary & Financial Advisor DBT, New Delhi	-	Member (Ex-officio)
Dr JR Gaur Principal Scientific Officer, BPR&D, New Delhi (Nominee of DG, BPR&D)	-	Member (Ex-officio)
Dr Suman Govil Advisor, DBT, New Delhi	-	Member (Ex-officio)
Dr J Gowrishankar Director, CDFD, Hyderabad	-	Member Secretary

MEMBERS OF CDFD RESEARCH AREA PANELS – SCIENTIFIC ADVISORY COMMITTEE (RAP-SAC)

Prof P Balaram Director, IISc, Bangalore	-	Chairman
Dr Ramakrishna Ramaswamy UoH, Hyderabad	-	Member
Dr Veena Parnaik CCMB, Hyderabad	-	Member
Dr SK Apte BARC, Mumbai	-	Member
Dr Ghanshyam Swarup CCMB, Hyderabad	-	Member
Dr Sandhya S Visweswaraiah IISc, Bangalore	-	Member
Dr Usha Vijayraghavan IISc, Bangalore	-	Member
Prof Sanjeev Galande IISER, Pune	-	Member
Dr Chetan E Chitnis ICGEB, New Delhi	-	Member
Dr Jaya Sivaswami Tyagi AIIMS, New Delhi	-	Member
Dr Joyoti Basu Bose Institute, Kolkata	-	Member
Dr Debasisa Mohanty NII, New Delhi	-	Member
Dr MK Mathew NCBS, Bangalore	-	Member
Dr Shubha R Phadke SGPGI, Lucknow	-	Member
Prof Umesh Varshney IISc, Bangalore	-	Member

Dr Suman Govil DBT, New Delhi (Nominee of DBT)	-	Member
Dr KV Prabhu NBPGR, New Delhi (Nominee of Director General, ICAR)	-	Member
Dr Vijay Kumar ICMR, New Delhi (Nominee of Director General, ICMR)	-	Member
Dr S Sathyan CFSL, Hyderabad (Nominee of Ministry of Home Affairs)	-	Member
Dr J Gowrishankar Director, CDFD, Hyderabad	-	Member Secretary

MEMBERS OF CDFD ACADEMIC COMMITTEE

Prof AS Raghavendra Dean, School of Life Sciences University of Hyderabad, Hyderabad	-	Chair
Prof Anil K Tyagi University of Delhi, South Campus, New Delhi	-	Member
Dr K Satyamoorthy Director, Manipal Life Sciences Centre Manipal University, Manipal	-	Member
Dr DP Kasbekar Haldane Chair, CDFD, Hyderabad	-	Member
Dr Ranjan Sen Staff Scientist, CDFD, Hyderabad	-	Member
Dr Sanjeev Khosla Staff Scientist & Co-ordinator (Academics) CDFD, Hyderabad	-	Member Convenor

MEMBERS OF THE INSTITUTIONAL BIO-SAFETY COMMITTEE

*** Dr J Nagaraju** Staff Scientist, CDFD, Hyderabad (Nominee of Director, CDFD)	-	Chairperson
Dr Rupinder Kaur Staff Scientist, CDFD, Hyderabad	-	CDFD Expert
Dr N Madhusudan Reddy Staff Scientist, CDFD, Hyderabad	-	CDFD Expert
Dr Ashwin Dalal Staff Scientist, CDFD, Hyderabad	-	Member with medical qualifications
Dr Imran Siddiqi Scientist, CCMB, Hyderabad	-	Outside Expert
Dr S Shivaji Scientist, CCMB, Hyderabad	-	DBT Nominee

*deceased Dec. 31, 2012

MEMBERS OF CDFD BUILDING COMMITTEE

Prof VS Chauhan Director, ICGEB, New Delhi	-	Chairman
Dr J Gowrishankar Director, CDFD, Hyderabad	-	Member
Shri S Raghavan Joint Secretary, DBT, New Delhi	-	Member
Shri VH Rao Senior Consultant, NIAB, Hyderabad	-	Member
Shri J Sanjeev Rao Head-Administration, CDFD, Hyderabad	-	Member
Shri BJ Acharyulu Head-F&A, CDFD, Hyderabad	-	Member
Shri K Ananda Rao Senior Consultant (Engg.), CDFD, Hyderabad	-	Member Convenor

MEMBERS OF CDFD MANAGEMENT COMMITTEE

Dr J Gowrishankar Director, CDFD, Hyderabad	-	Chairman
Dr J Nagaraju Staff Scientist, CDFD, Hyderabad	-	Member (deceased Dec. 31, 2012)
Dr DP Kasbekar Haldane Chair, CDFD, Hyderabad	-	Member (since Jan. 2013)
Dr Ranjan Sen Staff Scientist, CDFD, Hyderabad	-	Member
Dr MV Subba Reddy Staff Scientist, CDFD, Hyderabad	-	Member
Shri BJ Acharyulu Head-F&A, CDFD, Hyderabad	-	Member
Shri J Sanjeev Rao Head-Administration, CDFD, Hyderabad	-	Member Convenor

MEMBERS OF CDFD FINANCE COMMITTEE

Dr VS Chauhan Director, ICGEB, New Delhi	-	Chairman
Ms Anuradha Mitra JS&FA, DBT, New Delhi	-	Member (Ex-officio)
Dr Suman Govil Advisor, DBT, New Delhi (Nominee of Senior Scientist, DBT, New Delhi)	-	Member (Ex-officio)
Prof Dipankar Chatterji IISc, Bangalore	-	Member
Dr J Gowrishankar Director, CDFD, Hyderabad	-	Member
Shri BJ Acharyulu Head-F&A, CDFD, Hyderabad	-	Member Secretary

MEMBERS OF SEXUAL HARASSMENT COMPLAINTS COMMITTEE

Dr Gayatri Ramakrishna Staff Scientist, CDFD, Hyderabad	-	Chairperson (till Sep. 2012)
Shri J Sanjeev Rao Head-Administration, CDFD, Hyderabad	-	Member
Ms V Naga Sailaja Technical Officer, CDFD, Hyderabad	-	Member
Ms MV Sukanya Technical Officer, CDFD, Hyderabad	-	Member
Shri MSA Zaman Khan Section Officer, CDFD, Hyderabad	-	Member
Ms P Jamuna Gramya Resource Centre for Women, Hyderabad (Representing an NGO)	-	Member

सूचना अधिकार अधिनियम, 2005 का परिपालन
Implementation of RTI Act, 2005

IMPLEMENTATION OF RTI ACT, 2005

Appellate Authority: **J Sanjeev Rao**

Central Public Information Officer: **M Kavita Rao**

Quarter: 1st Quarter Year 2012-2013

Details about the requests and appeals

Progress during Quarter						
	Opening Balance as on beginning of 1st quarter	No. of applications received as transfer from other PAs u/s 6(3)	Received during the quarter (including cases transferred to other PAs)	No. of cases transferred to other PAs u/s 6(3)	Decisions where requests/appeals rejected	Decisions where requests/appeals accepted
Requests	0	0	9	0	1	5
First Appeals	0	N/A	0	N/A	0	0
	Total No. of CAPIOs designated		Total No. of CPIOs designated		Total No. of AAs designated	
	0		1		1	

Block-II Details about fee collected, penalty imposed and disciplinary action taken			
Registration Fee Collected (in Rs.) u/s 7(1)	Addl. Fee Collected (in Rs.) u/s 7(3)	Penalty Amount Recovered (in Rs.) as directed by CIC u/s 20(1)	No. of cases where disciplinary action taken against any officer u/s 20(2)
80	310	0	0

Quarter: 2nd Quarter Year 2012-2013

Progress during Quarter						
	Opening Balance as on beginning of 2nd quarter	No. of applications received as transfer from other PAs u/s 6(3)	Received during the quarter (including cases transferred to other PAs)	No. of cases transferred to other PAs u/s 6(3)	Decisions where requests/appeals rejected	Decisions where requests/appeals accepted
Requests	3	0	16	0	0	15
First Appeals	0	N/A	2	N/A	1	1
	Total No. of CAPIOs designated		Total No. of CPIOs designated		Total No. of AAs designated	
	0		1		1	

Block II - Details about fee collected, penalty imposed and disciplinary action taken			
Registration Fee Collected (in Rs.) u/s 7(1)	Addl. Fee Collected (in Rs.) u/s 7(3)	Penalty Amount Recovered (in Rs.) as directed by CIC u/s 20(1)	No. of cases where disciplinary action taken against any officer u/s 20(2)
160	98	0	0

Quarter: 3rd Quarter Year 2012-2013

Progress during Quarter						
	Opening Balance as on beginning of 3rd quarter	No. of applications received as transfer from other PAs u/s 6(3)	Received during the quarter (including cases transferred to other PAs)	No. of cases transferred to other PAs u/s 6(3)	Decisions where requests/appeals rejected	Decisions where requests/appeals accepted
Requests	4	0	5	0	4	5
First Appeals	0	N/A	3	N/A	2	0
	Total No. of CAPIOs designated		Total No. of CPIOs designated		Total No. of AAs designated	
	0		1		1	

Details about fee collected, penalty imposed and disciplinary action taken			
Registration Fee Collected (in Rs.) u/s 7(1)	Addl. Fee Collected (in Rs.) u/s 7(3)	Penalty Amount Recovered (in Rs.) as directed by CIC u/s 20(1)	No. of cases where disciplinary action taken against any officer u/s 20(2)
50	0	0	0

Quarter: 4th Quarter Year 2012-2013

Progress during Quarter						
	Opening Balance as on beginning of 4th quarter	No. of applications received as transfer from other PAs u/s 6(3)	Received during the quarter (including cases transferred to other PAs)	No. of cases transferred to other PAs u/s 6(3)	Decisions where requests/appeals rejected	Decisions where requests/appeals accepted
Requests	0	1	3	0	0	4
First Appeals	0	N/A	1	N/A	1	0
	Total No. of CAPIOs designated		Total No. of CPIOs designated		Total No. of AAs designated	
	0		1		1	

Details about fee collected, penalty imposed and disciplinary action taken			
Registration Fee Collected (in Rs.) u/s 7(1)	Addl. Fee Collected (in Rs.) u/s 7(3)	Penalty Amount Recovered (in Rs.) as directed by CIC u/s 20(1)	No. of cases where disciplinary action taken against any officer u/s 20(2)
30	0	0	0

बजट एवं वित्त
Budget and Finance

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS HYDERABAD

Budget & Finance 2012-13

Sources of Funds

The Financial resources of the Centre are the Core Plan Grant-in Aid provided by the Department of Biotechnology, Government of India as against Annual Budgetary projections made by the Institute. Other resources are in the form of Research Grants provided by various National and International agencies and also from Services rendered by CDFD. The components of the core grants are Plan (Recurring) essentially for meeting expenditures on salaries, Operating expenses etc., and Plan (Non-Recurring) for meeting expenses on account of Equipments, Infrastructure and Furnishing etc.,

Receipts during the year 2012-13

Particulars	Amount in Lakhs	Percentage- %
Plan Grant in Aid	3900.00	85.33
Sponsored Projects	586.52	12.83
CDFD Services	35.71	0.79
Misc Receipts	48.20	1.05
Total	**4570.43**	**100.00**

I. Application of Funds during 2012-13 (Plan Grant-in-Aid)

S.No.	Particulars	Amount in Lakhs	Percentage- %
1	**Recurring**		
	Salaries & Wages	949.37	23.16
	Operating Exp	1556.16	37.96
	Total	**2505.53**	**61.12**
2	**Non-Recurring**		
	Equipments,		
	Infrastructure & Furnishing	1593.81	38.88
	Total	**1593.81**	**38.88**
	Grand Total	**4099.34**	**100.00**

II. Application of Funds during 2012-13 (Extra Mural Projects)

S No	Particulars	Amount in Lakhs	Percentage- %
1	**Recurring**		
	Salaries & Wages	318.15	30.94
	Operating Exp	612.76	59.60
	Total	**930.91**	**90.54**
2	**Non-Recurring**		
	Equipments	97.29	9.46
	Total	**97.29**	**9.46**
	Grand Total	**1028.20**	**100.00**

लेखा परिक्षक की रिपोर्ट
Auditor's Report

K R Srinivasan & Co

Chartered Accountants

AUDITOR'S REPORT

Date: 04-07-2013

The Director,
Centre for DNA Fingerprinting and Diagnostics,
Nampally, Hyderabad - 500 001

We have audited the attached Balance Sheet of CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, Hyderabad, as at 31st March 2013 and also the Income & Expenditure Account for the year ended on that date annexed there to. These financial statements are the responsibility of the organization management. Our responsibility is to express an opinion on these financial statements based on our audit.

We report that:

1. We have obtained all the information and explanations, which are to the best of our knowledge and belief, were necessary for the purpose of our audit.
2. In our opinion, the organization has kept proper books of account as required by law so far, as appears from our examination of those books.
3. The Balance sheet and Income & Expenditure account dealt with by this report is in agreement with the books of account.
4. (a) The centre has maintained accounts on Accrual basis.

   (b) The Centre receives extra mural grants from various National & International agencies for specific research activities. The Centre has a policy of allocating the overheads and transfer of expenditure of CDFD to different projects at the end of the financial year after taking into account the amount of maximum permissible limit of overheads and also based on the approved budget estimates of the respective projects during the financial year.
5. In our opinion and to the best of our information and according to the explanations given to us, the said Balance sheet and the Income & Expenditure account read together with the notes thereon gives the required information in the manner so required and give a true and fair view.

   a) In so far it relates to the Balance sheet as at 31st March 2013 and

   b) In so far as it relates to the Income & Expenditure account excess of expenditure over income for the year ended on 31st March 2013.

for **K R Srinivasan & Co**
Chartered Accountants

Sd/-
[K R SRINIVASAN]

Place: Hyderabad
Date: 04/07/2013

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

BALANCE SHEET AS ON 31st MARCH, 2013

(Amount - Rs.)

CORPUS/CAPITAL FUND AND LIABILITIES	Schedule	Current Year	Previous Year
Corpus / Capital Fund	1	1142536939.00	996575609.00
Reserves and Surplus	2	0.00	276778938.00
Earmarked / Endowment funds	3	6531021.00	50698171.00
Secured Loans & Borrowings	4	0.00	0.00
Unsecured Loans & Borrowings	5	0.00	0.00
Deffered Credit Liabilities	6	0.00	0.00
Current Liabilities and Provisions	7	64750516.00	64107025.00
TOTAL		**1213818476.00**	**1388159744.00**
ASSETS			
Fixed Assets	8	932133417.00	1025989243.00
Investments- From Earmarked / Endowment Funds	9	62398273.00	62398273.00
Investments - Others	10	25159583.00	29159376.00
Current Assets, Loans, Advances etc.	11	194127203.00	270612851.00
TOTAL		**1213818476.00**	**1388159744.00**
Significant Accounting Policies	24		
Contingent Liabilities and Notes on Accounts	25		

DIRECTOR
CDFD

For K R SRINIVASAN & CO
CHARTERED ACCOUNTANTS
(K R SRINIVASAN)

HEAD - FINANCE & ACCOUNTS
CDFD

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

INCOME AND EXPENDITURE ACCOUNT FOR THE YEAR ENDING 31st MARCH, 2013 (Amount - Rs.)

INCOME	Schedule	Current Year	Previous Year
Income from Sales/Services	12	3571262.00	3158471.00
Grants/Subsides	13	210000000.00	210200000.00
Fees/Subscriptions	14	0.00	0.00
Income from Investments	15	2768470.00	10566572.00
Income from Royality, Publications etc.	16	0.00	0.00
Interest Earned	17	700706.00	1254141.06
Other Income	18	1350941.00	2842632.60
Increase/(decrease) in stock of Finished goods and works-in-progress	19	0.00	0.00
TOTAL (A)		**218391379.00**	**228021816.66**
EXPENDITURE			
Establishment Expenses	20	94843804.00	80052399.00
Administrative Expenses	21	143988338.00	143212816.86
Expenditure on Grants, Subsides etc.	22	0.00	0.00
Interest	23	0.00	0.00
Depreciation (Net Total at the year-end -corresponding to Schedule 8)		21763702.00	0.00
Less:Transferred to Grants-in-Aid		21763702.00	0.00
Provision For Salaries		6932849.00	0.00
TOTAL (B)		**245764991.00**	**223265215.86**
Balance being excess of Income over Expenditure (A-B)		-27373612.00	674552248.38
Transfer to Special Reserve (Specify each)			
Transfer to/from General Reserve			
BALANCE BEING SURPLUS/(DEFLICT) CARRIED TO CORPUS/CAPITAL FUND			
SIGNIFICANT ACOUNTING POLICIES	24		
CONTINGENT LIABILITIES AND NOTES ON ACCOUNTS	25		

DIRECTOR
CDFD

For K R SRINIVASAN & CO
CHARTERED ACCOUNTANTS
(K R SRINIVASAN)

HEAD - FINANCE & ACCOUNTS
CDFD

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

RECEIPTS AND PAYMENTS ACCOUNT FOR THE YEAR ENDED 31st MARCH 2013

(Amount - Rs.)

RECEIPTS	Current Year	Previous Year	PAYMENTS	Current Year	Previous Year
1.Opening Balances			**1. Expenses**		
a) Cash in hand	0.00	160550.00	a) Establishment Expenses (corresponding to Schedule 20)	94843804.00	80052399.00
b) Bank Balances			b) Administrative Expenses (corresponding to Schedule 21)	143988338.00	143212816.86
i) In current accounts	12333378.80	55687650.25	c) Schedule 22	0.00	0.00
ii) In deposit accounts	0.00	0.00			
iii) Savings accounts	73301897.29	7645412.22			
2.Grants Received			**2. Payments made against funds for various projects**		
a) From Government of India	390000000.00	380200000.00	(Name of the fund or project should beshown along with the		
b) From State government	0.00	0.00	particulars of payments made for each project)		
c) From other sources (details)			Projects (Annexure F)	102820071.00	154943838.00
(Grants for capital & revenue exp. To be shown seperately)			CSIR(Stipend)	12496276.00	10949949.00
			DBT(Stipend)	4595379.00	3239590.00
Research Associates - CSIR(Stipend)	13650331.00	5197614.00	DST(Stipend)	527012.00	247039.00
Research Associates - DBT(Stipend)	1292280.00	3477790.00	ICMR(Stipend)	2079781.00	1879593.00
Research Associates - DST(Stipend)	250400.00	250400.00	IISC(Stipend)	3083960.00	1869165.00
Research Associates - ICMR(Stipend)	2422008.00	665590.00	UGC(Stipend)	5164427.00	4282140.00
Research Associates - IISC(Stipend)	3693877.00	4385503.00			
Research Associates - UGC(Stipend)	5473330.00	8348180.00	**3. Investments and deposits made**		
			a) Out of Earmarked/Endowement funds	190000000.00	116714571.00
Projects (Annexure - C)	58652921.00	189431530.00	b) Out of Own Funds (Investments-Others)	0.00	0.00
3. Income on Investments from			**4. Expenditure on Fixed Assets & Capital Work-in-Progress**		
a) Earmarked/Endow. Funds	2768470.13	10566572.00	a) Purchases of Fixed Assets:		

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CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

RECEIPTS AND PAYMENTS ACCOUNT FOR THE YEAR ENDED 31st MARCH 2013

(Amount - Rs.)

RECEIPTS	Current Year	Previous Year	PAYMENTS	Current Year	Previous Year
b) Own Funds (Oth. Investment)			Books & Journals	707417.00	1185197.00
Investments EnCashed	190000000.00	132624298.00	Equipment -Lab/Office/Furniture	45729192.00	115062838.00
			b) Expenditure on Capital Work-in-Progress:	143151561.00	149823117.00
4. Interest Received					
a) On Bank deposits	0.00	290557.06	**5. Refund of surplus money/Loans**		
b) Loans, Advances etc			a) To the Government of India	0.00	0.00
Interest on LC	700706.00	963584.00	b) To the State Government	0.00	0.00
Interest on Computer Advance, Conveyance Advance and HBA	21531.00	26807.00	c) To other providers of funds	0.00	0.00
5. Other Income(Specify)			**6. Finance Charges (Interest)**	0.00	0.00
a) Analysis Charges	3571262.00	3324036.00			
			7. Other Payments (Specify)		
6. Any Other Receipts(Give Details)			Advances (Annexure-D)	32478185.00	62291324.00
I-Remittances (Annexure-A)	17787572.00	14050639.00	I-Remittances (Annexure-E)	17726793.00	13950648.00
			CPF A/c	11239240.00	7895131.00
CPF-SUB,Arrears and adv.Refund	16864561.35	7869743.00	New Pension Scheme	2123569.00	11649062.00
Sundry Receipts	1152808.30	8352499.60	Analysis Charges Paid/Refund	0.00	169325.00
Application Fee	69202.00	284300.00	Others	0.00	28278734.00
Provident Fund Salwage	0.00	0.00	**8. Closing Balances**		
Free Gifts - Donations	0.00	0.00	a) Cash in hand	0.00	0.00
Sale OF Tender Forms	63000.00	25000.00	b) Bank Balances		
Leave Salary-Pension Contribution	0.00	0.00	i) In current accounts	12223805.10	71591437.99
License Fee	44400.00	0.00	ii) In deposit accounts	0.00	0.00
Welfare Fund	0.00	0.00	iii) Savings accounts	20909457.77	13026015.28
New Pension Scheme	2123569.00	11649062.00			
Advance/Refunds/Recovery/Adj (Annexure-B)	49650763.00	146836613.00			
TOTAL	**845888267.87**	**992313930.13**	**TOTAL**	**845888267.87**	**992313930.13**

DIRECTOR
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For K R SRINIVASAN & CO
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CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2013

(Amount - Rs.)

		Current Year		Previous Year
SCHEDULE 1 - CORPUS/CAPITAL FUND :				
Balance as at the begining of the year		996575609.00		811485570.00
Add : Contribution towards Corpus/Capital Fund				
CDFD Core - Plan (Non-Recurring)	180000000.00		170000000.00	
Capitalised portion of Capital Expenditure of projects	9729088.00	189729088.00	15090039.00	185090039.00
Less : Lump Sum Depreciation For the Year 1996 to 2012	271409382.00			
Less : Depreciation For the Year 2012-2013	21763702.00	293173084.00		0.00
Add : Balance of net income/(Expenditure) transferred from the income and Expenditure Account		249405326.30		0.00
BALANCE AS AT THE YEAR - END		**1142536939.30**		**996575609.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2013

(Amount - Rs.)

	Current Year		Previous Year	
SCHEDULE 2 -RESERVES AND SURPLUS :				
1.Capital Reserve :				
As per last Account	0.00		0.00	
Addition during the year	0.00		0.00	
Less : Deductions during the year	0.00	0.00	0.00	0.00
2.Revolution Reserve :				
As per last Account	0.00		0.00	
Addition during the year	0.00		0.00	
Less : Deductions during the year	0.00	0.00	0.00	0.00
3.Special Reserves :				
As per last Account	0.00		0.00	
Addition during the year	0.00		0.00	
Less : Deductions during the year	0.00	0.00	0.00	0.00
4.General Reserve :				
As per last Account	276778938.30		272022337.50	
Addition during the year	0.00		4756600.80	
Less : Deductions during the year	27373612.00		0.00	276778938.30
	249405326.30			
Less : Transfer to Grant in Aid	249405326.30	0.00		
Total		**0.00**		**276778938.30**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2013

(Amount - Rs.)

SCHEDULE 3 - EARMARKED/ENDOWMENT FUNDS	Current Year		Previous Year	
(Refer Annexures)				
(a) Opening balance of the Funds		**50698171.20**		16210479.20
(b) Additions to the Funds :				
i. Donations /grants	58652921.00		189431530.00	
ii. Income from investments made on account of funds	0.00		0.00	
iii. Other additions	0.00	58652921.00	0.00	189431530.00
TOTAL (a+b)		109351092.20		205642009.20
(c) Utilisation/Expenditure towards objective of funds				
(i) Capital Expenditure (Refer Annexures I & II)				
- Fixed Assets	9551279.00		15090039.00	
- Others	177809.00	9729088.00	0.00	15090039.00
- Total				
(ii) Revenue Expenditure				
- Salaries, Wages and allowances etc.	31815150.00		33415240.00	
- Rent	0.00		0.00	
- Other Expenses	61275833.00	93090983.00	106438559.00	139853799.00
Total				
TOTAL (c)		102820071.00		154943838.00
NET BALANCE AS AT THE YEAR-END [(a + b)-c]		**6531021.20**		**50698171.20**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2013

(Amount - Rs.)

	Current Year		Previous Year	
SCHEDULE 4 - SECURED LOANS AND BORROWINGS:				
1. Central Government		0.00		0.00
2. State Government (Specify)		0.00		0.00
3. Financial Institutions				
(a) Term Loans	0.00		0.00	
(b) Interest accured and due	0.00	0.00	0.00	0.00
4. Banks				
(a) Term Loans	0.00		0.00	
- Interest accured and due	0.00		0.00	
(b) Other Loans (specify)	0.00		0.00	
- Interest accured and due	0.00	0.00	0.00	0.00
5. Other Institutions and Agencies		0.00		0.00
6. Debentures and Bonds		0.00		0.00
7. Others (Specify)		0.00		0.00
TOTAL		**0.00**		**0.00**
Note: Amount due within one year				

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2013

(Amount - Rs.)

	Current Year		Previous Year	
SCHEDULE 5 - UNSECURED LOANS AND BORROWINGS:				
1. Central Government		0.00		0.00
2. State Government (Specify)		0.00		0.00
3. Financial Institutions		0.00		0.00
4. Banks				
(a) Term Loans	0.00		0.00	
(b) Other Loans (specify)	0.00	0.00	0.00	0.00
5. Other Institutions and Agencies		0.00		0.00
6. Debentures and Bonds		0.00		0.00
7. Fixed Deposits		0.00		0.00
8. Others (Specify)		0.00		0.00
TOTAL		**0.00**		**0.00**
Note: Amounts due within one year				

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2013

(Amount - Rs.)

	Current Year		Previous Year	
SCHEDULE6 - DEFFERED CREDIT LIABILITIES:				
(a) Acceptances secured by hypothecation of capital equipment and other assets		0.00		0.00
(b) Others		0.00		0.00
TOTAL		0.00		0.00
Note: Amount due within one year				

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2013

(Amount - Rs.)

	Current Year		Previous Year	
SCHEDULE 7 - CURRENT LIABILITIES AND PROVISIONS				
A. CURRENT LIABILITIES				
1. Acceptances	0.00		0.00	
2. Sundry Creditors	0.00		0.00	
3. Advances Received	0.00		0.00	
4. Interest accured but not due on:	0.00		0.00	
5. Statutory Liabilities:	0.00		0.00	
6. Other current Liabilities				
CDFD.CP Fund A/C(Annexure-G)	35805401.67		29159376.32	
Out Standing Liabilities	1520556.00		11482970.44	
Collaboration -Workshop Funds	11300000.00		15302674.50	
House Building Advance	95087.00		95087.00	
TDS	478747.00		386081.00	
Income Tax	37355.00		76988.00	
Works Tax	234688.00		234176.00	
LIC	2550.00		2550.00	
GSLI	44390.00		27079.00	
Others (I-Remittances)	178985.00		0.00	
EMD	2898534.00		3138534.00	
Security Deposit	1708475.00		1639975.00	
Workshop & Conference	3161.00		0.00	
Royalty & Consultancy	2254740.00		1548122.00	
Professional Tax	99187.00		3302.00	
Lab Security Deposit & Hostel Security Deposit	1155810.00	57817666.67	1010110.00	
TOTAL (A)		57817666.67	64107025.26	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2013

(Amount - Rs.)

	Current Year		Previous Year	
SCHEDULE 7 - CURRENT LIABILITIES AND PROVISIONS				
B.PROVISIONS				
1. For Taxation	0.00		0.00	
2. Gratuity	0.00		0.00	
3. Superannuation/Pension	0.00		0.00	
4. Accumulated Leave Encashment	0.00		0.00	
5. Trade Warranties/Claims	0.00		0.00	
6. Others (Specify)	6932849.00	6932849.00	0.00	
TOTAL (B)	0.00	6932849.00	0.00	
TOTAL (A+B)	**0.00**	**64750515.67**	**64107025.26**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2013

(Amount - Rs.)

SCHEDULE 8 - FIXED ASSETS	GROSS BLOCK				DEPRECIATION				NET BLOCK	
	Cost / valuation as at beginning of the year	Additions during the year	Deductions during the year	Cost / Valuation at the year end	As at the beginning of the year	On Additions during the year	On Deductions during the year	Total up to the year end	As at the Current year end	As at the Previous year end
A. FIXED ASSETS:										
1. LAND:										
a) Freehold	3900000.00	0.00	0.00	3900000.00	0.00	0.00	0.00	0.00	3900000.00	3900000.00
b) Leasehold	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
2. BUILDINGS										
a) On Freehold Land	0.00	220052369.00	0.00	220052369.00	0.00	16503928.00	0.00	16503928.00	203548441.00	0.00
b) On Leasehold Land	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
c) Ownership Flats/Premises	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
d) Superstructures on Land not belongs to the entity	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
3. PLANT MACHINERY & EQUIPMENT	477308882.05	55128926.00	0.00	532437808.05	227497760.00	4700111.00	0.00	232197871.00	300239937.05	477308882.05
4. VEHICLES	4126158.00	5000.00	0.00	4131158.00	3366339.00	4999.00	0.00	3371338.00	759820.00	4126158.00
5. FURNITURE, FIXTURES	16445181.00	11700.00	0.00	16456881.00	9499432.00	585.00	0.00	9500017.00	6956864.00	16445181.00
6. OFFICE EQUIPMENT	11413499.00	134845.00	0.00	11548344.00	8194901.00	28361.00	0.00	8223262.00	3325082.00	11413499.00
7. COMPUTER/PERIPHERALS	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
8. ELECTRIC INSTALLATIONS	0.00				0.00	0.00	0.00	0.00		0.00
9. LIBRARY BOOKS	15081576.00	885226.00	0.00	15966802.00	15081576.00	525718.00	0.00	15607294.00	359508.00	15081576.00
10. TUBEWELLS & WATER SUPPLY	0.00				0.00	0.00	0.00	0.00		0.00
11. OTHER FIXED ASSETS	8857898.00	0.00	0.00	8857898.00	7769374.00	0.00	0.00	7769374.00	1088524.00	8857898.00
Airconditioning works		0.00	0.00		0.00	0.00	0.00	0.00		
Aluminium partition work		0.00	0.00		0.00	0.00	0.00	0.00		
DG Set		0.00	0.00		0.00	0.00	0.00	0.00		
Paintings		0.00	0.00		0.00	0.00	0.00	0.00		
Typewriters		0.00	0.00		0.00	0.00	0.00	0.00		
Miscellaneous non-consumables		0.00	0.00		0.00	0.00	0.00	0.00		
Other Assets		0.00	0.00		0.00	0.00	0.00	0.00		
EMB Net		0.00	0.00		0.00	0.00	0.00	0.00		
TOTAL	537133194.05	276218066.00	0.00	813351260.05	271409382.00	21763702.00	0.00	293173084.00	520178176.05	537133194.05
B. CAPITAL WORK-IN-PROGRESS	488856048.70	(76900808)	0.00	411955240.70	0.00	0.00	0.00	0.00	411955240.70	488856048.70
TOTAL	**1025989242.75**	**276218066.00**	**0.00**	**1225306500.75**	**271409382.00**	**21763702.00**	**0.00**	**293173084.00**	**932133416.75**	**1025989242.75**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2013

(Amount - Rs.)

SCHEDULE 9 - INVESTMENTS FROM EARMARKED/ENDOWMENT FUNDS	Current Year	Previous Year
1. In Government Securities	0.00	0.00
2. Other approved securities	0.00	0.00
3. Shares	0.00	0.00
4. Debentures and Bonds	0.00	0.00
5. Subsidiaries and Joint Ventures	0.00	0.00
6. Others (to be specified) - STDRs (Annexure-J)	62398273.00	62398273.00
TOTAL	**62398273.00**	**62398273.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2013

(Amount - Rs.)

SCHEDULE 10 - INVESTMENTS - OTHERS (Annexure-K)	Current Year	Previous Year
1. In Government Securities	0.00	0.00
2. Other approved securities	0.00	0.00
3. Shares	0.00	0.00
4. Debentures and Bonds : UTI Bonds	0.00	936360.00
5. Subsidiaries and Joint Ventures	0.00	0.00
6. Others (to be specified) - STDRs,(CPF),CDFD CP FUND A/C	25159583.00	28223016.00
TOTAL	**25159583.00**	**29159376.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2013

(Amount - Rs.)

SCHEDULE 11 - CURRENT ASSETS, LOANS, ADVANCES ETC.	Current Year		Previous Year	
A. CURRENT ASSETS:				
1. Inventors				
a) Stores and Spares	0.00		0.00	
b) Loose Tools	0.00		0.00	
c) Stock-in-trade				
Finished Goods	0.00		0.00	
Work-in-progress	0.00		0.00	
Raw Materials	0.00	0.00	0.00	0.00
2. Sundry Debtors:				
a) Debts Outstanding for a period exceeding six months			0.00	
b) Others-Life Membership Fees	165935.00	165935.00	165935.00	165935.00
3. Cash balances in hand (including cheques/drafts and imprest)				
4. Bank Balances:				
a) With Scheduled Banks:				
-On Current Accounts	12223805.10		71591437.99	
-On Deposit Accounts (includes margin money)	0.00		0.00	
-On Savings Accounts	20909457.77	33133262.87	13026015.28	84617453.27
b) With non-Schedules Banks:				
-On Current Accounts	0.00		0.00	
-On Deposit Accounts	0.00		0.00	
-On Savings Accounts	0.00	0.00	0.00	0.00
5. Post Office-Savings Accounts				
TOTAL (A)		**33299197.87**		**84783388.27**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2013

(Amount - Rs.)

SCHEDULE 11 - CURRENT ASSETS, LOANS, ADVANCES, ETC.	Current Year		Previous Year	
B.LOANS, ADVANCES AND OTHER ASSETS				
1. Loans:				
a) Staff	0.00		0.00	
b) Other Entities engaged in activities/objectives similar to that of the Entity	0.00	0.00	0.00	0.00
2. Advances and other amounts recoverable in cash or in kind or for value to be received				
a) On Capital Account (Annexure-H)	136321662.51	0.00	171246087.95	
b) Prepayments - Deposits (Annexure-I)	24506343.00	0.00	14583375.00	
c) Others	0.00	160828005.51		185829462.95
3. Income Accured:				
a) On Investments from Earmarked/Endowments Funds	0.00		0.00	
b) On Investments - Others	0.00		0.00	
c) On Loans and Advances	0.00		0.00	
d) Others	0.00	0.00	0.00	0.00
4. Claims Receivable				0.00
TOTAL (B)		160828005.51		185829462.95
TOTAL (A+B)		**194127203.38**		**270612851.22**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MARCH 2013

(Amount - Rs.)

SCHEDULE 12 - INCOME FROM SALES/SERVICES	Current Year	Previous Year
a) Sale of Finished Goods	0.00	0.00
b) Sale of Raw Material	0.00	0.00
c) Sale of Scraps	0.00	3760.00
2) Income from Services		
a) Labour and Processing Charges	0.00	0.00
b) Professional/Consultancy Services (Analysis Charges)	3571262.00	3154711.00
c) Agency Commission and Brokerage	0.00	0.00
d) Maintenance Services (Equpiment/Property)	0.00	0.00
e) Others (Specify)	0.00	0.00
TOTAL	**3571262.00**	**3158471.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MARCH 2013

(Amount - Rs.)

SCHEDULE 13 - GRANTS/SUBSIDIES	Current Year	Previous Year
(Irrevocable Grants & Subsidies Received)		
1) Central Government (DBT Plan Grant-in-Aid)	210000000.00	210200000.00
2) State Government(s)	0.00	0.00
3) Government Agencies	0.00	0.00
4) Institutions/Welfare Bodies	0.00	0.00
5) International Organisations	0.00	0.00
6) Others (Specify)	0.00	0.00
TOTAL	**210000000.00**	**210200000.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MARCH 2013

(Amount - Rs.)

SCHEDULE 14 - FEES/SUBSCRIPTIONS	Current Year	Previous Year
1) Entrance Fees	0.00	0.00
2) Annual Fees/Subscriptions	0.00	0.00
3) Seminar/Program Fees	0.00	0.00
4) Consultancy Fees	0.00	0.00
5) Others (Specify)	0.00	0.00
	0.00	0.00
TOTAL	**0.00**	**0.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MARCH 2013

(Amount - Rs.)

SCHEDULE 15 - INCOME FROM INVESTMENTS	Investment from Earmarked Fund		Investments - Others	
(Income on Invest from Earmarked/Endowment Funds transferred to Funds)	Current Year	Previous Year	Current Year	Previous Year
1) Interest:				
a) On Govt. Securities	0.00		0.00	
b) Other Bonds/Debentures	0.00	0.00	0.00	0.00
2) Dividends:				
a) On Shares	0.00	0.00	0.00	0.00
b) On Mutual Fund Securities	0.00	0.00	0.00	0.00
3) Rents 0.00	0.00	0.00	0.00	
4) Others (Specify) STDRs	2768470.13	10566572.00	0.00	0.00
TOTAL	**2768470.13**	**10566572.00**	**0.00**	**0.00**
TRANSFERRED TO EARMARKED/ENDOWMENT FUNDS				

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MARCH 2013

(Amount - Rs.)

SCHEDULE 16 - INCOME FROM ROYALITY, PUBLICATIONS ETC.	Current Year	Previous Year
1) Income from Royalty	0.00	0.00
2) Income from Publications	0.00	0.00
3) Others (Specify)	0.00	0.00
TOTAL	0.00	0.00

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MARCH 2013

(Amount - Rs.)

SCHEDULE 17 - INTEREST EARNED	Current Year	Previous Year
1) On Term Deposits		
a) With Schedule Banks	700706.00	963584.00
b) With Non-Scheduled Banks	0.00	0.00
c) With Institutions	0.00	0.00
d) Others	0.00	0.00
2) On Saving Accounts		
a) With Schedule Banks	0.00	290557.06
b) With Non-Scheduled Banks	0.00	0.00
c) post Office Savings Accounts	0.00	0.00
d) Others	0.00	0.00
3) On Loans		
a) Employees/Staff		
b) Others	0.00	0.00
4) Interest on Debtors and Other Receivables	0.00	0.00
TOTAL	**700706.00**	**1254141.06**
Note :- Tax deducted at source to be indicated		

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MARCH 2013

(Amount - Rs.)

SCHEDULE 18 - OTHER INCOME	Current Year	Previous Year
1) Profit on Sale/disposal of Assets:	0.00	0.00
a) Owned assets	0.00	0.00
b) Assets acquired out of grants, or received free of cost	0.00	0.00
2) Export Incentives realized	0.00	0.00
3) Fees for Miscellaneous Services	0.00	0.00
4) Miscellaneous Receipts	0.00	0.00
5) Other Receipts		
Sundry Receipts	1152808.30	2506525.60
Application Fee	69202.00	284300.00
Sales Of Tender Forms	63000.00	25000.00
Licence Fee	44400.00	0.00
Interest On Computer Advance,Conveyance Advance And HBA	21531.00	26807.00
Leave Salary-Pension Contribution	0.00	0.00
Provident Fund Salwage	0.00	0.00
Free.Gifts-Donations	0.00	0.00
TOTAL	**1350941.30**	**2842632.60**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MARCH 2013

(Amount - Rs.)

SCHEDULE 19 - INCREASE/(DECREASE) IN STOCK OF FINISHED GOODS & WORK IN PROGRESS	Current Year	Previous Year
a) Closing stock		
-Finished Goods	0.00	0.00
-Work-in-progress	0.00	0.00
Total (a)	0.00	0.00
b) Less: Opening Stock		
- Finished Goods	0.00	0.00
- Work-in-progress	0.00	0.00
Total (b)	0.00	0.00
NET INCREASE/(DECREASE) [a-b]	**0.00**	**0.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MARCH 2013

(Amount - Rs.)

SCHEDULE 20 - ESTABLISHMENT EXPENSES	Current Year	Previous Year
a) Salaries and Wages	54234162.00	74470200.00
b) Allowances and Bonus	33816395.00	1597702.00
c) Contribution to Provident Fund	2112193.00	2282201.00
d) Contribution to Other Fund (NPS)	1788473.00	0.00
e) Staff Welfare Expenses - Medical charges	2801565.00	1398440.00
f) Expenses on Employees Retirement and Terminal Benefits	91016.00	303856.00
g) Others (specify)	0.00	0.00
TOTAL	**94843804.00**	**80052399.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MARCH 2013

(Amount - Rs.)

SCHEDULE 21 - OTHER ADMINISTRATIVE EXPENSES, ETC.		Current Year	Previous Year
a)	Purchases	30974267.00	52186698.60
b)	Electricity and power	18257125.00	18343015.00
c)	Water charges	616153.00	0.00
d)	Insurance	80030.00	0.00
e)	Repairs and maintenance	18347984.00	21061051.00
f)	Rent, Rates and Taxes	20625866.00	17082514.00
g)	Vehicles Running and Maintenance	953329.00	873865.00
h)	Postage, Telephone and Communication Charges	3809722.00	3107079.00
i)	Printing and Stationary	1151153.00	1238899.00
j)	Travelling and Conveyance Expenses	6819565.00	6189789.26
k)	Expenses on Seminar/Workshops	1029747.00	611987.00
l)	Subscription Expenses	163532.00	21932.00
m)	Expenses on Fees	294361.00	348971.00
n)	Auditors Remuneration	28090.00	27395.00
o)	Hospitality Expenses	891110.00	1123155.00
p)	Professional Charges	3329870.00	2555345.00
q)	Advertisement and Publicity	4082079.00	3294255.00
r)	Bank Charges	35206.00	6864.00
s)	Security & Cleaning Contract Charges	16177366.00	14901941.00
t)	Training Course /Symposia	23752.00	168269.00

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MARCH 2013

(Amount - Rs.)

SCHEDULE 21 - OTHER ADMINISTRATIVE EXPENSES, ETC.		Current Year	Previous Year
u)	Other Contingencies	2178819.00	69792.00
v)	Liveries & Blankets	1170.00	0.00
w)	Other Research Expenses	14099459.00	0.00
x)	Office Books	18583.00	0.00
	TOTAL	**143988338.00**	**143212816.86**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MARCH 2013

(Amount - Rs.)

SCHEDULE 22 - EXPENDITURE ON GRANTS, SUBSIDES, ETC.	Current Year	Previous Year
a) Grants given to Institutions/Organisations	0.00	0.00
b) Subsidies given to Institutions/Organisations	0.00	0.00
TOTAL	**0.00**	**0.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MARCH 2013

(Amount - Rs.)

SCHEDULE 23 - INTEREST	Current Year	Previous Year
a) On Fixed Loans	0.00	0.00
b) On Other Loans (including Bank Charges)	0.00	0.00
c) Others	0.00	0.00
TOTAL	**0.00**	**0.00**

Schedule 24: Significant Accounting Policies, and Schedule 25: Contingent Liabilities & Notes on Account for the period ended 31/03/2013

1. Method of Accounting:

a. The accounting system adopted by the organization is on “Accrual basis”.

b. The organization has been allocating plan grant-in-aid under the “Non-recurring” & “Recurring” heads.

2. Revenue recognition:

Income comprises of Grant-in-Aid, Internal Resources through services and interest from short term deposits. Income accounted on the basis of the Cash/DD/Cheques/Cr notes received.

3. Fixed Assets:

(a) Fixed assets are stated at cost. Cost includes freight, duties, and taxes etc.,

(b) Depreciation: Based on the recommendation of the Finance Committee and approval of the Governing Body of the Institute, Depreciation Account on Fixed Assets from the financial year 1996-97 to 2011-12 of the institute has since been prepared at the rate prevailing to the concerned Fixed Assets as specified in the Income Tax Act, 1961 on Written Down Value Method of Depreciation. The accumulated depreciation from the financial year 1996-97 to 2011-12 has since been set off against the Grant in Aid (Non Recurring) in the concerned account.

(c) Capital work in progress has been entered to the extent of the last running account bills paid.

(d) Realization on sale of obsolete/surplus fixed assets which is not required for the purpose of research activities are adjusted against capital cost.

4. Inventories:

All purchases of chemicals, glassware and other consumables have been charged to consumption at the time of purchase.

5. Foreign Currency transactions:

Foreign Currency transactions are recognized in the books at the exchange rates prevailing on the date of transaction.

6. Investments:

Investments in STDR’s are stated at book values.

7. Advances:

It is observed from the objection book register that advances to suppliers for consumables & Equipments are to be reconciled and adjustment entries are to be passed in the books of accounts.

8. The previous year balances have been regrouped/rearranged, wherever necessary.

Director, CDFD | Head Finance & Accounts | for K R Srinivasan & Co
Chartered Accountants

Sd/-
[K R SRINIVASAN]

Place: Hyderabad
Date: 04/07/2013

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

CLARIFICATION ON NOTES ON ACCOUNTS: 2012-13

- Notes on Accounts 1 to 2 & 4 to 6: Method of Accounting/ Revenue recognition/Fixed Asset/ Inventories/ Foreign Currency transactions/Investments:
  These are all only informatory items.

- Notes on Accounts 3: Fixed Assets:
  Accumulated Depreciation for the period from 1996-97 to 2011-12 has been calculated on Written Down Value method and at the rates prevailing to the concerned Fixed Asset as specified on the Income Tax Act, 1961 and set off against the Grant-in-Aid (non-recurring) in the current financial year. The details of the Depreciation on Fixed Assets is at Schedule -8 is an integral part of the financial statements.

- Notes on Accounts 7: Advances:
  The observation of the audit has been noted. The action has already been initiated to reconcile the objection book register.

B J ACHARYULU
Head Finance & Accounts
CDFD

Annexure - I

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS
Details of closing balances of various Earmarked / Endowment Funds (Refer Sch-3)
for the year ended 31st March 2013

Amount in Rs.

Previous year	P No	Particulars	Current Year
-3110519.00	COE-I	COE for Genetics and Genomics of silkmoths	-9645531.00
-8969700.00	COE-II	DBT Centre of Excellence for Microbial Biology	-12818181.00
-630047.00	P-03	"Transgenesis and Genetic basis of Pathogen Resistance in the Silkworm, Bombyx Mori	-630047.00
244305.00	P-09	"NMITLI Project on – Latent M.Tuberculosis: New targets, Drug delivery systems, Bio enhancers & Therapeutics"	244305.00
-28332.00	P-10	"Role of upstream sequence elements in Hyper activation of transcription from Baculovirus polyhedrin gene promoter"	-28332.00
-335000.00	P-100	Effect of raective oxygen species on T-Cell immune response: An approach to understand the molecular mechanism of immunosuppression during tuberculosis - National Bioscience Award	-576590.00
13729401.00	P-101	Role of inositol pyrophosphates in cell physiology: Investigating the biochemical significance of protein pyrophosphorylation - Senior Fellowship	4364267.00
82654.00	P-102	Understanding the role of Mycobacterium tuberculosis heat shockprotein 60 as Th1/Th2 immuno modular	-430020.00
-300000.00	P-103	National Bioscience Award - Regulation of mast cell signaling, apoptosis and surface receptors	-600000.00
-1394866.00	P-104	Virtual Centre of Excellence on Epigenetics	-2017875.00
-90844.00	P-105	Cloning, Characterization and analysis of chromosomal rearrangements in human genetic disorders	-844946.00
190952.00	P-106	Clinical, Biochemical and molecular analysis of treatable lysosomal storage disorders	-189211.00
63600.00	P-107	IYBA Project - Mechanism and role of bacterial cell-cell signaling molecules in plant defense response	435.00
69925.00	P-108	Establishment of EBV transformed cell lines from families with rare genetic disorders	-392965.00
315626.00	P-109	Molecular dissection of PI3-Kinase/Akt pathway by suing proteomics based approach: A study to identify novel potential oncogenes and tumor suppressors	94426.00
-168679.00	P-110	India-Japan research project title"Identification and analysis of sex determining genes in silkmoths"	-191391.00
431731.00	P-111	Ramalingaswami Fellowship - Refractoriness mechanism in Mosquito: cracking molecular codes at genomic scale	550416.00
534630.00	P-113	Clinical and molecular genetic analysis of squamous cell carcinoma of the tongue	-1036754.00
51553.00	P-114	Evaluating the Calcineurin-NFAT Pathway and its regulators superoxide dismutase (SOD) AND RCAN1 (regular of Calcineurin) Down Syndrome	-450859.00
8039741.00	P-115	Setting up of the National Institute of Animal Biotechnology	-5.00
-288420.00	P-116	DBT-India and AIST - Japan : Understanding molecular mechanisms controlling dual role of Ras, Sirtuins and CARF in relation to cellular proliferation and senescence: Novel Strategy for developing cancer therapeutics	-1251366.00
-738605.00	P-119	Analysis of DNA copy number alterations in esophaeal cancer	-1132629.00
124600.00	P-120	Effect of reactive oxygen species on macrophage signalosome: impact on antigen presentation functions and T Cell priming responses	-600218.00
-597186.00	P-121	Identification and characterization of PTEN regulators	-1130866.00
11479043.00	P-122	Understanding the role of Hox genes in anterior-posterior axis determination of the central nervous system	13089682.00
2074056.00	P-123	Establish a Max Planck Partner Group for Genetic Diversity Studies at CDFD	1151969.00
167284.00	P-124	Preparation and characterization of peroxometal compounds and studies and their biological significance in cellular signalling	-549916.00
154000.00	P-125	Mechanistic studies on the role of protein kinase Snfilk in cell cycle and cancer	-480981.00
1581615.00	P-126	Rho-dependent transcription termination machinery: mechanism of action	-685428.00
5052715.00	P-127	Systematic studies on the functional network of phosphatases in cell life and death	4162538.00
2053587.00	P-128	Mechanism of iron acquisition and iron homeostasis in an opportunistic human pathogen Candida glabrata	537771.00
306000.00	P-129	Discovery of bioactive natural products from microbes especially actinomycetes in niche biotopes in Manipur	0.00
6737.00	P-13	"Programme to delineate gene functions in the post – genomics era by a systematic two gene knockout method"	6737.00
4187000.00	P-130	Comparative genetic analysis of sex chromosomes and sex determining genes in silkmoths	465973.00
1182935.00	P-131	Structural and functional studies of Acyl CoA Binding proteins from plasmodium falciparum	-768669.00
634323.00	P-132	Characterization of tumor suppressor function of ARIDIB, a component of the human SWI/SNF chromatin remodelling complex	-1228480.00
1549000.00	P-133	Investigating the role of Hox gene deformed in central nervous system patterning in Drosophila melanogaster	969489.00
254000.00	P-134	Exploration of wild silk moth biodiversity in Manipur and their genetic characterization using molecular markers	-141437.00
7418200.00	P-135	Sys TB: A Network Program for Resolving the Intracellular Dynamics of Host Phthogen Interaction in TB Infection	5376566.00
837200.00	P-136	Raf Kinase - a key target for modem-day theraphy against tumors	77980.00
1500000.00	P-137	Signaling pathways involved in down regulation of proinflammatory responses by PPE18 protein of Mycobacterium tuberculosis: Implication of PPE18 as therapeutics	685020.00
0.00	P-138	Co-evaluation of Dnmt3l and Genomic imprinting	903944.00

Annexure - I

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS
Details of closing balances of various Earmarked / Endowment Funds (Refer Sch-3)
for the year ended 31st March 2013

Amount in Rs.

Previous year	P No	Particulars	Current Year
2467200.00	P-139	Evaluating the role of Sirtuins and epigenetic changes during cellular senescense in context of p53 status	1223583.00
0.00	P-140	Development of baculovirus resistant silkworms strains through synthetic miRNA based knockdown of essential viral genes	556091.00
0.00	P-141	Evaluating the functional role of PTEN interacting proteins in cell survival signaling and tumor suppression	1463.00
0.00	P-142	Identification of H3K4 TRI Demethylase involved in erasing H3K4 trimethylation marks at E2F Responsive promoters	360148.00
0.00	P-143	Microarray based characterisation of squamous cell carcinoma of the tongue occuring in non smokers	146284.00
267184.00	P-144	Tri-National Training Program for Psychiatric Genetics	0.00
0.00	P-145	H3K4 HMT family regulatescell cycle progression	2208206.00
0.00	P-146	Role of MLL in ribosomal RNA transcription	812209.00
0.00	P-147	The Effect of Parental Education, Ethics of Research Participation and Array Comparative Genomic Hybridization in Subjects with Mental Retardation (MR) and /or Autism	315642.00
0.00	P-148	Transcriptional regulation of novel tumor suppressor genes in Pancreatic Cancer	20326.00
0.00	P-149	Role of SUMOylation in the pathobiology of Candida Glabrata	1770286.00
0.00	P-150	Genetic and genomic basis of the evolution of bombycid and sturniid silkmoths	164706.00
0.00	P-151	Human Exome Sequencing to Identify Novel Genes for Medelian Disorders	1993200.00
0.00	P-153	An attractive and promising stragegy for early cancer diagnosis through the assembly of the human cancer volatome"	3000000.00
0.00	P-155	Studies on thecellular roles of calcium signalling proteins in Neurospora crassa	335194.00
-687887.00	P-17	"Studies on inosital-phosphate synthesis – a novel enzyme from Mycobacterium tuberculosis H37RV" – Transfer from IMTECH, Chandigarh	-687887.00
-274286.00	P-18	"Mapping of receptor binding site on the Eythrocyte binding of malaria parasyte"	-274286.00
-1888111.00	P-20	"Genomic Micro array R&D Programmes on infectious diseases and Neurological Disorders"	-1888111.00
0.50	P-22	"Biotechnology for leather – towards cleaner processing"	0.50
-34495.00	P-23	"Development of PCR base assays for detection of GMO S"	-34495.00
-529111.00	P-25	"Functional studies of Human Immuno - deficiency Virus Type– 2 (HIV-2) Viral protien X (VPX)"	-529111.00
-79533.00	P-26	Occurrence of Mutations in Non dividing cells of Escherichia Coli"	-79533.00
-37624.00	P-28	Baculovirus resistance in transgenic silkworms	-37624.00
-310302.00	P-29	"Development of Hospital Surveillance system by advanced diagnostics method & Molecular DNA fingerprinting techniques"	-310302.00
2045696.00	P-30	Transcription termination and anti termination in E-coli	2045696.00
746453.00	P-31	Role of K-ras in Lung type II epithelial cells	746453.00
-234000.00	P-33	"Molecular and Epidemiological characterisation of cryptosporidium – An enteric protozoon parasite"	-234000.00
26334.00	P-34	"Molecular analysis of lepidopteran – specific immune protiens from silkmoths"	26334.00
-283883.00	P-35	"Identification, Characterization and Physical mapping of Z-Chromosome linked genes of the silk worm, Bombyxmori"	-283883.00
2073896.00	P-36	"Development of Artificial retina using Bacterio rhodospin and genetically engineered analogues "	2073896.00
-226058.00	P-40	"Antioxidants as a potential immuno adjuvant in anti tuberculosis immunotherapy"	-4058.00
1873605.00	P-41	"Construction, characterization and analysis of expressed sequences from silkworm "	1873605.00
-2237285.00	P-42	"Structural and functional studies on Mycobacterium tuberculosis heat shock proteins".	-2237285.00
685906.70	P-43	"A generalized mechanism of transcription termination in prokaryotes: a quest for mechanism based transcription inhibitors for microbial pathogens".	685906.70
-457538.00	P-44	"Understanding of role of Ras and NO / iNOS signalling in promotion of hepatocellular carcinomas with persistent HBV infection"	-457538.00
605714.00	P-45	Specialized chromatin structures as epigenetic imprints to distinguish parental alleles".	605714.00
-1586965.00	P-47	Research cum Training for DRDO Programme	-1586965.00
151826.00	P-48	'Molecular characterization of human liver stem cells for use in the treatment of hepatic diseases'.	151826.00
440950.00	P-49A	International Atomic Energy Agency (IAEA)	308361.00
-284065.00	P-51	"Understanding the mechanism of doxorubicin resistance in breast cancer celline MCF-7"	-284065.00
-1231118.00	P-52	"Nucleo Cytoplasmic transport of HIV – 1 Vpr"	-1231118.00
-37877.00	P-54	"Study of viability of Mycobacterium leprae in clinical samples and possibility of its presence in the environment using nucleic acid amplification techniques."	-37877.00
224.00	P-55	"Identification of DNA Markers for baculovirus resistance in silkworm, Bombyx mori"	224.00
-1231164.00	P-56	"Genetics of transcription-replication interplay and of stress adaptation in bacteria"	-1231164.00
-2215024.00	P-59	"An integrated Approach towards understanding the biology of Mycobacterium tuberculosis: Genetic, biochemical, immunological and structural analyses."	-2215024.00

Annexure - I

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS
Details of closing balances of various Earmarked / Endowment Funds (Refer Sch-3)
for the year ended 31st March 2013

Amount in Rs.

Previous year	P No	Particulars	Current Year
482124.00	P-60	"National Database of Prevalent Genetic Disorders in India: Development, Curation and Services"	482124.00
-280000.00	P-61	"Dissection of a novel phenotype of lethal accumulation of potassium in Escherichia coli mutants defective in thioredoxin/thioredoxin reductase and nucleoied protein H-NS"	-280000.00
-278928.00	P-62	"HIV – 1 Pathogenesis: Role of Integrase in Reverse Transciption and Nuclear Transport of Viral Genome"	-278928.00
-837574.00	P-63	"Upgradation of the existing computing infrastructure at the Bioinformatics facility at CDFD"	-837574.00
-158.00	P-64	Biotechnology for Leather: Towards cleaner processing phase-II	-158.00
-582647.00	P-65	"Molecular, genetic and functional analysis of the chromosomal plasticity region of the gastric pathogen Helicobater pylori"	-582647.00
18938021.00	P-65A	APEDA-CDFD Centre for Basmati DNA Analysis	19734821.00
-681246.00	P-66	Human Epigenome Variation: Analysis of CpG island methylation in chromosomes 18 and Y, and in some Hox, insulin signaling and chromatin reprogramming genes	-681246.00
-113545.00	P-67	Identification of novel Esophageal Squamous cell carcinoma (ESCC) genes by using a combination of array-based CGH and gene expression micro arrays	-113545.00
-59874.00	P-68	Identification of High risk individual with pre-cancerous states of esophageal cancer.	-59874.00
-21336.00	P-70	Identification of disease causing mutations in familial hypertrophic cardiomyopathy (FHC) patients from Andhra Pradesh	-21336.00
15829.00	P-71	Referral Centre for Genetic fidelity testing of tissue culture raised plants	0.00
-1421653.00	P-72	Nuances of non coding DNA near insulin-responsive genes.	-1421653.00
-857136.00	P-73	Identification and characterization of pancreatic cancer genes located within novel localized cpy number alterations	-857136.00
-10840.00	P-75	Preparing blueprint for the macromolecular crystallography beamline at Indus-II synchrotron source	-10840.00
-50234.00	P-76	A study of molecular markers in childhood autism with special references to nuclear factors - ± APPA B	-50234.00
124277.00	P-77	Functional characterization of Mycobacterium tuberculosis PE/PPE proteins having SH3 binding domain : Understanding their role in modulating macrophage functions	124277.00
1304.00	P-78	Task force- IMD Newborn screening for Congenital Hypothyroidism & Congenital Adrenal Hyperplasia: A multicentric study	1304.00
-105086.00	P-79	Understanding the role of AGE proteins in inducing inflammatory responses and its regulation	-105086.00
-608222.00	P-80	Referral centre for detection of genetically modified foods employing DNA-based markets	-608222.00
143470.00	P-81	Reconstructing Cellular Networks: Two-component regulatory systems	143470.00
62620.00	P-81A	Financial assistance for award of J C Bose Fellowship to Dr J Gowrishankar	562620.00
155859.00	P-82	Functional genomic analysis of Candida Glabrata-macrophage	-367721.00
-1155594.00	P-83	Prokaryotic Transcription termination factor, Rho: Mechanism of Action and Biology	-1155594.00
-126140.00	P-83A	Understanding the mechanism of Azadirachtin-mediated cell signaling: role in anti-inflammation and anti-tumorigenesis	0.00
-1150.00	P-84	Preparing for vaccine efficacy trials: Baseline epidemiology, improved diagnosis, markers of protection and phase I/II trials	-1150.00
-106479.00	P-84A	Human epigenetic to the rescue of human identification process: Enriching human DNA from DNA mixture employing antibodies directed against 5-methylcytosine followed by whole genome amplification	-106479.00
-1118755.00	P-85	IdeR associated gene regulatory network in mycobacteria	-1118755.00
-65698.00	P-87	Comparative genomics of wild silkmoths	-65698.00
0.00	P-88	Introduction of anti-baculoviral property in commercial silkworm strains by expression of multiple RNAi viral targets	218818.00
-636286.00	P-90	Role of Yapsins in the Pathobiology of Candida Glabrata	-636286.00
-1098900.00	P-91	DMMT3L: epigenetic correlation with cancer	-1098900.00
-1260461.00	P-92	Swarnajayanti fellowship proj on "Designing transcription anti-terminators: a novel approach for making new inhibitors of gene expression"	-3090255.00
-675810.00	P-93/A1	Virtual Centre of Excellence on multidisciplinary approaches aimed at interventions against tuberculosis	-661454.00
-831076.00	P-93/A2	Virtual Centre of Excellence on multidisciplinary approaches aimed at interventions against Mycobacterium tuberculosis	-2446997.00
-98464.00	P-97	Proteome-wide Analysis of Serine pyrophosphorylation by inositol pyrophosphates	-146870.00
-63019.00	P-98	Role of cell - cell signaling mediated by Diffusible signaling factor (DSF) in Xanthomonas virulence	-255844.00
-1261900.00	P-99	Role of inositol Pyrophosphates in eukaryotic cell growth, proliferation and ribosomae biogenesis	-315780.00
50698171.20			**6531021.20**

Annexure - II

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS
Details of Fixed Assets Fund (Capitalised portion of Project Grants)
for the year ended 31st March 2013

Amount in Rs.

Previous year	P No	Particulars	Current Year
11713327	COE-I	COE for Genetics and Genomics of silkmoths	11713327
10000000	COE-II	DBT Centre of Excellence for Microbial Biology	10000000
600000	P-03	"Transgenesis and Genetic basis of Pathogen Resistance in the Silkworm, Bombyx Mori	60000
329289	P-07	"Collection of well characterised clinical samples and strains of Mycobacterium tuberculosis and development of molecular techniques for detection of drug resistant strains – Multi Centric Project"	329289
588400	P-09	"NMITLI Project on – Latent M.Tuberculosis: New targets, Drug delivery systems, Bio enhancers & Therapeutics"	588400
47400	P-10	"Role of upstream sequence elements in Hyper activation of transcription from Baculovirus polyhedrin gene promoter"	47400
17784	P-100	Effect of raective oxygen species on T-Cell immune response: An approach to understand the molecular mechanism of immunosuppression during tuberculosis - National Bioscience Award	17784
6276263	P-101	Role of inositol pyrophosphates in cell physiology: Investigating the biochemical significance of protein pyrophosphorylation - Senior Fellowship	10645294
681121	P-102	Understanding the role of Mycobacterium tuberculosis heat shockprotein 60 as Th1/Th2 immuno modular	681121
1000000	P-107	IYBA Project - Mechanism and role of bacterial cell-cell signaling molecules in plant defense response	1000000
915278	P-109	Molecular dissection of PI3-Kinase/Akt pathway by suing proteomics based approach: A study to identify novel potential oncogenes and tumor suppressors	915278
268914	P-113	Clinical and molecular genetic analysis of squamous cell carcinoma of the tongue	670095
294008	P-114	Evaluating the Calcineurin-NFAT Pathway and its regulators superoxide dismutase (SOD) AND RCAN1 (regular of Calcineurin) Down Syndrome	475900
4580214	P-115	Setting up of the National Institute of Animal Biotechnology	4580214
800000	P-116	DBT-India and AIST - Japan : Understanding molecular mechanisms controlling dual role of Ras, Sirtuins and CARF in relation to cellular proliferation and senescence: Novel Strategy for developing cancer therapeutics	800000
183443	P-118	Construction of regulatory networks in Mycobacterium tuberculosis through analysis of gene expression data and transcription regulation predictions. (MOU with Russian Foundation)	183443
529750	P-12	Molecular genetics and Functional genomics of M.Tuberculosis patient isolates in India	529750
438084	P-122	Understanding the role of Hox genes in anterior-posterior axis determination of the central nervous system	459324
101800	P-123	Establish a Max Planck Partner Group for Genetic Diversity Studies at CDFD	453095
0	P-126	Rho-dependent transcription termination machinery: mechanism of action	385404
2225907	P-127	Systematic studies on the functional network of phosphatases in cell life and death	2897196
0	P-128	Mechanism of iron acquisition and iron homeostasis in an opportunistic human pathogen Candida glabrata	1594393
1334600	P-13	"Programme to delineate gene functions in the post – genomics era by a systematic two gene knockout method"	1334600
0	P-133	Investigating the role of Hox gene deformed in central nervous system patterning in Drosophila melanogaster	474792
5163243	P-14	"Comparitive and functional genomics approaches for the identification and characterization of genes responsible for multi drug resistance of mycobacterium tuberculosis"	5163243
0	P-142	Identification of H3K4 TRI Demethylase involved in erasing H3K4 trimethylation marks at E2F Responsive promoters	424914
0	P-146	Role of MLL in ribosomal RNA transcription	359711
6000000	P-15	"The Helicobacter Pylori genome programme – Genome sequencing, functional analysis and comparitive genomics of the strains obtained from Indian patients"	6000000
1814901	P-16	NMITLI Project on – Latent M.Tuberculosis: New targets, Drug delivery systems, Bio enhancers & Therapeutics	1814901
244400	P-17	"Studies on inosital-phosphate synthesis – a novel enzyme from Mycobacterium tuberculosis H37RV" – Transfer from IMTECH, Chandigarh	244400
344020	P-18	"Mapping of receptor binding site on the Eythrocyte binding of malaria parasyte"	344020
7246511	P-19	"Construction of Integrated RAPD, RFLP and Microsatellite linkage map of the Silkworm, Bombyx mori and its corelation with the Phenotypic linkage Map"	7246511
27331134	P-20	"Genomic Micro array R&D Programmes on infectious diseases and Neurological Disorders"	27331134
5300000	P-21	Development of Versatile, portable software for Bio-informatics	5300000
603747	P-22	"Biotechnology for leather – towards cleaner processing"	603747
375999	P-23	"Development of PCR base assays for detection of GMO S"	375999
600000	P-25	"Functional studies of Human Immuno - deficiency Virus Type– 2 (HIV-2) Viral protien X (VPX)"	600000
500000	P-26	Occurrence of Mutations in Non dividing cells of Escherichia Coli"	500000
260367	P-29	"Development of Hospital Surveillance system by advanced diagnostics method & Molecular DNA fingerprinting techniques"	260367
3746538	P-30	Transcription termination and anti termination in E-coli	3746538
3131006	P-31	Role of K-ras in Lung type II epithelial cells	3131006
4857938	P-36	"Development of Artificial retina using Bacterio rhodospin and genetically engineered analogues "	4857938
358470	P-39	"Computational analysis and functional characterization of mycobacterial protien(s) interacting with macrophase effector – APC functions – an approach to understand the molecular basis of pathogenesis of M. tuberculosis"	358470
49738	P-40	"Antioxidants as a potential immuno adjuvant in anti tuberculosis immunotherapy"	49738
3894086	P-41	"Construction, characterization and analysis of expressed sequences from silkworm "	3894086
9500000	P-42	"Structural and functional studies on Mycobacterium tuberculosis heat shock proteins".	9500000

Annexure - II

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS
Details of Fixed Assets Fund (Capitalised portion of Project Grants)
for the year ended 31st March 2013

Amount in Rs.

Previous year	P No	Particulars	Current Year
11970000	P-43	"A generalized mechanism of transcription termination in prokaryotes: a quest for mechanism based transcription inhibitors for microbial pathogens".	11970000
3331377	P-45	Specialized chromatin structures as epigenetic imprints to distinguish parental alleles".	3331377
416137	P-46	"Effect of reactive oxygen species (ROS) on immune response : Relevance in immunosuppression and Pathogenesis"	416137
377567	P-47	Research cum Training for DRDO Programme	377567
1413292	P-48	'Molecular characterization of human liver stem cells for use in the treatment of hepatic diseases'.	1413292
198095	P-50	"Cervical cancer prevention by multiple strategies in rural community in Andhra pradesh"	198095
401738	P-51	"Understanding the mechanism of doxorubicin resistance in breast cancer celline MCF-7"	401738
1359129	P-52	"Nucleo Cytoplasmic transport of HIV – 1 Vpr"	1359129
1114495	P-53	Collaborative research project on molecular ecology and systematics	1114495
1163764	P-56	"Genetics of transcription-replication interplay and of stress adaptation in bacteria"	1163764
2131403	P-57	Improved genome annotation through a combination of machine learning and experimental methods: Plasmodium falciparum as a case study.	2131403
63000	P-58	"Indo-Malaysian collaboration in Bioinformatics: Development and maintenance of a web-portal hosting databases and tools of common interest"	63000
32974662	P-59	"An integrated Approach towards understanding the biology of Mycobacterium tuberculosis: Genetic, biochemical, immunological and structural analyses."	32974662
5720800	P-60	"National Database of Prevalent Genetic Disorders in India: Development, Curation and Services"	5720800
4308314	P-62	"HIV – 1 Pathogenesis: Role of Integrase in Reverse Transciption and Nuclear Transport of Viral Genome"	4308314
9637574	P-63	"Upgradation of the existing computing infrastructure at the Bioinformatics facility at CDFD"	9637574
600585	P-64	Biotechnology for Leather: Towards cleaner processing phase-II	600585
260000	P-65	"Molecular, genetic and functional analysis of the chromosomal plasticity region of the gastric pathogen Helicobater pylori"	260000
16924622	P-65A	APEDA-CDFD Centre for Basmati DNA Analysis	16924622
264430	P-66	Human Epigenome Variation: Analysis of CpG island methylation in chromosomes 18 and Y, and in some Hox, insulin signaling and chromatin reprogramming genes	264430
622747	P-67	Identification of novel Esophageal Squamous cell carcinoma (ESCC) genes by using a combination of array-based CGH and gene expression micro arrays	622747
235593	P-69	ICMR adhoc New Scheme Understanding the role of PE/PPE family of M tuberculosis in the activation of HIV virus type I long terminal repeat (HIV-ILTP)	235593
1012807	P-70	Identification of disease causing mutations in familial hypertrophic cardiomyopathy (FHC) patients from Andhra Pradesh	1012807
1573795	P-71	Referral Centre for Genetic fidelity testing of tissue culture raised plants	1573795
45653	P-72	Nuances of non coding DNA near insulin-responsive genes.	45653
1000000	P-74	Molecular basic of insect plant interactions in rice under the national fund for basic and strategic research in agriculture	1000000
33672	P-75	Preparing blueprint for the macromolecular crystallography beamline at Indus-II synchrotron source	33672
245266	P-76	A study of molecular markers in childhood autism with special references to nuclear factors - ± APPA B	245266
1543605	P-77	Functional characterization of Mycobacterium tuberculosis PE/PPE proteins having SH3 binding domain : Understanding their role in modulating macrophage functions	1543605
496826	P-79	Understanding the role of AGE proteins in inducing inflammatory responses and its regulation	496826
4192480	P-80	Referral centre for detection of genetically modified foods employing DNA-based markets development of molecular	4192480
195728	P-81A	Financial assistance for award of J C Bose Fellowship to Dr J Gowrishankar	195728
1441427	P-82	Functional genomic analysis of Candida Glabrata-macrophage	1480220
912255	P-83	Prokaryotic Transcription termination factor, Rho: Mechanism of Action and Biology	912255
388583	P-83A	Understanding the mechanism of Azadirachtin-mediated cell signaling: role in anti-inflammation and anti-tumorigenesis	388583
44854	P-84	Preparing for vaccine efficacy trials: Baseline epidemiology, improved diagnosis, markers of protection and phase I/II trials	44854
1430573	P-84A	Human epigenetic to the rescue of human identification process: Enriching human DNA from DNA mixture employing antibodies directed against 5-methylcytosine followed by whole genome amplification	1430573
374630	P-89	Characterization of Mycobacterium tuberculosis transcription machinery and Bacteriophage metagenomics	374630
1376869	P-90	Role of Yapsins in the Pathobiology of Candida Glabrata	1376869
932151	P-91	DMMT3L: epigenetic correlation with cancer	932151
8500000	P-92	Swarnajayanti fellowship proj on "Designing transcription anti-terminators: a novel approach for making new inhibitors of gene expression"	8500000
2212534	P-93/A1	Virtual Centre of Excellence on multidisciplinary approaches aimed at interventions against tuberculosis	2212534
296034	P-93/A2	Virtual Centre of Excellence on multidisciplinary approaches aimed at interventions against Mycobacterium tuberculosis	655403
246320	P-95	Construction of regulatory networks in prokaryotes through protein: Protein interaction predictions and transcription regulation predictions. (MOU with Russian Foundation)	246320
918196	P-97	Proteome-wide Analysis of Serine pyrophosphorylation by inositol pyrophosphates	966602
2783795	P-98	Role of cell - cell signaling mediated by Diffusible signaling factor (DSF) in Xanthomonas virulence	2789420
2921729	P-99	Role of inositol Pyrophosphates in eukaryotic cell growth, proliferation and ribosomae biogenesis	2963482
254856786			**264585874**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS

FOR THE YEAR ENDED 31st MARCH 2013

Annexure: A Forming part of Receipts & Payment a/c

Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	I-Remittances	
4740809.00	TDS	4976630.00
5678791.00	Income Tax	6114373.00
14920.00	Works Tax	4586.00
1102504.00	LIC	1335912.00
225224.00	GSLI	219721.00
1574630.00	PPF	1904410.00
546897.00	Professional Tax	574296.00
166864.00	Service Tax	1979139.00
0.00	Others (I-Remittances)	678505.00
14050639.00		**17787572.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS

FOR THE YEAR ENDED 31st MARCH 2013

Annexure: B Forming part of Receipts & Payment a/c

Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	Advance refunds/recovery/Adjst.	
37500.00	Conveyance Advance	31080.00
41200.00	Computer Advance [Staff]	46200.00
201249.00	Computer Advance [Research Fellows]	70004.00
118725.00	Festival Advance	110625.00
157634.00	Others [Advances]	39075.00
14429932.00	General Deposits and Advances	1585218.00
310300.00	EMD	1800.00
533750.00	Security Deposit	71000.00
301909.00	Revolving Advance	307394.00
443063.00	Advance for purchases by Staff	239083.00
0.00	Workshop & Conference	536185.00
204860.00	LSD & HSD	220200.00
12500.00	Trainee Security Deposit	4000.00
233890.00	Royalty & Consultancy	1200000.00
107532410.00	Equipment	42903643.00
335803.00	LTC [Advance]	239061.00
4513584.00	TA-India & Abroad [Advance]	1690485.00
0.00	Other Advance recovery	355710.00
2644290.00	CDFD Staff reserve Fund	0.00
14201834.00	Chemicals (Advance)	0.00
582180.00	NIMS Advance	0.00
146836613.00		**49650763.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS

FOR THE YEAR ENDED 31st MARCH 2013

Annexure: C Forming part of Receipts & Payment a/c

Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	Projects - Receipts	
0	P-40	222000
5103400.00	P - 65A	1068000.00
1020000.00	P - 71	0.00
1795900.00	P- 79	0.00
1300000.00	P- 81A	1360000.00
839000.00	P- 82	0.00
0.00	P-83A	126140.00
0.00	P - 88	680000.00
300000.00	P - 89	0.00
618700.00	P - 90	0.00
3500000.00	P - 92	0.00
2010000.00	P - 93	645000.00
1452712.00	P - 96	0.00
532000.00	P - 97	0.00
1641200.00	P - 98	0.00
726299.00	P - 99	1217000.00
4470916.00	P - 101	0.00
1086164.00	P - 102	503782.00
0.00	P - 104	1437000.00
681000.00	P - 105	0.00
1602302.00	P - 106	505153.00
773000.00	P - 107	817000.00
470400.00	P - 108	0.00
742000.00	P - 109	566000.00
1511500.00	P - 111	1487000.00
1000000.00	P - 112	0.00
848689.00	P - 113	0.00
0.00	P - 114	760000.00
65500000.00	P - 115	143232.00
0.00	P - 119	1252800.00
13606258.00	P - 122	4880510.00
2884810.00	P - 123	1047000.00
819000.00	P - 124	0.00
764000.00	P - 125	0.00
2539300.00	P - 126	0.00
11097596.00	P - 127	4637410.00
2807200.00	P - 128	1017200.00
306000.00	P - 129	0.00
5987000.00	P - 130	0.00
1899200.00	P - 131	0.00

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS

FOR THE YEAR ENDED 31st MARCH 2013

Annexure: C Forming part of Receipts & Payment a/c

Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
929200.00	P - 132	
1849000.00	P - 133	763000.00
400000.00	P - 134	0.00
7943200.00	P - 135	0.00
837200.00	P - 136	0.00
1500000.00	P - 137	0.00
0.00	P-138	1799600.00
2467200.00	P - 139	500000.00
0.00	P-140	3700000.00
0.00	P-141	500000.00
0.00	P-142	1514000.00
0.00	P-143	714000.00
267184.00	P - 144	0.00
0.00	P-145	3885200.00
0.00	P-147	805900.00
0.00	P-148	700000.00
0.00	P-149	1979600.00
0.00	P-150	210000.00
0.00	P-151	1993200.00
0.00	P-153	3000000.00
0.00	P-155	335194.00
22433000.00	COE- I	4000000.00
8570000.00	COE- II	7881000.00
189431530.00		**58652921.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS
FOR THE YEAR ENDED 31st MARCH 2013

Annexure: D Forming part of Receipts & Payment a/c

Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	Advances	
35000.00	Computer Advance [Research Fellows]	100000.00
131250.00	Festival Advance	86250.00
376415.00	Others [Advances]	113479.00
9667900.00	General Deposits And Advances	1038800.00
2178922.00	EMD	241800.00
9750.00	Security Deposit	2500.00
223500.00	Revolving Advance	326500.00
264000.00	Advance for purchases by Staff	229702.00
538860.00	Workshop & Conference	1698172.00
129000.00	LSD & HSD	93000.00
11000.00	Trainee Security Deposit	12500.00
0.00	GDA [Others]	135277.00
1239852.00	Royalty & Consultancy	493382.00
28472236.00	Equipment	12673898.00
0.00	Office Equipment	22700.00
1118680.00	LTC [Advance]	1229250.00
0.00	Medical [Advance]	300000.00
3785265.00	TA-India & Abroad [Advance]	2876325.00
0.00	Honorarium [Advance]	5000.00
0.00	Chemicals [Advance]	9660410.00
13039405.00	Consumables, glassware and Spares [Advance]	714700.00
0.00	AMC for Equipment [Advance]	38250.00
0.00	Other Research Expenses [Advance]	28090.00
30000.00	Computer Advance [Staff]	210000.00
60000.00	Conveyance [Advance]	148200.00
64000.00	Rent [Advance]	0.00
916289.00	NIMS Advance	0.00
62291324.00		**32478185.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS

FOR THE YEAR ENDED 31st MARCH 2013

Annexure: E Forming part of Receipts & Payment a/c

Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	I-Remittances	
4709062.00	TDS	4883964.00
5622209.00	Income Tax	6154006.00
26093.00	Works Tax	4074.00
1099954.00	LIC	1335912.00
210600.00	GSLI	202410.00
1570900.00	PPF	2012875.00
544966.00	Professional Tax	478411.00
166864.00	Service Tax	2155621.00
0.00	Others (I-Remittances)	499520.00
13950648.00		**17726793.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS

FOR THE YEAR ENDED 31st MARCH 2013

Annexure: F Forming part of Receipts & Payment a/c

Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	Projects - Expenditure	
29363.00	P - 49A	132589.00
2547094.00	P - 65A	271200.00
412681.00	P - 71	15829.00
554228.00	P - 80	0.00
70745.00	P - 81	0.00
1345180.00	P - 81A	860000.00
1106732.00	P - 82	523580.00
783120.00	P - 84A	0.00
740000.00	P - 88	461182.00
802987.00	P - 90	0.00
311836.00	P - 91	0.00
3521916.00	P - 92	1829794.00
2832707.00	P - 93	2246565.00
424041.00	P - 95	0.00
796770.00	P - 96	0.00
1118988.00	P - 97	48406.00
1237665.00	P - 98	192825.00
1874442.00	P - 99	270880.00
35000.00	P - 100	241590.00
6430446.00	P - 101	9365134.00
558377.00	P - 102	1016456.00
300000.00	P - 103	300000.00
1692479.00	P - 104	2060009.00
917815.00	P - 105	754102.00
965294.00	P - 106	885316.00

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS

FOR THE YEAR ENDED 31st MARCH 2013

Annexure: F Forming part of Receipts & Payment a/c

Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
1311406.00	P - 107	880165.00
584498.00	P - 108	462890.00
1902478.00	P - 109	787200.00
193068.00	P - 110	22712.00
1568400.00	P - 111	1368315.00
1803726.00	P - 112	0.00
864774.00	P - 113	1571384.00
1481208.00	P - 114	1262412.00
62019564.00	P - 115	8182978.00
1981237.00	P - 116	962946.00
5251500.00	P - 117	0.00
1115770.00	P - 118	0.00
1298947.00	P - 119	1646824.00
492400.00	P - 120	724818.00
634282.00	P - 121	533680.00
2127215.00	P - 122	3269871.00
810754.00	P - 123	1969087.00
651716.00	P - 124	717200.00
610000.00	P - 125	634981.00
957685.00	P - 126	2267043.00
6044881.00	P - 127	5527587.00
753613.00	P - 128	2533016.00
0.00	P-129	306000.00
1800000.00	P - 130	3721027.00
716265.00	P - 131	1951604.00
294877.00	P - 132	1862803.00
300000.00	P - 133	1342511.00
146000.00	P - 134	395437.00
525000.00	P - 135	2041634.00
0.00	P-136	759220.00
0.00	P-137	814980.00
0.00	P-138	895656.00
0.00	P-139	1743617.00
0.00	P-140	1293909.00
0.00	P-141	498537.00
0.00	P-142	1153852.00
0.00	P-143	567716.00
0.00	P-144	267184.00
0.00	P-145	1676994.00
0.00	P-146	1037791.00
0.00	P-147	490258.00
0.00	P-148	679674.00
0.00	P-149	209314.00
0.00	P-150	45294.00
12344655.00	COE - I	10535012.00
12948013.00	COE - II	11729481.00
154943838.00		**102820071.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS

FOR THE YEAR ENDED 31st MARCH 2013

Annexure: G Forming part of Receipts & Payment a/c

Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	CDFD C.P.F ACCOUNT	
33724337.32	Opening Balance	29159376.32
	Add:	
7891447.00	Employee subscription/ refunds	5355840.00
62280.00	Transfer from other departments	0.00
3323326.00	Institute contribution (inc. Projects staff)	2112193.00
85173.00	Interest received	3277120.35
45086563.32	Less:	39904529.67
15927187.00	Advances/withdrawals/Transfer/Adjst	4099128.00
29159376.32		**35805401.67**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS

FOR THE YEAR ENDED 31st MARCH 2013

Annexure: H Forming part of Receipts & Payment a/c

Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	LOANS AND ADVANCES	
0.00	TA-India & Abroad [Advance]	1069515.56
0.00	Honorarium [Advance]	5000.00
304569.00	Rent [Advance]	304569.00
69666260.00	Chemicals [Advance]	79326670.00
982164.00	LTC [Advance]	1972353.00
0.00	Medical [Advance]	300000.00
0.00	Consumables, glassware and Spares [Advance]	714700.00
0.00	AMC for Equipment [Advance]	38250.00
0.00	Other Research Expenses [Advance]	28090.00
0.00	Trainee Security Deposit	27000.00
13414314.00	Research Fellows-Associates	8468959.00
68078113.45	Equipment [Advance]	37848368.45
0.00	Office Equipment [Advance]	22700.00
4310.00	GSLI Recovery	4310.00
355710.00	CDFD STAFF Reserve Fund	0.00
37913.00	Computer Advance [Research Fellows]	67909.00
77925.00	Festival Advance	53550.00
5258884.00	Others [Advances]	5333288.00
0.00	PPF	85575.00
72.00	Service Tax	176554.00
83237.00	Revolving Advance	102343.00
248219.50	Advance for purchases by Staff	238838.50
10334109.00	NIMS Advance	0.00
2400288.00	Workshop & Conference	0.00
0.00	Conveyance Advance	44620.00
0.00	Computer Advance [Staff]	88500.00
171246087.95		**136321662.51**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS

FOR THE YEAR ENDED 31st MARCH 2013

Annexure: I Forming part of Balance Sheet

Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	DEPOSITS	
14583375.00	General Deposits And Advances	24371066.00
0.00	GDA[Others]	135277.00
14583375.00		**24506343.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS

FOR THE YEAR ENDED 31st MARCH 2013

Annexure: J Forming part of Balance sheet

Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	INVESTMENT A/C	
51098273.00	Investments	51098273.00
11300000.00	Other Investments	11300000.00
62398273.00		**62398273.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS

FOR THE YEAR ENDED 31st MARCH 2013

Annexure: K Forming part of Balance sheet

Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	CDFD C.P.F INVESTMENT A/C	
29159376.32	Deposit with Banks	23202519.00
0.00	Employee subscription	7140112.00
		30342631.00
0.00	Less: Transfer to Bank A/c	5183048.00
29159376.32		**25159583.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-03: "Transgenesis and Genetic basis of Pathogen Resistance in the Silkworm, Bombyx Mori
P.I:
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	0.00	630047.00	Opening Balance	630047.00
0.00	Grant In Aid	0.00	0.00	Salaries - Manpower	0.00
			0.00	Consumables	0.00
			0.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
0.00		**0.00**	**630047.00**		**630047.00**
630047.00	Excess of Expenditure over Income	630047.00	0.00	Closing Balance	0.00
630047.00		**630047.00**	**630047.00**		**630047.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-09: "NMITLI Project on – Latent M.Tuberculosis: New targets, Drug delivery systems, Bio enhancers & Therapeutics"
P.I: Dr Seyed E Hasnain
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
244305.00	Opening Balance	244305.00			
0.00	Grant In Aid	0.00	0.00	Salaries - Manpower	0.00
			0.00	Consumables	0.00
			0.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
244305.00		**244305.00**	**0.00**		**0.00**
0.00	Excess of Expenditure over Income	0.00	244305.00	Closing Balance	244305.00
2443050.00		**244305.00**	**244305.00**		**244305.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-10: "Role of upstream sequence elements in Hyper activation of transcription from Baculovirus polyhedrin gene promoter"

P.I: Dr M D Bashyam

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	0.00	28332.00	Opening Balance	28332.00
0.00	Grant In Aid	0.00	0.00	Salaries - Manpower	0.00
			0.00	Consumables	0.00
			0.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
0.00		**0.00**	**28332.00**		**28332.00**
28332.00	Excess of Expenditure over Income	28332.00	0.00	Closing Balance	0.00
28332.00		**28332.00**	**28332.00**		**28332.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-13: "Programme to delineate gene functions in the post – genomics era by a systematic two gene knockout method"

P.I: Dr J Gowrishankar

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
6737.00	Opening Balance	6737.00			
0.00	Grant In Aid	0.00	0.00	Salaries - Manpower	0.00
			0.00	Consumables	0.00
			0.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
6737.00		**6737.00**	**0.00**		**0.00**
0.00	Excess of Expenditure over Income	0.00	6737.00	Closing Balance	6737.00
6737.00		**6737.00**	**6737.00**		**6737.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-17: "Studies on inosital-phosphate synthesis – a novel enzyme from Mycobacterium tuberculosis H37RV" – Transfer from IMTECH, Chandigarh
P.I: Dr Sekhar C Mande
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		687887.00		Opening Balance	687887.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**687887.00**			**687887.00**	
687887.00		Excess of Expenditure over Income	687887.00		0.00		Closing Balance	0.00	
687887.00			**687887.00**		**687887.00**			**687887.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-18: "Mapping of receptor binding site on the Eythrocyte binding of malaria parasyte"
P.I: Dr Akash Ranjan
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		274286.00		Opening Balance	274286.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**274286.00**			**274286.00**	
274286.00		Excess of Expenditure over Income	274286.00		0.00		Closing Balance	0.00	
274286.00			**274286.00**		**274286.00**			**274286.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-20: "Genomic Micro array R&D Programmes on infectious diseases and Neurological Disorders"
P.I: Dr Hasnain & Dr Bashyam
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		1888111.00		Opening Balance	1888111.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**1888111.00**			**1888111.00**	
1888111.00		Excess of Expenditure over Income	1888111.00		0.00		Closing Balance	0.00	
1888111.00			**1888111.00**		**1888111.00**			**1888111.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-23: "Development of PCR base assays for detection of GMO S"
P.I: Dr Nagaraju & Dr Niyaz Ahmed
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		34495.00		Opening Balance	34495.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**34495.00**			**34495.00**	
34495.00		Excess of Expenditure over Income	34495.00		0.00		Closing Balance	0.00	
34495.00			**34495.00**		**34495.00**			**34495.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-25: "Functional studies of Human Immuno - deficiency Virus Type– 2 (HIV-2) Viral protien X (VPX)"
P.I: Dr Mahalingam & Dr Mande
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		529111.00		Opening Balance	529111.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**529111.00**			**529111.00**	
529111.00		Excess of Expenditure over Income	529111.00		0.00		Closing Balance	0.00	
529111.00			**529111.00**		**529111.00**			**529111.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-26: Occurrence of Mutations in Non dividing cells of Escherichia Coli"
P.I:
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		79533.00		Opening Balance	79533.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**79533.00**			**79533.00**	
79533.00		Excess of Expenditure over Income	79533.00		0.00		Closing Balance	0.00	
79533.00			**79533.00**		**79533.00**			**79533.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-28: Baculovirus resistance in transgenic silkworms
P.I:
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		37624.00		Opening Balance	37624.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**37624.00**			**37624.00**	
37624.00		Excess of Expenditure over Income	37624.00		0.00		Closing Balance	0.00	
37624.00			**37624.00**		**37624.00**			**37624.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-29: "Development of Hospital Surveillance system by advanced diagnostics method & Molecular DNA fingerprinting techniques"
P.I: Dr K Prashanth
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		310302.00		Opening Balance	310302.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**310302.00**			**310302.00**	
310302.00		Excess of Expenditure over Income	310302.00		0.00		Closing Balance	0.00	
310302.00			**310302.00**		**310302.00**			**310302.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-30: Transcription termination and anti termination in E-coli
P.I: Dr Ranjan Sen
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
2045696.00	Opening Balance	2045696.00			
0.00	Grant In Aid	0.00	0.00	Salaries - Manpower	0.00
			0.00	Consumables	0.00
			0.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads 0.00	
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
2045696.00		**2045696.00**	**0.00**		**0.00**
0.00	Excess of Expenditure over Income	0.00	2045696.00	Closing Balance	2045696.00
2045696.00		**2045696.00**	**2045696.00**		**2045696.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-31: Role of K-ras in Lung type II epithelial cells
P.I: Dr Gayatri Ramakrishna
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
746543.00	Opening Balance	746453.00			
0.00	Grant In Aid	0.00	0.00	Salaries - Manpower	0.00
			0.00	Consumables	0.00
			0.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
746543.00		**746453.00**	**0.00**		**0.00**
0.00	Excess of Expenditure over Income	0.00	746543.00	Closing Balance	746453.00
746543.00		**746453.00**	**746543.00**		**746453.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-33: "Molecular and Epidemiological characterisation of cryptosporidium – An enteric protozoon parasite"
P.I: Dr Radha Rama Devi
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		234000.00		Opening Balance	234000.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**234000.00**			**234000.00**	
234000.00		Excess of Expenditure over Income	234000.00		0.00		Closing Balance	0.00	
234000.00			**234000.00**		**234000.00**			**234000.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-34: "Molecular analysis of lepidopteran – specific immune protiens from silkmoths"
P.I: Dr J Nagaraju
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
26334.00		Opening Balance	26334.00						
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
26334.00			**26334.00**		**0.00**			**0.00**	
0.00		Excess of Expenditure over Income	0.00		26334.00		Closing Balance	26334.00	
26334.00			**26334.00**		**26334.00**			**26334.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-35: "Identification, Characterization and Physical mapping of Z-Chromosome linked genes of the silk worm, Bombyxmori"
P.I: Dr J Nagaraju
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		283883.00		Opening Balance	283883.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**283883.00**			**283883.00**	
283883.00		Excess of Expenditure over Income	283883.00		0.00		Closing Balance	0.00	
283883.00			**283883.00**		**283883.00**			**283883.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-36: "Development of Artificial retina using Bacterio rhodospin and genetically engineered analogues "
P.I: Dr Sekhar C Mande
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
2073896.00		Opening Balance	2073896.00						
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
2073896.00			**2073896.00**		**0.00**			**0.00**	
0.00		Excess of Expenditure over Income	0.00		2073896.00		Closing Balance	2073896.00	
2073896.00			**2073896.00**		**2073896.00**			**2073896.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-40: "Antioxidants as a potential immuno adjuvant in anti tuberculosis immunotherapy"
P.I: Dr Sangita Mukhopadhyay
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	0.00	226058.00	Opening Balance	226058.00
0.00	Grant In Aid	222000.00	0.00	Salaries - Manpower	0.00
			0.00	Consumables	0.00
			0.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
0.00		**222000.00**	**226058.00**		**226058.00**
226058.00	Excess of Expenditure over Income	4058.00	0.00	Closing Balance	0.00
226058.00		**226058.00**	**226058.00**		**226058.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-41: "Construction, characterization and analysis of expressed sequences from silkworm "
P.I: Dr J Nagaraju
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
1873605.00	Opening Balance	1873605.00			
0.00	Grant In Aid	0.00	0.00	Salaries - Manpower	0.00
			0.00	Consumables	0.00
			0.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
1873605.00		**1873605.00**	**0.00**		**0.00**
0.00	Excess of Expenditure over Income	0.00	1873605.00	Closing Balance	1873605.00
1873605.00		**1873605.00**	**1873605.00**		**1873605.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-42: "Structural and functional studies on Mycobacterium tuberculosis heat shock proteins".
P.I: Dr Sekhar C Mande
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		2237285.00		Opening Balance	2237285.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**2237285.00**			**2237285.00**	
2237285.00		Excess of Expenditure over Income	2237285.00		0.00		Closing Balance	0.00	
2237285.00			**2237285.00**		**2237285.00**			**2237285.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-43: "A generalized mechanism of transcription termination in prokaryotes: a quest for mechanism based transcription inhibitors for microbial pathogens".
P.I: Dr Ranjan Sen
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
685906.70		Opening Balance	685906.70						
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
685906.70			**685906.70**		**0.00**			**0.00**	
0.00		Excess of Expenditure over Income	0.00		685906.70		Closing Balance	685906.70	
685906.70			**685906.70**		**685906.70**			**685906.70**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-44: "Understanding of role of Ras and NO / iNOS signalling in promotion of hepatocellular carcinomas with persistent HBV infection"
P.I: Dr Gayatri Ramakrishna
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		457538.00		Opening Balance	457538.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**457538.00**			**457538.00**	
457538.00		Excess of Expenditure over Income	457538.00		0.00		Closing Balance	0.00	
457538.00			**457538.00**		**457538.00**			**457538.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-45: Specialized chromatin structures as epigenetic imprints to distinguish parental alleles".
P.I: Dr Sanjeev Khosla
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
605714.00		Opening Balance	605714.00						
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
605714.00			**605714.00**		**0.00**			**0.00**	
0.00		Excess of Expenditure over Income	0.00		605714.00		Closing Balance	605714.00	
605714.00			**605714.00**		**605714.00**			**605714.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-47: Research cum Training for DRDO Programme
P.I: Dr Gowrishankar, Dr Mahalingam, Dr Mande, Dr Nagaraju, Dr Ni
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		1586965.00		Opening Balance	1586965.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**1586965.00**			**1586965.00**	
1586965.00		Excess of Expenditure over Income	1586965.00		0.00		Closing Balance	0.00	
1586965.00			**1586965.00**		**1586965.00**			**1586965.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-48: 'Molecular characterization of human liver stem cells for use in the treatment of hepatic diseases'.
P.I: Dr Sanjeev Khosla
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
151826.00		Opening Balance	151826.00						
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
151826.00			**151826.00**		**0.00**			**0.00**	
0.00		Excess of Expenditure over Income	0.00		151826.00		Closing Balance	151826.00	
151826.00			**151826.00**		**151826.00**			**151826.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-49A: International Atomic Energy Agency (IAEA)
P.I: J Nagaraju
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
470313.00	Opening Balance	440950.00			
0.00	Grant In Aid	0.00	0.00	Salaries - Manpower	0.00
			0.00	Consumables	0.00
			0.00	Contingencies	0.00
			29363.00	Travel	132589.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
470313.00		**440950.00**	**29363.00**		**132589.00**
0.00	Excess of Expenditure over Income	0.00	440950.00	Closing Balance	308361.00
470313.00		**440950.00**	**470313.00**		**440950.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-51: "Understanding the mechanism of doxorubicin resistance in breast cancer celline MCF-7"
P.I: Dr Sunil Kumar Manna
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	0.00	284065.00	Opening Balance	284065.00
0.00	Grant In Aid	0.00	0.00	Salaries - Manpower	0.00
			0.00	Consumables	0.00
			0.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
0.00		**0.00**	**284065.00**		**284065.00**
284065.00	Excess of Expenditure over Income	284065.00	0.00	Closing Balance	0.00
284065.00		**284065.00**	**284065.00**		**284065.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-52: "Nucleo Cytoplasmic transport of HIV – 1 Vpr"
P.I: Dr Mahalingam & Dr Manna
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		1231118.00		Opening Balance	1231118.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**1231118.00**			**1231118.00**	
1231118.00		Excess of Expenditure over Income	1231118.00		0.00		Closing Balance	0.00	
1231118.00			**1231118.00**		**1231118.00**			**1231118.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-54: "Study of viability of Mycobacterium leprae in clinical samples and possibility of its presence in the environment using nucleic acid amplification techniques."
P.I: Dr Niyaz Ahmed
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		37877.00		Opening Balance	37877.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**37877.00**			**37877.00**	
37877.00		Excess of Expenditure over Income	37877.00		0.00		Closing Balance	0.00	
37877.00			**37877.00**		**37877.00**			**37877.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-55: "Identification of DNA Markers for baculovirus resistance in silkworm, Bombyx mori"
P.I: Dr J Nagaraju
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
224.00		Opening Balance		224.00					
0.00		Grant In Aid		0.00		0.00	Salaries - Manpower		0.00
						0.00	Consumables		0.00
						0.00	Contingencies		0.00
						0.00	Travel		0.00
						0.00	Overheads		0.00
						0.00	Equipment		0.00
						0.00	Books		0.00
						0.00	AMC		0.00
						0.00	Others		0.00
						0.00	Transfer of Funds		0.00
224.00			**224.00**		**0.00**			**0.00**	
0.00		Excess of Expenditure over Income	0.00		224.00		Closing Balance	224.00	
224.00			**224.00**		**224.00**			**224.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-56: "Genetics of transcription-replication interplay and of stress adaptation in bacteria"
P.I: Dr Gowrishankar & Dr K Anupama
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance		0.00	1231164.00		Opening Balance	1231164.00	
0.00		Grant In Aid		0.00		0.00	Salaries - Manpower		0.00
						0.00	Consumables		0.00
						0.00	Contingencies		0.00
						0.00	Travel		0.00
						0.00	Overheads		0.00
						0.00	Equipment		0.00
						0.00	Books		0.00
						0.00	AMC		0.00
						0.00	Others		0.00
						0.00	Transfer of Funds		0.00
0.00			**0.00**		**1231164.00**			**1231164.00**	
1231164.00		Excess of Expenditure over Income	1231164.00		0.00		Closing Balance	0.00	
1231164.00			**1231164.00**		**1231164.00**			**1231164.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-59: "An integrated Approach towards understanding the biology of Mycobacterium tuberculosis: Genetic, biochemical, immunological and structural analyses."

P.I: Dr Hasnain, Dr Gowrishankar, Dr Mande, Dr Ranjan Sen

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	0.00	2215024.00	Opening Balance	2215024.00
0.00	Grant In Aid	0.00	0.00	Salaries - Manpower	0.00
			0.00	Consumables	0.00
			0.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
0.00		**0.00**	**2215024.00**		**2215024.00**
2215024.00	Excess of Expenditure over Income	2215024.00	0.00	Closing Balance	0.00
2215024.00		**2215024.00**	**2215024.00**		**2215024.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-60: "National Database of Prevalent Genetic Disorders in India: Development, Curation and Services"

P.I: Dr H A Nagarajaram

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
482124.00	Opening Balance	482124.00			
0.00	Grant In Aid	0.00	0.00	Salaries - Manpower	0.00
			0.00	Consumables	0.00
			0.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
482124.00		**482124.00**	**0.00**		**0.00**
0.00	Excess of Expenditure over Income	0.00	482124.00	Closing Balance	482124.00
482124.00		**482124.00**	**482124.00**		**482124.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-61: "Dissection of a novel phenotype of lethal accumulation of potassium in Escherichia coli mutants defective in thioredoxin/thioredoxin reductase and nucleoied protein H-NS"

P.I: Dr Abhijit A Sardesai

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance		0.00	280000.00		Opening Balance	280000.00	
0.00		Grant In Aid		0.00	0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**280000.00**			**280000.00**	
280000.00		Excess of Expenditure over Income	280000.00		0.00		Closing Balance	0.00	
280000.00			**280000.00**		**280000.00**			**280000.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-62: "HIV – 1 Pathogenesis: Role of Integrase in Reverse Transciption and Nuclear Transport of Viral Genome"

P.I: Dr S Mahalingam

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance		0.00	278928.00		Opening Balance	278928.00	
0.00		Grant In Aid		0.00	0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**278928.00**			**278928.00**	
278928.00		Excess of Expenditure over Income	278928.00		0.00		Closing Balance	0.00	
278928.00			**278928.00**		**278928.00**			**278928.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-63: "Upgradation of the existing computing infrastructure at the Bioinformatics facility at CDFD"

P.I: Dr Seyed E Hasnain

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		837574.00		Opening Balance	837574.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**837574.00**			**837574.00**	
837574.00		Excess of Expenditure over Income	837574.00		0.00		Closing Balance	0.00	
837574.00			**837574.00**		**837574.00**			**837574.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-64: Biotechnology for Leather: Towards cleaner processing phase-II

P.I: Dr J Gowrishankar

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		158.00		Opening Balance	158.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**158.00**			**158.00**	
158.00		Excess of Expenditure over Income	158.00		0.00		Closing Balance	0.00	
158.00			**158.00**		**158.00**			**158.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-65: "Molecular, genetic and functional analysis of the chromosomal plasticity region of the gastric pathogen Helicobater pylori"
P.I: Dr Ayesha Alvi
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		582647.00		Opening Balance	582647.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**582647.00**			**582647.00**	
582647.00		Excess of Expenditure over Income	582647.00		0.00		Closing Balance	0.00	
582647.00			**582647.00**		**582647.00**			**582647.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-65A: APEDA-CDFD Centre for Basmati DNA Analysis
P.I: Dr J Nagaraju
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
					0.00		Opening Balance	0.00	
16381715.00		Opening Balance	18938021.00		543948.00		Salaries - Manpower	271200.00	
0.00		Grant In Aid	0.00		2000000.00		Consumables	0.00	
1103400.00		Basmati Analysis Charges	1068000.00		0.00		Contingencies	0.00	
4000000.00		AMC Amount Received	0.00		0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Consultancy & Knowledge Fee	0.00	
					0.00		Vehicle	0.00	
					3146.00		Equipment	0.00	
21485115.00			20006021.00		2547094.00			271200.00	
		Excess of expenditure over income			18938021.00		Closing Balance	19734821.00	
21485115.00			**20006021.00**		**21485115.00**			**20006021.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-66: Human Epigenome Variation: Analysis of CpG island methylation in chromosomes 18 and Y, and in some Hox, insulin signaling and chromatin reprogramming genes

P.I: Dr Sanjeev Khosla

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		681246.00		Opening Balance	681246.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**681246.00**			**681246.00**	
681246.00		Excess of Expenditure over Income	681246.00		0.00		Closing Balance	0.00	
681246.00			**681246.00**		**681246.00**			**681246.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-67: Identification of novel Esophageal Squamous cell carcinoma (ESCC) genes by using a combination of array-based CGH and gene expression micro arrays

P.I: Dr M D Bashyam

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		113545.00		Opening Balance	113545.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**113545.00**			**113545.00**	
113545.00		Excess of Expenditure over Income	113545.00		0.00		Closing Balance	0.00	
113545.00			**113545.00**		**113545.00**			**113545.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-68: Identification of High risk individual with pre-cancerous states of esophageal cancer.
P.I: Dr Gayatri Ramakrishna
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		59874.00		Opening Balance	59874.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**59874.00**			**59874.00**	
59874.00		Excess of Expenditure over Income	59874.00		0.00		Closing Balance	0.00	
59874.00			**59874.00**		**59874.00**			**59874.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-70: Identification of disease causing mutations in familial hypertrophic cardiomyopathy (FHC) patients from Andhra Pradesh
P.I: Dr M D Bashyam
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		21336.00		Opening Balance	21336.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**21336.00**			**21336.00**	
21336.00		Excess of Expenditure over Income	21336.00		0.00		Closing Balance	0.00	
21336.00			**21336.00**		**21336.00**			**21336.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-71: Referral Centre for Genetic fidelity testing of tissue culture raised plants
P.I: Dr N M Reddy, Dr Nagaraju
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	15829.00	591490.00	Opening Balance	
1020000.00	Grant In Aid	0.00	187681.00	Salaries - Manpower	0.00
			200000.00	Consumables	0.00
			25000.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	15829.00
1020000.00		**15829.00**	**1004171.00**		**15829.00**
0.00	Excess of Expenditure over Income	0.00	15829.00	Closing Balance	0.00
1020000.00		**15829.00**	**1020000.00**		**15829.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-72: Nuances of non coding DNA near insulin-responsive genes.
P.I: Dr Nirmala Yabaluri
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	0.00	1421653.00	Opening Balance	1421653.00
0.00	Grant In Aid	0.00	0.00	Salaries - Manpower	0.00
			0.00	Consumables	0.00
			0.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
0.00		**0.00**	**1421653.00**		**1421653.00**
1421653.00	Excess of Expenditure over Income	1421653.00	0.00	Closing Balance	0.00
1421653.00		**1421653.00**	**1421653.00**		**1421653.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-73: Identification and characterization of pancreatic cancer genes located within novel localized cpy number alterations
P.I: Dr M D Bashyam
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		857136.00		Opening Balance	857136.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**857136.00**			**857136.00**	
857136.00		Excess of Expenditure over Income	857136.00		0.00		Closing Balance	0.00	
857136.00			**857136.00**		**857136.00**			**857136.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-75: Preparing blueprint for the macromolecular crystallography beamline at Indus-II synchrotron source
P.I: Dr Sekhar C Mande
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		10840.00		Opening Balance	10840.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**10840.00**			**10840.00**	
10840.00		Excess of Expenditure over Income	10840.00		0.00		Closing Balance	0.00	
10840.00			**10840.00**		**10840.00**			**10840.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-76: A study of molecular markers in childhood autism with special references to nuclear factors - ± APPA B

P.I: Dr S K Manna

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		50234.00		Opening Balance	50234.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**50234.00**			**50234.00**	
50234.00		Excess of Expenditure over Income	50234.00		0.00		Closing Balance	0.00	
50234.00			**50234.00**		**50234.00**			**50234.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-77: Functional characterization of Mycobacterium tuberculosis PE/PPE proteins having SH3 binding domain : Understanding their role in modulating macrophage functions

P.I: Dr Sangita Mukhopadhyay

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
124277.00		Opening Balance	124277.00						
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
124277.00			**124277.00**		**0.00**			**0.00**	
0.00		Excess of Expenditure over Income	0.00		124277.00		Closing Balance	124277.00	
124277.00			**124277.00**		**124277.00**			**124277.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-78: Task force- IMD Newborn screening for Congenital Hypothyroidism & Congenital Adrenal Hyperplasia: A multicentric study

P.I: Dr A Radha Rama Devi

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
1304.00		Opening Balance	1304.00						
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
1304.00			**1304.00**		**0.00**			**0.00**	
0.00		Excess of Expenditure over Income	0.00		1304.00		Closing Balance	1304.00	
1304.00			**1304.00**		**1304.00**			**1304.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-79: Understanding the role of AGE proteins in inducing inflammatory responses and its regulation

P.I: Dr S K Manna

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		1900986.00		Opening Balance	105086.00	
1795900.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
1795900.00			**0.00**		**1900986.00**			**105086.00**	
105086.00		Excess of Expenditure over Income	105086.00		0.00		Closing Balance	0.00	
1900986.00			**105086.00**		**1900986.00**			**105086.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-80: Referral centre for detection of genetically modified foods employing DNA-based markets
P.I: Dr Madhusudan Reddy
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		53994.00		Opening Balance	608222.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					554228.00		Transfer of Funds	0.00	
0.00			**0.00**		**608222.00**			**608222.00**	
608222.00		Excess of Expenditure over Income	608222.00		0.00		Closing Balance	0.00	
608222.00			**608222.00**		**608222.00**			**608222.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-81: Reconstructing Cellular Networks: Two-component regulatory systems
P.I: Dr Shekhar Mande
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
214215.00		Opening Balance	143470.00						
0.00		Grant In Aid	0.00		70745.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
214215.00			**143470.00**		**70745.00**			**0.00**	
0.00		Excess of Expenditure over Income	0.00		143470.00		Closing Balance	143470.00	
214215.00			**143470.00**		**214215.00**			**143470.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-81A: Financial assistance for award of J C Bose Fellowship to Dr J Gowrishankar
P.I: Dr J Gowrishankar
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
107800.00	Opening Balance	62620.00			
1300000.00	Grant In Aid	1360000.00	300000.00	Salaries - Manpower	300000.00
			650000.00	Consumables	342185.00
			0.00	Contingencies	60000.00
			335180.00	Travel	157815.00
			60000.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
1407800.00		**1422620.00**	**1345180.00**		**860000.00**
0.00	Excess of Expenditure over Income	0.00	62620.00	Closing Balance	562620.00
1407800.00		**1422620.00**	**1407800.00**		**1422620.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-82: Functional genomic analysis of Candida Glabrata-macrophage
P.I: Dr Rupinder Kaur
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
423591.00	Opening Balance	155859.00			
839000.00	Grant In Aid	0.00	228020.00	Salaries - Manpower	284787.00
			800000.00	Consumables	200000.00
			0.00	Contingencies	0.00
			0.00	Travel	0.00
			25091.00	Overheads	0.00
			53621.00	Equipment	38793.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
1262591.00		**155859.00**	**1106732.00**		**523580.00**
0.00	Excess of Expenditure over Income	367721.00	155859.00	Closing Balance	0.00
1262591.00		**523580.00**	**1262591.00**		**523580.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-83: Prokaryotic Transcription termination factor, Rho: Mechanism of Action and Biology
P.I: Dr Ranjan Sen
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		1155594.00		Opening Balance	1155594.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**1155594.00**			**1155594.00**	
1155594.00		Excess of Expenditure over Income	1155594.00		0.00		Closing Balance	0.00	
1155594.00			**1155594.00**		**1155594.00**			**1155594.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-83A: Understanding the mechanism of Azadirachtin-mediated cell signaling: role in anti-inflammation and anti-tumorigenesis
P.I: Dr Sunil Kumar Manna
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		126140.00		Opening Balance	126140.00	
0.00		Grant In Aid	126140.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**126140.00**		**126140.00**			**126140.00**	
126140.00		Excess of Expenditure over Income	0.00		0.00		Closing Balance	0.00	
126140.00			**126140.00**		**126140.00**			**126140.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-84: Preparing for vaccine efficacy trials: Baseline epidemiology, improved diagnosis, markers of protection and phase I/II trials

P.I: Dr Niyaz Ahmed

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		1150.00		Opening Balance	1150.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**1150.00**			**1150.00**	
1150.00		Excess of Expenditure over Income	1150.00		0.00		Closing Balance	0.00	
1150.00			**1150.00**		**1150.00**			**1150.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-84A: Human epigenetic to the rescue of human identification process: Enriching human DNA from DNA mixture employing antibodies directed against 5-methylcytosine followed by whole genome amplification

P.I: Dr Madhusudan Reddy

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
676641.00		Opening Balance	0.00				Opening Balance	106479.00	
0.00		Grant In Aid	0.00		248166.00		Salaries - Manpower	0.00	
					300000.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					60667.00		Overheads	0.00	
					174287.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
676641.00			**0.00**		**783120.00**			**106479.00**	
106479.00		Excess of Expenditure over Income	106479.00		0.00		Closing Balance	0.00	
783120.00			**106479.00**		**783120.00**			**106479.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-85: IdeR associated gene regulatory network in mycobacteria
P.I: Dr Akash Ranjan
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		1118755.00		Opening Balance	1118755.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**1118755.00**			**1118755.00**	
1118755.00		Excess of Expenditure over Income	1118755.00		0.00		Closing Balance	0.00	
1118755.00			**1118755.00**		**1118755.00**			**1118755.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-87: Comparative genomics of wild silkmoths
P.I: Dr J Nagaraju
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00		65698.00		Opening Balance	65698.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	0.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**65698.00**			**65698.00**	
65698.00		Excess of Expenditure over Income	65698.00		0.00		Closing Balance	0.00	
65698.00			**65698.00**		**65698.00**			**65698.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-88: Introduction of anti-baculoviral property in commercial silkworm strains by expression of multiple RNAi viral targets
P.I: Dr J Nagaraju
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
740000.00	Opening Balance	0.00			
0.00	Grant In Aid	680000.00	240000.00	Salaries - Manpower	200000.00
			0.00	Consumables	0.00
			0.00	Contingencies	0.00
			500000.00	Travel	261182.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
740000.00		**680000.00**	**740000.00**		**461182.00**
0.00	Excess of Expenditure over Income	0.00	0.00	Closing Balance	218818.00
740000.00		**680000.00**	**740000.00**		**680000.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-89: Characterization of Mycobacterium tuberculosis transcription machinery and Bacteriophage metagenomics
P.I: Dr Ranjan Sen
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	0.00	300000.00	Opening Balance	
300000.00	Grant In Aid	0.00	0.00	Salaries - Manpower	0.00
			0.00	Consumables	0.00
			0.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
300000.00		**0.00**	**300000.00**		**0.00**
0.00	Excess of Expenditure over Income	0.00	0.00	Closing Balance	0.00
300000.00		**0.00**	**300000.00**		**0.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-90: Role of Yapsins in the Pathobiology of Candida Glabrata
P.I: Dr Rupinder Kaur
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	0.00	451999.00	Opening Balance	636286.00
618700.00	Grant In Aid	0.00	141408.00	Salaries - Manpower	0.00
			300000.00	Consumables	0.00
			20000.00	Contingencies	0.00
			19425.00	Travel	0.00
			0.00	Overheads	0.00
			322154.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
618700.00		**0.00**	**1254986.00**		**636286.00**
636286.00	Excess of Expenditure over Income	636286.00	0.00	Closing Balance	0.00
1254986.00		**636286.00**	**1254986.00**		**636286.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-91: DMMT3L: epigenetic correlation with cancer
P.I: Dr Sanjeev Khosla
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	0.00	1098900.00	Opening Balance	1098900.00
0.00	Grant In Aid	0.00	0.00	Salaries - Manpower	0.00
			0.00	Consumables	0.00
			0.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
0.00		**0.00**	**1098900.00**		**1098900.00**
1098900.00	Excess of Expenditure over Income	1098900.00	0.00	Closing Balance	0.00
1098900.00		**1098900.00**	**1098900.00**		**1098900.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-92: Swarnajayanti fellowship proj on "Designing transcription anti-terminators: a novel approach for making new inhibitors of gene expression"

P.I: Dr Ranjan Sen

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	0.00	1238545.00	Opening Balance	1260461.00
3500000.00	Grant In Aid	0.00	635400.00	Salaries - Manpower	696542.00
			2300000.00	Consumables	1000000.00
			50000.00	Contingencies	0.00
			44674.00	Travel	133252.00
			120000.00	Overheads	0.00
			371842.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
3500000.00		**0.00**	**4760461.00**		**3090255.00**
1260461.00	Excess of Expenditure over Income	3090255.00	0.00	Closing Balance	0.00
4760461.00		**3090255.00**	**4760461.00**		**3090255.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P - 93: DBT Project on "Virtual Centre of Excellence on multidisciplinary approaches aimed at interventions against tuberculosis"

P.I.: Dr Shekar C Mande & Dr Sangita Mukhopadhyay

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
			684179.00	Opening Balance	1506886.00
0.00	Opening Balance	0.00	1560757.00	Salaries- Manpower	1341030.00
2010000.00	Grant in aid	645000.00	1050000.00	Consumables	546166.00
			100000.00	Contingencies	0.00
			2769.00	Travel	0.00
			0.00	Overheads	0.00
			119181.00	Equipment	359369.00
2010000.00		645000.00	3516886.00		3753451.00
1506886.00	Excess of expenditure over income	3108451.00		Closing Balance	
3516886.00		**3753451.00**	**3516886.00**		**3753451.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-95: Construction of regulatory networks in prokaryotes through protein: Protein interaction predictions and transcription regulation predictions. (MOU with Russian Foundation)

P.I: Dr Shekar C Mande

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
424041.00		Opening Balance		0.00					
0.00		Grant In Aid		0.00		0.00	Salaries - Manpower		0.00
						0.00	Consumables		0.00
						0.00	Contingencies		0.00
						0.00	Travel		0.00
						0.00	Overheads		0.00
						0.00	Equipment		0.00
						0.00	Books		0.00
						0.00	AMC		0.00
						0.00	Others		0.00
						424041.00	Transfer of Funds		0.00
424041.00				**0.00**	**424041.00**				**0.00**
0.00		Excess of Expenditure over Income		0.00		0.00	Closing Balance		0.00
424041.00				**0.00**	**424041.00**				**0.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-96: Molecular Characterization of sporadic colorectal cancer in the young from India

P.I: Dr M D Bashyam

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance		0.00		655942.00			
1452712.00		Grant In Aid		0.00		26700.00	Salaries - Manpower		0.00
						713546.00	Consumables		0.00
						0.00	Contingencies		0.00
						56524.00	Travel		0.00
						0.00	Overheads		0.00
						0.00	Equipment		0.00
						0.00	Books		0.00
						0.00	AMC		0.00
						0.00	Others		0.00
						0.00	Transfer of Funds		0.00
1452712.00				**0.00**	**1452712.00**				**0.00**
0.00		Excess of Expenditure over Income		0.00		0.00	Closing Balance		0.00
1452712.00				**0.00**	**1452712.00**				**0.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-97: Proteome-wide Analysis of Serine pyrophosphorylation by inositol pyrophosphates
P.I: Dr Rashna Bhandari
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
488524.00	Opening Balance	0.00		Opening Balance	98464.00
532000.00	Grant In Aid	0.00	198439.00	Salaries - Manpower	0.00
			575300.00	Consumables	0.00
			0.00	Contingencies	0.00
			24700.00	Travel	0.00
			0.00	Overheads	0.00
			320549.00	Equipment	48406.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
1020524.00		**0.00**	**1118988.00**		**146870.00**
98464.00	Excess of Expenditure over Income	146870.00	0.00	Closing Balance	0.00
1118988.00		**146870.00**	**1118988.00**		**146870.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-98: Role of cell - cell signaling mediated by Diffusible signaling factor (DSF) in Xanthomonas virulence
P.I: Dr Subhadeep Chatterjee
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	0.00	466554.00	Opening Balance	63019.00
1641200.00	Grant In Aid	0.00	149240.00	Salaries - Manpower	187200.00
			900000.00	Consumables	0.00
			10000.00	Contingencies	0.00
			19240.00	Travel	0.00
			0.00	Overheads	0.00
			159185.00	Equipment	5625.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
1641200.00		**0.00**	**1704219.00**		**255844.00**
63019.00	Excess of Expenditure over Income	255844.00	0.00	Closing Balance	0.00
1704219.00		**255844.00**	**1704219.00**		**255844.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-99: Role of inositol Pyrophosphates in eukaryotic cell growth, proliferation and ribosomae biogenesis

P.I: Dr Rashna Bhandari

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	0.00	113757.00	Opening Balance	1261900.00
726299.00	Grant In Aid	1217000.00	366800.00	Salaries - Manpower	206491.00
			800000.00	Consumables	0.00
			50000.00	Contingencies	20000.00
			8253.00	Travel	2636.00
			0.00	Overheads	0.00
			649389.00	Equipment	41753.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
726299.00		**1217000.00**	**1988199.00**		**1532780.00**
1261900.00	Excess of Expenditure over Income	315780.00	0.00	Closing Balance	0.00
1988199.00		**1532780.00**	**1988199.00**		**1532780.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-100: Effect of raective oxygen species on T-Cell immune response: An approach to understand the molecular mechanism of immunosuppression during tuberculosis - National Bioscience Award

P.I: Dr Sangita Mukhopadhyay

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	0.00	300000.00	Opening Balance	335000.00
0.00	Grant In Aid	0.00	30000.00	Salaries - Manpower	77479.00
			0.00	Consumables	164111.00
			5000.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
0.00		**0.00**	**335000.00**		**576590.00**
335000.00	Excess of Expenditure over Income	576590.00	0.00	Closing Balance	0.00
335000.00		**576590.00**	**335000.00**		**576590.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-101: Role of inositol pyrophosphates in cell physiology: Investigating the biochemical significance of protein pyrophosphorylation - Senior Fellowship

P.I: Dr Rashna Bhandari

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
15688931.00	Opening Balance	13729401.00			
4470916.00	Grant In Aid	0.00	1787120.00	Salaries - Manpower	1818930.00
			1100000.00	Consumables	2300000.00
			0.00	Contingencies	849721.00
			73814.00	Travel	27452.00
			584586.00	Overheads	0.00
			2884926.00	Equipment	4191222.00
			0.00	Books	177809.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
20159847.00		**13729401.00**	**6430446.00**		**9365134.00**
0.00	Excess of Expenditure over Income	0.00	13729401.00	Closing Balance	4364267.00
20159847.00		**13729401.00**	**20159847.00**		**13729401.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-102: Understanding the role of Mycobacterium tuberculosis heat shockprotein 60 as Th1/Th2 immuno modular

P.I: Dr Sangita Mukhopadhyay

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	82654.00	445133.00		
1086164.00	Grant In Aid	503782.00	289800.00	Salaries - Manpower	386400.00
			200000.00	Consumables	600000.00
			0.00	Contingencies	29605.00
			20627.00	Travel	451.00
			25000.00	Overheads	0.00
			22950.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
1086164.00		**586436.00**	**1003510.00**		**1016456.00**
0.00	Excess of Expenditure over Income	430020.00	82654.00	Closing Balance	0.00
1086164.00		**1016456.00**	**1086164.00**		**1016456.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-103: National Bioscience Award - Regulation of mast cell signaling, apoptosis and surface receptors
P.I: Dr Sunil Kumar Manna
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00				Opening Balance	300000.00	
0.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					300000.00		Consumables	300000.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**0.00**		**300000.00**			**600000.00**	
300000.00		Excess of Expenditure over Income	600000.00		0.00		Closing Balance	0.00	
300000.00			**600000.00**		**300000.00**			**600000.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-104: Virtual Centre of Excellence on Epigenetics
P.I: Dr Sanjeev Khosla
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
297613.00		Opening Balance	0.00				Opening Balance	1394866.00	
0.00		Grant In Aid	1437000.00		484709.00		Salaries - Manpower	452710.00	
					1100000.00		Consumables	1594206.00	
					70000.00		Contingencies	0.00	
					37770.00		Travel	13093.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
297613.00			**1437000.00**		**1692479.00**			**3454875.00**	
1394866.00		Excess of Expenditure over Income	2017875.00		0.00		Closing Balance	0.00	
1692479.00			**3454875.00**		**1692479.00**			**3454875.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-105: Cloning, Characterization and analysis of chromosomal rearrangements in human genetic disorders
P.I: Dr Ashwin B Dalal
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
145971.00	Opening Balance	0.00		Opening Balance	90844.00
681000.00	Grant In Aid	0.00	187200.00	Salaries - Manpower	126202.00
			700000.00	Consumables	600000.00
			20000.00	Contingencies	20000.00
			10615.00	Travel	7900.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
826971.00		**0.00**	**917815.00**		**844946.00**
90844.00	Excess of Expenditure over Income	844946.00	0.00	Closing Balance	0.00
917815.00		**844946.00**	**917815.00**		**844946.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-106: Clinical, Biochemical and molecular analysis of treatable lysosomal storage disorders
P.I: Dr Ashwin B Dalal
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	190952.00	446056.00		
1602302.00	Grant In Aid	505153.00	484977.00	Salaries - Manpower	409530.00
			450000.00	Consumables	450000.00
			30317.00	Contingencies	25786.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
1602302.00		**696105.00**	**1411350.00**		**885316.00**
0.00	Excess of Expenditure over Income	189211.00	190952.00	Closing Balance	0.00
1602302.00		**885316.00**	**1602302.00**		**885316.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-107: IYBA Project - Mechanism and role of bacterial cell-cell signaling molecules in plant defense response
P.I: Dr Subhadeep Chatterjee
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
602006.00	Opening Balance	63600.00			
773000.00	Grant In Aid	817000.00	187200.00	Salaries - Manpower	187200.00
			600000.00	Consumables	674153.00
			0.00	Contingencies	0.00
			0.00	Travel	18812.00
			54131.00	Overheads	0.00
			470075.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
1375006.00		**880600.00**	**1311406.00**		**880165.00**
0.00	Excess of Expenditure over Income	0.00	63600.00	Closing Balance	435.00
1375006.00		**880600.00**	**1375006.00**		**880600.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-108: Establishment of EBV transformed cell lines from families with rare genetic disorders
P.I: Dr Ashwin B Dalal
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
184023.00	Opening Balance	69925.00			
470400.00	Grant In Aid	0.00	187200.00	Salaries - Manpower	174737.00
			350000.00	Consumables	250000.00
			30000.00	Contingencies	25000.00
			17298.00	Travel	13153.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
654423.00		**69925.00**	**584498.00**		**462890.00**
0.00	Excess of Expenditure over Income	392965.00	69925.00	Closing Balance	0.00
654423.00		**462890.00**	**654423.00**		**462890.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-109: Molecular dissection of PI3-Kinase/Akt pathway by suing proteomics based approach: A study to identify novel potential oncogenes and tumor suppressors

P.I: Dr M Subba Reddy

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
1476104.00	Opening Balance	315626.00			
742000.00	Grant In Aid	566000.00	187200.00	Salaries - Manpower	187200.00
			800000.00	Consumables	580160.00
			0.00	Contingencies	0.00
			0.00	Travel	19840.00
			0.00	Overheads	0.00
			915278.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
2218104.00		**881626.00**	**1902478.00**		**787200.00**
0.00	Excess of Expenditure over Income	0.00	315626.00	Closing Balance	94426.00
2218104.00		**881626.00**	**2218104.00**		**881626.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-110: India-Japan research project title"Identification and analysis of sex determining genes in silkmoths"

P.I: Dr J Nagaraju

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
24389.00	Opening Balance	0.00		Opening Balance	168679.00
0.00	Grant In Aid	0.00	0.00	Salaries - Manpower	0.00
			0.00	Consumables	0.00
			0.00	Contingencies	0.00
			193068.00	Travel	22712.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
24389.00		**0.00**	**193068.00**		**191391.00**
168679.00	Excess of Expenditure over Income	191391.00	0.00	Closing Balance	0.00
193068.00		**191391.00**	**193068.00**		**191391.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-111: Ramalingaswami Fellowship - Refractoriness mechanism in Mosquito: cracking molecular codes at genomic scale
P.I: Dr Shweta Tyagi
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
488631.00	Opening Balance	431731.00			
1511500.00	Grant In Aid	1487000.00	1168400.00	Salaries - Manpower	1106000.00
			400000.00	Consumables	262315.00
			0.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
2000131.00		**1918731.00**	**1568400.00**		**1368315.00**
0.00	Excess of Expenditure over Income	0.00	431731.00	Closing Balance	550416.00
2000131.00		**1918731.00**	**2000131.00**		**1918731.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-112: Ramanujan Fellowship
P.I: Dr Rohit Joshi
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
803726.00	Opening Balance	0.00			
1000000.00	Grant In Aid	0.00	626400.00	Salaries - Manpower	0.00
			157326.00	Consumables	0.00
			0.00	Contingencies	0.00
			0.00	Travel	0.00
			20000.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			1000000.00	Transfer of Funds	0.00
1803726.00		**0.00**	**1803726.00**		**0.00**
0.00	Excess of Expenditure over Income	0.00	0.00	Closing Balance	0.00
1803726.00		**0.00**	**1803726.00**		**0.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-113: Clinical and molecular genetic analysis of squamous cell carcinoma of the tongue
P.I: Dr M D Bashyam
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
550715.00	Opening Balance	534630.00			
848689.00	Grant In Aid	0.00	519587.00	Salaries - Manpower	544619.00
			320000.00	Consumables	590000.00
			0.00	Contingencies	34084.00
			0.00	Travel	1500.00
			25187.00	Overheads	0.00
			0.00	Equipment	401181.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
1399404.00		**534630.00**	**864774.00**		**1571384.00**
0.00	Excess of Expenditure over Income	1036754.00	534630.00	Closing Balance	0.00
1399404.00		**1571384.00**	**1399404.00**		**1571384.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-114: Evaluating the Calcineurin-NFAT Pathway and its regulators superoxide dismutase (SOD) AND RCAN1 (regular of Calcineurin) Down Syndrome
P.I: Dr Gayatri Ramakrishna, Dr Ashwin Dalal
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
1532761.00	Opening Balance	51553.00			
0.00	Grant In Aid	760000.00	187200.00	Salaries - Manpower	112840.00
			1000000.00	Consumables	960000.00
			0.00	Contingencies	0.00
			0.00	Travel	7680.00
			0.00	Overheads	0.00
			294008.00	Equipment	181892.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
1532761.00		**811553.00**	**1481208.00**		**1262412.00**
0.00	Excess of Expenditure over Income	450859.00	51553.00	Closing Balance	0.00
1532761.00		**1262412.00**	**1532761.00**		**1262412.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-115: Setting up of the National Institute of Animal Biotechnology
P.I: Dr J Gowrishankar
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
4559305.00	Opening Balance	8039741.00			
65500000.00	Grant In Aid	143232.00	3276411.00	Salaries - Manpower	0.00
			6778000.00	Consumables	0.00
			4083820.00	Contingencies	0.00
			1301119.00	Travel	0.00
			0.00	Overheads	0.00
			4580214.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			42000000.00	Transfer of Funds	8182978.00
70059305.00		**8182973.00**	**62019564.00**		**8182978.00**
0.00	Excess of Expenditure over Income	5.00	8039741.00	Closing Balance	0.00
70059305.00		**8182978.00**	**70059305.00**		**8182978.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-116: DBT-India and AIST - Japan : Understanding molecular mechanisms controlling dual role of Ras, Sirtuins and CARF in relation to cellular proliferation and senescence: Novel Strategy for developing cancer therapeutics
P.I: Dr Gayatri Ramakrishna
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
1692817.00	Opening Balance	0.00		Opening Balance	288420.00
0.00	Grant In Aid	0.00	71961.00	Salaries - Manpower	144560.00
			1000000.00	Consumables	600000.00
			100000.00	Contingencies	100000.00
			9276.00	Travel	118386.00
			0.00	Overheads	0.00
			800000.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
1692817.00		**0.00**	**1981237.00**		**1251366.00**
288420.00	Excess of Expenditure over Income	1251366.00	0.00	Closing Balance	0.00
1981237.00		**1251366.00**	**1981237.00**		**1251366.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-117: Joint New Indigo Era-Net project titled "Mycobacterium Tuberculosis:bioinformatic and structural strategies towards treatment

P.I: Dr Shekhar C Mande

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
5251500.00	Opening Balance	0.00			
0.00	Grant In Aid	0.00	138667.00	Salaries - Manpower	0.00
			300000.00	Consumables	0.00
			25000.00	Contingencies	0.00
			140754.00	Travel	0.00
			50000.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			4597079.00	Transfer of Funds	0.00
5251500.00		**0.00**	**5251500.00**		**0.00**
0.00	Excess of Expenditure over Income	0.00	0.00	Closing Balance	0.00
5251500.00		**0.00**	**5251500.00**		**0.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-118: Construction of regulatory networks in Mycobacterium tuberculosis through analysis of gene expression data and transcription regulation predictions. (MOU with Russian Foundation)

P.I: Dr Shekhar C Mande

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
1115770.00	Opening Balance	0.00			
0.00	Grant In Aid	0.00	227877.00	Salaries - Manpower	0.00
			300000.00	Consumables	0.00
			10000.00	Contingencies	0.00
			98968.00	Travel	0.00
			35280.00	Overheads	0.00
			183443.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			260202.00	Transfer of Funds	0.00
1115770.00		**0.00**	**1115770.00**		**0.00**
0.00	Excess of Expenditure over Income	0.00	0.00	Closing Balance	0.00
1115770.00		**0.00**	**1115770.00**		**0.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-119: Analysis of DNA copy number alterations in esophaeal cancer
P.I: Dr M D Bashyam
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
560342.00	Opening Balance	0.00		Opening Balance	738605.00
0.00	Grant In Aid	1252800.00	247000.00	Salaries - Manpower	306453.00
			1000000.00	Consumables	1300000.00
			35000.00	Contingencies	25000.00
			16947.00	Travel	15371.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
560342.00		**1252800.00**	**1298947.00**		**2385429.00**
738605.00	Excess of Expenditure over Income	1132629.00	0.00	Closing Balance	0.00
1298947.00		**2385429.00**	**1298947.00**		**2385429.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-120: Effect of reactive oxygen species on macrophage signalosome: impact on antigen presentation functions and T Cell priming responses
P.I: Dr Sangita Mukhopadhyay
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
617000.00	Opening Balance	124600.00			
0.00	Grant In Aid	0.00	62400.00	Salaries - Manpower	143923.00
			400000.00	Consumables	580895.00
			30000.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
617000.00		**124600.00**	**492400.00**		**724818.00**
0.00	Excess of Expenditure over Income	600218.00	124600.00	Closing Balance	0.00
617000.00		**724818.00**	**617000.00**		**724818.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-121: Identification and characterization of PTEN regulators
P.I: Dr M Subba Reddy
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
37096.00	Opening Balance	0.00		Opening Balance	597186.00
0.00	Grant In Aid	0.00	187200.00	Salaries - Manpower	108680.00
			400000.00	Consumables	400000.00
			25000.00	Contingencies	25000.00
			12082.00	Travel	0.00
			10000.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
37096.00		**0.00**	**634282.00**		**1130866.00**
597186.00	Excess of Expenditure over Income	1130866.00	0.00	Closing Balance	0.00
634282.00		**1130866.00**	**634282.00**		**1130866.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-122: Understanding the role of Hox genes in anterior-posterior axis determination of the central nervous system
P.I: Dr Rohit Joshi
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	11479043.00			
13606258.00	Grant In Aid	4880510.00	660600.00	Salaries - Manpower	1340206.00
			835148.00	Consumables	1400000.00
			0.00	Contingencies	342745.00
			0.00	Travel	165680.00
			193383.00	Overheads	0.00
			438084.00	Equipment	21240.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
13606258.00		**16359553.00**	**2127215.00**		**3269871.00**
0.00	Excess of Expenditure over Income	0.00	11479043.00	Closing Balance	13089682.00
13606258.00		**16359553.00**	**13606258.00**		**16359553.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-123: Establish a Max Planck Partner Group for Genetic Diversity Studies at CDFD
P.I: Dr N Madhusudan Reddy
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	2074056.00			
2884810.00	Grant In Aid	1047000.00	185648.00	Salaries - Manpower	564208.00
			473306.00	Consumables	670000.00
			50000.00	Contingencies	200000.00
			0.00	Travel	183584.00
			0.00	Overheads	0.00
			101800.00	Equipment	351295.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
2884810.00		**3121056.00**	**810754.00**		**1969087.00**
0.00	Excess of Expenditure over Income	0.00	2074056.00	Closing Balance	1151969.00
2884810.00		**3121056.00**	**2884810.00**		**3121056.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-124: Preparation and characterization of peroxometal compounds and studies and their biological significance in cellular signalling
P.I: Dr Gayatri Ramakrishna
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	167284.00			
819000.00	Grant In Aid	0.00	111716.00	Salaries - Manpower	187200.00
			500000.00	Consumables	500000.00
			40000.00	Contingencies	30000.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
819000.00		**167284.00**	**651716.00**		**717200.00**
0.00	Excess of Expenditure over Income	549916.00	167284.00	Closing Balance	0.00
819000.00		**717200.00**	**819000.00**		**717200.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-125: Mechanistic studies on the role of protein kinase Snfilk in cell cycle and cancer
P.I: Dr M Subba Reddy
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	154000.00			
764000.00	Grant In Aid	0.00	110000.00	Salaries - Manpower	134981.00
			500000.00	Consumables	500000.00
			0.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
764000.00		**154000.00**	**610000.00**		**634981.00**
0.00	Excess of Expenditure over Income	480981.00	154000.00	Closing Balance	0.00
764000.00		**634981.00**	**764000.00**		**634981.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-126: Rho-dependent transcription termination machinery: mechanism of action
P.I: Dr Ranjan Sen
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	1581615.00			
2539300.00	Grant In Aid	0.00	111548.00	Salaries - Manpower	488532.00
			800000.00	Consumables	1381445.00
			30000.00	Contingencies	3081.00
			16137.00	Travel	8581.00
			0.00	Overheads	0.00
			0.00	Equipment	385404.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
2539300.00		**1581615.00**	**957685.00**		**2267043.00**
0.00	Excess of Expenditure over Income	685428.00	1581615.00	Closing Balance	0.00
2539300.00		**2267043.00**	**2539300.00**		**2267043.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-127: Systematic studies on the functional network of phosphatases in cell life and death
P.I: Dr M Subba Reddy
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	5052715.00			
11097596.00	Grant In Aid	4637410.00	269440.00	Salaries - Manpower	538921.00
			3000000.00	Consumables	3560000.00
			0.00	Contingencies	506524.00
			0.00	Travel	250853.00
			549534.00	Overheads	0.00
			2225907.00	Equipment	671289.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
11097596.00		**9690125.00**	**6044881.00**		**5527587.00**
0.00	Excess of Expenditure over Income	0.00	5052715.00	Closing Balance	4162538.00
11097596.00		**9690125.00**	**11097596.00**		**9690125.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-128: Mechanism of iron acquisition and iron homeostasis in an opportunistic human pathogen Candida glabrata
P.I: Dr Rupinder Kaur
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	2053587.00			
2807200.00	Grant In Aid	1017200.00	123613.00	Salaries - Manpower	85280.00
			600000.00	Consumables	800000.00
			30000.00	Contingencies	30000.00
			0.00	Travel	23343.00
			0.00	Overheads	0.00
			0.00	Equipment	1594393.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
2807200.00		**3070787.00**	**753613.00**		**2533016.00**
0.00	Excess of Expenditure over Income	0.00	2053587.00	Closing Balance	537771.00
2807200.00		**3070787.00**	**2807200.00**		**3070787.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-129: Discovery of bioactive natural products from microbes especially actinomycetes in niche biotopes in Manipur
P.I: Dr Shekhar C Mande
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	306000.00			
306000.00	Grant In Aid	0.00	0.00	Salaries - Manpower	0.00
			0.00	Consumables	0.00
			0.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	306000.00
306000.00		**306000.00**	**0.00**		**306000.00**
0.00	Excess of Expenditure over Income	0.00	306000.00	Closing Balance	0.00
306000.00		**306000.00**	**306000.00**		**306000.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-130: Comparative genetic analysis of sex chromosomes and sex determining genes in silkmoths
P.I: Dr J Nagaraju
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	4187000.00			
5987000.00	Grant In Aid	0.00	0.00	Salaries - Manpower	443341.00
			1750000.00	Consumables	2800000.00
			50000.00	Contingencies	100000.00
			0.00	Travel	377686.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
5987000.00		**4187000.00**	**1800000.00**		**3721027.00**
0.00	Excess of Expenditure over Income	0.00	4187000.00	Closing Balance	465973.00
5987000.00		**4187000.00**	**5987000.00**		**4187000.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-131: Structural and functional studies of Acyl CoA Binding proteins from plasmodium falciparum
P.I: Dr Akash Ranjan
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	1182935.00			
1899200.00	Grant In Aid	0.00	41265.00	Salaries - Manpower	414514.00
			650000.00	Consumables	1488971.00
			25000.00	Contingencies	29000.00
			0.00	Travel	19119.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
1899200.00		**1182935.00**	**716265.00**		**1951604.00**
0.00	Excess of Expenditure over Income	768669.00	1182935.00	Closing Balance	0.00
1899200.00		**1951604.00**	**1899200.00**		**1951604.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-132: Characterization of tumor suppressor function of ARIDIB, a component of the human SWI/SNF chromatin remodelling complex
P.I: Dr M D Bashyam, Dr Rohit Joshi
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	634323.00			
929200.00	Grant In Aid	0.00	84877.00	Salaries - Manpower	425016.00
			200000.00	Consumables	1400000.00
			10000.00	Contingencies	30000.00
			0.00	Travel	7787.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
929200.00		**634323.00**	**294877.00**		**1862803.00**
0.00	Excess of Expenditure over Income	1228480.00	634323.00	Closing Balance	0.00
929200.00		**1862803.00**	**929200.00**		**1862803.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-133: Investigating the role of Hox gene deformed in central nervous system patterning in Drosophila melanogaster

P.I: Dr Rohit Joshi

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	1549000.00			
1849000.00	Grant In Aid	763000.00	0.00	Salaries - Manpower	239394.00
			300000.00	Consumables	600000.00
			0.00	Contingencies	0.00
			0.00	Travel	28325.00
			0.00	Overheads	0.00
			0.00	Equipment	474792.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
1849000.00		**2312000.00**	**300000.00**		**1342511.00**
0.00	Excess of Expenditure over Income	0.00	1549000.00	Closing Balance	969489.00
1849000.00		**2312000.00**	**1849000.00**		**2312000.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-134: Exploration of wild silk moth biodiversity in Manipur and their genetic characterization using molecular markers

P.I: Dr K P Arun Kumar

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	254000.00			
400000.00	Grant In Aid	0.00	0.00	Salaries - Manpower	0.00
			131000.00	Consumables	350000.00
			15000.00	Contingencies	15000.00
			0.00	Travel	30437.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
400000.00		**254000.00**	**146000.00**		**395437.00**
0.00	Excess of Expenditure over Income	141437.00	254000.00	Closing Balance	0.00
400000.00		**395437.00**	**400000.00**		**395437.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-135: Sys TB: A Network Program for Resolving the Intracellular Dynamics of Host Phthogen Interaction in TB Infection
P.I: Dr. Sanjeev Kholsa
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	7418200.00			
7943200.00	Grant In Aid	0.00	0.00	Salaries - Manpower	0.00
			500000.00	Consumables	2000000.00
			25000.00	Contingencies	25000.00
			0.00	Travel	16634.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
7943200.00		**7418200.00**	**525000.00**		**2041634.00**
0.00	Excess of Expenditure over Income	0.00	7418200.00	Closing Balance	5376566.00
7943200.00		**7418200.00**	**7943200.00**		**7418200.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-136: Raf Kinase - a key target for modem-day theraphy against tumors
P.I: Dr Sunil Kumar Manna
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance	837200.00			
837200.00	Grant In Aid	0.00	0.00	Salaries - Manpower	162240.00
			0.00	Consumables	566980.00
			0.00	Contingencies	30000.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
			0.00	Books	0.00
			0.00	AMC	0.00
			0.00	Others	0.00
			0.00	Transfer of Funds	0.00
837200.00		**837200.00**	**0.00**		**759220.00**
0.00	Excess of Expenditure over Income	0.00	837200.00	Closing Balance	77980.00
837200.00		**837200.00**	**837200.00**		**837200.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-137: Signaling pathways involved in down regulation of proinflammatory responses by PPE18 protein of Mycobacterium tuberculosis: Implication of PPE18 as therapeutics

P.I: Dr Sangita Mukhopadhyay

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	1500000.00						
1500000.00		Grant In Aid	0.00		0.00		Salaries - Manpower	99840.00	
					0.00		Consumables	603140.00	
					0.00		Contingencies	112000.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
1500000.00			**1500000.00**		**0.00**			**814980.00**	
0.00		Excess of Expenditure over Income	0.00		1500000.00		Closing Balance	685020.00	
1500000.00			**1500000.00**		**1500000.00**			**1500000.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-138: Co-evaluation of Dnmt3l and Genomic imprinting

P.I: Dr Sanjeev Khosla

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00						
0.00		Grant In Aid	1799600.00		0.00		Salaries - Manpower	70656.00	
					0.00		Consumables	800000.00	
					0.00		Contingencies	25000.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**1799600.00**		**0.00**			**895656.00**	
0.00		Excess of Expenditure over Income	0.00		0.00		Closing Balance	903944.00	
0.00			**1799600.00**		**0.00**			**1799600.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-139: Evaluating the role of Sirtuins and epigenetic changes during cellular senescense in context of p53 status

P.I: Dr Gayatri Ramakrishna, Dr Sanjeev Khosla

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	2467200.00						
2467200.00		Grant In Aid	500000.00		0.00		Salaries - Manpower	80617.00	
					0.00		Consumables	1623000.00	
					0.00		Contingencies	40000.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
2467200.00			**2967200.00**		**0.00**			**1743617.00**	
0.00		Excess of Expenditure over Income	0.00		2467200.00		Closing Balance	1223583.00	
2467200.00			**2967200.00**		**2467200.00**			**2967200.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-140: Development of baculovirus resistant silkworms strains through synthetic miRNA based knockdown of essential viral genes

P.I: Dr K P Arun Kumar

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00						
0.00		Grant In Aid	1850000.00		0.00		Salaries - Manpower	193909.00	
					0.00		Consumables	1084288.00	
					0.00		Contingencies	0.00	
					0.00		Travel	15712.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**1850000.00**		**0.00**			**1293909.00**	
0.00		Excess of Expenditure over Income	0.00		0.00		Closing Balance	556091.00	
0.00			**1850000.00**		**0.00**			**1850000.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-141: Evaluating the functional role of PTEN interacting proteins in cell survival signaling and tumor suppression

P.I: Dr M Subba Reddy

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
	0.00	Opening Balance		0.00					
	0.00	Grant In Aid		500000.00		0.00	Salaries - Manpower		0.00
						0.00	Consumables		418537.00
						0.00	Contingencies		80000.00
						0.00	Travel		0.00
						0.00	Overheads		0.00
						0.00	Equipment		0.00
						0.00	Books		0.00
						0.00	AMC		0.00
						0.00	Others		0.00
						0.00	Transfer of Funds		0.00
	0.00			**500000.00**		**0.00**			**498537.00**
	0.00	Excess of Expenditure over Income		0.00		0.00	Closing Balance		1463.00
	0.00			**500000.00**		**0.00**			**500000.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-142: Identification of H3K4 TRI Demethylase involved in erasing H3K4 trimethylation marks at E2F Responsive promoters

P.I: Dr Shweta Tyagi

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
	0.00	Opening Balance		0.00					
	0.00	Grant In Aid		1514000.00		0.00	Salaries - Manpower		128938.00
						0.00	Consumables		600000.00
						0.00	Contingencies		0.00
						0.00	Travel		0.00
						0.00	Overheads		0.00
						0.00	Equipment		424914.00
						0.00	Books		0.00
						0.00	AMC		0.00
						0.00	Others		0.00
						0.00	Transfer of Funds		0.00
	0.00			**1514000.00**		**0.00**			**1153852.00**
	0.00	Excess of Expenditure over Income		0.00		0.00	Closing Balance		360148.00
	0.00			**1514000.00**		**0.00**			**1514000.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-143: Microarray based characterisation of squamous cell carcinoma of the tongue occuring in non smokers
P.I: Dr M D Bashyam
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00						
0.00		Grant In Aid	714000.00		0.00		Salaries - Manpower	163716.00	
					0.00		Consumables	404000.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
0.00			**714000.00**		**0.00**			**567716.00**	
0.00		Excess of Expenditure over Income	0.00		0.00		Closing Balance	146284.00	
0.00			**714000.00**		**0.00**			**714000.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-144: Tri-National Training Program for Psychiatric Genetics
P.I: Dr Ashwin B Dalal
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	267184.00						
267184.00		Grant In Aid	0.00		0.00		Salaries - Manpower	0.00	
					0.00		Consumables	213025.00	
					0.00		Contingencies	0.00	
					0.00		Travel	54159.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
					0.00		Books	0.00	
					0.00		AMC	0.00	
					0.00		Others	0.00	
					0.00		Transfer of Funds	0.00	
267184.00			**267184.00**		**0.00**			**267184.00**	
0.00		Excess of Expenditure over Income	0.00		267184.00		Closing Balance	0.00	
267184.00			**267184.00**		**267184.00**			**267184.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-145: H3K4 HMT family regulatescell cycle progression
P.I: Dr Shweta Tyagi
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
	0.00	Opening Balance		0.00					
	0.00	Grant In Aid		3885200.00		0.00	Salaries - Manpower		76994.00
						0.00	Consumables		1600000.00
						0.00	Contingencies		0.00
						0.00	Travel		0.00
						0.00	Overheads		0.00
						0.00	Equipment		0.00
						0.00	Books		0.00
						0.00	AMC		0.00
						0.00	Others		0.00
						0.00	Transfer of Funds		0.00
	0.00			**3885200.00**		**0.00**			**1676994.00**
	0.00	Excess of Expenditure over Income		0.00		0.00	Closing Balance		2208206.00
	0.00			**3885200.00**		**0.00**			**3885200.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-146: Role of MLL in ribosomal RNA transcription
P.I: Dr Shweta Tyagi
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
	0.00	Opening Balance		0.00					
	0.00	Grant In Aid		1850000.00		0.00	Salaries - Manpower		78080.00
						0.00	Consumables		600000.00
						0.00	Contingencies		0.00
						0.00	Travel		0.00
						0.00	Overheads		0.00
						0.00	Equipment		359711.00
						0.00	Books		0.00
						0.00	AMC		0.00
						0.00	Others		0.00
						0.00	Transfer of Funds		0.00
	0.00			**1850000.00**		**0.00**			**1037791.00**
	0.00	Excess of Expenditure over Income		0.00		0.00	Closing Balance		812209.00
	0.00			**1850000.00**		**0.00**			**1850000.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-147: The Effect of Parental Education, Ethics of Research Participation and Array Comparative Genomic Hybridization in Subjects with Mental Retardation (MR) and /or Autism

P.I: Dr Ashwin B Dalal

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
	0.00	Opening Balance		0.00					
	0.00	Grant In Aid		805900.00		0.00	Salaries - Manpower		40258.00
						0.00	Consumables		400000.00
						0.00	Contingencies		50000.00
						0.00	Travel		0.00
						0.00	Overheads		0.00
						0.00	Equipment		0.00
						0.00	Books		0.00
						0.00	AMC		0.00
						0.00	Others		0.00
						0.00	Transfer of Funds		0.00
	0.00			**805900.00**		**0.00**			**490258.00**
	0.00	Excess of Expenditure over Income		0.00		0.00	Closing Balance		315642.00
	0.00			**805900.00**		**0.00**			**805900.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD

P-148: Transcriptional regulation of novel tumor suppressor genes in Pancreatic Cancer

P.I: Dr K Jayaprakash Narayana

Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
	0.00	Opening Balance		0.00					
	0.00	Grant In Aid		700000.00		0.00	Salaries - Manpower		170484.00
						0.00	Consumables		0.00
						0.00	Contingencies		19081.00
						0.00	Travel		0.00
						0.00	Overheads		0.00
						0.00	Equipment		0.00
						0.00	Books		0.00
						0.00	AMC		0.00
						0.00	Others		0.00
						0.00	Transfer of Funds		490109.00
	0.00			**700000.00**		**0.00**			**679674.00**
	0.00	Excess of Expenditure over Income		0.00		0.00	Closing Balance		20326.00
	0.00			**700000.00**		**0.00**			**700000.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-149: Role of SUMOylation in the pathobiology of Candida Glabrata
P.I: Dr Rupinder Kaur
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
	0.00	Opening Balance		0.00					
	0.00	Grant In Aid		1979600.00		0.00	Salaries - Manpower		59314.00
						0.00	Consumables		100000.00
						0.00	Contingencies		50000.00
						0.00	Travel		0.00
						0.00	Overheads		0.00
						0.00	Equipment		0.00
						0.00	Books		0.00
						0.00	AMC		0.00
						0.00	Others		0.00
						0.00	Transfer of Funds		0.00
	0.00			**1979600.00**		**0.00**			**209314.00**
	0.00	Excess of Expenditure over Income		0.00		0.00	Closing Balance		1770286.00
	0.00			**1979600.00**		**0.00**			**1979600.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-150: Genetic and genomic basis of the evolution of bombycid and sturniid silkmoths
P.I: Dr J Nagaraju
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
	0.00	Opening Balance		0.00					
	0.00	Grant In Aid		210000.00		0.00	Salaries - Manpower		0.00
						0.00	Consumables		0.00
						0.00	Contingencies		0.00
						0.00	Travel		45294.00
						0.00	Overheads		0.00
						0.00	Equipment		0.00
						0.00	Books		0.00
						0.00	AMC		0.00
						0.00	Others		0.00
						0.00	Transfer of Funds		0.00
	0.00			**210000.00**		**0.00**			**45294.00**
	0.00	Excess of Expenditure over Income		0.00		0.00	Closing Balance		164706.00
	0.00			**210000.00**		**0.00**			**210000.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-151: Human Exome Sequencing to Identify Novel Genes for Medelian Disorders
P.I: Dr Ashwin B Dalal
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
	0.00	Opening Balance		0.00					
	0.00	Grant In Aid		1993200.00		0.00	Salaries - Manpower		0.00
						0.00	Consumables		0.00
						0.00	Contingencies		0.00
						0.00	Travel		0.00
						0.00	Overheads		0.00
						0.00	Equipment		0.00
						0.00	Books		0.00
						0.00	AMC		0.00
						0.00	Others		0.00
						0.00	Transfer of Funds		0.00
	0.00			**1993200.00**		**0.00**			**0.00**
	0.00	Excess of Expenditure over Income		0.00		0.00	Closing Balance		1993200.00
	0.00			**1993200.00**		**0.00**			**1993200.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-153: An attractive and promising stragegy for early cancer diagnosis through the assembly of the human cancer volatome"
P.I: Dr H A Nagarajaram
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
	0.00	Opening Balance		0.00					
	0.00	Grant In Aid		3000000.00		0.00	Salaries - Manpower		0.00
						0.00	Consumables		0.00
						0.00	Contingencies		0.00
						0.00	Travel		0.00
						0.00	Overheads		0.00
						0.00	Equipment		0.00
						0.00	Books		0.00
						0.00	AMC		0.00
						0.00	Others		0.00
						0.00	Transfer of Funds		0.00
	0.00			**3000000.00**		**0.00**			**0.00**
	0.00	Excess of Expenditure over Income		0.00		0.00	Closing Balance		3000000.00
	0.00			**3000000.00**		**0.00**			**3000000.00**

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
P-155: Studies on thecellular roles of calcium signalling proteins in Neurospora crassa
P.I: Dr D P Kasbekar
Receipts and Payments Account from 01/04/2012 to 31/03/2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
0.00		Opening Balance	0.00						
0.00		Grant In Aid	335194.00		0.00		Salaries - Manpower		0.00
					0.00		Consumables		0.00
					0.00		Contingencies		0.00
					0.00		Travel		0.00
					0.00		Overheads		0.00
					0.00		Equipment		0.00
					0.00		Books		0.00
					0.00		AMC		0.00
					0.00		Others		0.00
					0.00		Transfer of Funds		0.00
0.00			**335194.00**		**0.00**				**0.00**
0.00		Excess of Expenditure over Income	0.00		0.00		Closing Balance	335194.00	
0.00			**335194.00**		**0.00**			**335194.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
COE on Genetics and Genomic of Silkworms - P.I. Dr J Nagaraju
RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2012 TO 31.03.2013

Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year. Amount	Rs	Payments	Current Year Amount	Rs
					13198864.00		Opening Balance	3110519.00	
0.00		**Opening Balance**	0.00		8389307.00		Salaries- Manpower	7760392.00	
22433000.00		Grant in aid	4000000.00		3700000.00		Consumables	2429598.00	
					100000.00		Contingencies	100000.00	
					155348.00		Travel	245022.00	
					0.00		Workshop / Training	0.00	
					0.00		**Equipment Maintenance**	**0.00**	
					0.00		Books & Journals	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
22433000.00			4000000.00		25543519.00			13645531.00	
3110519.00		Excess of expenditure over income	9645531.00		0.00		Closing Balance	0.00	
25543519.00			**13645531.00**		**25543519.00**			**13645531.00**	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD
COE - II : DBT Project on " Centre of Excellence for Microbial Biology"
P.I: Dr J Gowrishankar, Dr K Anupama, Dr Abhijit A Sardesai, Dr Ranjan Sen and Dr Shekar C Mande
RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2012 TO 31.03.2013

Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
			4591687.00	Opening Balance	8969700.00
0.00	**Opening Balance**	0.00	7807713.00	Salaries- Manpower	8093406.00
8570000.00	Grant in aid	7881000.00	4400000.00	Consumables	1785000.00
			520000.00	Contingencies	41075.00
			220300.00	Travel	510000.00
			0.00	Training & Workshop	1300000.00
			0.00	Equipment	0.00
8570000.00		7881000.00	17539700.00		20699181.00
8969700.00	Excess of expenditure over income	12818181.00	0.00	Closing Balance	0.00
17539700.00		**20699181.00**	**17539700.00**		**20699181.00**

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Photo Gallery

Exposure visit for in-service biology teachers of Kendriya Vidyalaya Sangathan on 17 May 2012

Fire drill in the CDFD Administration Block on 30 May 2012

Signing of the MoU with the Government of Andhra Pradesh on 11 July 2012 to promote partnership in the area of DNA fingerprinting examination and training.

Flag hoisting on the occasion of Independence Day 2012

Celebration of Hindi Day on 14 September 2012

Lecture by Prof. Aravinda Chakravarti from the Johns Hopkins University School of Medicine, Baltimore, USA during the Mini-Symposium on 13 October 2012

Participants of the Seminar Workshop on Microbial Biology organized from 11-14 December 2012

Lecture by Prof. Ajit Varki, University of California, San Diego, USA on 5 February 2013

Glimpses of CDFD Foundation Day-2013

Dr. J. Gowrishankar, Director, CDFD being conferred with the Padma Shri Award-2013 by Hon'ble President of India Shri Pranab Mukherjee.