

# सी डी एफ डी CDFD

## वार्षिक प्रतिवेदन

अप्रैल 2009 से मार्च 2010 तक

## ANNUAL REPORT

April 2009 to March 2010



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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# Mandate



## 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.



## **From the Director's Desk**



## Director's Message

It is my pleasure to present the Annual Report of CDFD for the year ending 31 March, 2010. Established in 1996, this Centre has emerged as an institute of national and international renown that provides services and training in the areas of DNA profiling and diagnostic testing for genetic disorders, and also undertakes cutting edge basic research in diverse areas of molecular biology. With the induction of new groups, and an increasing awareness about CDFD's societal contributions, the Centre has been witnessing significant growth in all phases of activities, and several new frontiers of investigation have also



been initiated. A perusal of the Annual Report would, I trust, bring out the Centre's achievements in the current reporting year, and I would like to highlight a few of them below.

In the area of DNA profiling services, this year, CDFD was forwarded almost a hundred cases by the judiciary and law enforcing agencies of the Union and different State Governments. CDFD also undertook capacity building and training on DNA profiling for the state forensic science laboratories of Uttar Pradesh and Karnataka. The Medical Genetics Unit, which was set up in August 2009 and is operated jointly with the Nizam's Institute of Medical Sciences, Hyderabad, has been running effectively. This year the Diagnostics division had provided genetic evaluation and counselling to approximately 1800 patients.

This year, the APEDA-CDFD Centre for Basmati DNA Analysis tested around 350 basmati samples for purity. The CDFD is also a referral centre for genetic fidelity testing of tissue culture raised plants, and in this reporting year, two new whole genome scanning molecular markers [viz. inter-retrotransposon amplified polymorphism (IRAP) and retrotransposon microsatellite amplified polymorphism (REMAP)] were assessed for their utility in true-to-type testing.

In its efforts to apply RNAi technology in the control of baculovirus infection of silkmoths, the Laboratory of Molecular Genetics has been successful in transferring the transgene expressing dsRNA for essential viral genes into the commercial cultivar CSR2, which is a high yielding bivoltine strain that is extremely susceptible to baculovirus infection. In continued work on the gloverins, which are a family of antimicrobial peptides encoded in the *Bombyx* genome, the group has shown that loss of an intron from the ancestral gene leads to gain of function in overexpression during embryonic stage.

The Laboratory for Plant-Microbe Interactions has been engaged in studying interaction of different *Xanthomonas* pathogens with their cognate host plants. The group has made biosensors that can detect quorum sensing signal in *Xanthomonas* and *Pseudomonas* group of plant pathogens. The investigators in this laboratory have also isolated and characterized a novel gene called *motA*, required for virulence in *Xanthomonas*.

The Structural Biology group has undertaken global mapping of binding sites of GroEL1 protein on the *Mycobacterium tuberculosis* genome, resulting in formulation of a novel hypothesis regarding the pathogenetic role of PE-PGRS genes and their putative regulation by GroEL1. The successful determination of crystal structure of *M. tuberculosis* cAMP receptor protein (CRP<sub>Mt</sub>) in its apo-form has provided important insights into the allosteric transitions mediated by cAMP. In other *M. tuberculosis* related work, the Laboratory of Molecular Cell Biology has shown that the PPE18 protein encoded by this bacterium targets the host pathway involving SOCS3 to suppress production of proinflammatory cytokines, thereby contributing to the immune evasion strategy of the pathogen.

The Laboratory of Transcription is engaged in understanding the molecular basis of actions of Rho, NusG and a phage-encoded proteinaceous Rho-inhibitor, Psu. This laboratory has shown that the Rho protein from *M. tuberculosis* works via a mechanism which is distinct from that earlier characterized in other bacteria.

Improved computational substitution matrices have been developed and used by the Laboratory of Computational and Functional Genomics to assign novel functions to hypothetical proteins encoded in the *Plasmodium falciparum* genome. The Laboratory of Computational Biology has developed a novel hierarchical approach to protein fold recognition, resulting in improved prediction accuracy.

Work in the Mammalian Genetics laboratory has identified a correlation between the DNA methyltransferase *DNMT3L* and carcinogenesis through epigenetic reprogramming. Unlike other DNA methyltransferases, *Dnm2* is also apparently involved in RNA processing during cellular stress. The Molecular Oncology group has obtained the first molecular insights into the distinct clinical behaviour of colorectal cancers in young Indian patients, and has also identified a pattern of distinct genetic alterations in squamous cell carcinoma of the esophagus that distinguishes it from esophageal adenocarcinoma. In the Laboratory of Immunology, potential new mechanisms of anti-inflammatory and anti-tumour actions of azadirachtin (from neem extract) and thiadiazolidine have been characterized.

The mentoring of PhD scholars, postdoctoral fellows, summer trainees and project associates is a fundamental component of our research programme and activities, which needs a special mention here because they are the future leaders of science.

Finally, on behalf of all my colleagues, I express sincere gratitude to the Department of Biotechnology, as well as to the eminent members of the Society, Governing Council and RAP-SAC (Research Area Panels-Scientific Advisory Committee) of the Centre whose guidance and support have enabled CDFD's efforts to meet global standards in all its activities. As I have had occasion to record earlier, the combination of high-calibre services delivery and of research at the Centre has emerged as a unique model that strives for academic excellence tied to social relevance, in which each of the two sets of activities is enriched by, and in turn enriches, the other.

Happy reading!

**Dr. J. Gowrishankar**

March 31, 2010

# Services



## Laboratory of DNA Fingerprinting Services

<b>Scientist In-charge</b>	Madhusudan R Nandineni	Staff Scientist
<b>Other Members</b>	SPR Prasad	Technical Officer II
	V N Sailaja	Technical Officer II
	Ch V Goud	Technical Officer I
	D S Negi	Technical Officer I
<b>Coordinator</b>	J Nagaraju	Staff Scientist

### Objectives:

1. To provide DNA fingerprinting services in cases forwarded by law-enforcing agencies and judiciary of State and Federal Governments, relating to murder, 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
5. To create DNA marker databases of different caste populations of India.

### Summary of work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)

A total number of 91 cases were received for DNA fingerprinting examination during the period 01.04.2008 - 31.03.2009. Out of these, 49 cases are related to paternity/maternity/ biological relationship, 32 cases are related to identification of deceased, 05 cases are pertaining to rape, 02 cases are related to murder and 03 cases pertaining to wildlife poaching. 18 states of India availed DNA fingerprinting services of CDFD during this period. Rajasthan state forwarded the highest number (27) of cases followed by Andaman & Nicobar (5), Andhra Pradesh (7), Bihar (2), Chhattisgarh (5), Delhi (1), Himachal Pradesh (3), Karnataka (8), Kerala (6), Madhya Pradesh (5), Maharashtra (8), Puducherry (1), Punjab (4), Tamilnadu (1), Uttar Pradesh (6) and Uttarkhand (1).

### Details of services provided in the current reporting year ( April 1, 2009 - March 31, 2010).

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

Identity of deceased	47
Maternity / Paternity	49
Rape & Murder	03
Sexual Assault (Rape)	06
Kidney Transplantation	02
<b>Total No. of Cases</b>	<b>107</b>

### Deposition of evidence in Hon'ble Courts

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

### Training/Lectures/Workshops on DNA fingerprinting examination

Training on DNA fingerprinting examination has been provided to the scientists from the State Forensic Science Laboratory, Bangalore, Karnataka state and State Forensic Science Laboratory, Lucknow, Uttar Pradesh state.

### Lectures have been delivered for the benefit of the:

1. Foreign delegates from different countries, coordinated by the National Crime Records Bureau (NCRB), New Delhi
2. IPS and other senior police Officers from Sardar Vallabhbhai Patel National Police Academy, Hyderabad
3. Indian Air Force Officers from the Air Force Intelligence School, Pune
4. National Law School of India University, Bangalore.

### Summary of the state-wise breakup of DNA fingerprinting cases:

State-wise Case List	Identity of Deceased	Maternity and Paternity	Rape & Murder	Sexual Assault (Rape)	Kidney Transplant	Total No. of Cases
Andhra Pradesh	4	15	0	0	1	<b>20</b>
Bihar	0	1	0	0	0	<b>1</b>
Chhattisgarh	4	2	1	2	0	<b>9</b>
Himachal Pradesh	4	1	1	0	0	<b>6</b>
Jammu & Kashmir	0	1	0	0	0	<b>1</b>
Jharkhand	0	1	0	0	0	<b>1</b>
Karnataka	0	8	0	1	0	<b>9</b>
Kerala	0	3	0	0	0	<b>3</b>
Madhya Pradesh	1	0	0	2	0	<b>3</b>
Maharashtra	2	2	0	0	1	<b>5</b>
Meghalaya	0	1	0	0	0	<b>1</b>
Orissa	0	1	0	0	0	<b>1</b>
Rajasthan	24	11	1	0	0	<b>36</b>
Uttar Pradesh	7	1	0	1	0	<b>9</b>
Uttarkhand	1	0	0	0	0	<b>1</b>
West Bengal	0	1	0	0	0	<b>1</b>
<b>Total No. of Cases</b>	<b>47</b>	<b>49</b>	<b>3</b>	<b>6</b>	<b>2</b>	<b>107</b>

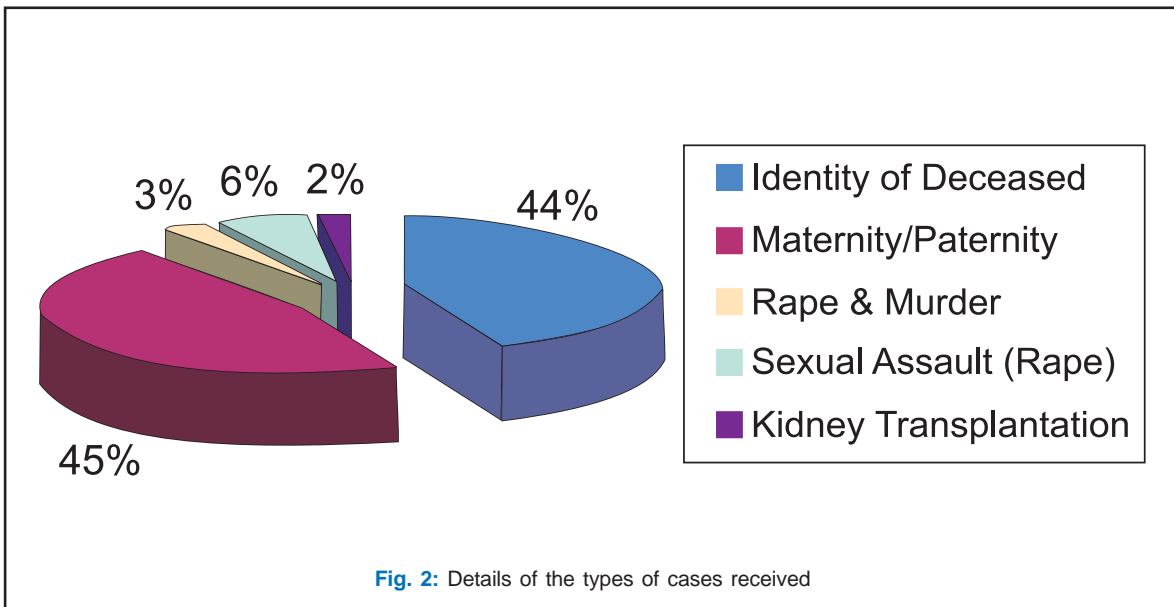
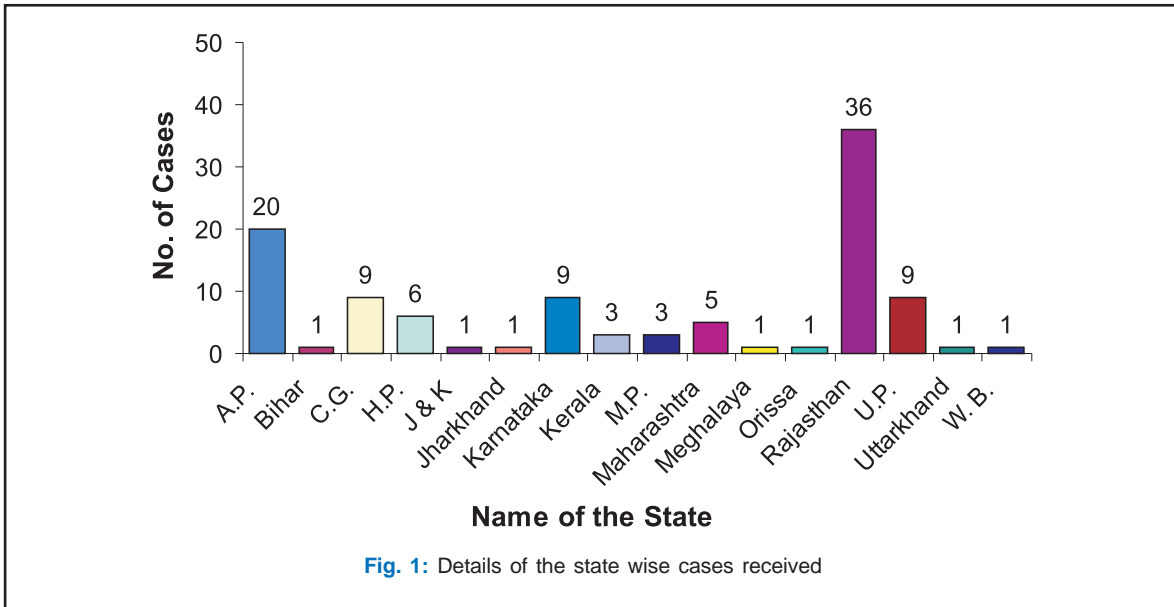
A total number of 107 cases were received for DNA fingerprinting examination during the period under report. Out of these, 49 cases were related to paternity / maternity, 47 cases were related to identification of deceased, 6 cases were pertaining to sexual assault (rape), 3 cases were related to murder and 2 cases pertaining to biological relationship (kidney transplantation). 15 states of India availed DNA fingerprinting services of CDFD during this period. Rajasthan State forwarded the highest number (36) of cases followed by Andhra Pradesh (20), Bihar (1), Chhattisgarh (9), Himachal Pradesh (6), Jammu & Kashmir (1), Karnataka (9),

Kerala (3), Madhya Pradesh (3), Maharashtra (5), Orissa (1), Uttar Pradesh (9), Uttarkhand (1) and West Bengal (1) (**Fig.1**).

During this reporting period, an amount of Rs. 18,39,545/- (Rupees eighteen lakhs thirty nine thousand and five hundred and forty five only) has been received towards DNA fingerprinting services, which is inclusive of service charge as levied by Govt. of India.

The cases involving paternity (45%) and identification of the deceased (44%), constituted the bulk of the cases received (**Fig. 2**).





**Publications:**

- Herráez DL, Bauchet M, Tang K, Theunert C, Pugach I, Li J, Nandineni MR, Gross A, Scholz M and Stoneking M (2009) Genetic variation and recent positive selection in worldwide human populations: evidence from nearly 1 million SNPs. *PLoS One* 4:e7888.
- Nandineni MR and Vedanayagam JP (2009) Selective enrichment of human DNA from non-human DNAs for DNA typing of decomposed skeletal remains (2009) *Forensic Science International: Genetics Supplement Series* 2: 520-521.

## Diagnostics Services

<b>Principal Investigator</b>	Ashwin Dalal	Staff Scientist
<b>Ph D Students</b>	Anusha Uttarilli	Junior Research Fellow
<b>Other Members</b>	P Rajitha	Technical Officer III
	G R Savithri	Technical Officer II
	R Angalena	Technical Officer II
	Usha Rani Dutta	Technical Officer I
	T Padma Priya	DBT Postdoctoral Fellow
	Jamal Md Nurul Jain	Technical Assistant
	C Krishna Prasad	Technician II
	R Sudheer Kumar	Technician II
<b>Collaborators</b>	MD Bashyam, Molecular Oncology, CDFD Suman Jain, Thalassemia Society, Hyderabad	

### 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
4. To impart training in genetic evaluation of patients with genetic disorders.

year 2009-10. These consisted of patients with chromosomal disorders, monogenic disorders, mental retardation, congenital malformations, multiple malformation syndromes, hemolytic anemias, short stature, skeletal dysplasias, myopathies, neurodegenerative disorders, ataxia, hypogonadism (male/female), ambiguous genitalia, inborn errors of metabolism, and familial disorders.

The Medical Genetics Unit established at Nizam's Institute of Medical Sciences, Hyderabad is running successfully and it is envisaged to create a Department of Medical Genetics in near future to provide services, training and conduct research in Medical Genetics. A total of 365 patients were examined and counseled in the unit during 2009-10.

### I. Services provided during the year 2009- 2010

#### Clinical Genetics

A total of 1826 patients attended the genetic clinic for genetic evaluation and counseling, during the

#### Genetic investigations done during 2009-10

Investigation	Total Cases	Positives
<b>Cytogenetics</b>	<b>693</b>	<b>50 (7.2 %)</b>
Proband	646	50 (7.7 %)
Prenatal	47	0 (0 %)
<b>Molecular Genetics</b>	<b>446</b>	<b>199 (44.6 %)</b>
Proband	421	191 (45.3 %)
Prenatal	25	8 (32 %)
<b>Biochemical Genetics</b>	<b>687</b>	<b>121 (17.6 %)</b>
Proband	685	121 (17.6 %)
Prenatal	2	0 (0 %)

## CYTOGENETICS

Disease	Abnormality	No. of Cases
Down Syndrome	Trisomy 21	16
	46,XY,rob(21;21)+21	1
Edwards Syndrome	47,XX+18	2
Turners Syndrome	Monosomy X (45,X)	5
	iso X,(46,X,i(X))	2
	Mosaic 45,X/46,XX	2
	46,X,del(X)(q25-qter)/45,X	1
	45,X/46,X,dup(X)(p22.1-pter)	1
	46,X,del(X)(q21.32;qter)	1
Klinefelter Syndrome	47,XXY	5
	48,XXX	1
Sex reversal	Phenotypic male with 46,XX	1
Triple X syndrome	47,XXX	1
Y mosaicism	46,XY/47,XYY	1
<b>Structural chromosomal abnormalities</b>		
<b>Inversions</b>		
	46,XY,inv(6)	1
<b>Translocations</b>		
	46,XX,t(X;20)(q13;p13) de novo	1
	45,XY,rob(13;14)	1
	46,XX,t(16;20)(p13.1;p13)	1
	46,XX,t(9;12)(p24;q24.1)	1
	46,XX,t(7;9)(p13;p22)	1
	46,XX,t(1;13)(q42.1;q14.3)	1
	47,XY+marker	1
<b>Duplications</b>		
	46,XX,dup(5)(q32→qter) de novo	1

## BIOCHEMICAL GENETICS

Disease	No. of Positives (%)
<b>Biochemical Tests (687)</b>	<b>121 (17.6%)</b>
Amino acid disorders (N=105)	11
Maple syrup urine disease	0
Non ketotic hyperglycinemia	1
Hyperornithinemia	3
Tyrosinemia	1
Hyperhomocysteinemia	4
Phenylketonuria	2 (1 Follow up)
<b>Lysosomal Storage Disorders (N=167)</b>	<b>47 (28 %)</b>
Hurler (11)	10
Hunter (14)	10
GM1-Gangliosidosis (25)	7
Chitotriosidase (18)	5
Gaucher's disease (9)	1
Krabbe's disease (6)	0
Sly disease (3)	0
Pompe disease (3)	0
Neuraminidase (1)	0
Arylsulphatase B (7)	3
Nieman pick disease (9)	3
Sanfilippo B (4)	0
Morquio A disease (6)	5
Mucopolipidosis (1)	1
Metachromatic leukodystrophy (25)	0
Hexosaminidase (23)	0
Tay Sachs's disease (1)	1
Sandhoff's disease (1)	1
<b>Metabolic Screening Tests</b>	
Newborn screening (N=35)	3
Urine metabolic screening (250)	14
Urine MPS screening (70)	34
Oligosaccharide screening (40)	8
Biotinidase (10)	3
GALT analysis (8)	1
<b>Prenatal Diagnosis (2)</b>	<b>0</b>
Tay Sachs disease (1)	0
Metachromatic leukodystrophy (1)	0

## FISH

Probe	Abnormality	No. of Cases
SEP (X)/(Y)	47,XXY/46,XX	4
LSI-21	Down 46,XY,t(Y;21)	5
Prader Willi syndrome	46,XY	1
Angelman syndrome	46,XX	1
WCP-22	46,XX,t(X;22), 46,XX,t(2;22)	2
WCP-2	46,XX,t(2;22)	1
Di George syndrome	Mental retardation	4
BCR/ABL	CML	2 (1 positive case)
Monosomy 1p	46,XX,t(9;12)	1

## QF-PCR (ANEUFAST)

Prenatal : 3 cases

## MOLECULAR GENETICS

Name Of Disorder	No. of Cases	Positive	Negative		
DMD/BMD	94	67	27		
DMD carrier analysis	06	04	02		
Spinal muscular atrophy	55	29	26		
SMA carrier analysis	03	02	01		
		<b>Normal</b>	<b>Homozygous</b>	<b>Heterozygous</b>	<b>Compound Heterozygous</b>
Thalassemia and sickle cell anemia	63	11	20	25	07
Factor V leiden	21	19	-	02	-
Factor II mutation	10	10	-	-	-
Cystic fibrosis	39	39	-	-	-
<b>Triplet Repeat Disorders</b>		<b>Positive</b>	<b>Negative</b>		
Fragile X syndrome	27	-	27		
Friedrichs ataxia	32	09	23		
Myotonic dystrophy	14	07	07		
Huntington disease	16	11	05		
SCA Panel (1,2,3,6 &7)	38	08	30		
DRPLA	03	-	03		
<b>Prenatal Diagnosis</b>					
DMD	06	04	02		
Spinal muscular atrophy	03	02	01		
		<b>Normal</b>	<b>Homozygous</b>	<b>Heterozygous</b>	<b>Compound Heterozygous</b>
Thalassemia	15	05	01	08	01
Cystic fibrosis	01	-	-	01	-

## II. RESEARCH

### 1. Research in single gene disorders

We conducted genetic analysis in patients with rare genetic disorders such as Giuffrè-Tsukahara syndrome, Progressive Pseudo-Rheumatoid Dysplasia (PPD) etc. Giuffrè-Tsukahara syndrome is characterized by microcephaly, mental retardation, radio-ulnar synostosis, short stature and scoliosis. The mode of inheritance of this disorder is not yet known and till date only five reports are available for this disease. The gene for this syndrome has not yet been identified. Earlier reports have proposed X linked dominant inheritance based on severe disease among males and report of a severely affected male and mildly affected mother showing skewed X inactivation. We provided further evidence for X-linked dominant mode of inheritance for this syndrome based on absence of skewed X-inactivation in our 8 year old female patient (Fig. 1).

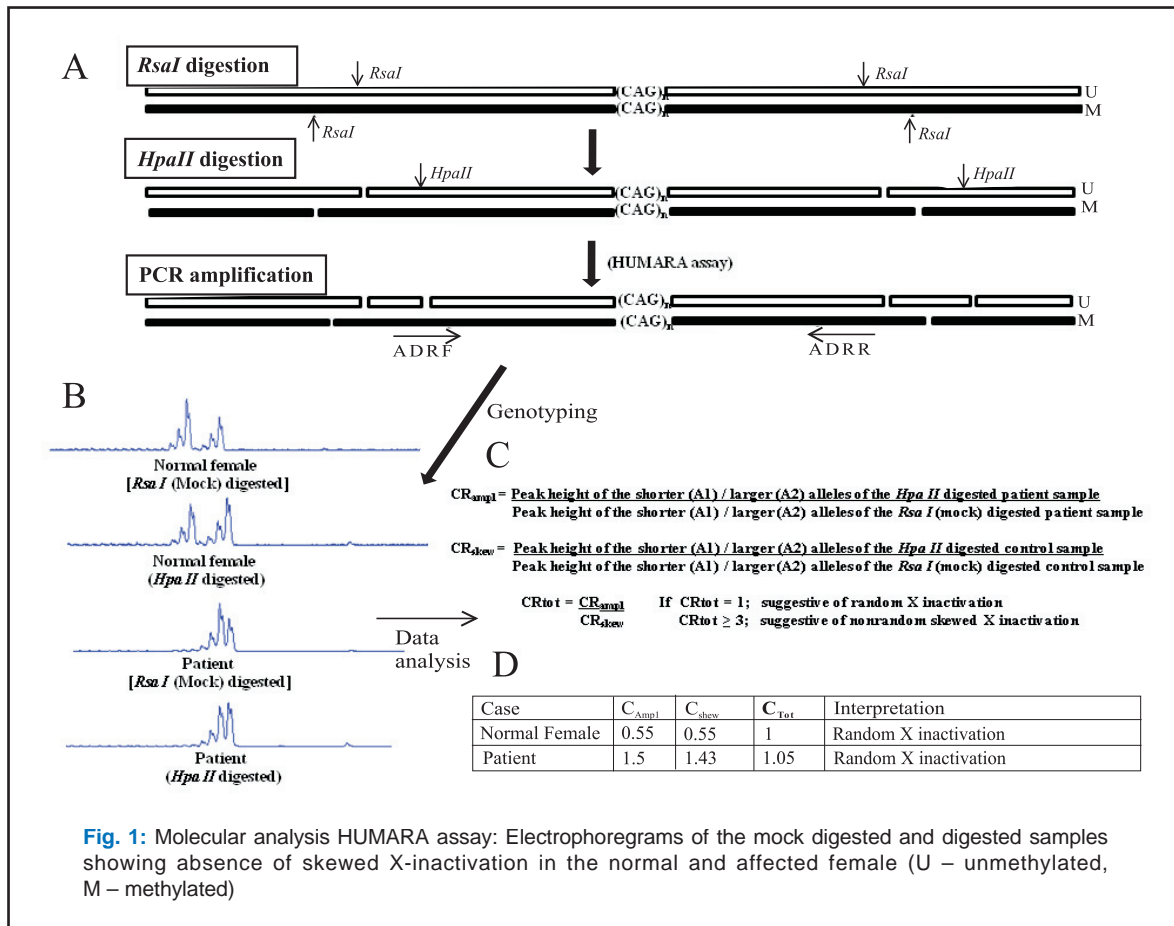
Progressive Pseudo-Rheumatoid Dysplasia (PPD) is an autosomal recessive genetic disease, caused

by mutations of the Wnt1-inducible signaling pathway protein 3 (*WISP3*), which is located on chromosome 6q22. We evaluated a patient with PPD and screened for mutations in *WISP3* gene. A novel mutation C145R (c.433T>C) in exon 3 was identified in a 30 year old male patient (Fig. 2). Mother of the patient was also found to be homozygous for the mutation. This was due to high degree of inbreeding in the family. His wife was normal for the mutation. Genetic analysis in this family helped the patient to take informed decision regarding reproductive options as he did not want to transmit his disease to his children.

### 2. Clinical, biochemical and molecular analysis of common lysosomal storage disorders

This is a new activity.

Lysosomal storage disorders are a heterogeneous group of disorders associated with specific lysosomal enzyme deficiency. Enzyme replacement therapy (ERT) is available for at least 5 of these disorders. The diagnosis and prenatal

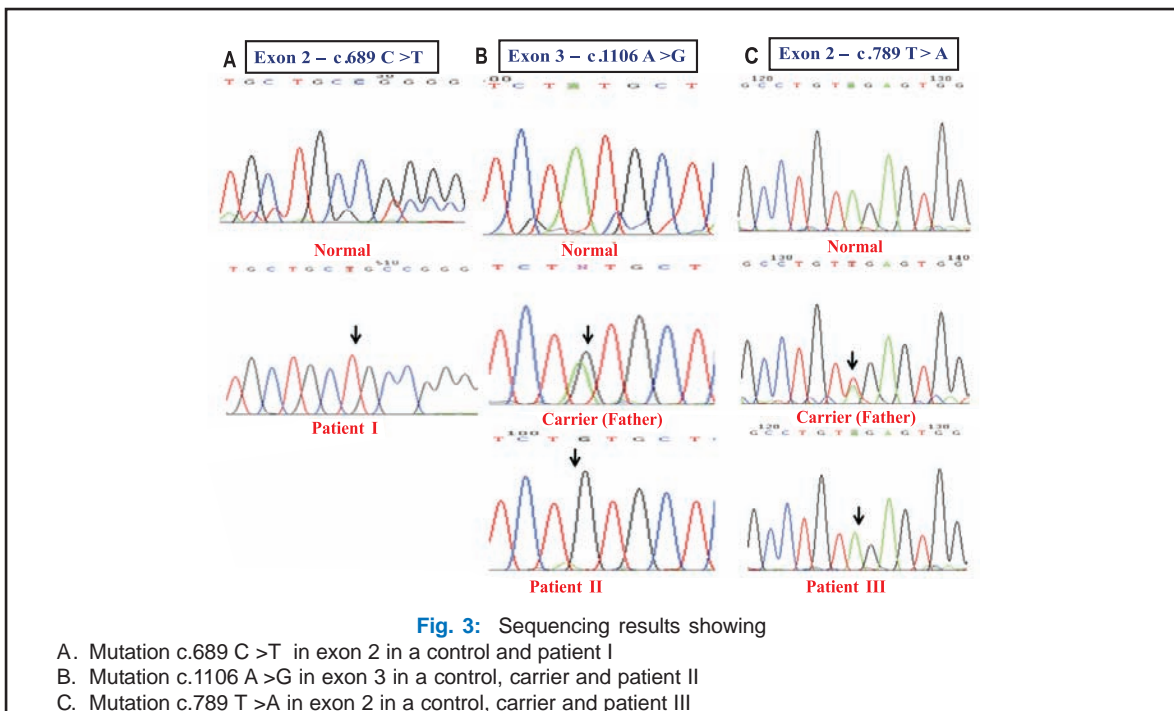
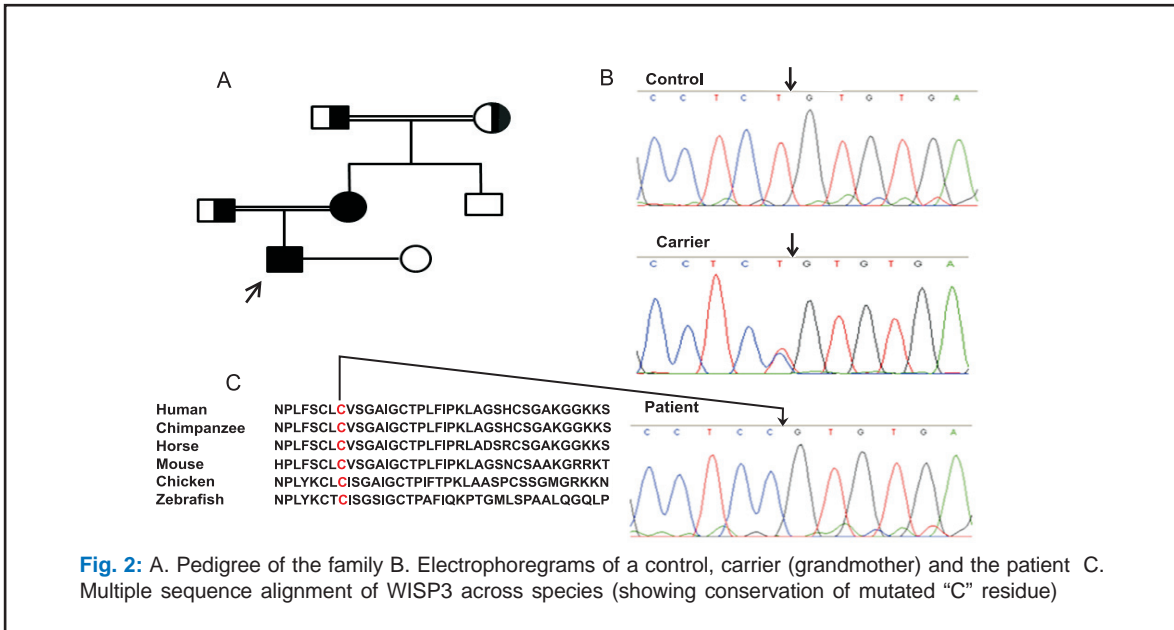


**Fig. 1:** Molecular analysis HUMARA assay: Electropherograms of the mock digested and digested samples showing absence of skewed X-inactivation in the normal and affected female (U – unmethylated, M – methylated)

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.

We screened 5 patients of Niemann-Pick disease for the mutations in all the six exons of *SMPD1* and found five novel mutations in exon two and three and two novel SNPs in exon two and six respectively (**Fig. 3**). We further correlated the mutation results with the enzyme assay results to look for any correlation.

We plan to study molecular aspects of other common lysosomal disorders in future.



## Publications

1. Angalena R, Chaudhary A, Bashyam MD and Dalal A (2009) Hemoglobin D (Iran) masquerading as hemoglobin E: An interesting case report. **Newsletter of Genetics Chapter of Indian Academy of Pediatrics** 2:11-12.
2. Dalal A (2009) Stem cell therapy: Current status. **Newsletter of Genetics Chapter of Indian Academy of Pediatrics** 2:5-7
3. Dalal A and Mehrotra RN (2009) Hypertrichosis, hyperkeratosis and mental retardation syndrome: further delineation of phenotype. **Clinical Dysmorphology** 18: 83-84.
4. Kumar R, Tamhankar PM, Panigrahi I, Dalal A and Agarwal S (2009) A novel beta-globin mutation (HBB:c.107A>G; or codon 35 beta (A→G)) at alpha-beta chain interfaces. **Annals of Hematology** 88: 1269-1271.
5. Priya TP and Dalal A (2009) Laboratory approach to neurogenetic disorders. Reviews in Neurology, **Indian Academy of Neurology** 12-25.
6. Girisha KM, Vahab SA, Dalal A, Gopinath PM and Satyamoorthy K (2010) Compound heterozygosity for HbD Punjab and polyadenylation signal mutation causes clinically asymptomatic mild hypochromia and microcytosis. **Annals of Hematology** 89: 625-626.
7. Agarwal S, Tamhankar PM, Kumar R and Dalal A (2010) Clinical and haematological features in a compound heterozygote (HBB:c.92 + 5G > C/HBB:c.93-2A > C) case of thalassaemia major. **International Journal of Laboratory Hematology** (In press).
8. Angalena R, Prabitha KN, Chaudhary AK, Bashyam MD, Jain S and Dalal A (2010) A novel homozygous point mutation at codon 82 (HBB:c.247 A>T) in the beta-globin gene leads to thalassemia major. **International Journal of Laboratory Hematology** (In press).
9. Priya TP, Philip N, Molho-Pessach V, Busa T, Dalal A and Zlotogorski A (2010) H syndrome: novel and recurrent mutations in SLC29A3. **British Journal of Dermatology** (In press).
10. Priya TP and Dalal A (2010) Molecular diagnosis of triplet repeat disorders by triple prime PCR (TP-PCR) based approach. **Newsletter of Genetics Chapter of Indian Academy of Pediatrics** (In press).
11. Rajita P and Dalal A (2010) Partial monosomy 7q: case report. **Indian Pediatrics** (In press).



# Research



## Laboratory of Molecular Genetics

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

<b>Principal Investigator</b>	J Nagaraju	Staff Scientist
<b>Ph D Students</b>	Jayendranath S	Senior Research Fellow
	Jyoti Singh	Senior Research Fellow
	Asha Minz	Senior Research Fellow
	Chandrapal Singh	Senior Research Fellow
	S Suresh Kumar	Senior Research Fellow
	Deepa Badrinarayan	Junior Research Fellow
	G Gopinath	Junior Research Fellow
	T R Sitalakshmi	Junior Research Fellow
<b>Others</b>	Varsha	Staff Scientist
	V V Satyavathi	Technical Officer IV (CoE)
	A Sobhan Babu	Technical Officer I
	M Muthulakshmi	Technical Officer I
	S Annapurna	Technical Officer I (CoE)
	Archana Tomar	Bioinformatician (CoE)
	R Lakshmi Vaishna	Technical Assistant (CoE)
	M J Reddy	Technical Assistant (CoE)
	N Mrinal	Research Associate
	P Nagamanju	Project Associate
	A Kaliappan	Project Assistant (till Oct. 2009)
	K Vijayasarathy	Project Assistant (till July 2009)
	K Adarsh Gupta	Project Assistant
	Santhosh R Jadhav	Project Assistant (till Feb. 2010)
	S Venkateswari	Project Assistant (till Dec. 2009)
	M Nagamuralidhar	Project Assistant

#### Objectives

1. Generation of transgenic silkworms resistant to *Bombyx mori* nucleopolyhedrosis virus (BmNPV) using RNAi strategy and introduction of anti-baculoviral property to commercial silkworm strains by expression of multiple RNAi viral targets
2. Identification and functional characterization of novel genes involved in immune response pathways of silkmoths.

#### Summary of the work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)

- We have generated several transgenic silkworm lines expressing dsRNA for multiple essential baculoviral genes using *piggyBac* transposon-based germline transgenesis. To commercially exploit these transgenics, we introduced the transgenes from Nistari which is a non-diapausing low yielding strain to the diapausing, high yielding and baculovirus susceptible strain, CSR2.



X

Select for *red eye* individuals



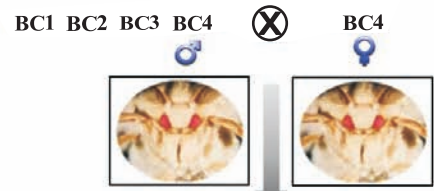
Back Cross

F1

BC1  
BC2  
BC3  
BC4



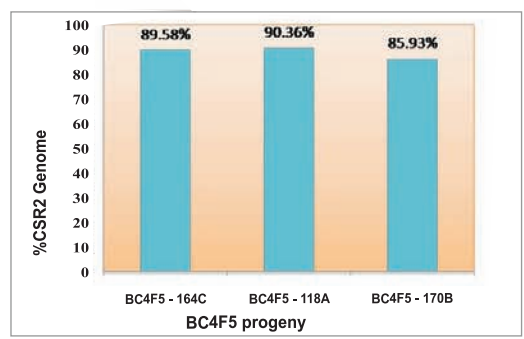
Selection for DsRed reporter phenotype (red eye colour) and microsatellite alleles specific to CSR2 line



Sib mated

BC4 F1 - 1<sup>st</sup> Inbred generation

BC4 F5 - 5<sup>th</sup> Inbred generation



Percentage of CSR2 genome in the BC4F5 progeny as evaluated by genome-wide microsatellite markers

**Fig. 1:** Schematic diagram showing transfer of transgene (dsRNA for multiple essential baculoviral genes) from transgenic Nistari lines to CSR2 line

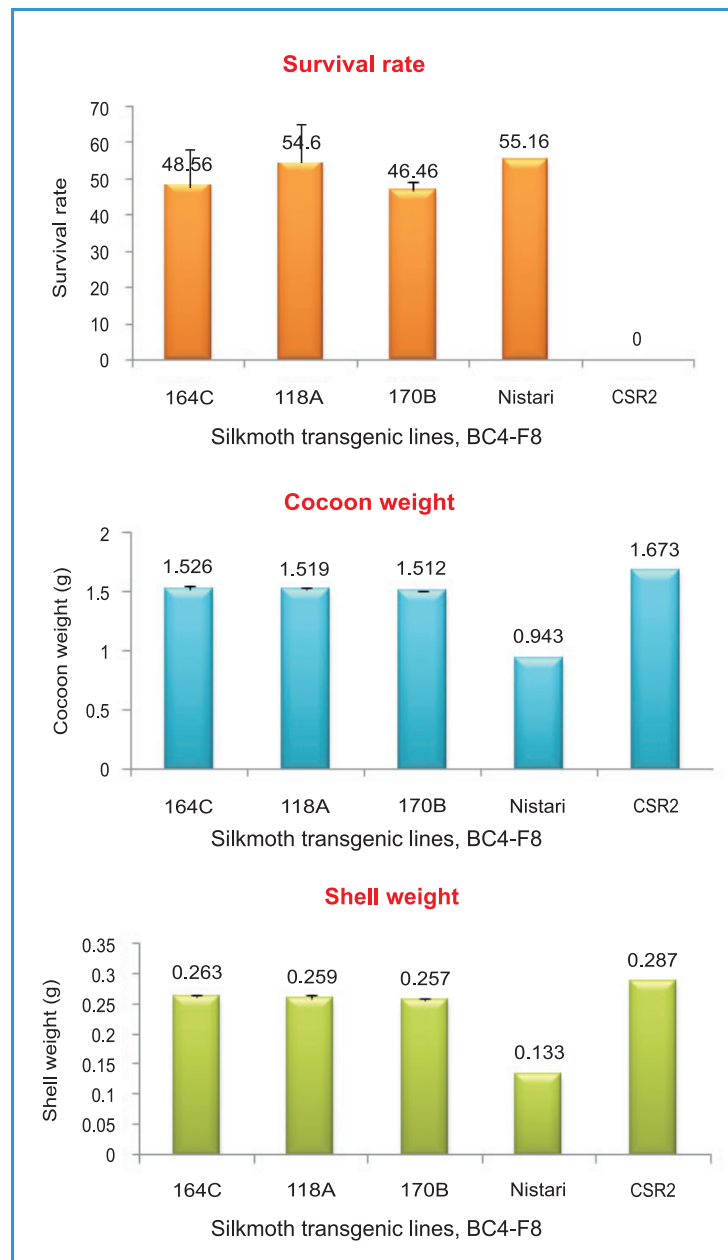
- In an attempt to understand the evolution of immune system in insects, we investigated the role of gene duplication in the evolution of a gloverin family of antibacterial genes (*Bmglv1*, *Bmglv2*, *Bmglv3*, and *Bmglv4*) in the silkworm, *B. mori*.

**Details of progress made in the current reporting year (April 1, 2009 - March 31, 2010)**

**Project: Development of RNAi-based baculovirus resistant transgenic silkmoths**

We initiated work to transfer the anti-viral property

of the baculoviral resistant transgenics in the Nistari genetic background to the existing high yielding CSR2 strain. CSR2 strains are highly susceptible to baculovirus infection. The transgenic lines were used as donor parents to introduce the transgenes to the high yielding baculovirus susceptible CSR2 strains by recurrent backcross strategy. Transfer of BmNPV resistance gene from transgenic Nistari lines to CSR2 is pictorially represented in **Fig. 1**. The screening of backcross lines with appropriate controls was carried out by feeding baculovirus polyhedral inclusion bodies *per os* (40,000



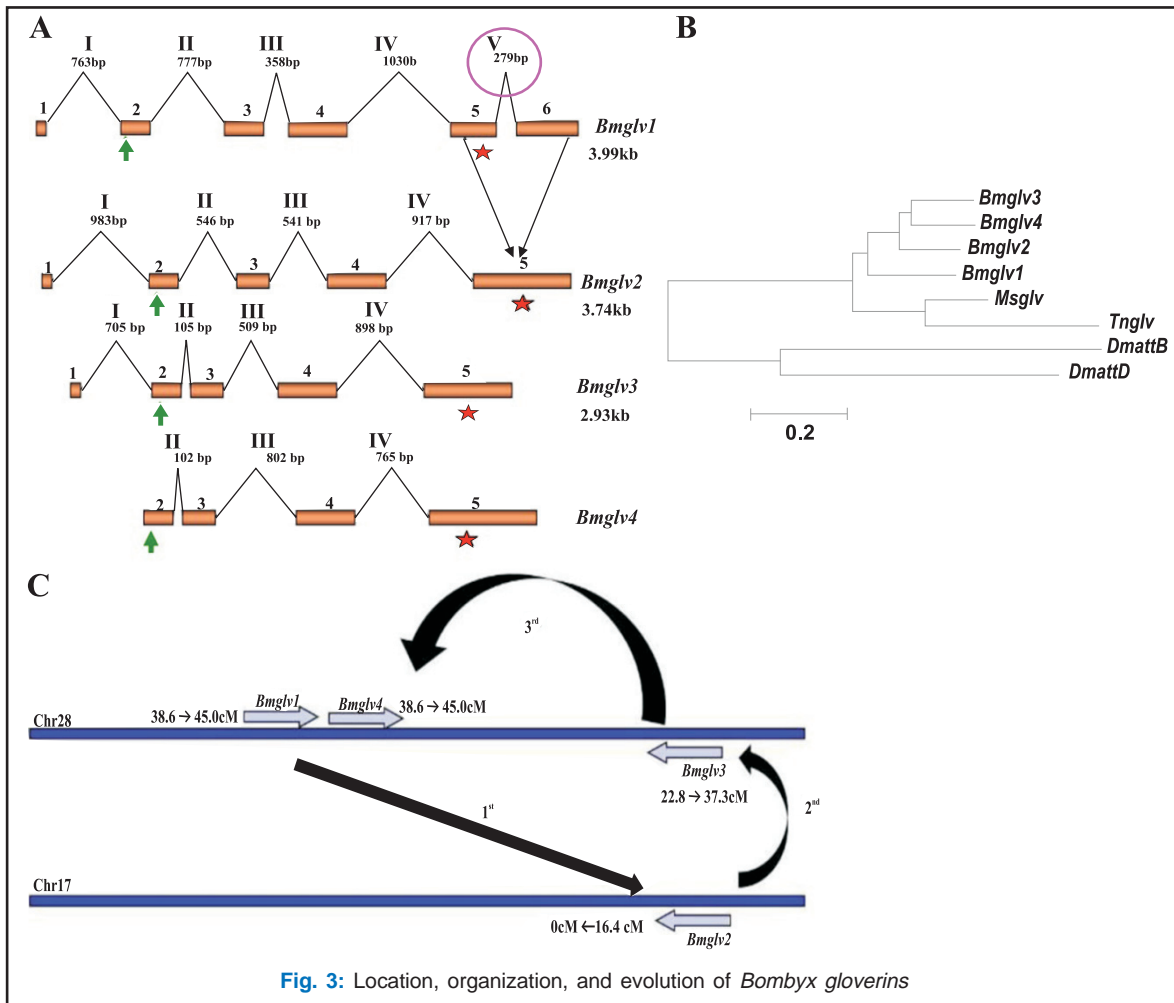
**Fig. 2:** Characteristics of transgenic lines derived from backcross breeding

polyhedra/larvae @ 1ml for 100 larvae) and recording the survival rate of the infected lines. We have earlier developed and successfully identified many microsatellite markers that are polymorphic between Nistari and CSR2. The backcross offspring were screened for the transgene along with the reporter gene coupled with genome-wide distributed microsatellite marker alleles specific to the recurrent parent CSR2 strain. The backcross offspring that carried transgene and CSR2-specific microsatellite markers were only selected. In addition, backcross transgenic breeds were selected based on survival rate, cocoon weight and shell weight. After four backcrosses, the progeny were sib-mated for four generations (BC4F5). In the BC4F5 progeny, 85.93 to 90.36% CSR2 genome was found to be incorporated as screened by microsatellite markers. The survival rate, cocoon weight and shell weight of the transgenic lines derived from these backcrosses followed by sib-mating are given in **Fig. 2**. When these backcross derived transgenic lines were challenged with 40,000 polyhedra/larvae,

all the CSR2 moths were dead due to baculovirus infection whereas the backcross derived transgenic CSR2 lines reported survival rate ranging from 46.46 to 54.6%.

**Project: Molecular characterization of immune response proteins of silkmoths**

Silkworm has four *gloverin* genes, *Bmgvl1*, *Bmgvl2*, *Bmgvl3* and *Bmgvl4* and we made an interesting observation of the presence of an intronV only in *Bmgvl1* and not in others. Phylogenetic analysis of the four *gloverins* suggested *Bmgvl1* as the ancestral gene (**Figs. 3A and 3B**). The genes *Bmgvl2-4* have evolved as a result of three gene duplication events. During the first duplication, intronV of *Bmgvl1* was lost leading to fusion of exon5 and exon6, as a result of which the derived gene *Bmgvl2* has only five exons. Overall the gene size has become smaller with each round of duplication, because of erosion in intronic regions of the genes (*Bmgvl1* (3.9kb)→*Bmgvl3* (2.9kb)). We also mapped the physical location of the four *gloverins*;

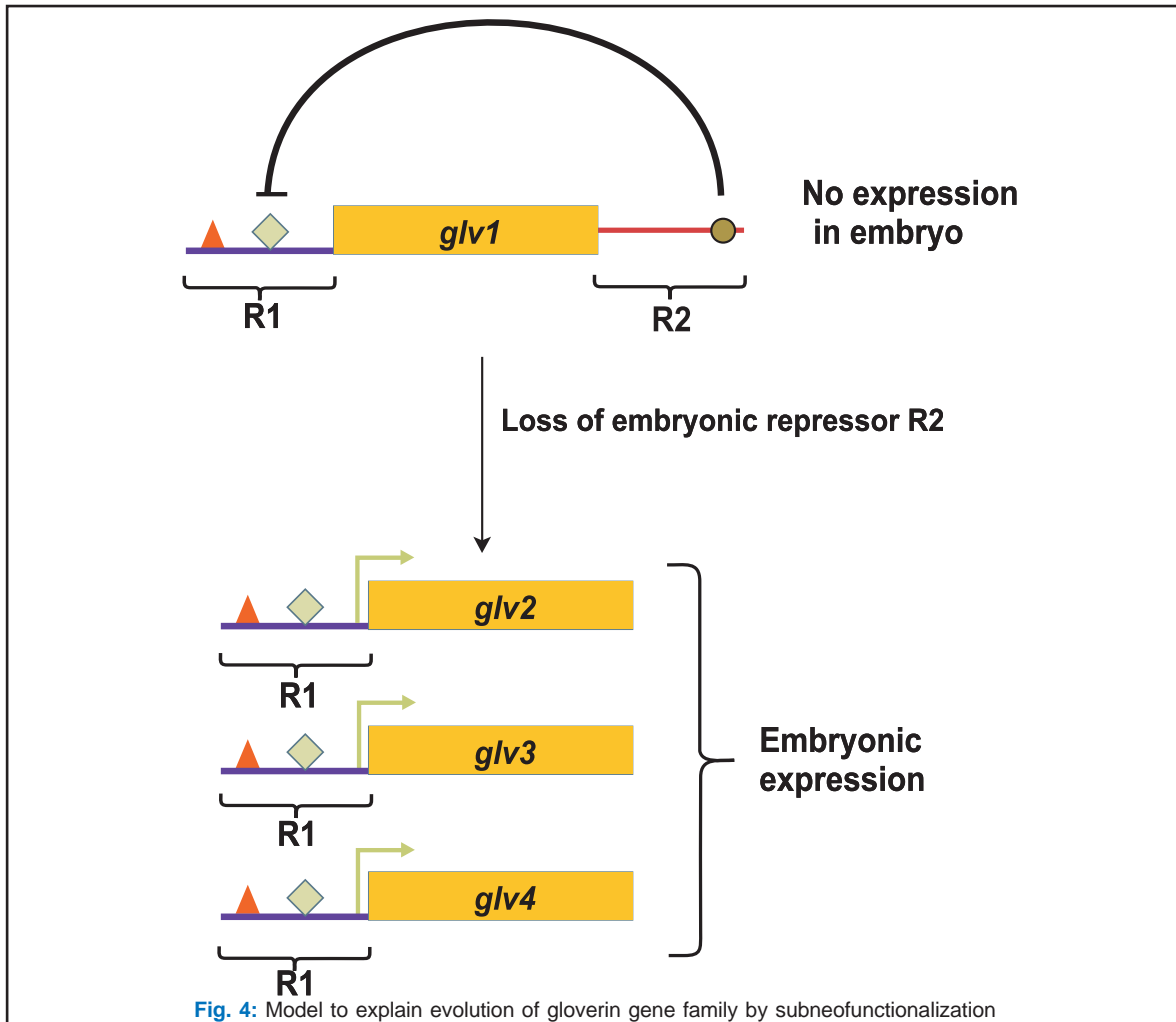


**Fig. 3:** Location, organization, and evolution of *Bombyx gloverins*

*Bmglv1*, *Bmglv3*, and *Bmglv4* to chromosome 28, and *Bmglv2* to chromosome 17 (**Fig. 3C**). *Bmglv1* and *Bmglv4* are present as tandemly duplicated genes on positive strand at 38.6→45.0 cM, and *Bmglv2* and *Bmglv3* are present on the complementary strand at 0cM←16.4 cM on chromosome 17, and at 22.8→37.3 cM on chromosome 28, respectively.

We observed a significant difference in the embryonic expression profile of these *gloverin* genes. *Bmglv2-4* expressed during the embryonic stages and in the adult stage but not in the larval stages. *Bmglv1* on the other hand, expressed in larval stage, but not in embryonic stage or adult. Since *Bmglv1* and *Bmglv2* genes were quite distinct in their embryonic expression pattern, we examined the differences between the two genes to gain insight into their embryonic regulation. We investigated whether a certain regulatory motif in the promoter of *Bmglv2* affected its expression in embryo. We found loss of intronV located in 3'UTR

of *Bmglv1* during *Bmglv1* to *Bmglv2* duplication changed developmental regulation of *Bmglv2* resulting in acquisition of new function by the latter in embryonic development. IntronV of *Bmglv1* is 279bp long and to characterize the motif regulating embryonic expression of upstream ORF, EMSA was done with different fragments of intronV generated by restriction digestion. The fragment corresponding to the last 40bp of the intron, which has a putative CF2 (Chorion Factor 2) binding site, showed specific shift in EMSA. The CF2 complex retarded with nuclear extracts from adult ovary, testis and embryonic extracts but not from tissues of larval origin. The *Bmglv1* expression was not seen in the tissues where CF2 is expressed. By gel mobility shift, chromatin immunoprecipitation, and immunodepletion assays, we identified CF2 as the repressor molecule that bound to a 10-bp regulatory motif in intronV of *Bmglv1* and repressed its transcription. *Gloverin* paralogs that lacked intronV were independent of CF2 regulation and thus expressed during embryonic stages. This study



**Fig. 4:** Model to explain evolution of gloverin gene family by subneofunctionalization

suggested the presence of two regulatory elements (i) promoter (R1) and (ii) intronV (R2) in ancestral gloverin (*Bmglv1*). The promoter regulation is same for both the ancestral (*Bmglv1*) and the duplicated copy (*Bmglv2*), but the expression of *Bmglv1* was not observed in embryonic stages because of the inhibition of *Bmglv1* transcription by CF2. The CF2-mediated repression was mediated by intronV, which is present only in *Bmglv1*, the ancestral copy. Thus we identified intronV as the second regulator (R2) and also showed that R2 is dominant over R1 in embryonic stages. During the first duplication, intronV (R2) was lost resulting in embryonic

expression of daughter gene *Bmglv2*. We proposed a model to explain the evolution of gloverin gene family by subneofunctionalization as shown in **Fig. 4**. Embryonically expressing paralog *Bmglv2* controls embryonic development, a feature not observed in *Bmglv1*, suggesting gain of function for *Bmglv2* (neofunctionalization).

#### **Publications:**

1. Mrinal N and Nagaraju J (2008) Intron loss is associated with gain of function in the evolution of the gloverin family of antibacterial genes in *Bombyx mori*. **Journal of Biological Chemistry** 283: 23376-23387.



## APEDA-CDFD Centre for Basmati DNA Analysis

<b>Principal Investigator and Consultant</b>	J Nagaraju	Staff Scientist
<b>Other Members</b>	A Srividya D Swarna Kumari Revathi Nagaraja	Research Associate Project Assistant (till Aug. 2009) Project Assistant

### Objectives

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

### Services provided in the current reporting year 2009 - 2010

During the period under report, a total of 349 Basmati samples were analyzed and the number of samples indicating the percentage of adulteration with non-basmati rice is shown in **Fig. 5**.

### Basmati rice genetics and genomics

**Project: Fine-mapping and positional cloning of candidate genes in a promising region on chromosome 5 for grain quality traits of Basmati rice.**

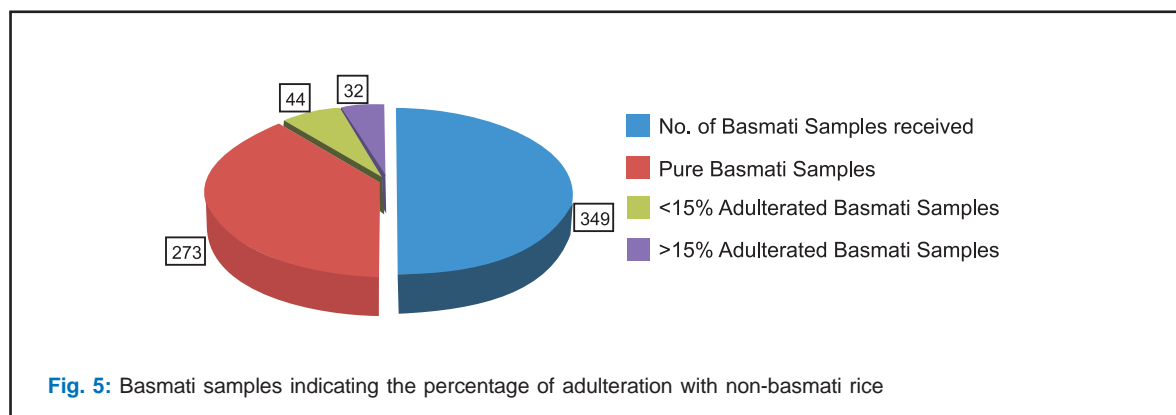
**Summary of the work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)**

In order to fine map and mine candidate genes of

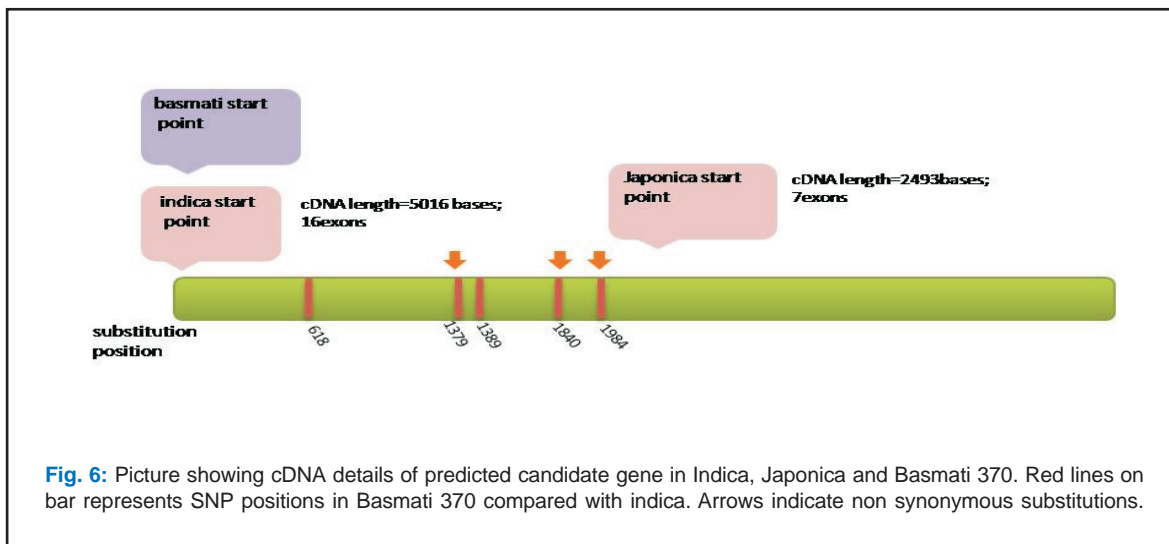
grain appearance traits of Basmati, a total of 47 QTLs for 16 different agronomic and quality traits were mapped in an F<sub>2</sub> mapping population, derived from a cross of traditional Basmati variety, Basmati 370 and a semi dwarf variety, Jaya. Interestingly, a single region on chromosome 5 was found to be controlling important grain appearance traits viz., grain length, grain breadth, length-breadth ratio and grain elongation ratio. Further fine mapping of this region using additional SSRs, Indels and ESTs has been attempted.

### Details of progress made in the current reporting year (April 1, 2009 - March 31, 2010)

Two predicted candidate genes were sequenced to find DNA variation between Basmati 370 and Jaya. One of these two genes showed five SNPs; one each in first, sixth and seventh exons, while two in the fourth. Within these five, three SNPs are non-synonymous (**Fig. 6**). The consistency of these SNPs was confirmed using four other traditional Basmati varieties. Currently, sequencing of this region employing non-aromatic long grain varieties is going on. Upon identification of Basmati specific sequence, further confirmation will be made by expression analysis and transgenic studies.



**Fig. 5:** Basmati samples indicating the percentage of adulteration with non-basmati rice



## Publications

1. Arunkumar KP, Mita K and Nagaraju J (2009) Silkworm Z chromosome is enriched in testis-specific genes. *Genetics* 182: 493-501.
2. Beech CJ, Nagaraju J, Vasan SS, Rose RI, Othman RY, Pillai V and Saraswathy TS (on behalf of the working groups) (2009) Risk analysis of a hypothetical open field release of a self-limiting transgenic *Aedes aegypti* mosquito strain to combat dengue. *Asia Pacific Journal of Molecular Biology and Biotechnology* 17: 99-111.
3. Beech CJ, Vasan SS, Quinlan MM, Capurro ML, Alphey L, Bayard V, Bouari M, McLeod MC, Kittayapong P, Lavery JV, Lim HL, Marrelli MT, Nagaraju J, Ombongi K, Othman RY, Pillai V, Ramsey J, Reuben R, Rose RI, Tyagi BK and Mumford J (2009) Deployment of innovative genetic vector control strategies: Progress on regulatory and biosafety aspects, capacity building and development of best-practice guidance. *Asia Pacific Journal of Molecular Biology and Biotechnology* 17: 75-85.
4. Johny S, Chakraborty S, Gadagkar R and Nagaraju J (2009) Polymorphic microsatellite loci for primitively eusocial wasp *Ropalidia marginata*. *Molecular Ecology Resources* 9:1172-1175.
5. Shimomura M, Minami H, Suetsugu Y, Ohyanagi H, Satoh C, Antonio B, Nagamura Y, Kadono-Okuda K, Kajiwara H, Sezutsu H, Nagaraju J, Goldsmith MR, Xia Q, Yamamoto K and Mita K (2009) KAIKObase: An integrated silkworm genome database and data mining tool. *BMC Genomics* 10: 486.
6. Mrinal N and Nagaraju J (2010) Dynamic repositioning of dorsal to two different kappaB motifs controls its autoregulation during immune response in *Drosophila*. *Journal of Biological Chemistry* (In press).

## Laboratory of Genomics and Profiling Applications

<b>Principal Investigator</b>	Madhusudan R Nandineni	Staff Scientist
<b>Ph D Students</b>	Anujit Sarkar	Junior Research Fellow
<b>Other Members</b>	Aruna Devi	Project Assistant
	Vishaka Sharma	Project Assistant
	Gadde Srinath	Project Assistant
	Sreeja Reddy	Project Assistant (since Feb. 2010)
	Jeffrey Pratap	Project Assistant (till June 2009)

### Objectives:

1. Development, standardization and validation of DNA markers for genetic fidelity testing of tissue culture raised plants and for phylogenetic studies
2. Development of novel strategies/methodologies for enrichment of human DNA from mixtures containing human and non-human DNAs for DNA profiling-based human identification
3. To study the human genetic diversity among various population groups of India.

### Project 1: Development and validation of DNA-based markers for genetic fidelity testing of tissue culture-raised plants and for phylogenetic studies.

#### Summary of work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)

As a referral centre for the genetic fidelity testing of tissue culture raised plants employing DNA markers, one of our laboratory's focus has been to develop DNA-based molecular markers which could be useful for true-to-type testing of important tissue culture raised crop plants like banana, black pepper, potato, sugarcane and vanilla. We had proposed to isolate microsatellite or simple sequence repeat (SSR) markers, which are highly polymorphic, using a selective hybridization procedure, and to check their utility for the above-mentioned purpose. In the meantime, we had tested some of the whole genome scanning molecular markers such as inter-simple sequence repeats (ISSR) for true-to-type testing. We had previously reported about the progress of work with ISSR markers and the efforts regarding SSR isolation.

### Details of progress made in the current reporting year (April 1, 2009 - March 31, 2010)

#### (A) Whole genome scanning molecular marker-based assay for genetic fidelity testing:

While the isolation of SSRs from these crops was in progress, we wished to check the suitability of whole genome scanning molecular markers (like ISSRs) for genetic fidelity testing of tissue culture raised plants. ISSR markers are less demanding as compared to SSRs, both technically as well as cost wise. Thirty ISSR primers derived from University of British Columbia (UBC) list were screened to select the most suitable primers that show polymorphism amongst different varieties of each crop. The markers which are able to distinguish between different varieties were used for assessing the clonal fidelity of the micropropagated plants. In our studies, few of the ISSR markers have been found to be useful for the purpose, while some of them have shown inconsistency in the pattern of amplified fragments among the tested plant varieties. Thus alternative multi-locus marker systems were explored for genetic fidelity testing. We are presently exploring the feasibility of employing some of the other whole genome scanning DNA-markers like the retrotransposon-based molecular markers, viz. inter-retrotransposon amplified polymorphism (IRAP) and retrotransposon microsatellite amplified polymorphism (REMAP) for true-to-type testing, as they offer more advantages than ISSR assays.

IRAP and REMAP are dominant, multi-locus marker system that examines variation in retrotransposons' insertion sites. Ubiquitous distribution, high copy number and widespread chromosomal dispersion of these mobile elements in most plant genomes provide an excellent potential for developing DNA-based marker systems for genetic fidelity testing and phylogenetic studies. The genetic stability of

tissue culture raised clones mainly depends on genotype, the chimeric nature of the explant used, tissue culture conditions, maintenance of cultures and number of subcultural passages. Retrotransposons are generally thought to be activated by tissue culture conditions employed for micropropagation of plants and it has been demonstrated that the copy number of some retrotransposons (e.g. *Tos 17* in rice, *Tto1* in tobacco), which are normally inactive elements, increases 10-fold during tissue culture. Since the idea is to assess the genetic fidelity (true-to-typeness) of tissue culture raised micropropagules, we hypothesized that the retrotransposon-based markers are well-suited for the purpose.

The IRAP fragments between two retrotransposons are generated by PCR, using outward-facing primers annealing to long terminal repeat (LTR) target sequences, whereas the REMAP fragments between retrotransposons and SSRs are generated by PCR, using one primer complimentary to the LTR target sequences and other one to a nearby SSR motif. Thus depending on the SSR loci (di-, tri-, tetra-, etc), various combinations of REMAP assays are possible for each LTR primer. The PCR amplicons are separated by high-resolution agarose gel-electrophoresis to visualize and score the bands.

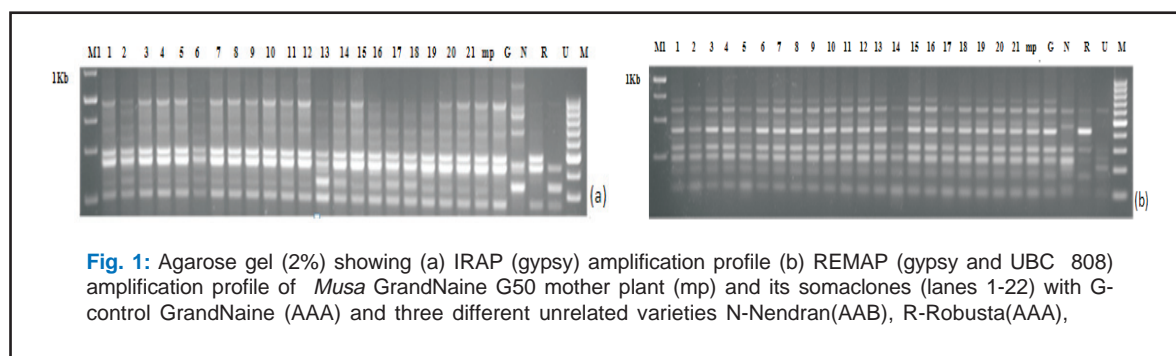
#### Varietal and clonal typing studies using the retrotransposon-based marker systems:

In IRAP analysis, various LTR primers reported previously were tested in different combinations to screen for the most suitable IRAP primer pairs, which show good reproducibility for phylogenetic studies of different varieties and true-to-type testing of micropropagated plants of banana, potato and sugarcane. In REMAP analysis, different combinations of LTR primers and thirty ISSR primers (which included di, tri and tetra nucleotide repeats) from the UBC list were used to screen for the suitable primer combinations for the above

crops. Standardization and testing these primer combinations for the intended purposes are currently under progress. **Fig.1** shows the representative preliminary results of IRAP and REMAP primers in banana clones and varieties. As can be gleaned from the figure, these retrotransposon-based markers were able to distinguish between different varieties and were also amenable for clonal fidelity testing in banana micropropagules. Further work is in progress to standardize these conditions for genetic fidelity testing.

#### (B) Isolation of microsatellite markers from sugarcane

SSRs are extremely valuable markers for genetic diversity analysis, phylogenetic studies, clonal fidelity testing, etc. In the present study, the method described by Glenn and Schable was followed for SSR isolation from sugarcane, which included the construction of a sub-genomic library. The amplicons from the insert containing (positive) clones were sequenced and mined for the presence of SSRs. More than seventy insert-containing (recombinant) clones were recovered in the initial rounds of enrichment, which were sequenced in both directions. The clone sequences when screened for the presence of microsatellite repeats have shown that a total of 54 clones contained SSR motifs, with the repeat size ranging from 12-40 nucleotides long. Primers were designed complementary to the 5' and 3' flanking genomic sequences of these repeats to standardize the PCR conditions for amplification of these markers and to test their polymorphic potential in different varieties of sugarcane. In future studies, they would be tested for their utility as markers in clonal fidelity studies. Since it is desirable to isolate multiple SSRs, which are polymorphic and informative, the above strategy would be adopted to isolate more number of microsatellites in sugarcane and as well as in other crop plants like banana, potato, black pepper and vanilla.



### (C) Employing previously known SSR markers for genetic fidelity testing

Numerous SSR primers reported in the literature for the above-mentioned crops were tested for their utility in genetic fidelity testing. PCR conditions were standardized for these primer pairs and the informative SSRs were tested in different varieties of tissue-culture raised plants for their applicability in genetic fidelity testing. Some of these SSR markers have shown high degree of polymorphism in all varieties tested so far. The agarose gel electrophoresis of clones of tissue-culture raised banana plants using the Ma-1-32 and MaCIR 150 SSR markers is depicted in **Fig. 2** and polyacrylamide gel electrophoresis (PAGE) with the Ma-1-27 SSR marker in 24 different varieties of banana is shown in **Fig. 3**. Future experiments will focus to validate informative SSRs by PAGE and capillary electrophoresis-based genotyping analysis and multiplexing of many loci for assessing the clonal fidelity of the micropropagated plants and also for phylogenetic studies of different crop plant genotypes.

#### Project 2: Development of novel strategies/methodologies for enrichment of human DNA from mixtures containing human and non-human DNAs for human identification

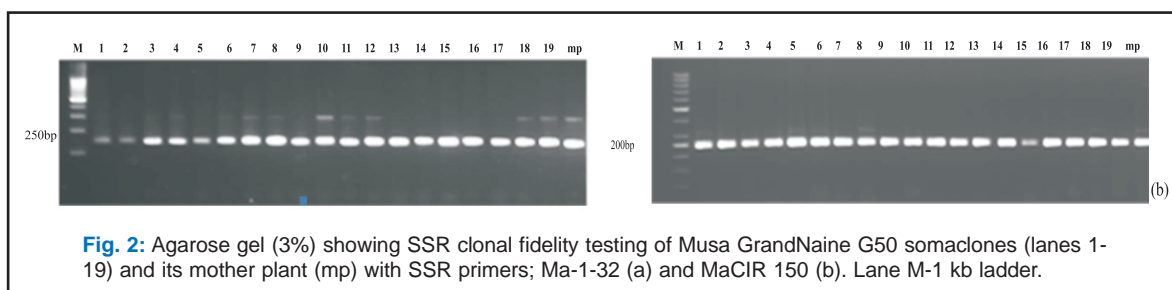
##### Summary of work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)

One of the major problems in obtaining good DNA profile for human identification (ID) purposes from old forensic skeletal exhibits has been that the DNA

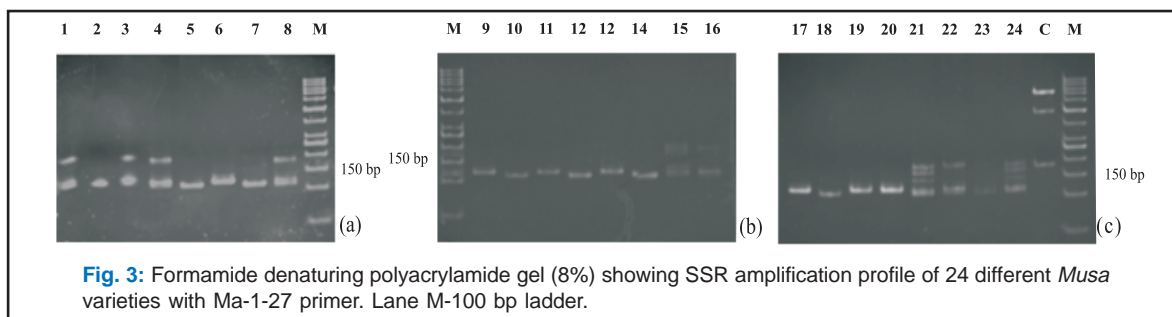
isolated from such sources is often highly fragmented/ degraded and contaminated with non-human DNAs. As mentioned in our previous reports, we sought to enrich the human DNA from such sources by two different approaches. In one approach, we have used biotinylated oligos to 'capture' the regions of microsatellites or short tandem repeat (STR) loci currently used for human ID purposes. In the second approach, we have employed antibodies directed against 5-methyl cytosine (5-mC) bases to 'pull down' human DNA containing 5-mC bases. The DNA segments pulled down by both these approaches were subjected to genotyping employing universally accepted commercial kits used for human ID purposes. In the first approach, by employing ten biotinylated oligos with sonicated human DNA, we have in our previous report demonstrated the specific amplification of all the ten corresponding STRs from the captured DNA fragments. In the case of 'pull down' with monoclonal and polyclonal antibodies directed against 5-mC residue, only a few loci could be amplified from the immunoprecipitated DNA; with few allele and locus dropouts.

##### Details of progress made in the current reporting year (April 1, 2009 - March 31, 2010)

To the previous list of ten primers described last year, we have designed six additional biotinylated oligos to complete the set of 16 loci required for unambiguous ID of humans by DNA testing and performed the hybrid-capture experiment with human DNA. The enriched DNA was used as



**Fig. 2:** Agarose gel (3%) showing SSR clonal fidelity testing of *Musa* GrandNaine G50 somaclones (lanes 1-19) and its mother plant (mp) with SSR primers; Ma-1-32 (a) and MaCIR 150 (b). Lane M-1 kb ladder.



**Fig. 3:** Formamide denaturing polyacrylamide gel (8%) showing SSR amplification profile of 24 different *Musa* varieties with Ma-1-27 primer. Lane M-100 bp ladder.



template for genotyping. By employing 16 oligos which are 3' biotinylated, we have been able to amplify all the forensically relevant STR loci by the protocol described in the previous reports. We have also been successful in minimizing the recovery of non-template DNA in our enriched product by using biotinylated oligos for various loci (**Nandineni and Vedanayagam, 2009**).

We performed reconstitution experiments by mixing human DNA with excess of bacterial DNA to simulate the natural conditions of mixed DNAs most often observed with DNA recovered from challenging forensic human skeletal samples. We mixed sonicated human DNA (of ~500 base pairs long) with varying amounts of bacterial DNA (*Escherichia coli*, MC4100), to get 1:1, 1:10, 1:50 and 1:100 ratios of human to bacterial DNA by weight and performed the enrichment procedure using the 3'-biotinylated oligos by following the protocol described in the previous reports. It is worthwhile to mention here that the human genome size is ~1000 times that of the *E. coli* genome and hence a ratio of 1:1 by weight would actually correspond to a ratio of 1:1000 genome copies of human DNA to bacterial DNA. The results showed that though the amplification of targeted loci was successful at lower bacterial concentrations (up to 1:50 ratio by weight), but at high bacterial concentration (1:100 by weight), the peak heights of targeted loci have decreased considerably along with the loss of one or more alleles.

Hence in order to increase the efficiency and specificity of the enrichment method, we decided to modify and adopt the primer extension capture (PEC) method for this purpose (*Briggs et al, Science 17, 2009, 325: 318-321*). In this method, after the hybridization step, the biotinylated oligos bind to the complementary regions upstream of their corresponding STR loci, a single cycle of extension will be carried out wherein the 5' biotinylated oligos will act as primers, and in the presence of dNTPs and Taq polymerase, the oligos will undergo an extension step to produce a long, double stranded hybrid molecule which will be captured subsequently by streptavidin-coated magnetic beads. The longer double stranded DNA molecule thus obtained during the single extension step will be able to withstand a more stringent final wash at higher temperature, and thus are expected to remain tightly bound to the beads, while the other non-specific DNA fragments would be washed away at high stringency conditions.

In the second approach using antibodies against 5-mC bases we had pulled down the human sonicated DNA with antibodies and subjected it to the whole genome amplification step using Genomiphi kit (GE Healthcare) followed by genotyping. It was observed that the peaks for the various STR loci were obtained, but were not ideal for human DNA typing suggesting that the strategy may have to be revisited. Presently, we are evaluating the efficiency of the antibody pull-down strategy to decide the future course of experiments.

### **Project 3: To study human genetic diversity in various population group in India**

#### **Summary of work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)**

One of the objectives of our laboratory is to access genetic diversity among different population groups in India and to address questions related to the phenotypic effects of genetic variation(s) within and between population groups; and also to address how such genetic variation is correlated with demographic distribution/stratification of various population groups in the country. In the initial phase, we are interested to validate the putative genetic variants (single nucleotide polymorphisms, SNPs) that play an important role in determining the pigmentation make up in different population groups in India. Previous studies on different world populations have revealed that skin pigmentation is a polygenic trait involving more than thirty genes. Our preliminary studies on some of these loci had given some interesting insights accounting for this difference.

#### **Details of progress made in the current reporting year (April 1, 2009 - March 31, 2010)**

During the current year, more phenotypic traits (like body-mass index, hair thickness etc) have been included during sampling for the genetic variation studies. Genetic variants associated with these traits have been reported in literature for different world populations, but there is scant information with relation to Indian populations. As was performed with skin pigmentation loci, we wish to test the association of these genetic variants (SNPs) with the phenotypes for the Indian populations.

We are in the process of collecting samples from subjects after informed consent from different locations in India for the initial set of studies. During sampling, skin melanin index values (a quantitative measure of darkness of the skin) are being

collected from the subjects. In future experiments, we would like to genotype large number of individuals for the various SNPs to correlate the genotypes to the actual phenotype (as determined by skin melanin index) to understand the complex phenotype of skin pigmentation.

Further, we wish to include ancestry informative markers (AIMs) (which are primarily linked SNPs in mitochondrial DNA and Non-Recombining region of Y-chromosome, NRY; carrying the information regarding a person's lineage and ancestry), in our panel of SNPs for genetic variation studies. The understanding and validation of these variants, apart from holding great implications in studies related to human evolutionary, migratory and forensic genetics, would also be of profound importance in forensic DNA testing to track or shortlist the

culprit(s) within a large population where only biological evidence is recovered from the crime scene without a suspect.

#### Publications:

1. Herráez DL, Bauchet M, Tang K, Theunert C, Pugach I, Li J, Nandineni MR, Gross A, Scholz M and Stoneking M (2009) Genetic variation and recent positive selection in worldwide human populations: evidence from nearly 1 million SNPs. *PLoS One* 4:e7888.
2. Nandineni MR and Vedanayagam JP (2009) Selective enrichment of human DNA from non-human DNAs for DNA typing of decomposed skeletal remains (2009) *Forensic Science International: Genetics Supplement Series* 2: 520-521.

## Laboratory of Fungal Pathogenesis

### Understanding the pathobiology of an opportunistic human fungal pathogen, *Candida glabrata*

<b>Principal Investigator</b>	Rupinder Kaur	Staff Scientist
<b>Ph D Students</b>	Gaurav	Senior Research Fellow
	Maruti Nandan Rai	Senior Research Fellow
	Sapan Borah	Junior Research Fellow
<b>Other members</b>	G Neelima	Project Assistant
	Sriram Balusu	Project Assistant (since Sep. 2009)
	Shivarathri Raju	Project Assistant (since Oct. 2009)
	DPSS Lakshmi	Technical Assistant

*Candida glabrata* is an opportunistic fungal pathogen of humans and accounts for about 12% of total blood stream *Candida* infections. It currently ranks as the second or third most common yeast pathogen found in blood stream infections depending upon the geographical location. *C. glabrata* is a haploid budding yeast and is more closely related to the model yeast *Saccharomyces cerevisiae* than to its highly pathogenic counterpart *C. albicans*. Despite its reduced virulence potential, *C. glabrata* infections are usually associated with a high mortality rate, probably, in part, due to its innate resistance to the most widely used anti-fungal drug, fluconazole. Research in our laboratory is centered on elucidating the molecular basis of high intrinsic resistance of *C. glabrata* towards fluconazole and its interaction with the host immune cells.

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

##### Objectives:

1. Analysis of intra-cellular behavior
2. Screening of *C. glabrata* mutant library for altered survival profiles
3. Identification and analysis of the genes required for survival *in vitro*.

##### Summary of the work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)

An *in vitro* system consisting of human monocytic cell line THP1 was established and infection studies of PMA (Phorbol-12 Myristate 13-acetate) differentiated THP1 cells with *C. glabrata* cells revealed that wild-type cells undergo a moderate

5-7 fold replication over a period of 24 hr while a *C. glabrata* strain disrupted for putative cell surface associated aspartyl proteases was rapidly killed by macrophages displaying a viability of 1.34% after 24 hr of co-incubation with macrophages. Next, conditions were standardized to use this *in vitro* system to screen a *C. glabrata* mutant library (18,432 mutants; generated by homologous recombination of *in vitro* generated Tn7 insertions in *C. glabrata* genomic clones) for altered survival profiles in macrophages via a modified version of signature tagged mutagenesis (STM) approach. These mutants have been assembled in a total of 192 pools wherein each pool is comprised of 96 mutants. Each of these pools carries the same set of 96 tags but within a pool each mutant carries a different tag thereby allowing a parallel analysis of 96 mutants at once. For a pool of tagged mutants, the ratio of hybridization in the output and input pools reflects any shift in the representation of the corresponding mutant in the pool. A total of 48 mutant pools were screened in differentiated THP1 cells for altered survival phenotypes using hybridization-based STM approach.

##### Details of the progress made in the current reporting year (April 1, 2009 - March 31, 2010)

The STM screen for altered survival profiles was extended to additional 144 pools and mutants with an output/input ratio of  $\geq 6.0$  and  $\leq 0.1$  were selected as 'up' (increased survival) and 'down' (reduced survival) mutants respectively. Using this ratio as cut-off criteria, a total of 175 mutants were identified that displayed altered survival profiles in differentiated THP1 cells (**Table 1**). Next, mutants were retested for survival defects in macrophages



Table 1: Summary of the STM screen

Total number of mutants screened	18,432
Mutants selected with a cut-off value of $\leq 0.1$ and $\geq 6.0$	175
Number of Up mutants identified	69
Number of Down mutants identified	106
Number of mutants rescued	133
Number of genes identified	102
Number of mutants with Tn7 insertion in the inter-genic regions	8

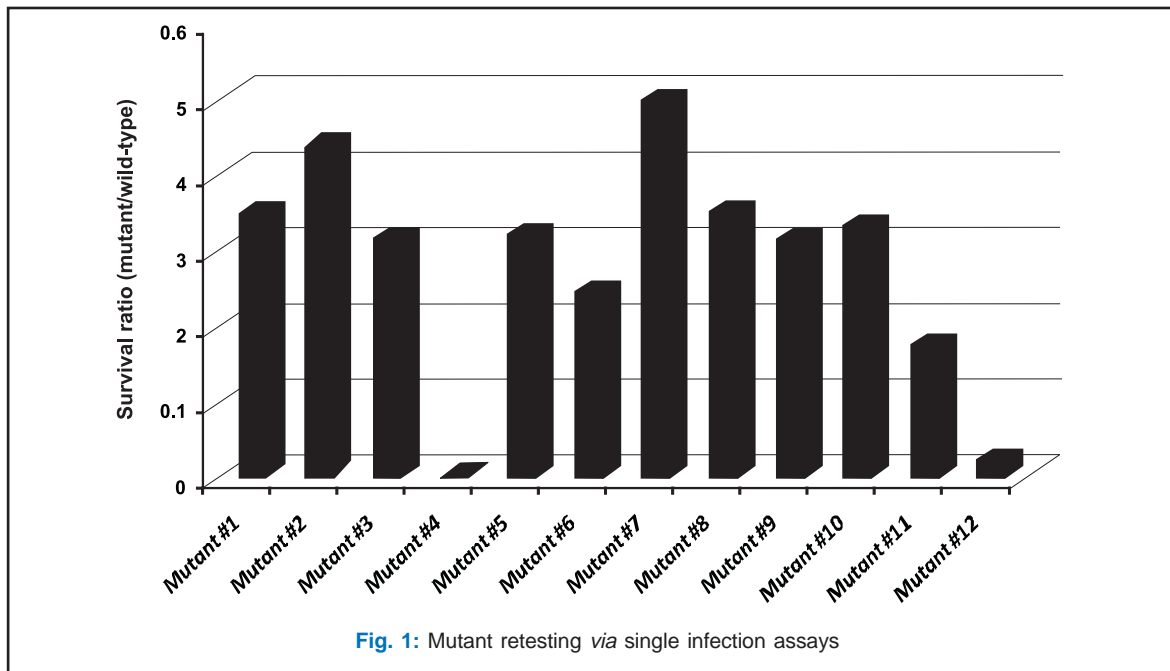


Fig. 1: Mutant retesting via single infection assays

by single infection assays and survival ratio was calculated by dividing the colony forming units (CFUs) obtained for a mutant with those obtained for the wild-type strain after 24 hr of co-incubation with macrophages (Fig. 1). Tn7 insertion mapping and sequence analyses of the mutants identified a set of 102 genes in *C. glabrata* that are required for its survival/replication in cultured human macrophages. Functional categorization of the genes into biological processes was carried out based upon the Gene Ontology (GO) annotations of their *S. cerevisiae* homologs in the Saccharomyces Genome Database (SGD).

To obtain a preliminary understanding of their role in intracellular survival, all the 175 mutants were tested for growth defects under a wide variety of conditions such as acidic pH, alkaline pH, high temperature, oxidative stress, starvation stress, osmotic stress, cell wall stress *etc.* This profiling

revealed the diverse nature/phenotypes of the identified mutants (Table 2) and overlapping sensitivities to different stresses were seen for very few mutants. Two of the down rescued mutants (T42-19 and T42-25) that were exquisitely sensitive to sodium chloride, were selected for further analysis. Insertion in these mutants was mapped to the *C. glabrata* ORF, *CAGL0K12034g* which is an ortholog of *Saccharomyces cerevisiae* *ENA1*. *ENA1* codes for an ATPase that acts as a sodium-lithium transporter and is required to survive salt and alkaline pH stress in *S. cerevisiae*. This protein has yet not been characterized in *C. glabrata* and intriguingly, *Ena1* has recently been reported to be required for virulence in a murine model of systemic infection for another fungal pathogen, *Cryptococcus neoformans*. Future efforts will be focused on elucidating the role of the identified genes in the survival and interaction of *C. glabrata* with the host cells.

**Table 2:** Phenotypic profiling summary

Total number of mutants profiled	175
Sensitive to salt	5
Sensitive to SDS	19
Sensitive to low pH	3
Sensitive to pH 7.0	5
Sensitive to caffeine	7
Sensitive to high temperature (42°C)	1
Sensitive to ER stress	9
Sensitive to cell wall stress	4
Sensitive to oxidative stress	4
Sensitive to RPMI medium + serum	6

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

### Objectives

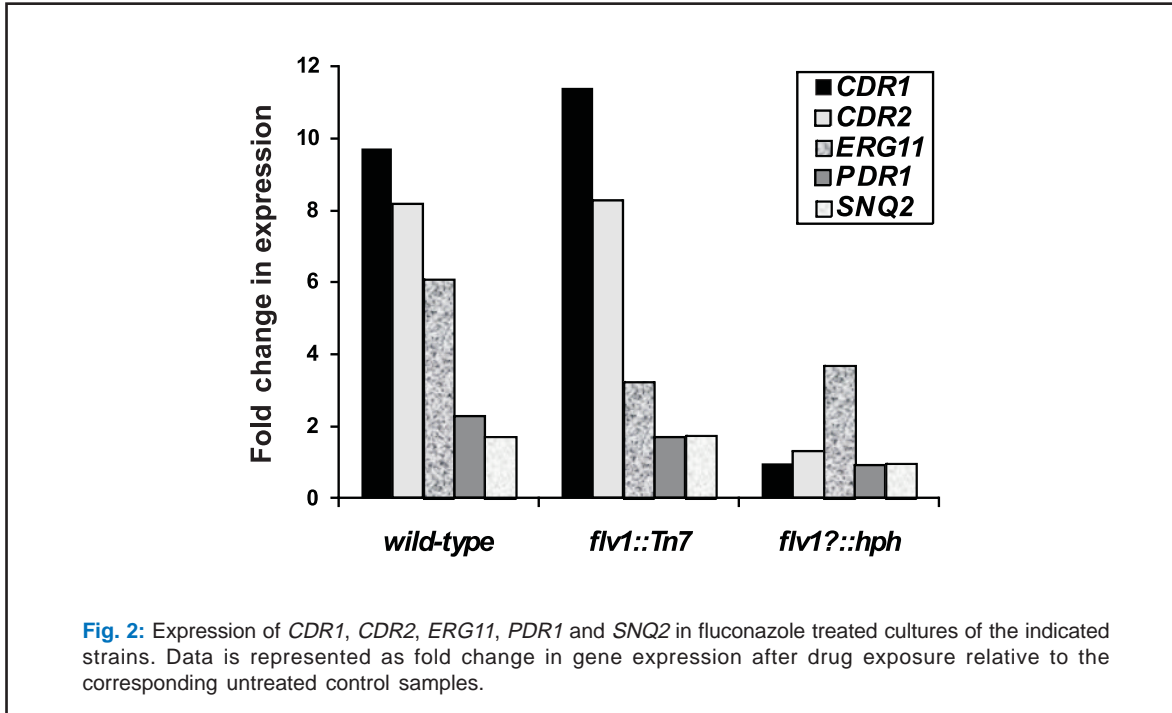
1. Identification and characterization of fluconazole sensitive mutants
2. Understanding the molecular basis of high innate resistance of *C. glabrata*.

### Summary of the work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)

To better understand the inherent low fluconazole susceptibility of *C. glabrata*, fluconazole sensitive mutants were tested for their inability to survive fluconazole stress by CFU assay. One of the mutants carrying Tn7 insertion in the *FLV1* (fluconazole loss of viability) gene was found to lose viability upon fluconazole exposure and also displayed sensitivity to several other stress causing agents. Surprisingly, contrary to the insertional mutant (*flv1::Tn7*, YRK25) phenotype, the *flv1* deletion strains (*flv1Δ::hph*), generated by both one step and two-step gene replacement methodology, showed elevated resistance to the azole compounds including fluconazole. This resistance towards fluconazole was neither due to the loss of mitochondrial function nor due to the strain specific variations because of different parental strain backgrounds. As a control, *FLV1* disruption in the knock-out strains was confirmed by Southern analysis and fluconazole resistance of *flv1Δ::hph* strains was complemented by expressing *FLV1* ectopically from a plasmid.

### Details of the progress made in the current reporting year (April 1, 2009 - March 31, 2010)

To investigate the potential molecular mechanism for differential susceptibility of a *flv1::Tn7* insertional mutant (YRK25) and a *flv1* knock-out strain (*flv1Δ::hph*, YRK304) towards fluconazole, we decided to examine the expression of five genes, that have been reported to contribute to azole resistance/hypersusceptibility in *C. glabrata*, in these mutant backgrounds. These five genes, *CDR1*, *CDR2* and *SNQ2*, *PDR1* and *ERG11*, code for plasma membrane ATP-binding cassette transporters, Zinc finger transcriptional regulator of pleiotropic drug resistance genes, and Lanosterol 14- $\alpha$ -demethylase (target of fluconazole) respectively. As shown in figure 2, wild-type cells respond to fluconazole exposure by elevating the expression of genes coding for drug transporters (*Cdr1* and *Cdr2*) by eight to ten-fold. Similar expression profiles were seen for *flv1::Tn7* mutant (YRK25). A modest 1.8-fold induction was seen in the expression levels of the third drug-transporter, *Snq2*, in both the strain backgrounds (**Fig. 2**). In contrast, untreated cells of *flv1* deletion mutant (*flv1Δ::hph*, YRK304) strain showed constitutive high expression of *CDR1* and *CDR2* and no further induction was seen upon fluconazole exposure. In consistence with earlier reports, a three to six-fold increase was observed for *ERG11* transcript levels after fluconazole treatment (**Fig. 2**) in different strain backgrounds indicating that cells respond to drug exposure by elevating the expression of its target



enzyme. Collectively, the real time RT-PCR results suggest that constitutive high expression of the drug efflux pumps accounts for the fluconazole resistance phenotype of the *flv1* deletion mutants.

In the original mutant screen for altered fluconazole susceptibility profiles, Tn7 insertion was mapped initially in a single *flv1* mutant (YRK25) and was found to be in the C-terminal domain of the Flv1 protein. To conduct a structure-function analysis on Flv1, we decided to map Tn7 insertions in additional *flv1* fluconazole sensitive mutants. Tn7 rescue and sequencing analysis of these mutants revealed Tn7 insertions to be scattered throughout the Flv1 protein revealing the significance of one particular domain of Flv1 for survival under fluconazole stress. Intriguingly, overexpression of

*FLV1* in the wild-type background led to sensitivity to higher temperature and fluconazole, phenotypes exhibited by *flv1::Tn7* insertional mutants. Preliminary data suggests that dysregulation of the Protein kinase C-mediated cell integrity signaling pathway accounts for the differential fluconazole susceptibility profiles of *flv1* mutants. Experiments are currently underway to identify the down-stream components of this stress signaling cascade and to establish a direct link between Flv1 function and dysregulation of the PKC-MAPK signaling pathway.

#### Other publications

1. Kaur R (2009) Review of: Lilavati's daughters: The women scientists of India. Rohini Godbole and Ram Ramaswamy (eds),. **Current Science** 96: 1137-1138.

## Laboratory of Immunology

### Understanding the role of nuclear factor kappaB in doxorubicin-mediated cell death and chemoresistance: regulation to improve chemotherapy

<b>Principal Investigator</b>	Sunil K Manna	Staff Scientist
<b>Ph D Students</b>	Charitha Gangadharan	Senior Research Fellow
	Maikho Thoh	Senior Research Fellow
	Sidharth Mahali	Junior Research Fellow
	S Adeel Husain Zaidi	Junior Research Fellow
	Reveendra B Mokhamatar	Junior Research Fellow
<b>Other Members</b>	Nune Raviprakash	Project Assistant
	Damodar Edupalli	Project Assistant
	T Navaneetha	Technical Assistant
	A Jagan	Technician II
<b>Collaborators</b>	GT Ramesh	Norfolk University, USA
	Chitta S Kumar	SK University, AP, India

#### Objectives

1. Understanding the mechanism of doxorubicin-mediated cell death and drug-resistance
2. Detection of the molecular mechanisms mediated by novel small molecules to induce anti-inflammatory and anti-tumorigenic responses
3. Regulation of cytokine receptors to regulate tumorigenesis and inflammatory responses.

#### Summary of work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)

The RelA (p65) is a subunit of nuclear transcription factor kappa B (NF- $\kappa$ B) and actively participates in expression of NF- $\kappa$ B-dependent genes involved in inflammation and tumorigenesis. Hence, the regulation of p65 is an important strategy to regulate those responses. Our data suggested that the dichlorophenyl derivative of 1,2,4-thiadiazolidine (known as P<sub>3</sub>-25) induced cell death in NF- $\kappa$ B-expressing and doxorubicin-resistant cells. P<sub>3</sub>-25 inhibited NF- $\kappa$ B-dependent gene expression completely and inhibited phosphorylation of RelA (p65) by inhibiting activity of protein kinase A (PKA), having an IC<sub>50</sub> at 10.5 nM. P<sub>3</sub>-25 potentiated different chemotherapeutic agents-mediated cell death. Our results suggest that P<sub>3</sub>-25 inhibits PKA activity followed by decreased phosphorylation of p65 and transcriptional activity of NF- $\kappa$ B thereby decreasing antiapoptotic proteins resulting in induction of

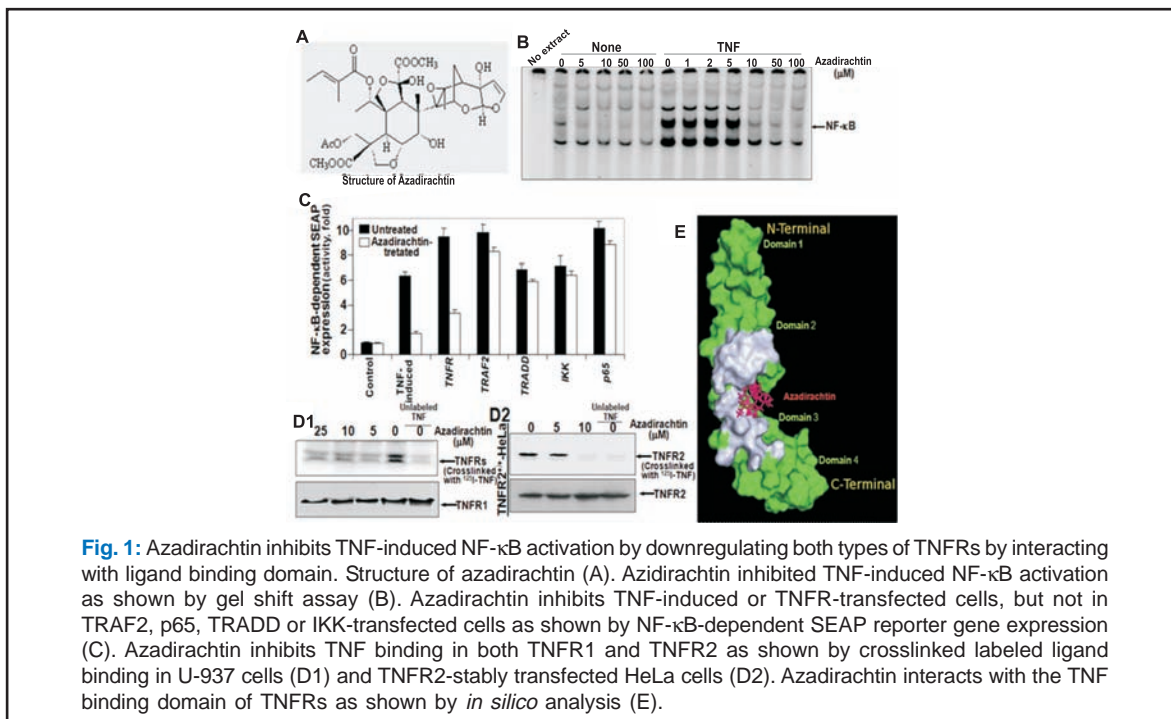
apoptosis in NF- $\kappa$ B-expressing and doxorubicin-resistant cells (**Mol. Immunol. 2009, 46: 1340-1350**). P<sub>3</sub>-25 is a potential inducer of cell death by arresting cell cycle at G1 phase and by decreasing the amounts of cyclin D1 and cyclin E without interfering p16 and p27. It decreased c-Myc level and thereby inhibited DNA binding ability of Myc-Max complex. P<sub>3</sub>-25 dephosphorylated Rb and Akt facilitating nuclear translocation of FKHR which led to the expression of FasL. Activated FasL inhibited cell proliferation and induced cell death. Our results suggest that P<sub>3</sub>-25 derivative exerts anti-tumor activities by decreasing Myc-mediated response and increasing FasL expression, which may help in designing drugs for tumor therapy (**Biochem. Pharmacol. 2009, 78: 495-503**). Overall, these studies might help to understand the mechanism of P<sub>3</sub>-25-mediated apoptosis and to design it as new chemotherapeutic drug for tumor therapy. A dihydrobenzofuran lignan, the dimerization product of caffeic acid methyl ester, has shown pronounced anti-leishmanial and anti-plasmodial activities. Our study showed the effect of this compound on cell cycle (G2/M arrest) and apoptosis was via mitochondrial controlled pathway (**J. Med. Chem. 2009, 52: 3184-3180**). These findings open promising avenues, as to how this specific dihydrobenzofuran lignan mediates cytotoxicity and may prove a molecular rationale for future therapeutic interventions in carcinogenesis.

**Details of progress in the current reporting year  
(April 1, 2009 - March 31, 2010)**

**(A) Azadirachtin interacts with the TNF binding domain of its receptors and inhibits TNF-induced biological responses**

The role of azadirachtin, an active component of a medicinal plant *Neem* (*Azadirachta indica*), on TNF-induced cell signaling in human cell lines was investigated. Azadirachtin (**Fig. 1A**) blocks TNF-induced activation of NF- $\kappa$ B (**Fig. 1B**) and expression of NF- $\kappa$ B-dependent genes such as adhesion molecules and cyclooxygenase 2. Azadirachtin inhibits inhibitory subunit of NF- $\kappa$ B ( $\text{I}\kappa\text{B}\alpha$ ) phosphorylation and thereby its degradation and RelA (p65) nuclear translocation. It blocks  $\text{I}\kappa\text{B}\alpha$  kinase (IKK) activity *ex vivo*, but not *in vitro*. Surprisingly, azadirachtin blocks NF- $\kappa$ B DNA binding activity in transfected cells with *TNF receptor associated factor (TRAF) 2*, *TNF receptor associated death domain (TRADD)*, *IKK* or *p65*, but not with TNFR (**Fig. 1C**), suggesting that its effect is at TNFR level. Azadirachtin blocks binding of TNF, but not IL-1, IL-4, IL-8, or TNF-related apoptosis inducing ligand (TRAIL) with its respective receptors. Azadirachtin inhibits TNF binding in both TNFR1 and 2 as shown by crosslinking experiment (**Fig. 1D1 & 1D2**). Further, *in silico* data suggest that azadirachtin strongly binds in the TNF binding site of TNFR (**Fig. 1E**). We demonstrate a novel action of azadirachtin against TNF-mediated

biological responses in mammalian cells through inhibition of NF- $\kappa$ B, thereby regulation of inflammation and tumorigenesis. We are reporting for the first time that it inhibits inflammatory responses in diverse mammalian cell types. Azadirachtin interacts with TNFRs and prevents TNF binding thereby downstream signaling like IKK activation,  $\text{I}\kappa\text{B}\alpha$  degradation, p65 nuclear translocation and NF- $\kappa$ B-dependent genes transcription. Even azadirachtin treatment at 4°C also supports the effect of azadirachtin on TNFRs levels. *In silico* data for TNF binding site at TNFRs and interaction of azadirachtin on this binding site might help to address this issue further. Though Th2 cytokine, IL-4 sheds both types of TNFRs from cell membrane, but azadirachtin does not do so. These data further suggest that azadirachtin-mediated interaction lies within TNFRs. As TNF is the most potent inducer of NF- $\kappa$ B, blocking TNF receptors is expected to control inflammation and tumorigenesis. Azadirachtin-mediated interaction with TNFRs and the decrease in TNF-induced biological activities in diverse cell types are novel findings. Azadirachtin-mediated inhibition of inflammatory responses might be the basis of the folklore use of neem products against many diseases. Hence, understanding the azadirachtin (an active component of neem products) mediated inhibition of TNF-induced inflammatory responses might help in exploring its use as medicine against several inflammatory diseases.





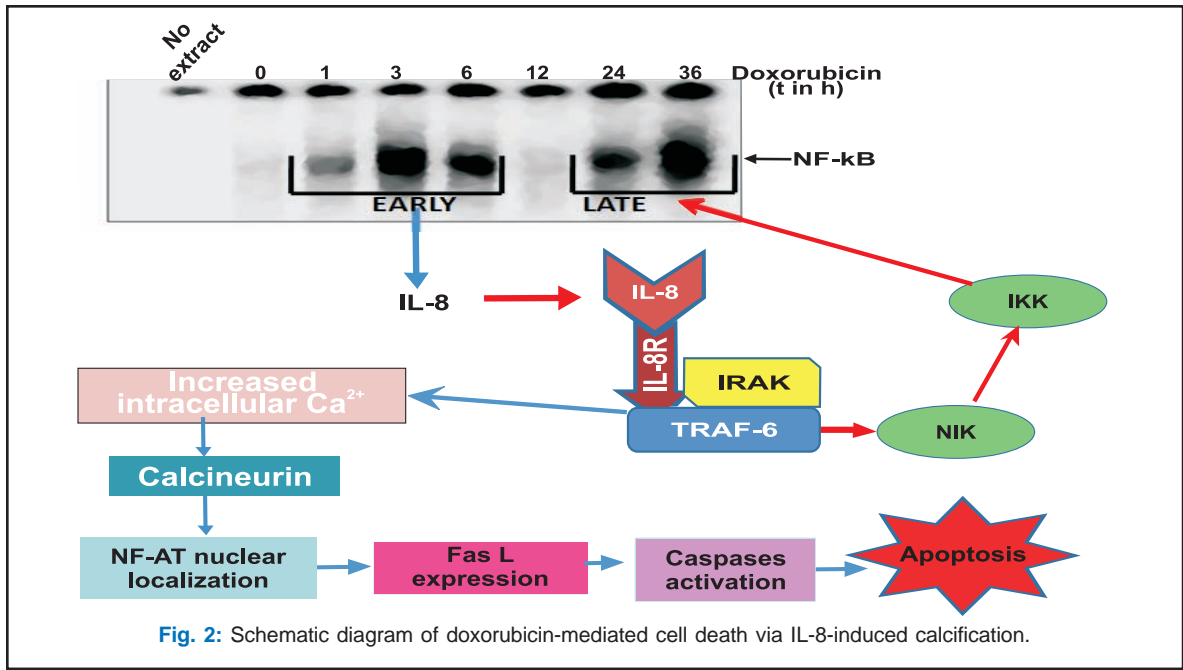
**(B) Late phase activation of nuclear transcription factor kappaB by doxorubicin is mediated by interleukin-8 and induction of apoptosis via FasL**

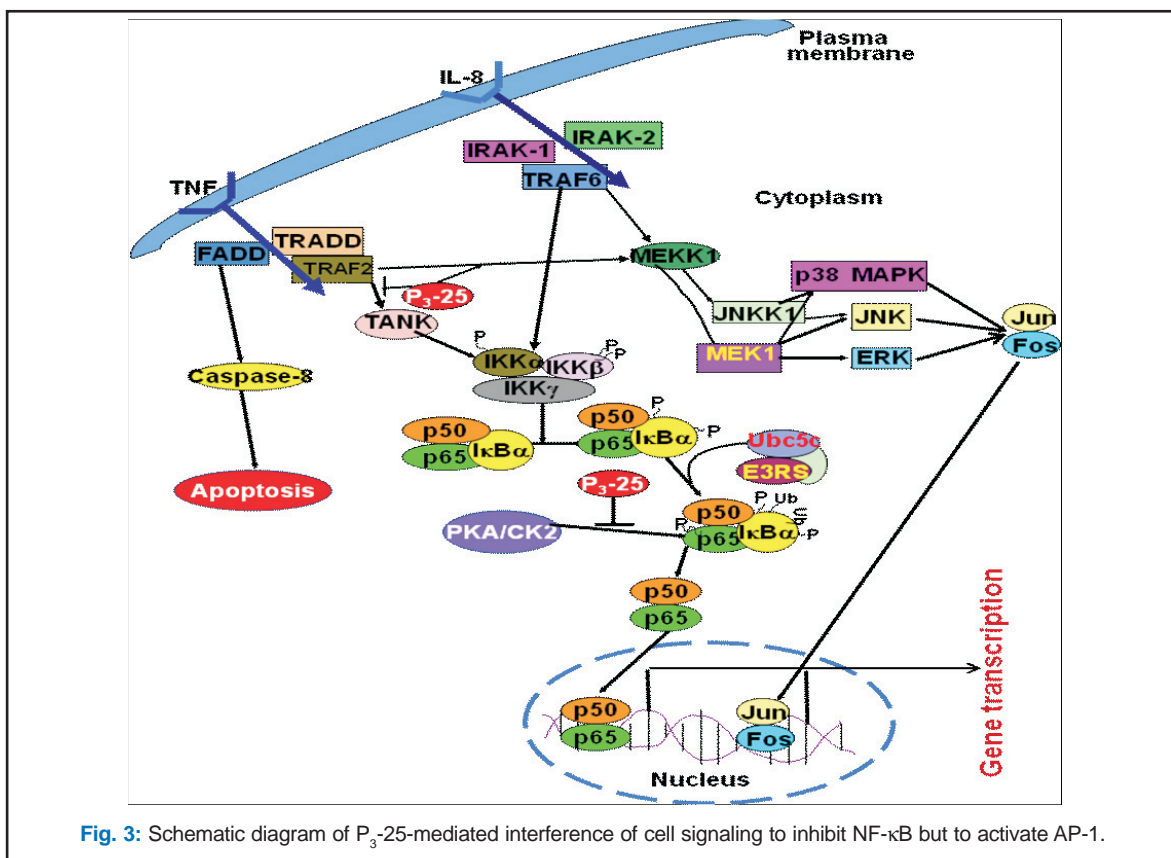
Doxorubicin is one of the most effective molecules used in the treatment of various tumors. Contradictory reports often open windows to understand the effect of doxorubicin-mediated signaling on apoptosis. In this report, we provide evidence that doxorubicin induced biphasic induction of nuclear factor kappaB (NF-κB); immediate activation is followed by decrease in the amount of RelA (p65) subunit possibly by inducing the activity of proteasome, but not proteases. Further induction of NF-κB was observed through expression of interleukin 8 (IL-8) by doxorubicin treatment. Increased amount of IL-8 induced apoptosis via increase in the release of intracellular Ca<sup>2+</sup>, activation of calcineurin, nuclear translocation of nuclear factor activated T-cell (NF-AT), and NF-AT-dependent FasL expression (**Fig. 2**). Anti-IL-8 or -FasL antibody, dominant negative TRAF6 (*TRAF6-DN*), or TRAF6 binding peptide (TRAF6-BP) inhibited doxorubicin-mediated late phase induction of NF-κB and diminished cell death. Thus, our study clearly demonstrated that doxorubicin-mediated cell death is obtained through the expression of IL-8. IL-8-mediated calcification is required for enhancement of doxorubicin-mediated cell death. Overall, this study will help us to understand the mechanism of doxorubicin-mediated

cell signaling cascade in chemotherapy.

**(C) Inhibiting TNF receptor associated factor 2-mediated activation of nuclear factor kappaB facilitates induction of activator protein-1**

The compound P<sub>3</sub>-25 is known to possess anti-bacterial, anti-fungal, and anti-tubercular activities. In this report we provide evidence that P<sub>3</sub>-25 inhibits nuclear transcription factor kappaB (NF-κB), which is known to induce inflammatory and tumorigenic responses. It activates activator protein (AP)-1, another transcription factor, and inhibits TNF receptor associated factor (TRAF) 2-mediated NF-κB activation, but not TRAF6-mediated NF-κB DNA binding by preventing its association with TANK (TRAF for NF-κB). It facilitates binding of mitogen activated protein kinase kinase kinase (MEKK) 1 with TRAF2 and thereby activates c-Jun-terminal kinase (JNK) and AP-1. In this report, first time we provide evidences that the dimethyl form of 1,2,4 thiazolidine (P<sub>3</sub>-25), a synthetic derivative, interacts with TRAF2 in such manner where recruitment of TANK is completely inhibited and thereby inhibiting recruitment of IKKs. Thus, P<sub>3</sub>-25 inhibits IκBα degradation thereby resulting in the arrest of NF-κB in cytoplasm. Though TRAF6- or IL-8-mediated IKKs activation is unaffected by P<sub>3</sub>-25 treatment, but it blocks NF-κB-dependent gene transcription by inhibiting p65 phosphorylation. Thus, double sword mechanism of P<sub>3</sub>-25 completely shuts down NF-κB functions (**Fig. 3**).





## Publications

1. Bose JS, Gangan V, Jain SK and Manna SK (2009) Downregulation of inflammatory responses by novel caffeine acid ester derivative by inhibiting NF-kappaB. *Journal of Clinical Immunology* 29: 90-98.
2. Bose JS, Gangan V, Jain SK and Manna SK (2009) Novel caffeic acid ester derivative induces apoptosis by expressing FasL and downregulating NF-kappaB: Potentiation of cell death mediated by chemotherapeutic agents. *Journal of Cellular Physiology* 218: 653-662.
3. Bose JS, Gangan V, Prakash R, Jain SK and Manna SK (2009) A dihydrobenzofuran lignan induces cell death by modulating mitochondrial pathway and G2/M cell cycle arrest. *Journal of Medicinal Chemistry* 52: 3184-3190.
4. Gangadharan C, Thoh M and Manna SK (2009) Inhibition of constitutive activity of nuclear transcription factor kappaB sensitizes doxorubicin-resistant cells to apoptosis. *Journal of Cellular Biochemistry* 107: 203-213.
5. Manna SK and Gangadharan C (2009) Decrease in RelA phosphorylation by inhibiting protein kinase A induces cell death in NF-kappaB-expressing and drug-resistant tumor cells. *Molecular Immunology* 46:1340-1350.
6. Raghavendra PB, Pathak N and Manna SK (2009) Novel role of thiadiazolidine derivatives in inducing cell death through Myc-Max, Akt, FKHR, and FasL pathway. *Biochemical Pharmacology* 78: 495-503.
7. Gangadharan C, Thoh M and Manna SK (2010) Late phase activation of nuclear transcription factor kappaB by doxorubicin is mediated by interleukin-8 and induction of apoptosis via FasL. *Breast Cancer Research and Treatment* 120: 671-683.
8. Thoh M, Kumar P, Nagarajaram HA and Manna SK (2010) Azadirachtin interacts with the TNF binding domain of its receptors and inhibits TNF-induced biological responses. *Journal of Biological Chemistry* 285: 5888-5895.
9. Manna SK, Babajan B, Raghavendra PB, Raviprakash N and Kumar CS (2010) Inhibiting TNF receptor associated factor 2-mediated activation of nuclear factor kappaB facilitates induction of activator protein-1. *Journal of Biological Chemistry* (In press).

## Laboratory of Bacterial Genetics

### Studies on gene regulation, transcription termination, and amino acid and ion-transport in *Escherichia coli*

<b>Principal Investigator</b>	J Gowrishankar	Director and Staff Scientist
	Abhijit A Sardesai	Staff Scientist
	R Harinarayanan	Staff Scientist
<b>Ph D Students</b>	Syeda Aisha Haneea	Senior Research Fellow
	Shivalika Saxena	Senior Research Fellow
	Carmelita N Marbaniang	Senior Research Fellow
	L Shanthy	Junior Research Fellow
	Amit Pathania	Junior Research Fellow
	Aanisa Nazir	Junior Research Fellow
	Amar Deep Lakra	Junior Research Fellow (since Jan. 2010)
<b>Other Members</b>	V K Mishra	Staff Scientist
	K Anupama	Staff Scientist
	J Krishna Leela	Technical Officer III
	T S Shaffiqu	Technical Assistant
	Vimala Allada	Project Associate
	P Hima Bindu	Project Associate
	S Mahalakshmi	Project Assistant (since Nov. 2009)

#### Objectives

1. To study the ArgP regulon and the mechanism of ArgP-mediated transcriptional regulation of the arginine exporter ArgO
2. To test the model of and mechanisms mediating R-loop formation from nascent untranslated transcripts
3. To investigate an unusual phenomenon of K<sup>+</sup> toxicity in *hns trx* double mutant strains
4. To investigate the physiological roles of the stringent response factors DksA/(p)ppGpp.

#### Summary of work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)

1. Several years ago, a novel arginine exporter ArgO of *E. coli* and a regulator protein ArgP involved in the transcriptional regulation of *argO* were reported from our laboratory. Mutations in *argP* also contributed to an osmosensitivity phenotype, which was inferred to be caused by a decrease in glutamate dehydrogenase

activity in the mutant strains. In vitro experiments had demonstrated that ArgP binds the *argO* regulatory region to recruit RNA polymerase to the promoter in the presence of either arginine or lysine; and that whereas Arg-mediated recruitment leads to activation of *argO* transcription, Lys-mediated recruitment leads to trapping of RNA polymerase at the promoter and hence to *argO* transcriptional inactivation. The latter was the first known instance of an environmental signal regulating bacterial transcription at the final stage of promoter escape (i.e., after open complex formation) by RNA polymerase. The effect of ArgP on transcriptional regulation of *gdhA* (encoding glutamate dehydrogenase, required for glutamate synthesis and osmoregulation) was also investigated with the aid of *gdhA-lac* fusions. The results demonstrated that *gdhA* transcription is independently and additively affected by ArgP and osmolarity of the growth medium, which provides an explanation for the osmosensitivity associated with *argP* mutations. Functional studies on the



mechanism of ArgO-mediated export of arginine were also initiated, by the approach of obtaining novel *argO* mutants with altered transporter characteristics.

2. *E. coli* missense *rho* and *nusG* mutants are known to be defective in factor-dependent transcription termination, and we had recently identified a new missense mutation in *nusA* that also confers the phenotype of defective transcription termination. Mutations in the gene for the nucleoid protein H-NS were able to restore the efficiency of transcription termination in *rho*, *nusG* or *nusA* mutant strains. We have earlier also proposed that the nascent untranslated transcripts which fail to undergo termination in the *rho* or *nusG* mutants are prone to generating RNA-DNA hybrids (R-loops) in the DNA upstream of the moving RNA polymerase, and had obtained evidence that such R-loop formation in the mutants could serve to bypass the essential role of RNase E-mediated mRNA turnover in *E. coli*.
3. A novel phenotype of potassium toxicity in *E. coli* strains doubly defective for the nucleoid protein H-NS and reduced cytoplasmic thioredoxin (through mutation in either the *trxA* or *trxB* genes encoding thioredoxin and thioredoxin reductase, respectively) was identified. These strains were unable to grow in minimal media containing 40 mM or more of K<sup>+</sup> (including minimal A medium, which has around 115 mM K<sup>+</sup>), whereas they grew quite normally in media in which K<sup>+</sup> has been substituted with Na<sup>+</sup>. A genetic suppressor approach was initiated in an attempt to understand the mechanism of K<sup>+</sup> toxicity of these mutants.

### Work undertaken in the current reporting year (April 1, 2009 - March 31, 2010)

#### 1. ArgP regulon and mechanism of ArgO exporter function

- a. From a microarray-based comparison of mRNA abundances between an *argP*<sup>+</sup> strain and an *argP* mutant, the *lysP* gene was chosen for further study as a candidate member of the ArgP regulon on the considerations that (i) its mRNA abundance was approximately 4-fold elevated in *argP*<sup>+</sup> relative to the *argP* mutant; and (ii) it encodes a permease for L-lysine, which was earlier shown to be a co-effector in ArgP-mediated regulation of *argO*.

By the following tests, we were able to establish that *lysP* is a new member of the ArgP regulon.

- (i) The *cis* regulatory region upstream of the *lysP* open-reading frame was cloned as a 264-bp fragment in a single-copy-number *lacZ* reporter gene plasmid vector pMU575. The expression of *lysP-lac* was unaffected by arginine but was repressed approximately 5-fold by lysine-supplementation in the wild-type (*ArgP*<sup>+</sup>) strain. In the *argP* mutant, *lysP-lac* expression was down-regulated 25-fold relative to *argP*<sup>+</sup> in unsupplemented medium, and there was no change in expression with either arginine or lysine supplementation.
- (ii) It is known that *lysP* mutants are resistant to the lysine analogue thialysine. We were able to show that an *argP lysP*<sup>+</sup> strain is also thialysine-resistant, and that the resistance levels are not further increased in the *argP lysP* double mutant.

These results indicate that *lysP* transcription is activated by ArgP, and further that ArgP mediates the repressive effect of lysine on *lysP* much as it does the repressive effect of this amino acid on other genes such as *argO*, *gdhA*, and *dapB*.

We had earlier obtained and characterized several dominant gain-of-function mutations in *argP* (designated *argP*<sup>d</sup>) that conferred (relative to *argP*<sup>+</sup>) vastly increased expression as well as loss of lysine repression of *argO*. We tested this panel of *argP*<sup>d</sup> mutations for their effect on *lysP* transcription. Our results indicate that whereas some of the *argP*<sup>d</sup> mutations confer loss of lysine repression of *lysP* nearly completely (P108S, L294F, R295C) or partially (A68V, S94L), several others (V144M, P217L, P274S) are as proficient as *argP*<sup>+</sup> for lysine repression.

Since a recent report from another group had implicated the global regulator Lrp in regulation of *argO*, we also tested the effects if any of *lrp* mutation on *lysP-lac* expression. It was observed that *lysP* transcription is reduced about two-fold in Lrp-deficient strains but that this reduction is not additive to that elicited by  $\Delta argP$  mutation.

Our aim now is to undertake in vitro studies to examine the binding of ArgP to the *lysP* regulatory region, and to attempt reconstitution of *lysP* transcriptional regulation by ArgP in a purified system.

- b. To study the mechanism of ArgO exporter function, we have identified, from a mutagenized library using a two-step procedure, ArgO

variants with impaired exporter function (that is, which confer less resistance to the arginine analogue canavanine than does the *argO*<sup>+</sup> parent). The parental ArgO used in these experiments was a derivative tagged with an HA epitope that did not perturb its exporter function. Bioinformatic analysis of ArgO has suggested that it possesses six transmembrane stretches with three cytoplasmic and four periplasmic hydrophilic loops. From a collection of fifty mutants being studied, we have obtained multiple amino acid substitutions in the putative first, second, fourth, and fifth transmembrane segments and one alteration in the putative fourth periplasmic hydrophilic loop. To obtain further insight into the topological distribution of residues critical for ArgO function, we have initiated a genetic analysis of the topology of ArgO in the inner membrane.

## 2. Studies on *rho* and *nusG* mutants and the R-loop model

- a. In our report last year, we had described our findings that RNase E truncated for its C-terminal half (*rne-ΔCTH*) is synthetically lethal in combination with deficiency of the RNA 5'-pyrophosphohydrolase RppH (*ΔrppH*), and that the synthetic lethality is suppressed by *rho* or *nusG* mutations. It is known that the endonuclease activity of RNase E is stimulated by 5'-monophosphate group on RNA (that is generated by action of RppH on 5'-triphosphate ends in RNA).

In the current year, the following additional results were obtained in this line of work:

- (i) The CTH of RNase E serves as a scaffold for assembly of a macromolecular complex called the degradosome. However, unlike with *rne-ΔCTH*, *ΔrppH* was not synthetic lethal with *ΔrhIB Δpnp* (that encode other major components of the degradosome).
- (ii) Suppression of *ΔrppH rne-ΔCTH* synthetic lethality by *rho* or *nusG* was independent of RNase G (which is an RNase E paralogue).
- (iii) A variety of *rho* or *nusG* missense mutations defective in transcription termination were capable of suppressing the synthetic lethality.
- (iv) In a "reduced-genome" *E. coli* strain MDS42 in which NusG is dispensable for viability, the *ΔnusG* mutation could also suppress *ΔrppH-rne-ΔCTH* lethality.

- (v) Suppression by *rho* or *nusG* of *ΔrppH-rne-ΔCTH* inviability was dependent on the presence of RNase H1 (which degrades RNA in R-loops), i.e., suppression was not seen in an *mhA* mutant derivative. In the resulting quadruple mutant *ΔrppH rne-ΔCTH rho/nusG mhA* which is inviable, ectopic expression of the phage T4-encoded R-loop helicase UvsW restored viability.
- (vi) An RNase E variant with a combined deletion of its CTH and an R169Q substitution in its "5'-sensor-domain" was associated with inviability, suppressible by *rho* or *nusG*.
- (vii) Likewise, the *rho* or *nusG* mutations could restore viability in strains completely deficient in RNase E and RppH.

Our results above provide support to the following major conclusions, namely (i) that the essential function of RNase E is in catalyzing mRNA turnover; (ii) that the enzyme has two pathways for endonucleolytic cleavage, one of which is rendered defective by C-terminal truncation and the other by either the R169Q alteration in its 5'-sensor-domain or by RppH deficiency; and (iii) that the *rho* and *nusG* mutations restore viability in RNase E- and RppH- deficient bacteria by providing a bypass route for mRNA turnover, through the formation of R-loops from nascent untranslated transcripts that fail to be terminated in these strains.

- b. In the context of our studies on the interplay between Rho-dependent transcription termination and RNase E-mediated RNA degradation, we have also undertaken studies on the effects of heterologous expression in *E. coli* of *Bacillus subtilis* RNase J1, which is a 5'-3' exonuclease. Native *E. coli* has several 3'-5' exoribonucleases but none with a 5'-3' polarity. We had earlier obtained five plasmid clones expressing RNase J1 from an arabinose-inducible promoter in *E. coli* following PCR amplification of the gene from *B. subtilis*, but all of them carried different mutations in the open-reading frame and conferred lethality upon 0.2% arabinose-supplementation. These observations indicated that heterologous expression of RNase J1 is quite toxic in *E. coli*.

In the current year, we have taken several approaches to achieve levels of RNase J1 activity below the threshold of toxicity, including (i) modulating the concentration of inducer (arabinose) in strain derivatives carrying a constitutively

expressed arabinose-transporter so that an all-or-none phenomenon of induction is avoided and graded induction is obtained; (ii) introduction of mutations in *pcnB* or *dnaC* leading to reduction in copy number of the plasmid clones; and (iii) integration of the constructs in single copy into the chromosome as part of a lambda prophage.

With the use of these approaches, we have been able to study the phenotypic effects of RNase J1 expression in *E. coli*. In summary, our results support two important conclusions: (i) RNase J1 expression is apparently able to compensate for the inviability associated with the absence of RNase E (which is otherwise considered as an essential enzyme in *E. coli*); and (ii) RNase J1 toxicity in *E. coli* is alleviated by the absence of reduced activity of RNase E. It may be noted that *B. subtilis* does not have an RNase E ortholog, and hence our observations suggest that the RNA turnover mechanisms mediated by RNase E and by RNase J1 have evolved to be mutually exclusive in the different bacterial genera.

Future work in this area aims at investigating the interplay, if any, between RNase J1 expression and Rho-dependent termination of transcription in *E. coli*.

- c. We had earlier found that the transcription termination-defective (i.e., polarity-relief) phenotypes conferred by recessive missense mutations in *rho* or *nusG* are suppressed by expression of a dominant-negative variant of the nucleoid protein H-NS that represents the N-terminal 64 codons of the 137 amino acid-long open reading frame (H-NS $\Delta$ 64); a recessive mutation in the gene encoding the transcription elongation factor NusA was also identified that suppressed the effect of H-NS $\Delta$ 64 and restored polarity-relief in these derivatives.

In the current year, we identified the alteration in NusA as a Arg-to-Cys substitution at residue 258 (R258C). The *nusA* mutation was shown by itself to confer a polarity-relief phenotype *in vivo* although it did not affect the rate of transcription elongation in the strain. It was also synthetically lethal with the *rho* or *nusG* missense mutations in the absence of H-NS $\Delta$ 64.

In an attempt to understand the mechanism by which H-NS $\Delta$ 64 restores transcriptional polarity in the *rho* and *nusG* mutants, we have tested its dependence on the proteins of the “H-NS family” including wild-type H-NS itself, its paralog StpA,

and its interacting partners YdgT and Hha. It was found that suppression of polarity relief in *rho* or *nusG* mutants by H-NS $\Delta$ 64 is dependent on the presence of the genes *ydgT* or *Hha* on the chromosome, and furthermore that multicopy-*ydgT* by itself can substitute for H-NS $\Delta$ 64 in eliciting the suppression phenotype.

These results indicate (i) that NusA function is needed, in addition to those of NusG and Rho, for efficient (factor-dependent) transcription termination; (ii) that the structure of the nucleoid is a determinant in the efficiency of the process, and (iii) that an entire spectrum of efficiencies of Rho-dependent termination can be generated by various combinations of perturbations in the genes encoding Rho, NusA, NusG, and the H-NS family of proteins, with the corresponding phenotypes extending from polarity through polarity relief to lethality.

Another mutation that had been obtained earlier as a suppressor of the H-NS $\Delta$ 64 effect in *rho* or *nusG* mutants was shown to be a gain-of-function mutation in *clpA*, which encodes a component of the ClpAP protease complex. It is possible that this mutant exhibits accelerated degradation of the YdgT and/or the Hha proteins in *E. coli*.

### 3. Potassium toxicity in *hns* *trx* mutants

To gain insight into the mechanism of K<sup>+</sup> toxicity in the *trx hns* (TH) mutants, we have obtained and characterized a variety of suppressors of the toxicity phenotype (some of which had been listed by us in last year's Report). The expanded list of suppressors includes loss-of-function mutations in *rpoS*, *ptsP*, *ptsO* (also called *npr*), *ahpC*, *fabF*, *cspC*, *ycgO*, *yajC*, *grxA*, and *glpR*; an insertion in the promoter region of *acpP* possibly leading to down-regulation of its expression; and a constitutive active allele of *oxyR* (*oxyR2*). Supplementation of the medium with methionine or cysteine, or introduction of plasmid pBR322 (whose *tet* gene encodes a K<sup>+</sup>-carrier function) also suppressed K<sup>+</sup>-sensitivity in the TH strain. Further, it was established that the K<sup>+</sup>-sensitivity phenotype is dependent on the presence of the *spoT1* allele in the TH strain, and is lost upon introduction of either *spoT*<sup>+</sup> or loss-of-function mutations in *spoT*.

Since SpoT is involved in ppGpp metabolism (with *spoT1* associated with increased intracellular ppGpp levels), we measured steady-state intracellular [ppGpp] in the TH mutant, its parent and the various suppressor derivatives. The results indicate that the K<sup>+</sup>-toxicity phenotype is correlated

with increased ppGpp levels, and that the ppGpp levels are once again lowered in several of the suppressor strains (such as *acpP* and *glpR*).

The products of two of the suppressors identified above *ptsP* and *ptsO* are part of a sequential phosphotransfer cascade to PtsN, whose phosphorylation substrate remains unidentified. Deletion of *ptsN* by itself conferred a K<sup>+</sup>-sensitive phenotype, much like that of the TH strain, and several suppressors of the TH strain phenotype also suppressed K<sup>+</sup> sensitivity in the *ptsN* mutant: these included *spoT*, *yajC*, *glpR*, *fabF*, *ycgO*, and pBR322. These observations indicate that strong similarities exist between the mechanism of K<sup>+</sup>-toxicity in the two mutants TH and *ptsN*.

Altogether, the results above suggest a very complex metabolic interplay that is responsible for the K<sup>+</sup>-toxicity phenotype, and our preliminary model is that this is related to intracellular K<sup>+</sup> accumulation to abnormally high levels in the mutants. We intend to measure intracellular [K<sup>+</sup>] in the different strains, and also to undertake studies to decipher how the suppressors are acting to exert their phenotypic effects.

#### 4. Physiological roles of the stringent response factors DksA/(p)ppGpp

This is a newly initiated project, whose aim is to use genetic approaches to understand the role of (p)ppGpp and its functionally related protein factor DksA in *E. coli* physiology. Two specific aspects that have been investigated relate to the metabolic role of transketolases and of SsrA/SmpB proteins, as briefly described below.

*E. coli* has two transketolase isoenzymes encoded by *tktA* and *tktB*, respectively. Transketolase activity provides the crucial link between two important metabolic routes in the cell, namely, glycolysis and the pentose phosphate pathway. It was shown earlier that a ppGpp<sup>0</sup> mutant ( $\Delta relA \Delta spoT$ ) is synthetically lethal with  $\Delta tktA$ , and it was also observed that  $\Delta tktA \Delta tktB$  strains are severely comprised for growth on rich media such as LB. We have set out to understand the cause of slow growth in LB by using two genetic approaches, namely (i) isolating and characterizing suppressor mutations, that is, mutations that rescue the growth defect in LB in the knock-out strain, and (ii) looking for growth rescue using a multi-copy genomic library of *E. coli*. Several suppressors have been isolated, and their characterization is in progress.

In *E. coli* and many other bacteria, ribosomes stalled during the process of translation are rescued and

the truncated polypeptide so synthesized is tagged at the C-terminal end and directed for degradation. This process is carried out by the *ssrA/smpB* system. We have found that, unlike in a wild-type strain where this system is dispensable, in a ppGpp<sup>0</sup> strain these factors perform an essential function, that is, ppGpp<sup>0</sup> *ssrA* or a ppGpp<sup>0</sup> *smpB* mutant cannot survive. We have also found that the growth defect is rescued by increasing the growth temperature or by addition of certain antibiotics (at sub-inhibitory concentrations) that target translation. In ongoing work, we are testing the hypothesis that a translation/transcription defect (since the two are coupled in bacteria) in the ppGpp<sup>0</sup> strain makes the *ssrA/smpB* system indispensable for viability.

#### Publications

1. Dutta D, Bandyopadhyay K, Datta AB, Sardesai AA and Parrack P (2009) Properties of HflX, an enigmatic protein from *Escherichia coli*. **Journal of Bacteriology** 191: 2307-2314.
2. Kumar CMS, Khare G, Srikanth CV, Tyagi AK, Sardesai AA and Mande SC (2009) Facilitated oligomerization of mycobacterial GroEL: evidence for phosphorylation-mediated oligomerization. **Journal of Bacteriology** 191: 6525-6538.
3. Kumar S, Balakrishna K, Agarwal GS, Merwyn S, Rai GP, Batra HV, Sardesai AA and Gowrishankar J (2009) Th1-type immune response to infection by pYV-cured *phoP-phoQ* null mutant of *Yersinia pseudotuberculosis* is defective in mouse model. **Antonie Van Leeuwenhoek** 95: 91-100.
4. \*Lee SJ, Trostel A, Le P, Harinarayanan R, Fitzgerald PC and Adhya S (2009) Cellular stress created by intermediary metabolite imbalances. **Proceedings of the National Academy of Sciences of the USA** 106: 19515-19520.

\* Work done elsewhere.

#### Other publications

1. Gowrishankar J (2009) Regulation of genetically modified organisms: has the time come to amend the law? **Current Science** 96: 1574.
2. Gowrishankar J (2009) Swine flu: perhaps to do nothing is the best strategy for India? **The Hindu**, 2 July 2009.
3. Gowrishankar J (2009) H1N1: Option for India. **Biotech News** (2009) 4: 44-47.
4. Gowrishankar J (2010) Extramural research funding by institutions that undertake intramural research. **Current Science** 98: 478.



## Laboratory of Computational Biology

### Protein structure prediction, modeling and analysis of protein-protein interactions

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	H Rachita	Junior Research Fellow
	Manjari	Junior Research Fellow

#### Objectives

1. Analysis of distribution, abundance and polymorphism of simple sequence repeats (SSRs) in prokaryotic genomes
  2. Development of methods for protein structure prediction and modeling
  3. Prediction and modeling of deleterious (disease) human nsSNPs
  4. Studies on protein-protein interaction networks focusing evolution of protein-protein functional linkages in biochemical pathways and viral-human interactions.
3. Efforts were made to find out a set of sequence-structure based features that characterize distinctly disease and benign nsSNPs from each other. Investigations were carried out on a set of known nsSNPs comprising of 326 disease and 333 benign mutations mapping on to TM regions of 55 human transport proteins.
  4. Efforts were made to understand the design principles of protein-protein functional linkages in biochemical pathways. Phylogenetic-Profile method was used to construct genome-wide network for *Escherichia coli* K12 substrate. MG1655 using a reference set of 79 organisms. The number of interactions inferred by this approach was too large (more than 200,000) to be biologically feasible. Moreover, manually curated public databases such as KEGG contain pathway information for organisms. Hence, it was planned to take a different approach for the construction of enzyme-centric Metabolic Networks.

#### Summary of work done until the beginning of this reporting year (April 1, 2008 – March 31, 2009)

1. We have been studying distribution, abundance and polymorphism of simple sequence repeats in known Mycobacterial and Yersinia genomes. All these genomes characteristically harbor short repeat tracts indicating SSR tract expansions have not been favored in these genomes. Cross-genome comparative analysis of equivalent SSRs lead to the discovery of several hundreds of SSRs which have undergone length polymorphism leaving behind interesting changes to nearby coding regions and these seem to aid pathogens for their survival and adaptation.
2. We have developed a new method for protein fold-recognition which uses secondary structural and solvent accessibility state frequencies of amino acids and amino acid pairs as fold-discriminatory features. Performance evaluation of the new method was carried out on a benchmark data set of proteins comprising of 27 folds. Further efforts were

made to increase the fold-coverage of the new method from 27 folds to 711 folds.

#### Details of progress made in the current reporting year (April 1, 2009 - March 31, 2010)

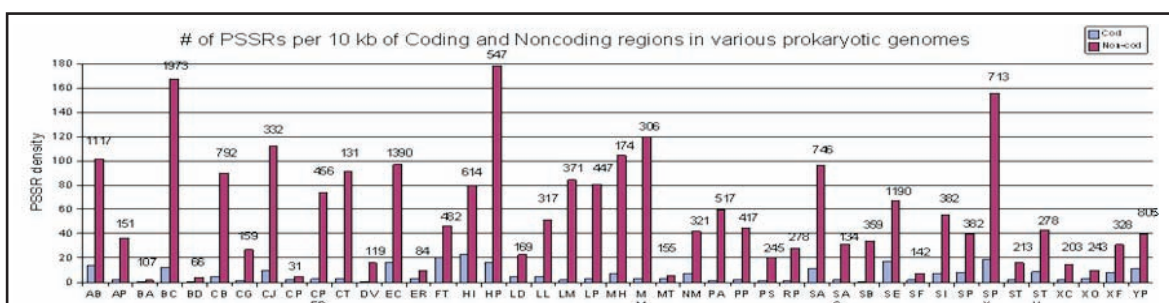
##### Project 1: Analysis of simple sequence repeats (SSRs) polymorphism in fully sequenced prokaryotic genomes

Availability of whole genome sequences of several prokaryotes led us to make a systemic study on SSRs which have undergone length polymorphism. Cross-genome comparisons of SSRs belonging to 43 difference species of prokaryotes revealed 18351 PSSRs. Of these 7075 were found in coding regions and 11276 in non-coding regions indicating restrained SSR polymorphism in coding regions as

compared to non-coding regions (**Fig. 1**) for genome-wise distribution of PSSRs in coding and non-coding regions). Interestingly, about 90% of the PSSRs found in coding regions were causing frame shift mutations. Distribution of PSSRs along the lengths of ORFs was analyzed. It was found that middle parts of the genes harbor PSSRs much less than expected whereas both the 5' and 3' parts harbor more number of PSSRs than expected. Furthermore, PSSR distribution pattern in relation to transcription and replication directions were studied. It was revealed that the regions where transcription and replication happen head-on (i.e.,

their directions are opposite to each other) harbor more number of PSSRs than the regions where the two processes happen in the same direction.

Mutational bias towards expansion or contraction of SSRs, which is also referred to as directionality of SSR evolution, in relation to presence or absence of MMR system was also studied by considering the PSSRs in non-coding regions. It was found that SSR mutations are biased towards contraction in MMR proficient genomes whereas they are biased towards expansions in MMR deficient strains (**Table 1**).



**Fig. 1:** Tract densities of PSSRs in coding (blue bar) and non-coding (magenta bar) regions in various prokaryotic species. The number of PSSRs found in each species is shown on each magenta colored bar.

**(Foot note)** AB = *Acinetobacter baumannii*, AP = *Actinobacillus Pleuropneumoniae*, BA= *Bacillus anthracis*, BC = *Bocillus cereus*, CB = *Classtridium botulinum*, CG = *Caryncbacterium glutomicum*, CJ = *Compylalbacter jejuni*, cp = *Chlamydoiphita pnevmanios*, CPER = *Clastridium perfringens*, CT = *Chlamyala, trachomatis*, DV = *Desulfavibria vulgaris*, EC = *Escherichia cali*, ER = *Ehrlichia ruminontium*, FT = *Francisella tuforensia*, HI = *Haemoplus infiuenzue*, HP = *Heinobacter pylor*, LL = *Lactococcus lactis*, LM = *Lintezio monocyogenes*, LP = *Legionella pnevmophilla*, MH = *Mycopiasno hypneumniae*, MM = *Methunococcus marigaludii*, MT = *Mycobacterium tuberculosis* and *Mycobacterium bavis*, NM = *Neiseria meningiorts*, FA = *Pseudomanos ogrvginasa*, PP = *Pseudomonos putida*, PS = *Pseudorsonos syringue*, RP = *Rhavapseudomonos Palustris*, SA = *Stophylococcus oureus*, SAG = *Streptococcus ogatactiae*, SB = *Shewaarlla baltica*, SE = *Salmonella enterica*, SF = *Shigella flexneri*, SI = *Sulphalobus isfandicus*, SP = *Streptacoccus pneumoniue*, SPY = *Streptococcus pyogenes*, ST = *Salmanetto typhi*, STH = *Streptococcus thermaphifus*, XC = *xanthamonas compestris*, XO = *Xonthomanas myzag*, XF = *Xylello fastidiosus*, YP = *Yersinio pestis*.

Species Name	Name of strain(s)	#PSSR	Cont	Exp	Cont/Exp	$\chi^2$ 1:1	P-value
<i>Acinetobacter baumannii</i>	AB0057, SDF, AB307_0294, ACICU and SDF	331	180	132	1.36	7.38	<b>&lt;0.006</b>
	ATCC_17978 (MMR-)	139	76	63	1.20	1.22	NS
<i>Haemophilus influenzae</i>	RD_KW20, 86_028NP and PittEE	103	71	32	2.21	14.17	<b>0.0002</b>
	PittGG (MMR-)	79	43	36	1.2	0.62	NS
<i>Staphylococcus aureus</i>	MRSA252, MSSA476, MW2, JH1, Mu3, Mu50, N315, COL, Newmann, NCTCT, USA300	312	183	129	1.41	9.35	<b>0.002</b>
	RF122 (MMR-)	180	89	91	1.0	0.02	NS

**Table 1:** PSSRs found in MMR proficient and deficient strains of *Acinetobacter baumannii*, *Haemophilus influenza* and *Staphylococcus aureans*. Number of instances of PSSR expansions and contractions are also given. The significant one is indicated as bold. "NS" means not significant

## Project 2: A knowledge-based approach to protein fold recognition

The new fold recognition method was trained and tested for a set comprising of more than 700 folds which included orphan folds. However, increase in the number of folds led to a drop in prediction accuracy. In order to deal with the complexity involved in learning large number of folds a hierarchical approach for protein fold recognition (abbreviated as HPFP: Hierarchical Protein Fold Prediction) was developed in which first structural class of the protein is predicted followed by fold prediction within predicted structural class. A new SVM-based method was also developed for structural class prediction, which uses combination of secondary structural content and secondary structural state frequencies of amino acids as discriminatory features.

HPFP currently gives overall prediction accuracies of 87.4%, 85.6%, 78.0% and 87.4% for all- $\alpha$  class, all- $\beta$  class,  $\alpha/\beta$  class and  $\alpha+\beta$  class folds, respectively. HPFP has been implemented as a web server at <http://cdfd.org.in/HPFP/>.

## Project 3: Classification of nsSNPs into deleterious (disease) and benign categories and mapping of nsSNPs on human protein-protein interaction network

A new method was developed which classifies nsSNPs into deleterious (disease) and benign mutations. This new method essentially calculates an estimated position specific probability of the mutated amino acid residue at a given position  $i$  using Dirichlet mixture of priors as follows:

$$\hat{p}_i = \frac{X_i}{\sum_{k=1}^{20} X_k}$$

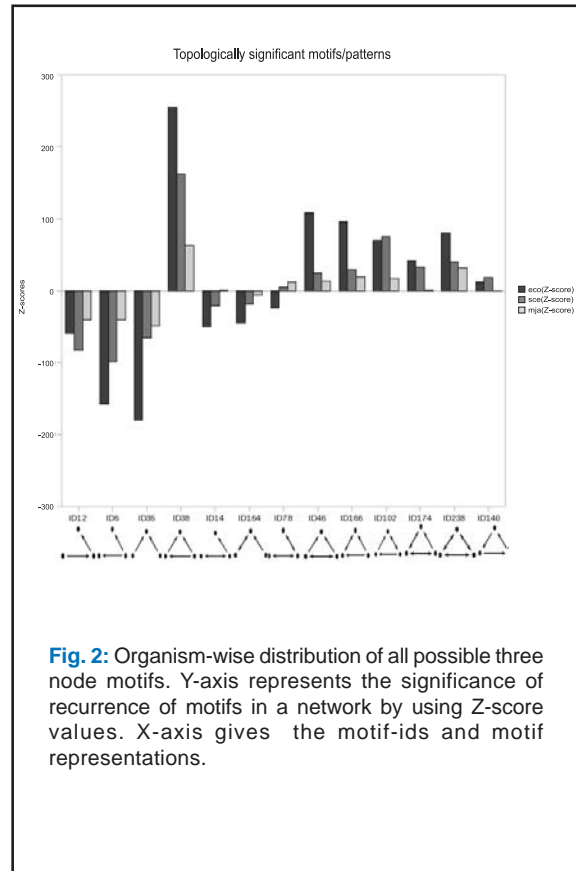
$$\text{Where } X_i = \sum_{j=1}^l q_j e^{(\log B(\vec{a}_j + \vec{n}) - \log B(\vec{a}_j))} \times \frac{\alpha_{j,i} + n_i}{|\vec{a}_j| + |\vec{n}|} \quad (2)$$

Where  $q_j$  is the mixture coefficient of the component  $j$ , the parameters  $\vec{a}_j$  ( $a_{j,1} \dots a_{j,20}$ ) for each component  $j$  of the Dirichlet mixture,  $l$  is the number of components,  $B$  is the beta function,  $\vec{n}$  is the observed amino acid count vector. A probability score less than and greater than 0.05 respectively indicates deleterious and acceptable/benign mutations. When known disease nsSNPs mapping on to human membrane proteins were tested it was found that 97.5% of them were correctly identified as deleterious. We also calculated ( $\hat{p}_i$ ) values for all the known disease (3103) and benign (18407)

nsSNPs mapping on to various human proteins and found that more than 80%, of disease and 60% benign mutations can be correctly predicted.

## Project 4: Evolutionary dynamics of protein-protein functional linkage networks: analysis of biochemical pathways

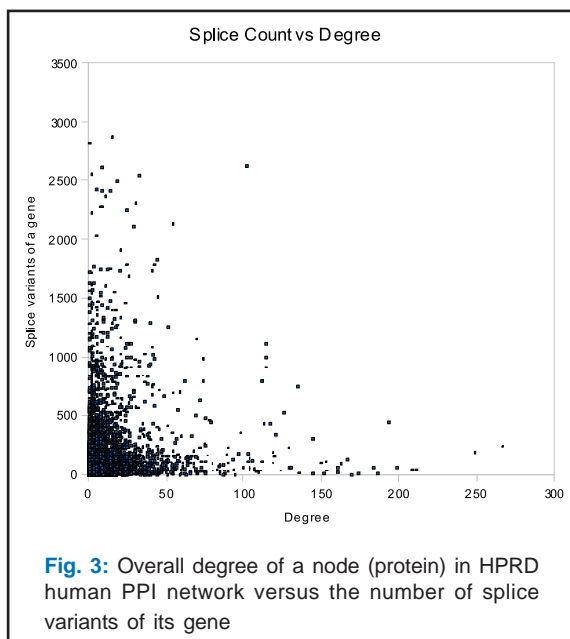
The KGML files of the model organisms *E. coli* DH10B, *Saccharomyces cerevisiae* and *Methanococcus jannaschii* from the three Kingdoms Prokarya, Eukarya and Archea respectively were parsed using R and PERL. The parsed data was used to construct an enzyme-centric network for each of the organisms followed by calculation of its topological properties viz., degree distribution, betweenness distribution, and motif abundances. As expected, all the networks were in general showed scale-free nature although with differences in the values of the power law exponent. Next, the Betweenness Centrality of each of the nodes was calculated and was found to be poorly correlated to node degree. Analysis of network motifs revealed that some three node-motifs are over-represented/under-represented in these enzyme-centric networks (**Fig. 2**).



**Fig. 2:** Organism-wise distribution of all possible three node motifs. Y-axis represents the significance of recurrence of motifs in a network by using Z-score values. X-axis gives the motif-ids and motif representations.

## 2. Characterization of “HUB” proteins in PPI networks of *Homo sapiens*

The hub proteins in the human protein-protein interaction network were examined in relation to the number of their splice variants. Manually curated HPRD (Human Protein Reference Database) PPI dataset was used for construction of network and analysis of its topological properties and ASD (Alternative Splicing Database) flat-files from ENSEMBLE was used to get the number of splice variants for proteins. Contrary to the speculations, no significant linear correlation between the number of splice variants of a gene and its degree in PPI networks was found (**Fig. 3**).



### Future plans and directions

1. Analysis of protein-protein interaction networks after mapping deleterious nsSNPs onto human proteins
2. Comparative analysis of enzyme centric PPI networks of *E. coli*, *S. cerevisiae* and *M. jannaschii* and analysis of viral and human protein-protein interaction networks.

### Publications

1. Achary MS and Nagarajaram HA (2009) Effects of Disease Causing Mutations on the essential Motions in proteins. *Journal of Biomolecular Structure and Dynamics* 26:609-624.
2. Korupolu, RV, Achary MS, Aneesa F, Sathish K, Wasia R, Sairam M, Nagarajaram, HA and Singh SS. (2009) Profilin oligomerization and its effect on poly (l-proline) binding and phosphorylation *International Journal of Biological Macromolecules* 45: 265-273.
3. Mudunuri SB, Rao AP, Pallamsetty S, Mishra P and Nagarajaram HA (2009) VMD: Viral Microsatellite Database - A Comprehensive Resource for All Viral Microsatellites. *Journal of Computer Science and Systems Biology* 22: 283-000. doi:10.4172/jcsb.1000043: 001-004.
4. Mudunuri SB, Rao AP, Mishra P and Nagarajaram HA (2010) Comparative Analysis of Microsatellite Detecting Software: A Significant Variation in Results and Influence of Parameters. *Proceedings of International Symposium on Biocomputing*, (ISB 2010), Kerala, February 15-17, 2010. (Link to ACM Digital Library)
5. Thoh M, Kumar P, Nagarajaram HA and Manna SK (2010) Azadirachtin interacts with the TNF binding domain of its receptors and inhibits TNF-induced biological responses. *Journal of Biological Chemistry* 285: 5888-5895.
6. Purushotham K, Madhumohan, Anwaruddin M, Nagarajaram HA, Hariram VD, Narasimhan C, Bashyam MD (2010). The MYH7 p.R787H mutation causes hypertrophic cardiomyopathy in two unrelated families. *Experimental & Clinical Cardiology* (In press).

### Patents filed

1. Nagarajaram HA and Shamim MTA. Fold-wise classification of proteins. USPTO Patent Application No. 20100057419.



## Laboratory of Molecular Cell Biology

### Signal transduction pathways in macrophages and host-pathogen interaction in tuberculosis

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	Khalid Hussain Bhat	Senior Research Fellow
	G Sreejit	Senior Research Fellow
	Nazia Parveen	Junior Research Fellow
	Atul Udgata	Junior Research Fellow
	Arghya Dash	Junior Research Fellow
	Gouranga Pradhan	Junior Research Fellow
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	V Valluri, Blue Peter Research Centre, Hyderabad	

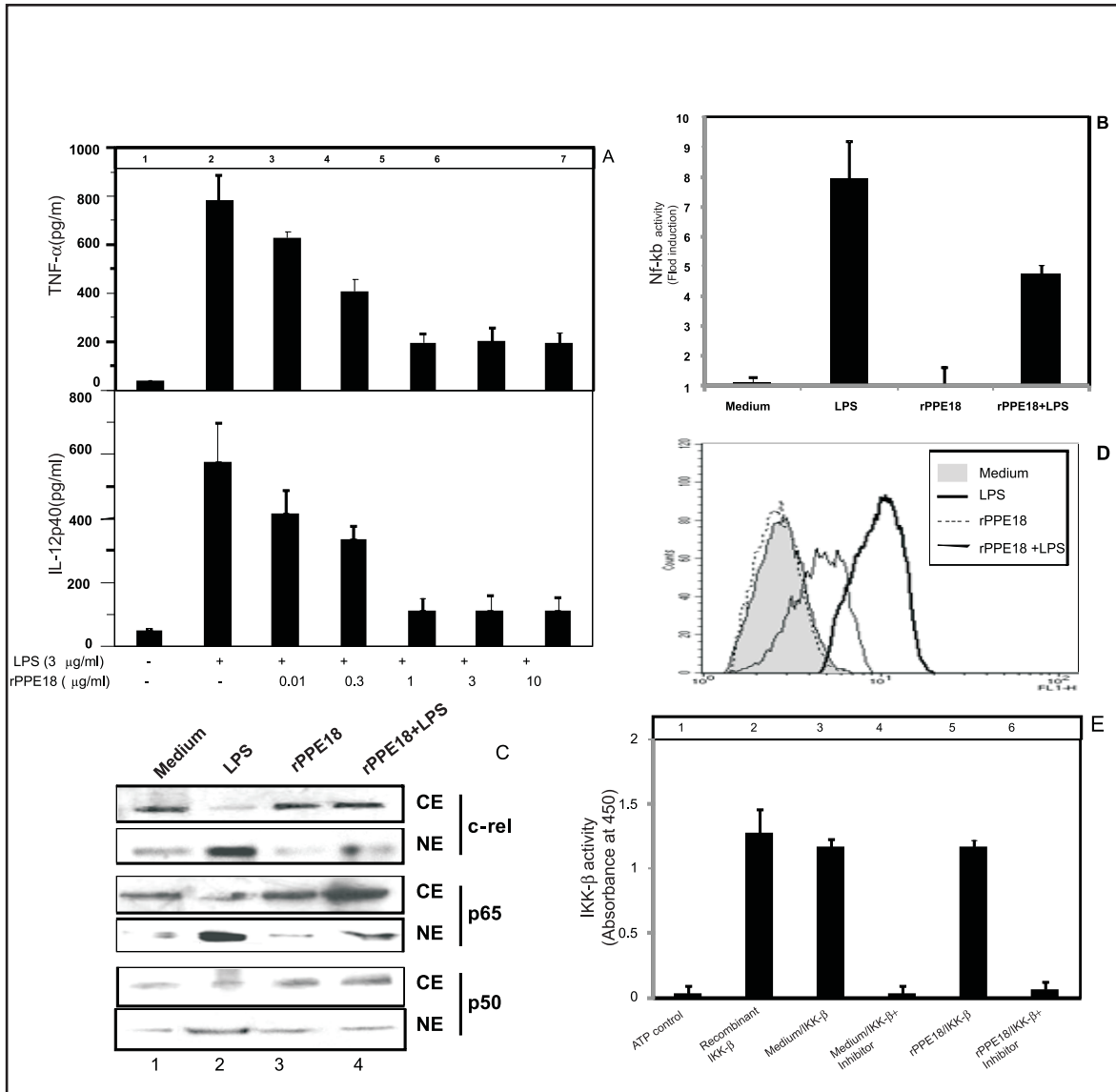
#### Objectives

1. Signal transduction pathways in macrophages regulating its innate-effector functions
2. Studying how various candidate proteins of *Mycobacterium tuberculosis* interfere with macrophage signaling cascades to suppress host's protective responses against the bacilli
3. Role of the PPE proteins in the activation of HIV-1 LTR.

#### Summary of work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)

The macrophage elicits various anti-mycobacterial mechanisms during its innate phase of activation which play crucial roles in deciding outcome of *Mycobacterium tuberculosis* (Mtb) infection in the host. Among these, productions of proinflammatory cytokines (IL-12 and TNF- $\alpha$ ) are critical for mounting an optimal defense against the Mtb infection. Regulation of proinflammatory responses often

involves diverse signaling cascades and the pathogenic *M. tuberculosis* bacteria have evolved several mechanisms to modulate these signaling pathways to suppress IL-12 and TNF- $\alpha$  production to favor its survival and persistence inside the host. In our earlier studies, we have demonstrated that a member of the PPE (proline-proline glutamic acid) family of protein of *M. tuberculosis*, PPE18 is exposed to the cell surface and could modulate the host immune responses by interacting with the macrophage surface components. PPE18 is one of the highly expressed genes in *M. tuberculosis* as compared to *M. bovis*. A comparative genome analyses of the avirulent H37Ra strain versus virulent H37Rv strain revealed presence of 53 insertions and 21 deletions in H37Ra relative to H37Rv. Interestingly, PPE18 harbors one of those deletions in H37Ra, indicating that this gene may be pathophysiologically important. We observed that PPE protein triggers an anti-inflammatory response by activating IL-10 and concurrently decreases the



**Fig. 1:** rPPE18 protein of *M. tuberculosis* inhibits proinflammatory cytokines by attenuating NF-κB activity and phosphorylation of IκBα in LPS-activated macrophages.

- A)** THP-1 macrophages were pretreated with PPE18 at at varying concentrations as indicated and then stimulated with LPS and cultured for 48 hours to measure IL-12 p40 and TNF-α by EIA.
- B)** PMA-differentiated THP-1 macrophages were transfected with either the vector control alone (pCONA) or the NF-κB luciferase reporter plasmid (3Xlg -ConA-Luc) along with pSV-β-Galactosidase plasmid. After 24 hours, the macrophages were treated for 1 hour with either medium or rPPE 18 (3 μg/ml) and then stimulated with LPS for another 1 hour. Transcriptional activity of NF-κB was measured by luciferase and β-galactosidase assays. Data are shown as fold inductions over basal activity and represent as mean SD of three independent experiments performed in triplicate.
- C)** Cytoplasmic and nuclear extracts were prepared from PMA-differentiated THP-1 macrophages stimulated with LPS in presence of either medium or rPPE18 (3 μg/ml) and levels of p50, p65 and c-rel transcription factors were measured by Western blotting using rabbit anti-p50 or anti-p65 or anti-c-rel Ab respectively.
- D)** PMA-differentiated THP-1 macrophages were stimulated with LPS in the absence or presence of rPPE18 (3 μg/ml). The phosphorylation of IκBα in various groups at 15 minutes time point was analyzed by flow cytometry.
- E)** Whole cell extracts were prepared from PMA-differentiated THP-1 macrophages either treated with medium alone or rPPE18 (3 μg/ml). Equal amounts of total protein were used to immunoprecipitate IKK-α using anti-IKK-α/αAb bound to sepharose-protein G beads and the immunoprecipitated IKK-α was used to assess the IκBα phosphorylation using the kit obtained from Calbiochem, USA.

levels of proinflammatory indicators like IL-12 p40 in activated macrophages. The recombinant PPE18 was found to directly interact with the TLR2 on macrophages to induce IL-10 and the results are also suggestive of a critical role of p38 MAPK for IL-10 activation. Interestingly, the anti-inflammatory effect of PPE18 is in contrast to the actions of other TLR2 ligands (Pam<sub>3</sub>CSK<sub>4</sub>) which induce a proinflammatory response such as production of TNF- $\alpha$ . A detailed study by us indicated that the site of interaction between the PPE18 and the TLR2 ectodomain encompasses the region that lies between LRR 11~15 on the convex face, a region that does not overlap with the binding site for the synthetic lipopeptide Pam<sub>3</sub>CSK<sub>4</sub>. A deletion in the LRR 11~15 domain abolished the binding of PPE18 to TLR2 indicating that PPE18 specifically interacts with TLR2 through this region. Interestingly, while PPE18 activates p38 MAPK, Pam<sub>3</sub>CSK<sub>4</sub> is known to induce predominantly ERK 1/2. Thus, we conclude that different TLR2 ligands interact with different ligand-specific sites on TLR2 ectodomain which may trigger specific conformational changes in TLR2 leading to different downstream signaling. We are now studying in detail the downstream signaling pathways involved in the PPE18-mediated downregulation of proinflammatory cytokines mainly the IL-12 and TNF- $\alpha$ .

#### Details of progress made in the current reporting year (April 1, 2009 - March 31, 2010)

##### Project 1. Understanding roles of the PPE18 protein in the pathogenesis of *Mycobacterium tuberculosis*

The recombinant PPE18 (rPPE18) protein of *M. tuberculosis* inhibits proinflammatory cytokines by attenuating NF- $\kappa$ B/rel activity and phosphorylation of I $\kappa$ B $\alpha$  in LPS-activated macrophages. We observed earlier that the purified recombinant PPE18 protein of *M. tuberculosis* inhibited LPS-induced IL-12 p40 and TNF- $\alpha$  cytokines in dose dependent manners. The concentrations at which rPPE18 inhibited IL-12 p40 and TNF- $\alpha$  induction by 50%, (IC<sub>50</sub>; calculated based on linear interpolation) was found to be 257.8 ng/ml  $\pm$  21.4 (6.59 picomole) and 292 ng/ml  $\pm$  64.2 (7.49 picomole) respectively (**Fig. 1A**). The NF- $\kappa$ B transcription factors are known to play essential roles in the induction of proinflammatory cytokines as the promoters of IL-12 p40 and TNF- $\alpha$  contain NF- $\kappa$ B binding sites and transcription of these genes are critically dependent on binding of NF- $\kappa$ B/rel transcription factors to these sites. Therefore, we

measured if NF- $\kappa$ B activity was lower in LPS-treated macrophages in the presence of rPPE18 by carrying out the luciferase assay for NF- $\kappa$ B activity. We found that the recombinant PPE18 protein attenuated 58% of LPS-stimulated NF- $\kappa$ B activity ( $p < 0.001$ ) (**Fig. 1B**). PPE18 was found to inhibit the cyto-nuclear translocation of NF- $\kappa$ B/rel transcription factors in LPS-activated macrophages (**Fig. 1C**). The inhibition of translocation of NF- $\kappa$ B/rel correlated well with the three fold down-regulation of LPS-induced I $\kappa$ B $\alpha$  phosphorylation (**Fig. 1D**) at Ser32/36 residues (which is a crucial event for NF- $\kappa$ B translocation and subsequent activation of target genes). This was well correlated with the observation that I $\kappa$ B $\alpha$  was poorly degraded in the rPPE18 and LPS co-treated group compared to the group treated with LPS alone. Further, we noted that PPE18 did not affect the IKK- $\beta$  activity since there was no difference in the ability of IKK- $\beta$  to phosphorylate GST-I $\kappa$ B $\alpha$  in the presence or absence of rPPE18 (**Fig. 1E**). These results suggest that PPE18 inhibits the cyto-nuclear translocation of NF- $\kappa$ B by inhibiting phosphorylation and subsequent degradation of I $\kappa$ B $\alpha$  without affecting the IKK- $\beta$  activity.

The rPPE18 targets the SOCS3 signaling to downregulate LPS-induced I $\kappa$ B $\alpha$  phosphorylation and translocation of NF- $\kappa$ B subunits to nucleus *vis-à-vis* induction of proinflammatory cytokines. Since mycobacteria are known to increase the levels of SOCS3 proteins and several studies have implicated a role of SOCS3 in attenuation of proinflammatory signaling, we speculated that probably SOCS3 is involved in the observed PPE18-mediated down-regulation of proinflammatory responses. The rPPE18 was found to increase expression of SOCS3 mRNA in a time-dependent manner (1-24 hours). The mRNA levels for SOCS3 were also found to be well correlated with the levels of SOCS3 protein in macrophages. Also, a significant increase in the SOCS3 expression in macrophages infected with *M. smegmatis* expressing PPE18 was observed as compared to the macrophages infected with *M. smegmatis* harbouring only the control pMV261 vector. To validate the fact that PPE18 targets SOCS3 to downregulate IL-12 and TNF- $\alpha$  induction, we suppressed SOCS3 expression by using SOCS3-specific siRNA and examined the effect of PPE18 on I $\kappa$ B $\alpha$  phosphorylation and NF- $\kappa$ B activity in LPS-stimulated THP-1 macrophages. Specific knock down of SOCS3 by siRNA enhanced I $\kappa$ B $\alpha$  phosphorylation leading to increased nuclear levels of NF- $\kappa$ B/rel proteins *vis-à-vis* an increase in IL-12 p40 and TNF- $\alpha$  induction ( $p < 0.0001$  in both

the cases) in LPS-activated macrophages in response to rPPE18. These results indicate that PPE18 probably targets the SOCS3 signaling to inhibit I $\kappa$ B $\alpha$  phosphorylation and consequent nuclear translocation of NF- $\kappa$ B/rel transcription factors and thus resulting in poorer transactivation of the IL-12 p40 and TNF- $\alpha$  genes.

### **Project 2. Understanding the role of *M. tuberculosis* PPE proteins in the activation of HIV-1 long terminal repeat (HIV-1 LTR)**

Due to the high incidence of both HIV and *Mycobacterium* sp. infection in the developing countries, tuberculosis (TB) has emerged to be the most common opportunistic infection in HIV-infected patients worldwide. Recent reports have demonstrated that an increased level of HIV replication is observed where lymphoid cells were incubated with purified protein derivatives (PPD) or during phagocytosis of *M. tuberculosis* bacteria suggesting that *M. tuberculosis* probably accelerate HIV-1 replication in dually infected individuals. Although the involvement of *M. tuberculosis* in the activation of HIV-LTR is well established, the mycobacterial components and the detailed pathways by which these proteins can activate HIV-LTR transcription have not been fully elucidated. The progression of retroviral replication within infected host cells is mainly dependent on the transcriptional activation of HIV-LTR by various host cellular transcription factors. The PE and PPE genes are thought to play major roles in mycobacterial pathogenesis and preliminary work carried out in our laboratory indicated that some of the PE/PPE proteins could modulate the intracellular signaling cascades in macrophages but no data are available as whether these proteins are also involved in upregulation of HIV replication and disease progression. Thus, we intended to examine whether PE/PPE protein(s) mediated modulations in the intracellular signalling cascades(s) play any role in enhancing HIV-1 pathogenesis by activating the regulatory elements in HIV-1 LTR.

In this report, we describe importance of one of the PPE proteins, the Rv1168c in the activation of HIV-1 LTR. LTR activation by Rv1168c was demonstrated by transfection experiments in which the LTR directed the expression of the bacterial enzyme chloramphenicol acetyltransferase (CAT). To examine the effect of the Rv1168c in the activation of HIV-LTR, the THP-1 cells were transfected with the HIV-LTR plasmid construct and after 6 hours, cells were treated with either various concentrations

of the recombinant Rv1168c (rRv1168c) or the BSA protein (control group). The LTR activation was determined by measuring CAT expression by ELISA. It could be observed that rRv1168c potently stimulated CAT expression in THP-1 cells. The Rv1168c enhanced LTR activity in dose-dependent manner and maximum activity was observed by 3  $\mu$ g/ml of Rv1168c protein. Hence, 3  $\mu$ g/ml protein concentration was used in all the subsequent experiments. BSA did not increase CAT level indicating that the LTR activation is Rv1168c specific. In order to prove that the effect of Rv1168c on LTR activation is not due to any LPS contamination but specific to the protein, we used heat-treated rRv1168c. It was found that denaturation of rRv1168c protein by autoclaving abrogated LTR activation by rRv1168c.  $\beta$ -galactosidase protein expression was found to be equivalent in all the groups indicating equal transfection efficiency. We found that the Rv1168c protein is a potent transactivator of HIV-1 LTR and can substitute for HIV-1 Tat.

**Future plans:** We would like to study in detail the mechanisms involved in the SOCS3-mediated regulation of I $\kappa$ B-NF- $\kappa$ B/rel activity by PPE18. Also we will be studying pathways involved in HIV-1 LTR activation by some *M. tuberculosis* PPE proteins.

### **Publications**

1. Nair S, Ramaswamy PA, Ghosh S, Joshi DC, Pathak N, Siddiqui I, Sharma P, Hasnain SE, Mande SC and Mukhopadhyay S (2009) The PPE18 of *Mycobacterium tuberculosis* interacts with TLR2 and activates IL-10 induction in macrophage. *Journal of Immunology* 183: 6269- 6281.
2. Alam K, Ghousunnissa S, Nair S, Valluri VL and Mukhopadhyay S (2010) Glutathione-redox balance regulates c-rel-driven IL-12 production in macrophages: possible implications in antituberculosis immunotherapy. *Journal of Immunology* 184: 2918-2929.
3. Bashir N, Kounsar F, Mukhopadhyay S and Hasnain SE (2010) *Mycobacterium tuberculosis* conserved hypothetical protein rRv2626c modulates macrophage effector functions. *Immunology* 130: 34-45.

### **Patents filed**

1. Mukhopadhyay S, Bhat K. H and Khan N. Inhibitors of Rv0256c. USPTO Patent Application No. 20100129809.

## Laboratory of Structural Biology

### Structural and biochemical characterization of some *M. tuberculosis* proteins

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#### Objectives

1. Identification of important proteins of *Mycobacterium tuberculosis* for crystallographic and biochemical analysis
2. Expression and biochemical characterization of the chosen proteins. X-ray structural analysis of the chosen proteins
3. Develop applications of graph theory to understand genome-wide protein: protein interactions.

#### Summary of work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)

Two broad categories of proteins from *Mycobacterium tuberculosis* were chosen for biochemical and structural work. Refer **Table 1**

#### Chaperonins:

We had earlier reported a detailed study to address why the *M. tuberculosis* chaperonins are unable to complement the loss of GroEL in *E. coli*. Through these studies, we had concluded that the recombinant *M. tuberculosis* chaperonins do not form canonical tetradecamers, and that by facilitating their tetradecamer formation, these attain an identical function as that of *E. coli* GroEL. Surprisingly, sequence analysis of the available GroEL sequences reported by us earlier had indicated that the *M. tuberculosis* groEL genes have not turned into pseudo genes, despite one of them exhibiting accelerated evolution. We had also carried out experiments to test oligomeric properties of *M. tuberculosis* GroELs in their native condition. For this, the whole cell lysates of *M. tuberculosis*

**Table 1**

<b>Heat Shock Proteins</b>	<ul style="list-style-type: none"> <li>● Chaperonin-60 family (Cpn60.1, Cpn60.2 and Cpn10)</li> <li>● Heat shock protein 70 family (Hsp70, Hsp40)</li> </ul>
<b>Other proteins including those involved in transcription processes</b>	<ul style="list-style-type: none"> <li>● HrcA and HspR: transcriptional repressors of the Hsp60 and Hsp70 operons respectively</li> <li>● YefM: YoeB toxin-antitoxin complex</li> <li>● cAMP Receptor Protein</li> </ul>



were fractionated by gel filtration chromatography, and various fractions were tested for the presence of GroELs by Western blotting. Interestingly, it was observed that GroEL1 exists as a monomer, dimer, heptamer and tetradecamer. Further, by probing with anti-phosphoserine, anti-phosphothreonine and anti-phosphotyrosine antibodies, it was revealed that only the tetradecameric fraction is phosphorylated on a Ser-residue. We thus concluded that oligomerization of GroEL1 under native condition is mediated by specific phosphorylation on Ser-residues.

In the previous report, we had also shown that *M. tuberculosis* GroEL-1 possesses an unusual property as a DNA-binding protein. We had hypothesized that this property might be due to participation of GroEL-1 in nucleoid formation in *M. tuberculosis*. The purified nucleoids of *M. tuberculosis* showed presence of GroEL1 molecule when probed with anti-GroEL1 antibodies. Imaging by fluorescence microscopy further confirmed that GroEL1 of *M. tuberculosis* colocalises with its nucleoids.

#### Details of progress made in the current reporting year (April 1, 2009 - March 31, 2010)

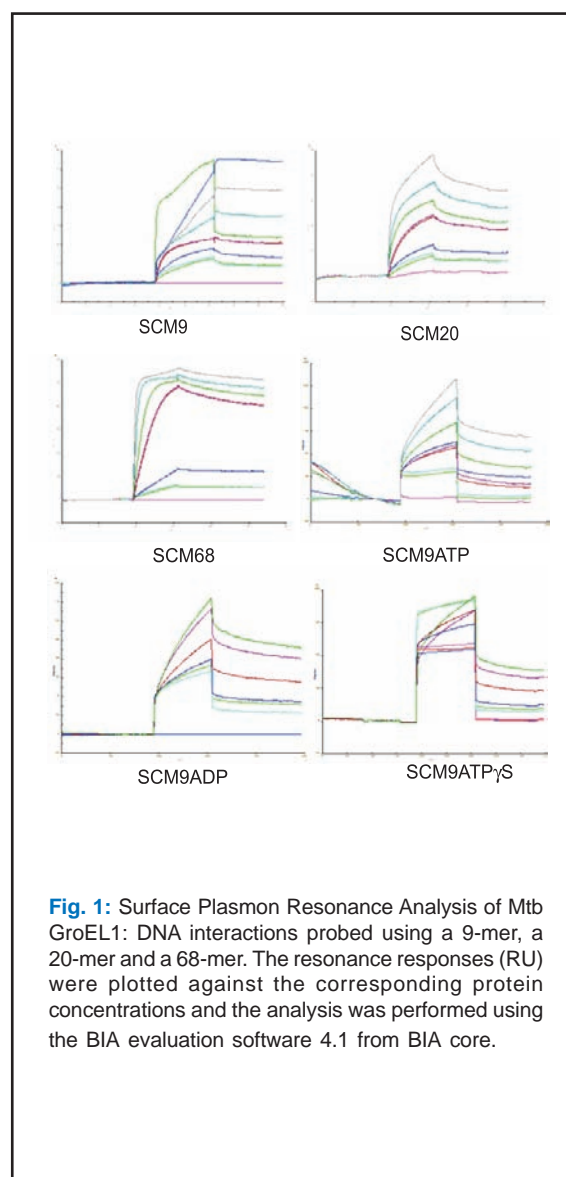
##### Project 1: Molecular characterization of Chaperonins

During the period under review, we sought to determine the binding sites of GroEL1 on *M. tuberculosis* chromosome through genome-wide ChIP-chip analysis. For this, we treated mycobacterial cells with formaldehyde, harvested and lysed them gently. The chemically crosslinked DNA-protein complexes were immunoprecipitated using monoclonal anti-GroEL1 antibody, which was custom generated from Bangalore Genei. Whole cell extract DNA was used as the control in the ChIP-chip experiments. The immunoprecipitated DNA was hybridized on a high density microarray chip containing approximately 240,000 overlapping probe DNA fragments, each of about 60 oligonucleotide length. The scanned microarray data were analysed using Chip Analytics software of Agilent Technologies, and by locally written scripts.

The analysis of microarray data revealed that out of the 240,000 probes, approximately 2400 probes are enriched for binding. Gene-based enrichment showed that this corresponds to 357 genes out of the ~4000 genes in the genome of *M. tuberculosis*. An interesting outcome of this analysis was that the GroEL1 binds predominantly to the coding

region, and to GC-rich regions. Enrichment in the coding region of the PE-PGRS genes was also observed. The results of ChIP-chip were confirmed by PCR amplifications of the bound probes, and by electrophoretic mobility shift assays of identified consensus sequences.

The kinetics and affinity of GroEL1 binding to DNA was tested using surface plasmon resonance with biotinylated 9-mer, 20-mer and 68-mer oligonucleotides. The sequences of these oligonucleotides were derived from consensus obtained from ChIP-chip analysis. Binding kinetics was also obtained for the 9-mer oligonucleotide in the presence of 1mM ATP, ADP and ATP $\gamma$ S. Results of Surface Plasmon Resonance analyses are shown in **Fig. 1**.



**Fig. 1:** Surface Plasmon Resonance Analysis of Mtb GroEL1: DNA interactions probed using a 9-mer, a 20-mer and a 68-mer. The resonance responses (RU) were plotted against the corresponding protein concentrations and the analysis was performed using the BIA evaluation software 4.1 from BIA core.

The SPR analysis resulted in the following kinetic parameters:

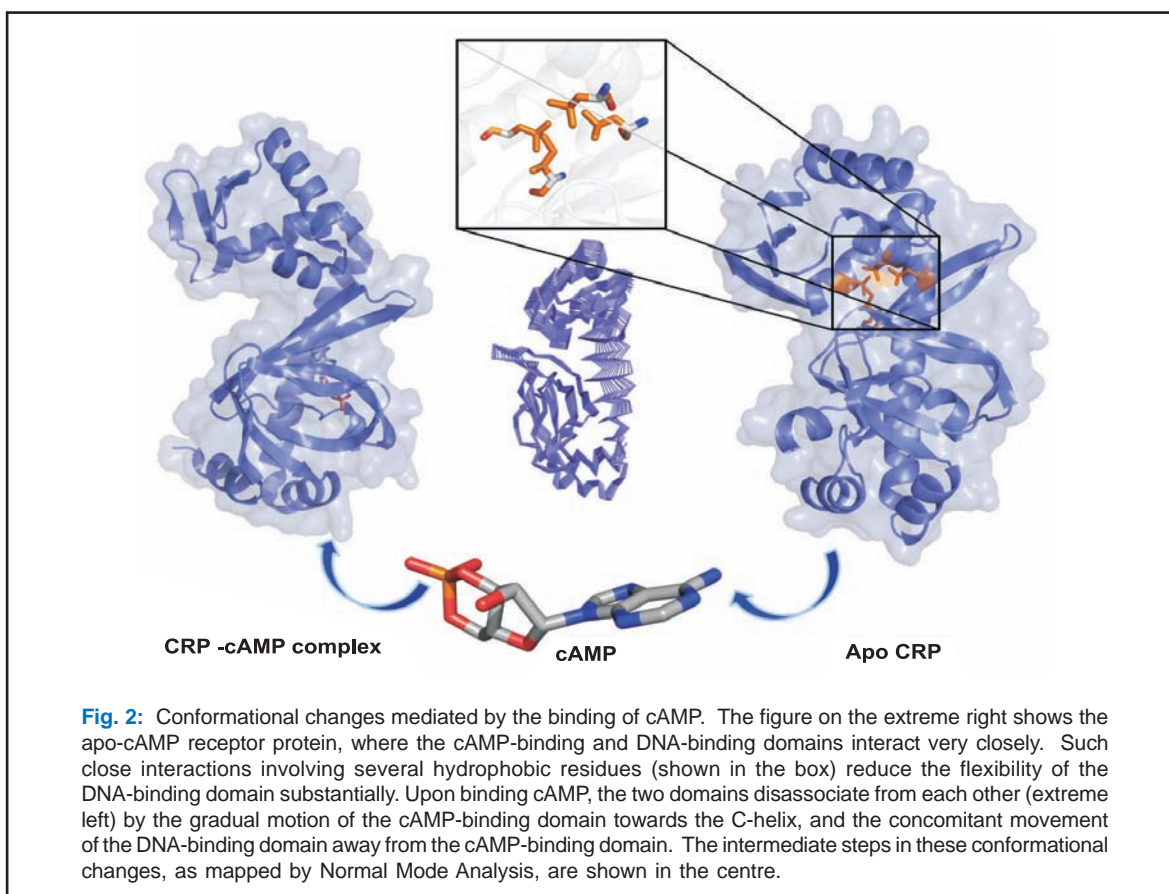
Oligos	$k_{on}$	$k_{off}$	$K_a$	$K_d$
SCM9	$5.5e^3$	$1e^{-5}$	$5.5e^8$	$1.8e^{-9}$
SCM20	$2.9e^4$	$9e^{-4}$	$3.1e^9$	$3.2e^{-8}$
SCM68	$2.9e^4$	$1.51e^{-3}$	$1.92e^7$	$5.68e^{-8}$
SCM9ATP	$2.57e^3$	$2.32e^{-3}$	$1.11e^6$	$9.04e^{-7}$
SCM20ADP	$1.56e^3$	$9.91e^{-4}$	$1.57e^6$	$6.36e^{-7}$
SCM9ATP $\gamma$ S	$2.9e^3$	$1.67e^{-3}$	$1.74e^6$	$5.74e^{-7}$

It can be clearly seen that the affinity of GroEL1: DNA binding reduces in the presence of ATP, ADP or ATP $\gamma$ S.

### Project 2: Structural studies on cyclic AMP receptor protein

During the period under review, the crystal structure of *M. tuberculosis* cAMP receptor protein (CRP<sub>MT</sub>) was determined. Diffraction data on these crystals were collected in the previous year, and the structure was determined using molecular replacement. These crystals are devoid of cAMP, thus enabling us to make comparisons with the structures in the presence of cAMP, and thereby allowing us to

hypothesize the allosteric transitions mediated by cAMP. The crystallographic data were complemented using Normal Mode Analysis in order to map paths of conformational changes. The overall hypothesis that we have proposed includes the changes brought about by cAMP binding in the following sequence (**Fig. 2**) subtle changes in the orientation of side chains in the cAMP binding site, drawing closer of the cAMP binding domain towards the C-helix, reduced interactions between the cAMP binding and DNA binding domains, enhanced flexibility of the DNA-binding domain resulting in sequence specific recognition of the cognate DNA.



### Project 3: Application of graph theory to genome-wide protein:protein interactions

During the period under review, we have attempted to make predictions of genome-wide functional linkages of *M. tuberculosis*. These have been attempted by the use of Support Vector Machine, with positive data from curated literature, and negative data from the assumed pairs which are not colocalised in the same sub-cellular compartment. The features to train SVM include, phylogenetic profile, frequency of occurrence on operons and correlation from large scale gene expression studies. Our predictions yield approximately 40,000 functional linkages. Further analysis of these by the use of graph theory methods are in progress.

#### Future plans and directions

We plan to analyse the results of CHIP-chip using GroEL1 binding sites. Possible biological hypothesis will be attempted to be proposed based on these results.

The genome-wide functional linkages will be analysed in the light of dormancy regulons, and attempts will be made to propose hypothesis on the onset of dormancy.

#### Publications

1. Basu D, Khare G, Singh S, Tyagi A, Khosla S and Mande SC (2009) A novel nucleoid-

associated protein of *Mycobacterium tuberculosis* is a sequence homolog of GroEL. ***Nucleic Acids Research*** 37:4944-4954.

2. Kumar CMS, Khare G, Srikanth CV, Tyagi AK, Sardesai AA and Mande SC (2009) Facilitated oligomerization of mycobacterial GroEL: evidence for phosphorylation-mediated oligomerization. ***Journal of Bacteriology*** 191: 6525-6538.
3. Manimaran P, Hegde SR and Mande SC (2009) Prediction of conditional gene essentiality through graph theoretical analysis of genome-wide functional linkages. ***Molecular Biosystems*** 5: 1936- 1942.
4. Nair S, Ramaswamy PA, Ghosh S, Joshi DC, Pathak N, Siddiqui I, Sharma P, Hasnain SE, Mande SC and Mukhopadhyay S (2009) The PPE18 of *Mycobacterium tuberculosis* interacts with TLR2 and activates IL-10 induction in macrophage. ***Journal of Immunology*** 183: 6269- 6281.
5. Kumar P, Joshi DC, Akif Mohd, Akhter Y, Hasnain SE and Mande SC (2010) Mapping conformational transitions in cyclic AMP receptor protein: crystal structure and normal-mode analysis of *Mycobacterium tuberculosis* apo-cAMP receptor protein. ***Biophysical Journal*** 98: 305- 314.



## Laboratory of Mammalian Genetics

### Epigenetic mechanisms underlying developmental pathways

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	Amitava Basu	Junior Research Fellow
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#### **Project 1: DNMT3L: epigenetic correlation with cancer**

##### **Summary of work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)**

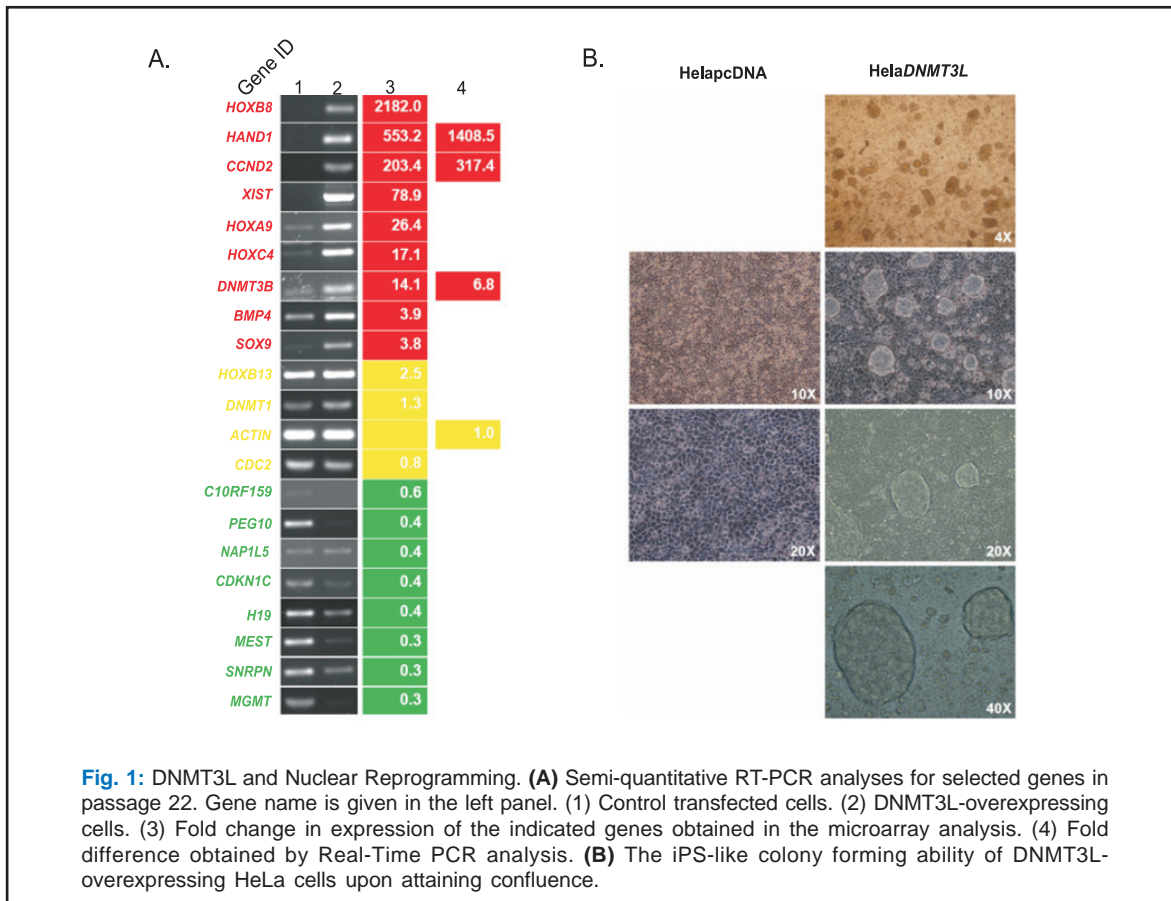
Previously, we had reported loss of DNA methylation at the promoter of the DNA methyltransferase, *DNMT3L*, in cervical cancer samples. This loss of *DNMT3L* promoter DNA methylation correlated with its expression. Furthermore, *DNMT3L* overexpression stimulated cellular proliferation in HeLa and SiHa cells and induced nuclear reprogramming. The nuclear reprogramming was apparent due to change in the morphology of the transfected cells after 20 generations.

##### **Details of progress made in the current reporting year (April 1, 2009 - March 31, 2010) DNMT3L and Nuclear Reprogramming**

To test if the morphological changes observed in *DNMT3L* overexpressing cells were due to genome-wide nuclear reprogramming, microarray analysis

was done as reported in the last report. We observed change in the expression level of several families of genes. Importantly, 24 out of the 36 HOX genes were found to be upregulated in *DNMT3L*-overexpressing cells. Hox genes have been shown to be upregulated in several cancers especially leukemias. Imprinted genes are the known targets of *DNMT3L*. We found several of the imprinted genes to be down regulated. In addition, several epigenetic effectors like DNMT3B, DNMT3A, DNMT1 and cell cycle regulators like CDC2, 5, 6, 7, 14A, 16, 20, 23, 34 and CDKN2C, 1A, 1B, 1C were also misregulated. The microarray data for many of the genes was validated by semi-quantitative RT-PCR and Quantitative Real-time PCR (**Fig.1A**).

Interestingly, we found that confluent cultures of *DNMT3L*-overexpressing cells formed colonies (**Fig.1B**) which were morphologically very similar to iPS or ES cells. However, at the molecular level only the stem cell marker SOX2 was upregulated, indicating that DNMT3L overexpression could reprogram cells only into a partial pluripotent state.



## Project 2: Role of *Dnmt2* in mammalian cells

### Summary of work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)

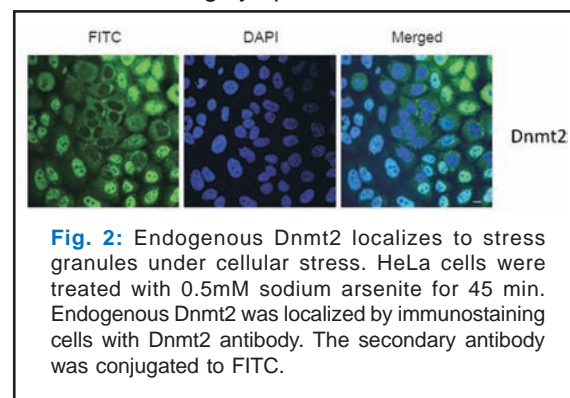
Though it has all the domains specific for methyltransferases, *Dnmt2* has failed to show significant DNA methylation *in vitro* and *in vivo* conditions. Previously we had reported identification of proteins involved in RNA processing to be the interacting partners of *Dnmt2* by Yeast-two hybrid and immuno-precipitation experiments. Moreover, we had found that *Dnmt2* localises to cytoplasm only during cellular stress and under normal conditions it is localized in the nucleus.

### Details of progress made in the current reporting year (April 1, 2009 - March 31, 2010)

#### *Dnmt2* is part of RNA processing during cellular stress

We had previously identified several *Dnmt2*-interacting proteins that are involved in RNA processing. Some of these interactions were validated by GST-pull down and Mammalian Two-hybrid assays. We have probed the interaction of *Dnmt2* with a few of these proteins further. *HnrnpK*

interacts with *Dnmt2* in the nucleus as they colocalise in the nucleus whereas, *G3BP* over expression causes *Dnmt2* to translocate to the stress granules. That *Dnmt2* is part of stress granules was also confirmed by growing cells under conditions of stress. For example, sodium arsenite causes oxidative stress to the cell and when cells were grown in its presence, *Dnmt2* relocates to the cytoplasmic foci from its nuclear location (**Fig. 2**) Furthermore, inhibitors of translation, which can modulate the size and numbers of stress granules, also lead to change in the number and size of *Dnmt2* containing cytoplasmic foci.



### Project 3: Host epigenetic response to infection

#### Summary of work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)

In order to respond to the challenge by an environmental cue (in this case infection by *Mycobacterium tuberculosis*), the cells would have to reprogram the epigenetic markings at several loci in the genome so that the affected gene may be appropriately modulated. In a preliminary experiment, using AIMS (Amplification of InterMethylated Sites) that can identify DNA methylation differences on a genome-wide basis, we had detected difference in the DNA methylation profile of uninfected cells versus cells infected with *M. bovis*.

#### Details of progress made in the current reporting year (April 1, 2009 - March 31, 2010)

The role of epigenetic events in the regulation of gene expression at the level of DNA methylation, histone modifications etc. are well known. Several studies have shown a correlation between environment and epigenetic circuitry. Infection by *M. tuberculosis* is analogous to an environmental cue to which the host cell(s) respond by various mechanisms. Presence or absence of certain gene products in the host may be required, as these might enhance the process of infection. This project was undertaken to:

- a) Examine epigenetic changes in the host upon infection with *M. tuberculosis* and identify the genetic loci where these changes are brought about.
- b) Identify genes or gene products synthesized by the mycobacterium that directly affect the epigenetic circuitry of the host.

This, we believe, will provide us important evidence on the genes in the host that might be participating in a response to mycobacterial infection. Our previous preliminary analysis had already shown that differences do exist in the DNA methylation of the host cells before and after infection with *M. bovis*. We now are extending this study to THP1 cells infected with Rv strain of *M. tuberculosis*.

A bioinformatic analysis of the *M. tuberculosis* genome identified 29 genes that have a putative methyltransferase function. This function is based on these genes having a SAM-binding domain. Several of them also have nucleic acid binding domain. Based on past literature, this list was pruned down to 21 by removing those genes which

are known to be methyltransferases for other proteins. All these 21 genes were taken forward for analysis. To further narrow down our search, the following criterion was set:

- a) The gene should be a DNA methyltransferase
- b) The gene product should be secreted out of the mycobacterium
- c) Upon infection it should also localize to the nucleus.

To test the genes for these characteristics, 17 of the 21 genes have been cloned. For purification and DNA methyltransferase assay, 10 of them have been cloned as a His-tagged fusion protein in to the bacterial expression vector PET28a+. For secretion studies, their GFP-fusion construct was cloned into a mycobacterial vector pVV16. For nuclear localization, all the 17 have been cloned into mammalian vector pCDNA3.1 in fusion with GFP.

### Project 4: Specialized chromatin structures as epigenetic imprints to distinguish parental alleles

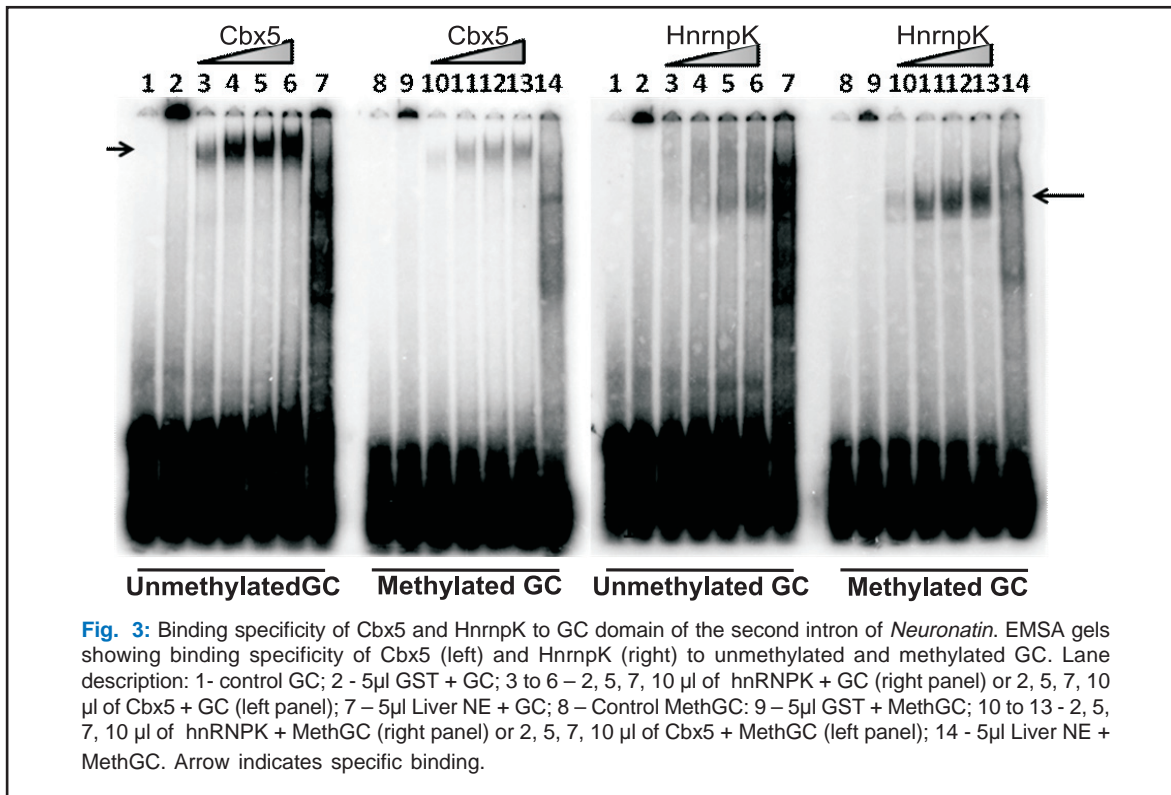
#### Summary of work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)

Previously, we had reported methylation-restricted protein binding to a GC-rich motif within the transcription-independent, parental-allele-specific, DNase I hypersensitive site present in the second intron of the imprinted mouse *neuronatin* gene. Our last report described the identification of GC-rich motif binding proteins using yeast One-hybrid assay and affinity chromatography using Biotin-tagged GC motif in conjugation with peptide fingerprinting (mass spectroscopy). Furthermore, we had initiated experiments to examine whether the 250bp second intron of *Neuronatin* has any regulatory effect on the transcription of a reporter gene using P-element transposition strategy in *Drosophila*.

#### Details of progress made in the current reporting year (April 1, 2009 - March 31, 2010)

##### Characterization of GC-binding proteins :

From the list of several proteins that were identified as binding to GC-rich region from within the second intron of *Neuronatin*, *HnrnpK* and *Cbx5* were taken up for further characterization. We find that both these proteins can discriminate between methylated and unmethylated form of the GC region. While *Cbx5* binds with a higher affinity to unmethylated DNA, *Hnrnpk* preferred methylated GC (**Fig. 3**). Further work is in progress to examine these interactions.



### Functional analysis of neuronatin's second intron

*Drosophila* transgenic for a white-eye gene construct had shown that the second intronic region of *Neuronatin* is a transcriptional activator. To test whether the same is true in mammals, mice in which the second intron of *Neuronatin* has been deleted were generated in collaboration with NCBS, Bangalore and Centre for Developmental Biology, Kobe. For the analysis, these mice have now been crossed with wild type mice producing offspring inheriting either a maternal or a paternal copy of the deletion. This should enable us to examine whether this intronic region has any role in establishing or maintaining the imprinting status of *neuronatin*. In wild type animals, *Neuronatin* is paternally expressed. Therefore, should the second intron play a role in imprinting, heterozygotes inheriting the deleted locus from the father would be expected to show loss of *Neuronatin* expression, whereas mice inheriting the deletion from mother would not show any effect on *Neuronatin* expression. In addition, this would also be suggestive of its role in maintaining the paternal allele in a transcriptionally active state. Alternatively, inheritance of the deleted *Neuronatin* allele from father may have no effect but inheritance from mother may result in expression of the gene from

the maternal allele in addition to the normally expressed paternal allele. This would indicate that intron 2 of *Neuronatin* normally exerts a silencing effect on the maternal allele of *Neuronatin* gene. *Neuronatin* intron 2 deleted mice will also be analyzed for the effect of deletion on methylation and nucleosomal organisation within *Neuronatin* locus. Changes in these epigenetic modifications would be useful in assessing the role of *Neuronatin*'s second intron in imprint maintenance.

### Publications

1. Basu D, Khare G, Singh S, Tyagi A, Khosla S and Mande SC (2009) A novel nucleoid-associated protein of *Mycobacterium tuberculosis* is a sequence homolog of GroEL. *Nucleic Acids Research* 37:4944-4954.
2. Gokul G, Ramakrishna G and Khosla S (2009) Reprogramming of HeLa cells upon DNMT3L overexpression mimics carcinogenesis. *Epigenetics* 4: 322-329.
3. Manderwad GP, Gokul G, Kannabiran C, Honavar SG, Khosla S and Vemuganti G (2010) Hypomethylation of the DNMT3L promoter in ocular surface squamous neoplasia (OSSN). *Archives of Pathology & Laboratory Medicine* (In press).



## Laboratory of Molecular Oncology

### Genomics and molecular genetics of cancer and human genetic disorders

<b>Principal Investigator</b>	Murali D Bashyam	Staff Scientist
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	R A Sastry and Ravikant, NIMS, Hyderabad	
	S Pattnaik and M Vamsy, IACHRC, Hyderabad	
	T K Chattopadhyay, S Pal and S D Gupta, AIIMS, New Delhi	
	S Nampoothiri and S Vaidyanathan, AIMS, Cochin	
	R Puri and I C Verma, Sir Ganga Ram Hospitals, Delhi	
	A R Ramadevi, Sandor Proteomics	
	V Hariram, UMCC, Hyderabad	

### Objectives

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

### Summary of work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)

#### Colorectal cancer

Work on the identification and characterization of major deregulated pathway(s) in young colorectal cancer patients was continued. Initial analysis revealed a statistically significant difference in the proportion of Wnt positive tumors between young (<50 yrs) and older (>60 yrs) patients. Several novel APC mutations were identified in Wnt+ tumors. Fourteen CRC samples were analyzed by aCGH; gain of Wnt5B and CyclinD1 genes in Wnt positive tumors and co-amplification of ErbB2 and GrB7 in Wnt negative tumors were observed.

#### Esophageal cancer

Screening for p53 and Wnt status was carried out on esophageal squamous and adenocarcinoma samples. The results indicated a significantly high association of deregulated Wnt signaling with adenocarcinoma but not with squamous cell carcinoma samples. In addition, determination of gene copy alterations in esophageal cancer genomes was initiated; preliminary results indicated amplification of cyclin D1 in both subtypes whereas a novel amplification at 10q21 was detected in squamous cell carcinoma samples. Genome wide transcript profiling revealed elevated expression of genes located within the 10q21 amplification.

#### Phenylketonuria (PKU)

Molecular genetic analysis of three PKU families revealed novel mutations in the phenylalanine hydroxylase gene (*PAH*) viz. c.168-2A>G (IVS2-2A>G), c.60+5G>A (IVS1+5G>A) and c.1177insT. The IVS2-2A>G resulted in activation of an alternative 3' splice site within the second intron that gen-

erated a premature termination codon (PTC) in the mutated transcript thereby triggering nonsense mediated decay resulting in degradation of the transcript. Degradation of the mutated transcript was confirmed by quantitative reverse transcription polymerase chain reaction (Q-RT-PCR).

### Familial hypertrophic cardiomyopathy (FHC)

We detected the p.R787H mutation in four independent FHC families. Interestingly, probands in two families harbored the mutation in heterozygous condition and harbored a second independent heterozygous mutation; one harbored a novel *MYBPC3* p.S1212X mutation and the other harbored the *MYBPC3* p.G757D mutation. We detected the p.C1124X and IVS7+1 mutations in the *MyBPC3* gene and a novel p.S322F in the *MYH7* gene in three families, respectively. In addition, we identified the previously reported common g.21003\_21028del25 mutation in the *MYBPC3* gene in four families; the mutation was detected at an allele frequency of 2.5% in the normal population. We also detected a novel polymorphism viz. *MyBPC3* IVS19+7G>A.

### Details of progress made in the current reporting year (April 1, 2009 - March 31, 2010)

#### Project 1: Molecular genetic analyses of sporadic colorectal cancer occurring in the young

The main objective of this project is to understand the biology of sporadic colorectal cancers occurring in the young in India. We previously reported that unlike older patients, a significantly less proportion of young colorectal cancer patients appeared to harbor deregulated Wnt signaling. During the current reporting year, we have re-analyzed the data and also repeated the immunohistochemistry experiments using more appropriate controls. The results are shown in Table 1a; the difference

between young and older patients with respect to Wnt status is statistically significant ( $p < 0.016$ ; fisher's exact test). Although we excluded patients with family history from the analysis, it is possible that some of the MSI-H patients might be positive for family history (they may belong to the HNPCC category). However, the difference in Wnt signaling status between young and older patients is still significant if all MSI-H samples are removed from the analysis. None of the other parameters exhibited a significant difference between the two age groups (**Table 1a**). As a first step to determine the deregulated pathway(s) that lead to tumor initiation and progression in young colorectal cancer patients that did not harbor a deregulated Wnt signaling pathway, we have begun to analyse the status of other canonical pathways. Interestingly, there appeared to be no significant difference in p53 status between Wnt- and Wnt+ tumors; MSI-H status was predominantly associated with Wnt- status as expected (**Table 1b**). We have performed array based comparative genomic hybridization (aCGH) to compare genetic lesions in Wnt- and Wnt+ tumors. Last year we analyzed fourteen samples using aCGH, this year we have added an additional eighteen samples (four Wnt+, three moderately Wnt+, seven Wnt- and four samples could not be classified appropriately). A recurrent deletion at 1p36.21 and a recurrent amplification at 19q13.12-13.32 were identified specifically in Wnt- samples. In addition, we also identified several known and a few presumptive novel copy number polymorphisms.

#### Project 2: Comparative analysis of esophageal squamous cell carcinoma and adenocarcinoma

We had earlier commenced molecular analysis of differences between esophageal adenocarcinoma and squamous cell carcinoma. We have now extended the analysis to a larger cohort of samples.

**Table 1a:** CRC patient data stratified based on age with respect to various criteria

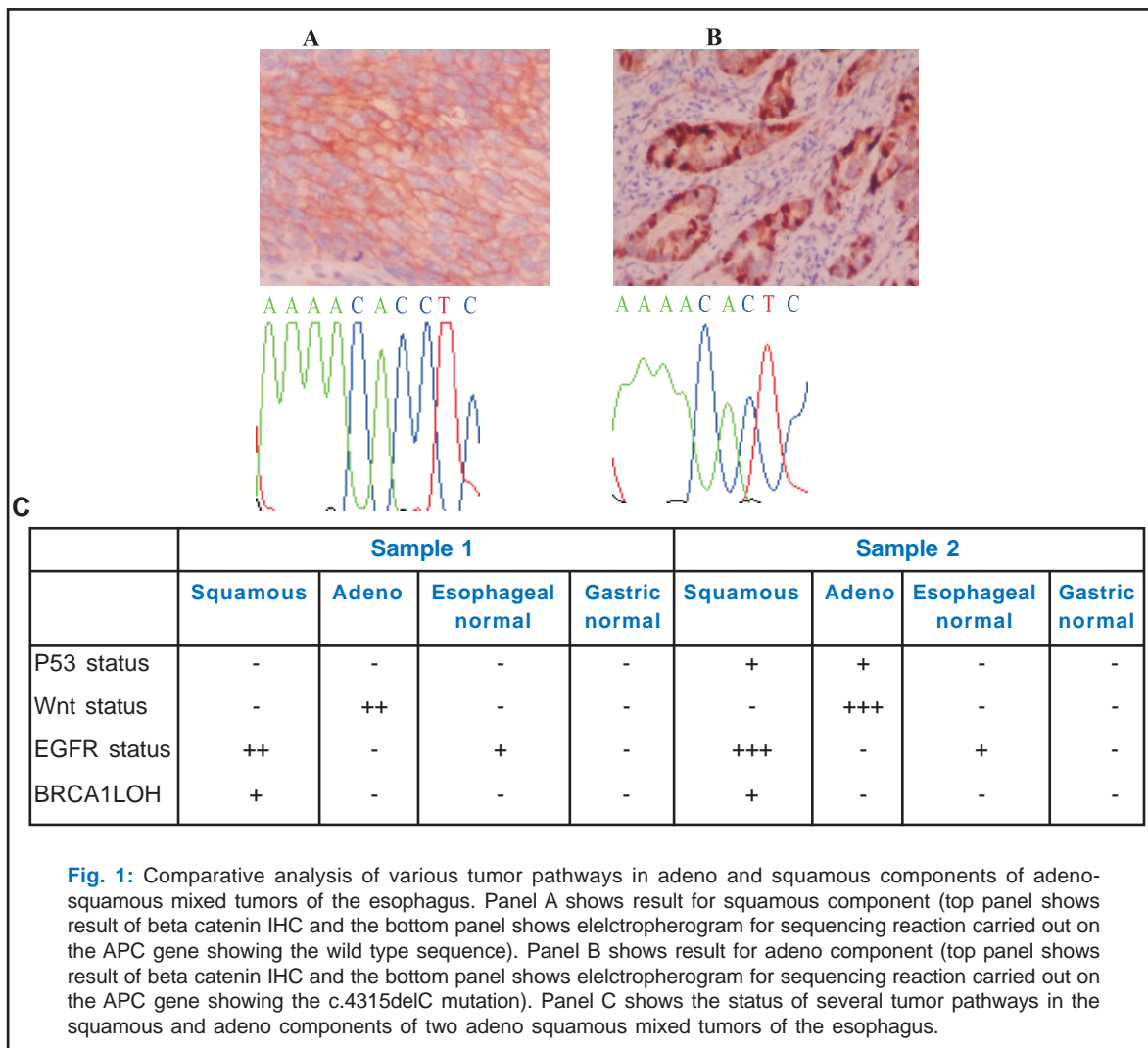
Age	Male	Female	Wnt-	Wnt+	Grade I	Grade II	Grade III	MSI-L/ MSS	MSI-H
Young	44	46	47	42	46	13	1	20	11
Old	33	17	13	31	20	7	2	11	2

**Table 1b:** CRC patient data stratified based on Wnt status with respect to various criteria

Wnt status	P53-	P53+	MSI-I/MSS	MSI-H	Grade I	Grade II	Grade III
Negative	9	24	12	9	32	10	3
Positive	13	23	12	6	57	13	1

P53 immunohistochemistry (IHC) revealed nuclear staining in a significant proportion of adenocarcinoma (17/35; 49%) and squamous cell carcinoma samples (60/98; 61%), confirming earlier observations that p53 inactivation may be a common event in both subtypes. We however detected a significant difference ( $p=0.001$ ; fisher's exact test) in the status of Wnt signaling between the two subtypes; ESCC (6/98; 6%), Ea (18/35; 51%). We also detected elevated expression of EGFR in all of 27 ESCC samples tested (using IHC) but in only 9 out of 24 Ea samples. 5 out of 18 ESCC samples and 1 out of 5 Ea samples exhibited microsatellite instability high (MSI-H) status. Loss of heterozygosity (LOH) at the BRCA1 locus was detected in 2 out of 18 ESCC samples. We next analyzed the status of these pathways in squamous and adeno components of two independent esophageal adeno-squamous mixed tumors. Deregulated Wnt activa-

tion (using IHC for beta catenin) was detected in the adeno component but not in the squamous component in both samples (**Fig. 1A and B**). DNA isolated from microdissected tumor cells from the adeno component and not from the squamous component revealed presence of the APC c.4315delC mutation in one sample validating the IHC result (**Fig. 1A and B**). In contrast, EGFR over expression was detected in the squamous component but not in the adeno component (**Fig. 1C**). Microsatellite instability in two of nine markers tested as well as BRCA1 LOH was detected in DNA isolated from microdissected tumor cells from the squamous component and not from the adeno component (**Fig. 1C**). These results indicate that even in esophageal mixed tumors, the individual components maintain their respective biologies suggesting perhaps that the components arose independently. However, more work needs to be done to conclusively prove this inference.



### Project 3: Molecular genetic analyses of Phenylketonuria (PKU)

During the current reporting year, we have analyzed four PKU families in addition to the three analyzed previously. The mutations detected included c.976delT, c.842+1G>A (IVS7+1G>A), c.526C>T (p.R176X), and c.1503A>G. Among these, the c.1503A>G mutation was detected in a heterozygous state and we were unable to detect the second mutation in this sample. In addition, we also detected a novel single nucleotide polymorphism (SNP) viz. c.2220T>C located downstream of the mRNA cleavage site in the 3' UTR. In total, we have analyzed seven PKU cases so far and four out of seven mutations were novel, which was surprising given that more than 500 mutations in the *PAH* gene have been reported from PKU patients worldwide. More importantly, we did not detect a single missense mutation (the most common form of mutation in patients from other populations). At least five out of the seven mutations are expected to alter the *PAH* mRNA (rather than the protein). The c.1177insT and c.976delT mutations are expected to generate PTCs located 21 and 44 nucleotides upstream of the subsequent exon-exon junction and therefore are less likely to trigger nonsense mediated decay (NMD). The resultant truncated proteins would however be devoid of part of the catalytic domain and the complete C-terminal tetramerization domain. The c.526C>T mutation generates a PTC located 178 nucleotides upstream of the subse-

quent exon-exon junction and is expected to activate NMD. This is the first molecular genetic analysis of PKU from the Indian population and is also the first report of role of NMD in PKU.

### Project 4: Molecular genetic analyses of Familial Hypertrophic Cardiomyopathy (FHC)

We have so far screened 55 FHC patients for presence of mutations in the two main genes viz. *MYH7* and *MYBPC3*; mutations were identified in 19 patients (34.5%) and four patients exhibited compound heterozygosity. This is in contrast with results obtained from the western population where the two genes account for about 75-80% of FHC cases. In all we report 13 independent mutations out of which only four were located in *MYH7* (the rest were in the *MYBPC3*) in contrast to the western population where *MYH7* is the major FHC gene. The mutation and associated clinical details for each of the 19 patients is given in **Table 2**. The *MYBPC3* p.R787H mutation was identified in four independent families as described in last year's report; two patients exhibited compound heterozygosity. The *MYBPC3* c.459delC mutation was detected in two patients; in one it was associated with the *MYBPC3* p.Glu708Lys mutation. Five patients harbored the *MYBPC3* g.21003\_21028del25 intronic deletion mutation reported previously to occur with a high frequency in the Indian sub-continent. In addition, we identified a novel SNP located in *MYBPC3* viz. c.4106delA located in the 3' UTR in three patients and also in five out of ninety four samples screened.

**Table 2:** Clinical and molecular analysis of FHC patients.

S.No	Gender (M/F)	Age (Years)	IVS (Cm)	LVPW (Cm)	LVEF (%)	ace	Mutation
1	M	44	2.4	1.4	68	DD	MYBPC3 c.459delC
2	M	40	2.3	1.3	65	ID	MYBPC3 IVS7+1G>A
3	F	50	1.4	0.9	58	ID	MYBPC3 IVS25+1G>A
4	F	41	2.4	1.6	60	ID	MYBPC3 IVS25+1G>A
5	M	3	1.7	0.7	70	DD	MYBPC3 p.C1124X
6	M	21	1.8	0.8	65	ID	MYBPC3 p.G757D
7	M	40	1.8	1.1	65	ID	MYBPC3 p.E708L, MYBPC3 c.459delC
8	M	57	1.7	1.1	60	II	MYBPC3 g.21003_21028del25
9	M	68	1.8	0.9	60	II	MYBPC3 g.21003_21028del25 + MYBPC3 p.L1218P
10	M	60	1.5	1			MYBPC3 g.21003_21028del25
11	M	54	2	1.1	60	ID	MYBPC3 g.21003_21028del25
12	F	47	1.8	0.8	65	II	MYBPC3 g.21003_21028del25
13	F	47	1.8	1.1	60	II	MYH7 p.S322F, novel
14	M	54	1.7	1	70	ID	MYH7 p.R663H
15	M	21	1.9	0.9	66	ID	MYH7 p.M659I
16	M	52	1.5	1.2	65	II	MYH7 p.R787H
17	F	63	2.1	1	55	ID	MYH7 p.R787H
18	M	64	1.7	1.2	60	ID	MYH7 p.R787H and MYBPC3 p.S1212 X, novel
19	F	66	1.8	1.4	60	II	MYH7 p.R787H and MYBPC3 p.G757D



### Future plans and direction

1. Microarray based CGH and expression profiling will be carried out to determine deregulated pathway(s) in Wnt negative CRC samples
2. We plan to screen more esophageal cancer samples to determine status of Wnt/MSI/EGFR/p53 pathways. In addition, microarray based CGH and expression profiling will be undertaken to determine important deregulated pathways in squamous cell carcinoma of the esophagus and to classify tumors based on EGFR/p53/Wnt/MSI status.

### Publications

1. Angalena R, Chaudhary A, Bashyam MD and Dalal A (2009) Hemoglobin D (Iran) masquerading as hemoglobin E: An interesting case report. **Newsletter of Genetics Chapter of Indian Academy of Pediatrics** 2:11-12.
2. Bashyam MD (2009) Nonsense-mediated decay: linking a basic cellular process to human disease. **Expert Review of Molecular Diagnostics** 9:299-303.
3. Bashyam MD (2009) Studies on nonsense mediated decay reveal novel therapeutic options for genetic diseases. **Recent Patents on DNA & Gene Sequences** 3:7-15.
4. Kumar MS, Ramachandran A, Hasnain SE and Bashyam MD (2009) Octamer and heat shock elements regulate transcription from the AcMNPV polyhedrin gene promoter. **Archives of Virology** 154: 445-456.
5. Angalena R, Prabitha KN, Chaudhary AK, Bashyam MD, Jain S and Dalal A (2010) A novel homozygous point mutation at codon 82 (HBB:c.247 A>T) in the beta-globin gene leads to thalassemia major. **International Journal of Laboratory Hematology** (In press).
6. Bashyam MD, Chaudhary A, Reddy E, RamaDevi A, Savithri G, Ratheesh R, Bashyam L, Mahesh E, Sen D, Puri R, Verma I, Nampoothiri S, Vaidyanathan S, Chandrasekhar M, Kantheti P (2010) Phenylalanine hydroxylase gene mutations in phenylketonuria patients from India: identification of novel mutations that affect PAH RNA. **Molecular Genetics and Metabolism** (In press).
7. Purushotham G, Madhumohan K, Anwaruddin M, Nagarajaram HA, Hariram V, Narasimhan C and Bashyam MD (2010). The MYH7 p.R787H mutation causes hypertrophic cardiomyopathy in two unrelated families. **Experimental & Clinical Cardiology** (In press).

## Laboratory of Cancer Biology

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<b>Collaborators</b>	Pavani Sowjanya, Medciti Group, Medchal	
	Nashreen Islam, Tejpur University, Assam	

### Project A: Understanding the mechanism of cellular senescence

#### Objective:

Telomere attrition is a well-known cause for cellular senescence. However, oxidative damage can accelerate ageing leading to premature senescence. In this context, our earlier work has thrown light on involvement of wild type Ras in growth arrest and cellular senescence (**Arvind *et al*, FASEB 2005; Sujoy *et al*, JGH, 2010**). Infact senescence is now considered an important mechanism in inhibiting neoplastic transformation. We are currently focusing on two main aspects (a) to understand the role of histone deacetylases, Sirtuins (SIRT7), in context of both cellular proliferation and senescence and (b) role of redox in accelerating senescence.

### Project A1: Understanding role of SIRT7 in cellular proliferation and premature senescence

Amongst the various histone deacetylases members of the silent information regulator 2 (Sirtuins) 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 functions of the various isoforms in context of cell proliferation and ageing are still unclear in higher organisms. In this context, we intend to take a detailed study on the role of Sirtuins and in particular Sirt7 in relation to cell growth and senescence.

### Summary of work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)

Earlier we reported subtle changes in mRNA expression of SIRT7 in 10 human cancerous cell lines of various origins. All these cell lines were then tested for presence of mutation in the coding sequence of SIRT7. We reported the presence of a mutation E256K (G to A transition) in exon 7 of

SIRT7 in lung carcinoma cell line A549 while no mutations were detected in the other cell types.

### Details of progress made in the current reporting year (April 1, 2009 - March 31, 2010)

1. To check for expression level of SIRT7 in relation to ageing:

Since in organisms like yeasts and worms there is a close connection between ageing and SIR2, we asked the question if the expression of SIRT7 varies during the process of ageing. Using two approaches, we checked the expression of SIRT7: (a) in mice tissues from different age groups and organs (b) during replicative senescence in primary fibroblasts.

#### (a) Expression level of SIRT7 in mice of various age groups

The endogenous expression of SIRT7 was checked in different organs by both semiquantitative PCR and real time PCR from male mice belonging to different age groups (1week, 6 months and 1 year old). In all the five different organs tested viz., liver, lungs, heart, kidney and spleen, we did not find any significant alteration in levels of SIRT7 with increasing age.

#### (b) Expression level of SIRT7 in young vs senescent fibroblasts

Primary cell cultures undergo senescence with repeated passaging because of telomere attrition. We used the human amniotic fluid fibroblasts as a source of primary cell culture. The human fibroblasts were passaged till they stopped dividing and showed typical senescent characteristic markers viz. enlarged morphology and positivity for beta-galactosidase. RNA was collected from three different passages and expression of SIRT7 was compared by semi quantitative RT-PCR. We found a significant decline in level of SIRT7 expression in ageing fibroblasts (**Fig. 1**).

Expression endogenous Sirt7 following replicative senescence in three different human primary fibroblast cultures (PC)

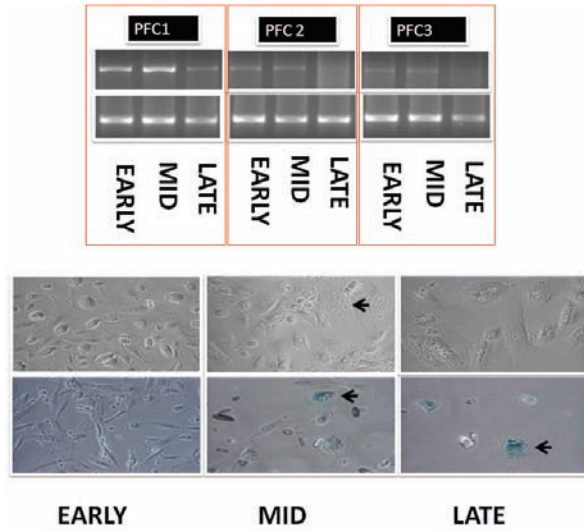


Fig. 1: Expression of endogenous SIRT7 and beta-galactosidase in young (early) and senescent (late) cells

2. Role of SIRT7 in cellular proliferation

Based on our observation on declining levels of SIRT7 expression in senescent cells, we hypothesize that SIRT7 may have a role in cellular proliferation. In order to gain insight if SIRT7 gives any growth advantage, we cloned human SIRT7 in EGFP-C3 mammalian expression vector and overexpressed it in HEK293 cells. We compared the growth rates of HEK clones with varying levels of SIRT7-GFP expression. We isolated two clones

each with varying levels of SIRT7, high-SIRT7-GFP clones with two fold higher levels of SIRT7 expression and low-SIRT7-GFP. While both control and low-SIRT7-GFP HEK clones showed similar growth rate, the high-SIRT7-GFP clones showed faster growth rate (Fig. 2). The asynchronous cell cultures of both high and low-SIRT7-GFP clones did not show any changes in the cell cycle profile. However, when they were synchronized by serum starvation and then stimulated, more cells

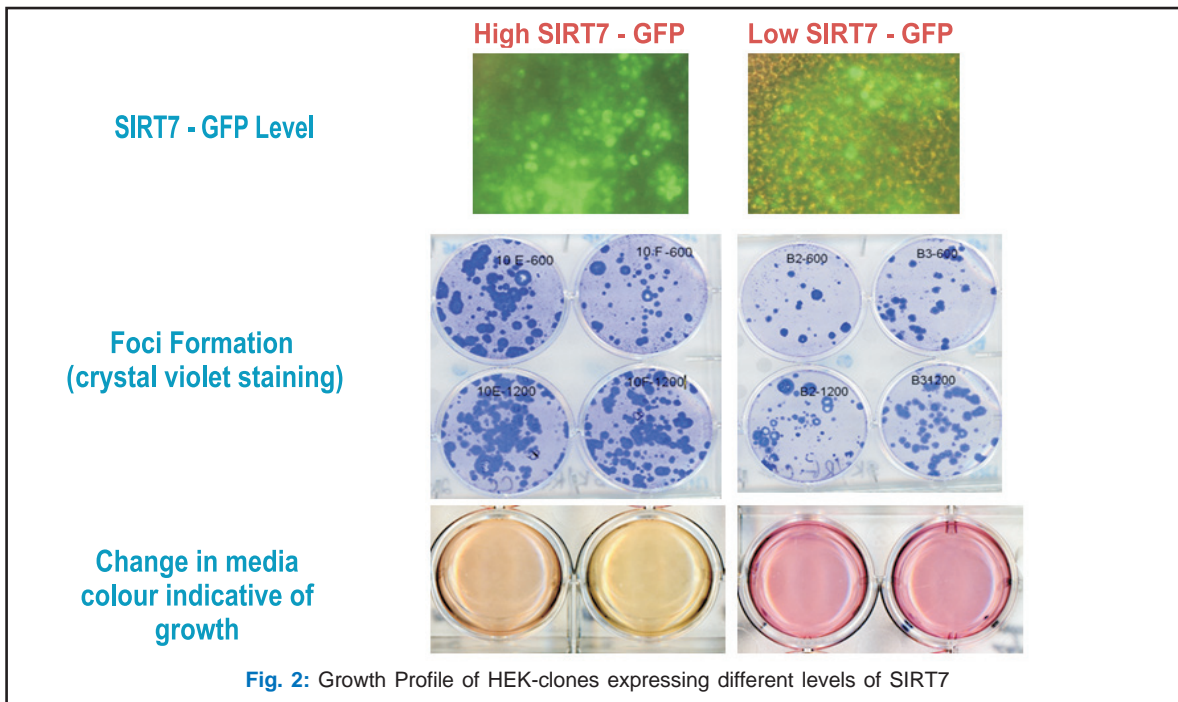


Fig. 2: Growth Profile of HEK-clones expressing different levels of SIRT7

accumulated in G2/M phase of cell cycle in the High-SIRT7-GFP clones. Studies are now underway to clone the SIRT7 in retroviral plasmids so that the role of SIRT7 in proliferation/senescence can be studied using the primary and immortalized cell culture systems.

### Project A2: Cellular Models with changes in redox states to study cellular senescence

This is a new activity.

In continuation with the previous studies on SIRT7 and ageing, we are also trying to establish cell culture systems where senescence can be induced to study various biochemical and cellular changes associated with ageing. Experimentally, one can induce premature senescence in cell culture conditions by treating with high concentrations of  $H_2O_2$  which is cytotoxic to cells and is also easily degraded by endogenous catalase.  $H_2O_2$  is believed to change the redox state in the cell which accelerates changes associated with ageing. Professor T. Ramasarma is advising us on the use of small molecules that can efficiently alter the cellular redox states and also more stable at physiological pH compared to  $H_2O_2$ . We are in the process of evaluating few such small molecules synthesized in the laboratory of Prof. Nashreen Islam, Tejpur University. One such chemical compound is diperoxovanadate (DPV), a complex of  $H_2O_2$  with orthovanadate, which is catalase

resistant and known to substitute for  $H_2O_2$  in peroxidative activities at concentrations order of magnitudes lower than  $H_2O_2$ . DPV causes cytoskeletal disruption and efficiently induces premature cellular senescence at concentrations lower than  $H_2O_2$  (Fig. 3). Currently studies are underway to study the mechanism by which DPV induces senescence.

### Project B: Cervical cancer screening programme in peri urban Medchal Mandal, Hyderabad

In an ongoing collaborative project with a rural hospital based in outskirts of Hyderabad an attempt is being made to evaluate the feasibility of three different methods viz, Cytopathology, HPV detection and Visual Inspection by acetic acid (VIA) for effective strategy in cancer cervix screening programme.

### Summary of work done until the beginning of this reporting year (April 1, 2008 – March 31, 2009)

A total of 2374 women attending the cancer detection clinic of Medciti hospital at Medchal Mandal were screened for HPV. We found HPV prevalence close to 11% in the community based screening programme. Majority of the women showed a clearance on follow up. Also we had reported that it is feasible for the women to self-collect vaginal samples for screening of HPV.

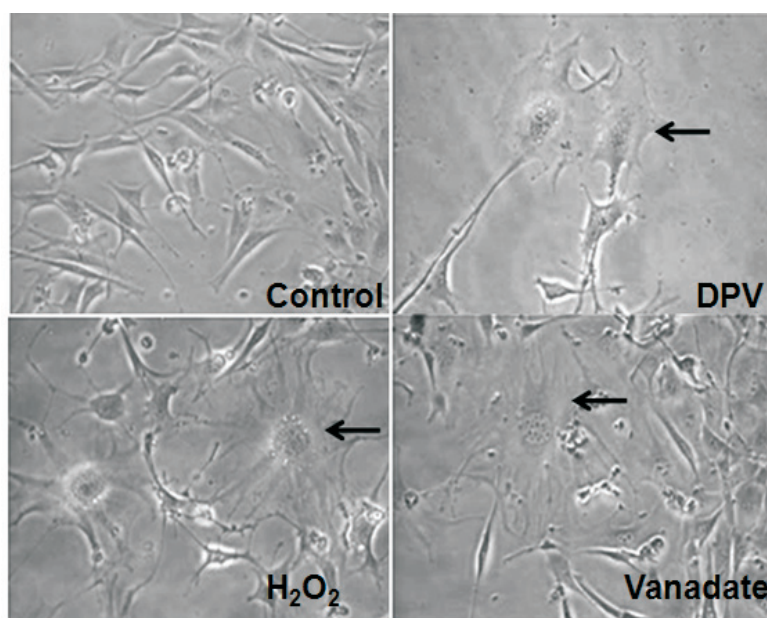


Fig. 3: Stress induced senescence like morphology following treatment with (DPV  $\mu$ M),  $H_2O_2$  (250  $\mu$ M) and Vanadate (25 $\mu$ M). Senescence is characterized by appearance of flat, enlarged and multinucleate cells



## Details of progress made in the current reporting year (April 1, 2009 - March 31, 2010)

### Objectives:

Visual inspection of the cervix after acetic acid application (VIA) is widely recommended as the method of choice in cervical cancer screening programs in resource-limited settings, because of its simplicity and ability to link with immediate treatment. In testing the effectiveness of VIA, HPV DNA testing, and Pap cytology in a population-based study in a peri-urban area in Andhra Pradesh, India, we found the sensitivity of VIA for detection of cervical intraepithelial neoplasia grade 2 and worse (CIN2+) to be 26.3%, much lower than the 60-90% reported in the literature. We therefore investigated the determinants of VIA positivity in our study population.

### Methods:

We evaluated VIA positivity by demographics and reproductive history, results of clinical examination, and results from the other screening methods.

### Results:

Of the 19 women diagnosed with CIN2+, only 5 were positive by VIA (positive predictive value = 3.1%). In multivariate analysis, VIA-positivity (12.74%) was associated with older age, positive Pap smear, visually apparent cervical inflammation and inter-observer variation. Cervical inflammation of unknown cause was present in 21.62 % of women. In disease-negative women, cervical inflammation was associated with an increase in VIA-positivity from 6.1% to 15.5% ( $P < 0.001$ ). Among the six gynecologists who performed VIA, the positivity rate varied from 4% to 31%.

### Conclusions:

The interpretation of VIA is subjective and its performance cannot be readily evaluated against objective standards.

### Impact:

VIA is not a robust screening test and we caution against its use as the primary screening test in resource-limited regions. From our earlier studies we conclude that HPV-DNA testing in conjunction with cytopathology is a better screening strategy.

### Publications

1. Gokul G, Ramakrishna G and Khosla S (2009) Reprogramming of HeLa cells upon DNMT3L overexpression mimics carcinogenesis. *Epigenetics* 4: 322-329.
2. Sowjanya AP, Paul P, Vedantham H, Ramakrishna G, Vidyadhari D, Vijayaraghavan K, Lakshmi S, Sudula M, Ronnett BM, Das M, Shah KV, Gravitt PE and on behalf of the Community Access to Cervical Health Study Group (2009) Suitability of self-collected vaginal samples for cervical cancer screening in periurban villages in Andhra Pradesh, India. *Cancer Epidemiology, Biomarkers & Prevention* 18:1373-1378.
3. Bose S, Sakhuja P, Bezawada L, Agarwal AK, Kazim SN, Khan LA, Sarin SK and Ramakrishna G (2010) Hepatocellular carcinoma with persistent hepatitis B virus infection shows unusual downregulation of Ras expression and differential response to Ras mediated signaling. *Journal of Gastroenterology and Hepatology* (In press).

# Laboratory of Computational and Functional Genomics

## Computational and functional genomics of microbial pathogens

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	Vijaykumar Muley	Senior Research Fellow
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	Bhavik Sawhney	Junior Research Fellow
	Ajit Roy	Junior Research Fellow
	Suhail Yousuf	Junior Research Fellow
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	Manju Shukla	Project Assistant
	Vaishnavi Vishnudas	Project Assistant
	Eliza Dewangan	Project Assistant
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	Niyaz Ahmed, University of Hyderabad, Hyderabad	
	Vijaya Lakshmi Valluri, Blue Peter Research Centre, Hyderabad	

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

#### 1. Reconstruction of a genome-wide protein-protein functional linkage map: A machine learning approach to understand cellular physiology

Cellular responses to environmental conditions are governed by the fine-tuning of functional and physical interactions in the proteome. A number of methods have been proposed for the prediction of these protein-protein interactions (PPI), which are based on genomic contexts and expression similarity (ESM).

#### Objectives

1. To develop an integrated approach for the prediction of functional and physical interactions in the proteome
2. To assess the performance of the combination of genomic context, expression similarity and machine learning method.

### Summary of the work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)

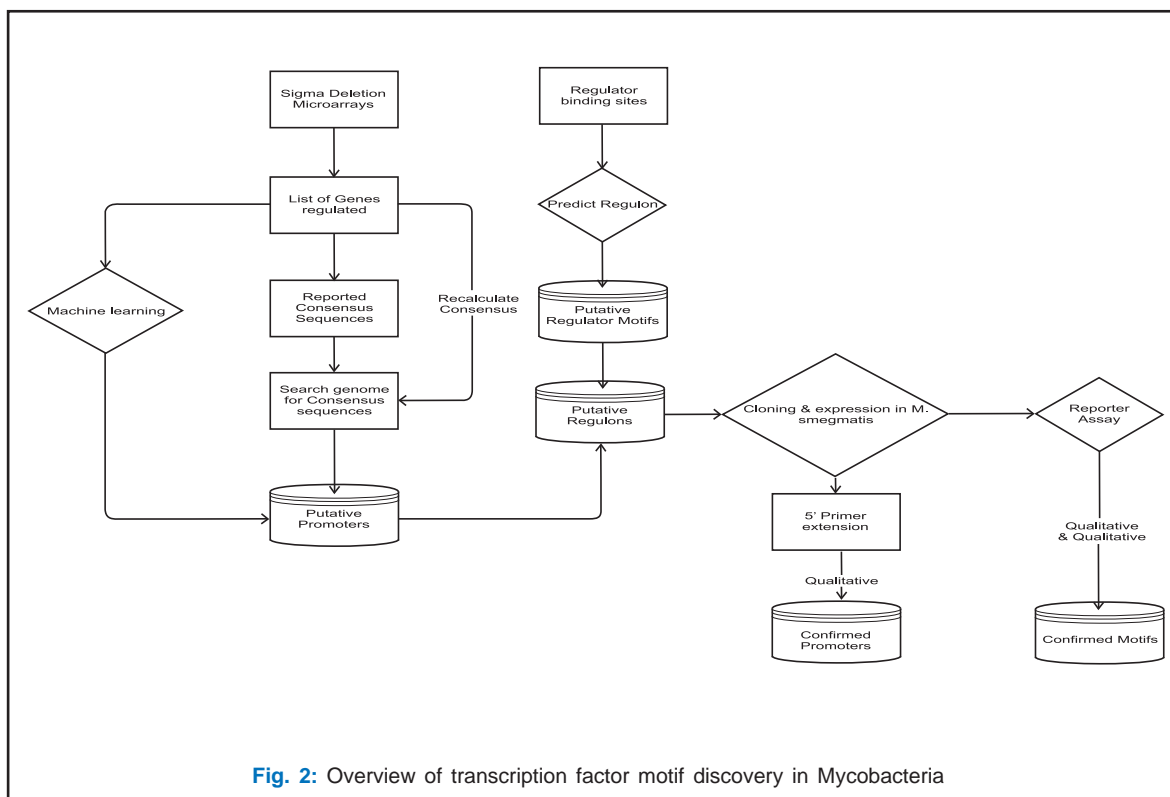
We have systematically identified GGDEF, EAL, HD-GYP and PilZ domain containing proteins and other additional domains co-occurring with them on the same proteins in 779 bacteria. This resulted in the identification of total 124 domains in 16179 bacterial proteins.

#### Details of progress in the current reporting year (April 1, 2009 - March 31, 2010)

We derived the whole genome protein functional linkage map of *Escherichia coli* K12 using a combination of seven MLMs. Integration of six features and high-quality gold standard dataset for training of MLMs resulted in combined average balanced accuracy, sensitivity and specificity of over 93%, 87% and 99% respectively during a ten-fold validation run. A functional and topological analysis of the predicted consensus interactions along with a comparison to previously proposed approaches showed higher quality and utility of our approach.







of *M. tuberculosis* could be generated. The PredictRegulon webserver was used to identify new possible binding sites for the iron dependent regulator, IdeR. As an *in vivo* verification of the regulatory significance of these motifs, it is proposed to clone them upstream of a promoterless reporter gene within the *M. smegmatis* model system. We have designed primers to amplify these regions, and we are currently cloning them into pSD5B, a mycobacterial shuttle vector that contains a promoterless full-length *lacZ* (Fig. 2).

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

### 1. Amino Acid substitutions in *P. falciparum*

The extreme compositional bias (AT bias) of genomes like *P. falciparum* has considerably complicated the sequencing and annotation efforts.

#### Objectives

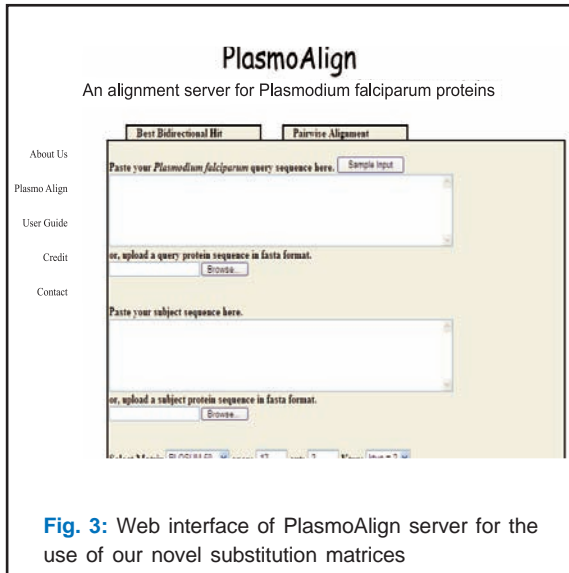
1. To develop web application that uses new substitution matrices to show better sequence alignment
2. To use the improved substitution matrices for assigning functions to the hypothetical proteins of this parasite.

### Summary of the work done until the beginning of this reporting year (April 1, 2008 – March 31, 2009)

Using the new improved substitution matrices, we attempted the annotation of *P. falciparum* proteins. An effort was made to assign functions to the hypothetical proteins of this parasite.

### Details of progress in the current reporting year (April 1, 2009 – March 31, 2010)

We developed PlasmoAlign, a protein alignment server, that has been designed specifically for aligning *P. falciparum* proteins with its potential orthologs using a novel parasite specific asymmetric substitution matrix (PfFSmat60) developed by us. The webserver also provides the user with the option to search for potential orthologs of this parasite in other organisms based on bi-directional best hits using our symmetric matrices, Smat. The alignments of *Plasmodium* proteins achieved with our matrices have been shown to be both statistically significant and biologically meaningful. This tool is expected to be of immense value to an experimental biologist interested in aligning the candidate proteins of *Plasmodium* that show poor sequence alignments with the existing matrices (Fig. 3).



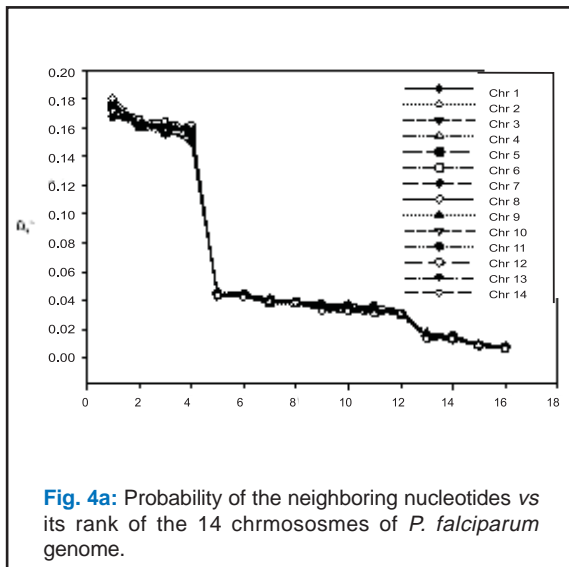
**Fig. 3:** Web interface of PlasmoAlign server for the use of our novel substitution matrices

## 2. Nucleotide correlations and amino acid usage in an AT biased genome: *P. falciparum* as a case study

The *P. falciparum* 3D7 nuclear genome is extremely AT rich with an overall (A+T) composition of 80.6%. The high AT content of its genome and more specifically in the intronic and intergenic regions makes it an organism of interest to be studied

### Objectives

1. To perform frequency analysis and correlations studies in the neighboring nucleotides of the *P. falciparum* genome
2. To study the effect of these correlations on the amino acid composition of *P. falciparum*.



**Fig. 4a:** Probability of the neighboring nucleotides vs its rank of the 14 chromosomes of *P. falciparum* genome.

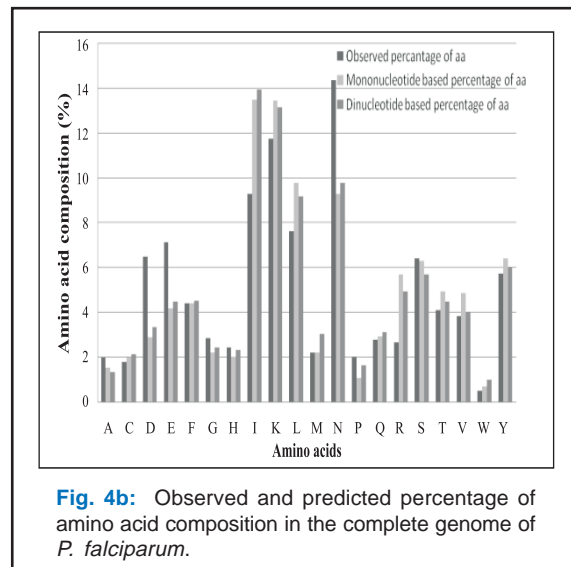
## Summary of the work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)

We have calculated the relative abundance (R) of each of the dinucleotides and have observed correlations ( $R > 1.2$ ) in the dinucleotides of the three datasets for phase 0, 1 and 2. Our results show that there is an increase in the correlations from phase 0 to 2, which suggests that phase 2 shows maximum number of correlations between the nucleotides of the exons.

## Details of progress in the current reporting year (April 1, 2009 - March 31, 2010)

Our work suggests that the correlations follow a similar pattern as that of natural language and there has been an influence of AT% on these correlations (**Fig. 4a**). The existence of these correlations in the genome is a result of the expansion and modification of some regions of the genome, which in the due course of evolution have led to the occurrence of correlations in the genomes.

The plots of the observed to predicted amino acid composition suggests that amino acids ADEGHNP have observed values higher than the mono/dinucleotide predicted values (**Fig. 4b**). This could imply that these amino acids have selection pressure at the amino acid level whereas the predicted mono/dinucleotide values for the other amino acids are more than the observed values suggesting that they might have selection pressure at the nucleotide level, which is influencing the usage of particular amino acids being coded only by the AT rich codons.



**Fig. 4b:** Observed and predicted percentage of amino acid composition in the complete genome of *P. falciparum*.

### 3. Role of multiple Acyl CoA binding protein paralogues in *P. falciparum*

Acyl-coenzyme A binding proteins (ACBPs) are a family of 86 to 103 residues (~10 kD) proteins with conserved amino acid sequences. There are experimental evidences from diverse sources suggesting their role in modulation of fatty acid biosynthesis, regulation of the intracellular acyl-CoA pool size and many more.

#### Objectives

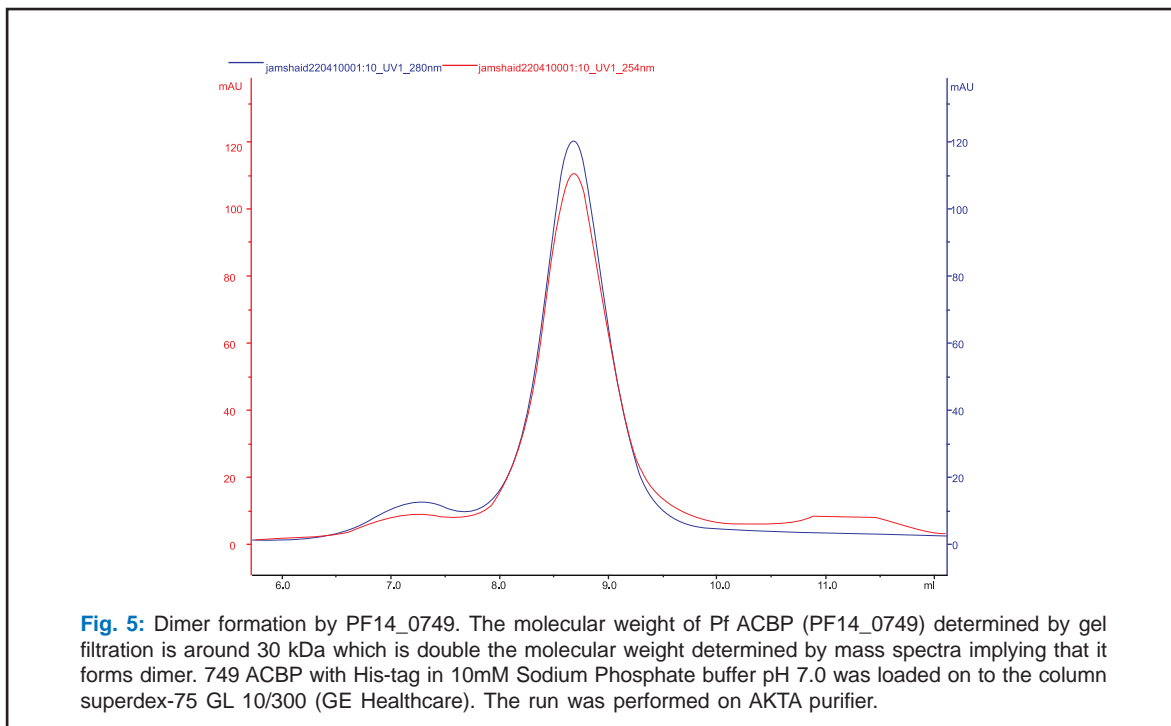
1. To study the binding preferences of all Pf ACBPs and also to study stage specific expression of different Pf *acbp* genes
2. To study the oligomerisation state of ACBPs by mass spectrometry and gel filtration chromatography.

#### Summary of the work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)

We have cloned and expressed all the four ACBPs as histidine-tagged recombinant proteins and purified them by Ni-NTA affinity chromatography. The ACBPs were further purified by gel filtration on Superdex-75 column.

#### Details of progress in the current reporting year (April 1, 2009 - March 31, 2010)

Human ACBP is known to form dimer in the presence of its ligand acyl CoA, but for *P. falciparum*, ACBP (PF14\_0749) the crystal structure have been solved, which was found to be in monomeric form. Here, we report that the same ACBP can also form dimer under certain conditions. In addition, we have found that at least one more Pf ACBP (PF08\_0099) also forms a dimer under the same conditions. In size exclusion chromatography, carbonic anhydrase (29 kDa) was used as marker (**Fig. 5**).



## Laboratory of Transcription

### Mechanism of transcription termination and antitermination in *Escherichia coli*

<b>Principal Investigator</b>	Ranjan Sen	Staff Scientist
<b>Ph D Students</b>	Jisha Chalisery	Senior Research Fellow (till March 2010)
	Ghazala Muteeb	Senior Research Fellow
	Amitabh Ranjan	Junior Research Fellow
	Rajesh Sashni	Junior Research Fellow
	Sourav Mishra	Junior Research Fellow
<b>Other Members</b>	Nanci R Kolli	Technical Assistant
	Nisha C	Postdoctoral Fellow
	Kalyani B	Senior Project Assistant
	Jisha V	Project Assistant (till July 2009)
	Shalini Mohan	Project Assistant
	Shrutika Wadgaonkar	Project Assistant (since Oct. 2009)
<b>Collaborator</b>	Udayaditya Sen, Saha Institute of Nuclear Physics, Kolkata.	

#### Objectives

Transcription must terminate at the end of each operon. In *E. coli*, end of 50% of the operons consist of intrinsic termination signal that codes for a hairpin followed by a U-rich stretch in mRNA. Rest of the operons does not have any signature sequence and it is possible that termination of these operons depend on a factor called Rho. On the other hand, these termination signals can be overcome in response to certain type of modifications in the elongation complex and process is termed as antitermination. Mechanism of these termination and antitermination processes is still not very clear and offers an exciting subject for study. In our laboratory, studies in the following area are in progress.

- 1) Mechanism of action of transcription termination factor, Rho
- 2) Molecular basis of Rho-NusG interaction
- 3) Mechanism of transcription antitermination by N protein at Rho-dependent terminators
- 4) Mechanism of action of transcription antitermination of Rho-dependent termination by an anti-rho factor Psi
- 5) Physiological significance of Rho dependent termination.

#### Summary of the work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)

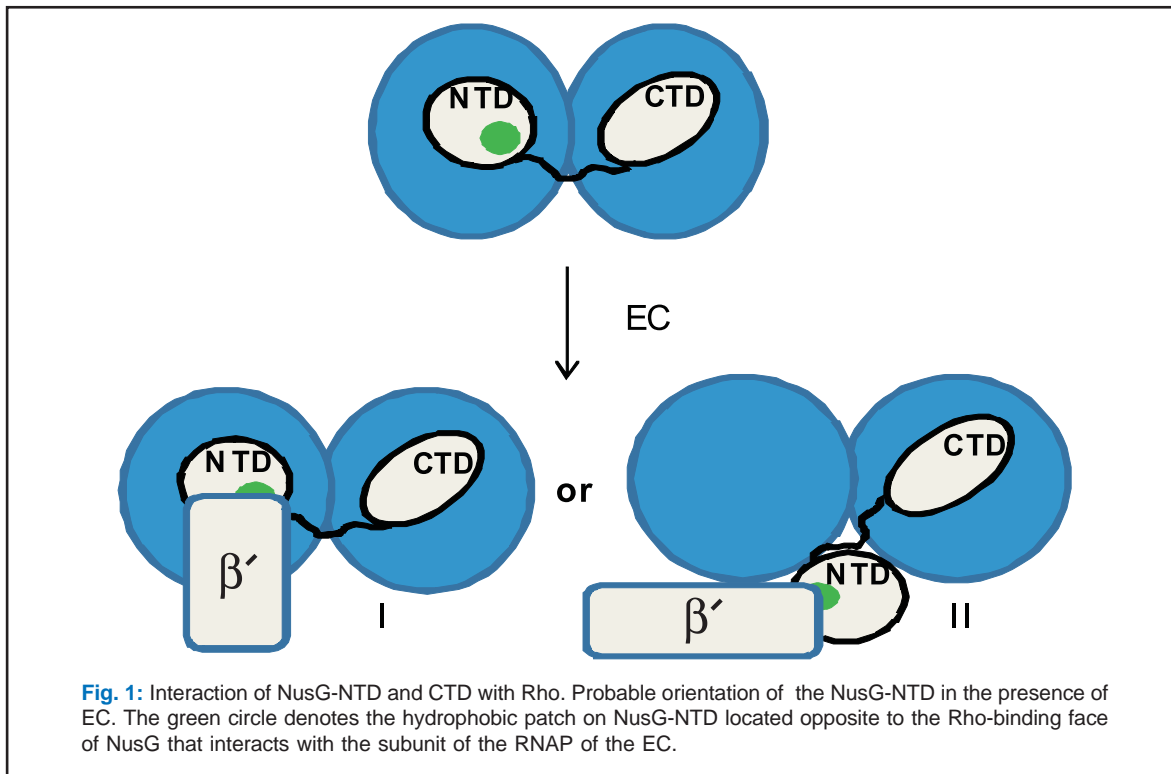
We have described the isolation of and characterization of different Psi (an inhibitor of Rho) mutants both in *vivo* and in *vitro*. Location of these mutants together with the cross-linking data, we have described the interaction surface of Psi required to form complex with Rho (**JMB, 2009**).

We have defined the interacting region of the transcription elongation factor NusG with Rho using mutational and biochemical analysis. Further work to identify the interacting regions on Rho was initiated.

#### Details of the progress in the current reporting year (April 1, 2009 - March 31, 2010)

##### A) Interaction surface required for the complex formation between a transcription terminator and an antiterminator.

The Rho-dependent transcription termination requires the interaction between the terminator, Rho and the antiterminator, NusG. The interaction surface of the Rho-NusG complex is unknown. We show that the  $\beta$ -sheet bundle of the NusG-CTD has the major binding determinants for the Rho. Di-sulphide bridges can be engineered from the NusG-CTD with



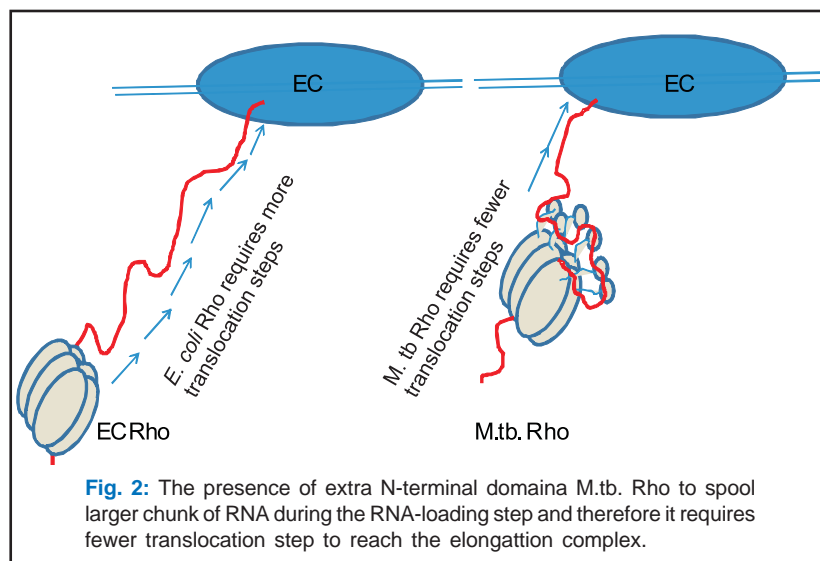
the surface exposed amino acids 217, 221 and 224 of Rho, belonging to its P-loop domain, and a hydrophobic pocket located behind these amino acids in Rho is the likely docking site for NusG. However, in the absence of transcription elongation complex (EC), a part of the NusG-NTD, located on the same face of the Rho-binding region of the NusG-CTD, also comes within the interacting distance with this hydrophobic pocket of Rho located on the adjacent subunit. We propose that in the absence of EC one face of NusG interacts with Rho and its opposite face binds to the EC via its NTD. **Fig.1** describes the proposed model.

**B) A bacterial transcription terminator with inefficient molecular motor action but with a robust transcription termination function.**

The molecular motors like helicases/translocases are capable of translocating along the single stranded nucleic acids and unwinding DNA or RNA duplex substrates using the energy derived from their ATPase activity. Bacterial transcription terminator, Rho, is a hexameric helicase and releases RNA from the transcription elongation complexes by an unknown mechanism. It has been proposed, but not directly demonstrated, that kinetic energy obtained from its molecular motor

action (helicase / translocase activities) is instrumental in dissociating the transcription elongation complex. Here, we report a hexameric Rho analogue (Rv1297, *M. tb* Rho) from *Mycobacterium tuberculosis* having poor RNA-dependent ATP hydrolysis and inefficient DNA:RNA unwinding activities. However, compared to the *E. coli* Rho it exhibited very robust and earlier transcription termination from the elongation complexes of the *E. coli* RNA polymerase. Bicyclomycin, an inhibitor of ATPase as well as RNA release activities of the *E. coli* Rho, inhibited the ATPase activity of the *M. tb* Rho with comparable efficiency but was not efficient in inhibiting its transcription termination function. Unlike *E. coli* Rho, the *M. tb* Rho was capable of releasing RNA in the presence of non-hydrolysable analogues of ATP quite efficiently. Also this termination function most likely does not require NusG, an RNA-release facilitator, as this Rho was incapable of binding to the NusG either of *M. tb* (Rv0639) or *E. coli*. These results strongly suggest that ATPase activity of the *M. tb* Rho is uncoupled from its transcription termination function and this function may not be dependent on its helicase / translocase activity. A model for the proposed mechanism of action of *M.tb*. Rho is described in **Fig. 2**.

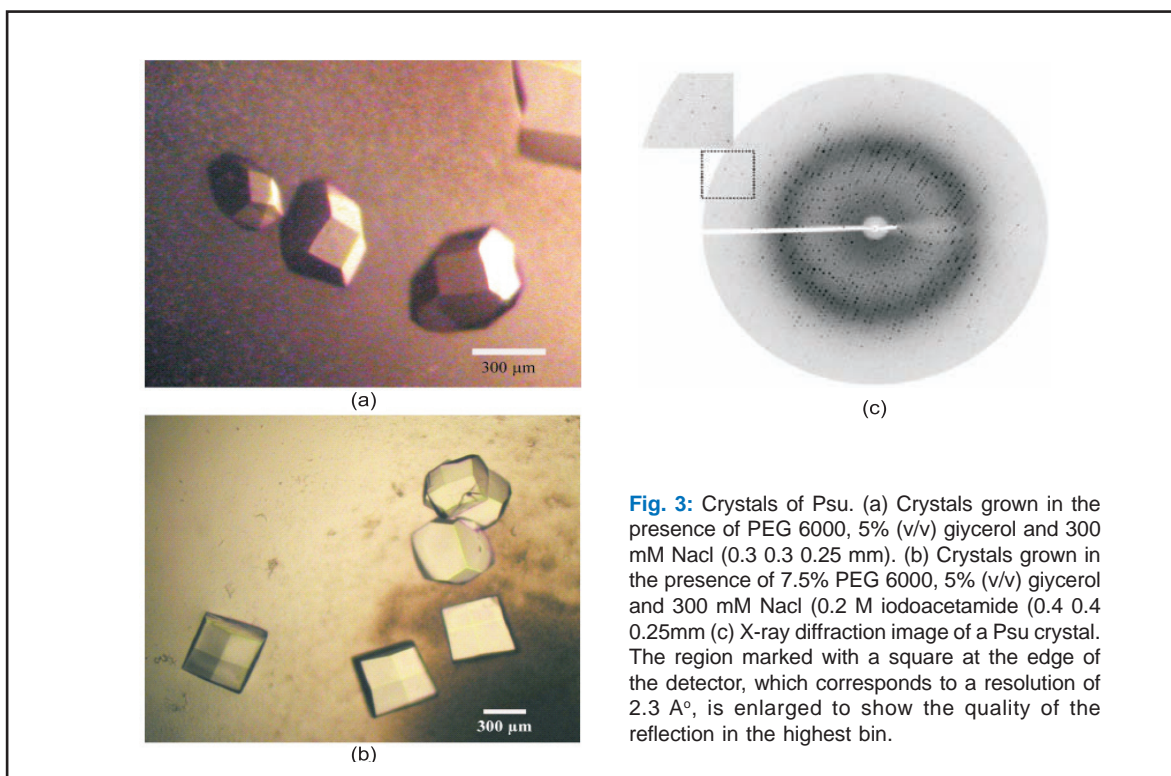




**C) Crystallization and Preliminary Crystallographic Analysis of Psu, an inhibitor of bacterial transcription terminator Rho.**

Psu, a coat protein from bacteriophage P4, inhibits Rho-dependent transcription termination both *in vivo* and *in vitro*. Psu protein is  $\alpha$ -helical in nature and appeared to be a dimer in solution. It interacts with Rho and affects the ATP binding and RNA-dependent

ATPase activity of Rho, which in turn reduces the rate of RNA release from the elongation complex. Crystals of Psu were grown in space group I4 in the presence of PEG, with unit-cell parameters,  $a=b=148.76$  and  $c=63.38$  Å and a calculated Matthews coefficient of  $2.19$  Å<sup>3</sup> Da<sup>-1</sup> (43.9% solvent content) with two molecules per asymmetric unit. A native dataset of Psu has been collected upto  $2.3$  Å (**Fig. 3**).





## Publications

1. Pani B, Ranjan A and Sen R (2009) Interaction surface of bacteriophage P4 protein Psi required for the complex formation with the transcription terminator Rho. ***Journal of Molecular Biology*** 389: 647-660.
2. Khamurai S, Ranjan A, Pani B, Sen R and Sen U (2010) Crystallization and preliminary X-Ray analysis of Psi, an inhibitor of bacterial transcription terminator Rho. ***Acta Crystallographica Section F Structural Biology and Crystallization Communication*** 66: 204-206.
3. Nisha CK, Ranjan A, Kalyani S, Wal M and Sen R (2010) A bacterial transcription terminator with inefficient molecular motor action but with a robust transcription termination function. ***Journal of Molecular Biology*** 395: 966-982.
4. Muteeb G and Sen R (2010) Random mutagenesis using mutator strain, in *In Vitro Mutagenesis Protocols: Third Edition*, Braman, J (ed.), ***Methods in Molecular Biology***, 634 (In press).

## Laboratory of Cell Signalling

### Investigating the role of inositol pyrophosphates in eukaryotic cell physiology

<b>Principal Investigator</b>	Rashna Bhandari	Staff Scientist
<b>Ph D Students</b>	Swarna Gowri Thota	Junior Research Fellow
	Jadav Rathan Singh	Junior Research Fellow
	CVL Manasa	Junior Research Fellow
<b>Other Members</b>	L Padmavathi	Scientist B (since Nov. 2009)
	Ruth Manorama Ravoori	Technical Assistant
	P Srilakshmi	Research Associate
	Dhananjay Shukla	DBT Postdoctoral Fellow
	Dharmika Kumar	Project Assistant (since Oct. 2009)
<b>Collaborators</b>	Umesh Varshney, IISc, Bangalore	
	Satish Kumar, CCMB, Hyderabad	
	Keykavous Parang, University of Rhode Island, USA	

### Objectives

1. Examine the role of inositol pyrophosphates in eukaryotic cell growth, proliferation and ribosome biogenesis
2. Understand the cellular functions of mammalian inositol hexakisphosphate kinase 1 (IP6K1)
3. Generate tools to detect inositol pyrophosphate mediated protein pyrophosphorylation.

### Summary of the work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)

Inositol pyrophosphates are derivatives of inositol that contain pyrophosphate or diphosphate moieties in addition to monophosphates. They include diphosphoinositol pentakisphosphate (PP-IP<sub>5</sub>, or IP<sub>7</sub>) and bis-diphosphoinositol tetrakisphosphate ([PP]<sub>2</sub>-IP<sub>4</sub> or IP<sub>8</sub>), which are implicated in diverse biological functions, including cell growth, vesicular trafficking, apoptosis, DNA recombination and osmotic regulation. We have earlier demonstrated that 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 and vesicular trafficking. 5PP-IP<sub>5</sub> (IP<sub>7</sub>) is synthesised from inositol hexakisphosphate (IP<sub>6</sub>) and ATP by IP<sub>6</sub> kinases, three isoforms of which are present in mammals

(IP6K1, IP6K2 and IP6K3). IP6K1 knockout mice display low body weight compared with wild type mice, low insulin levels and defective spermatogenesis.

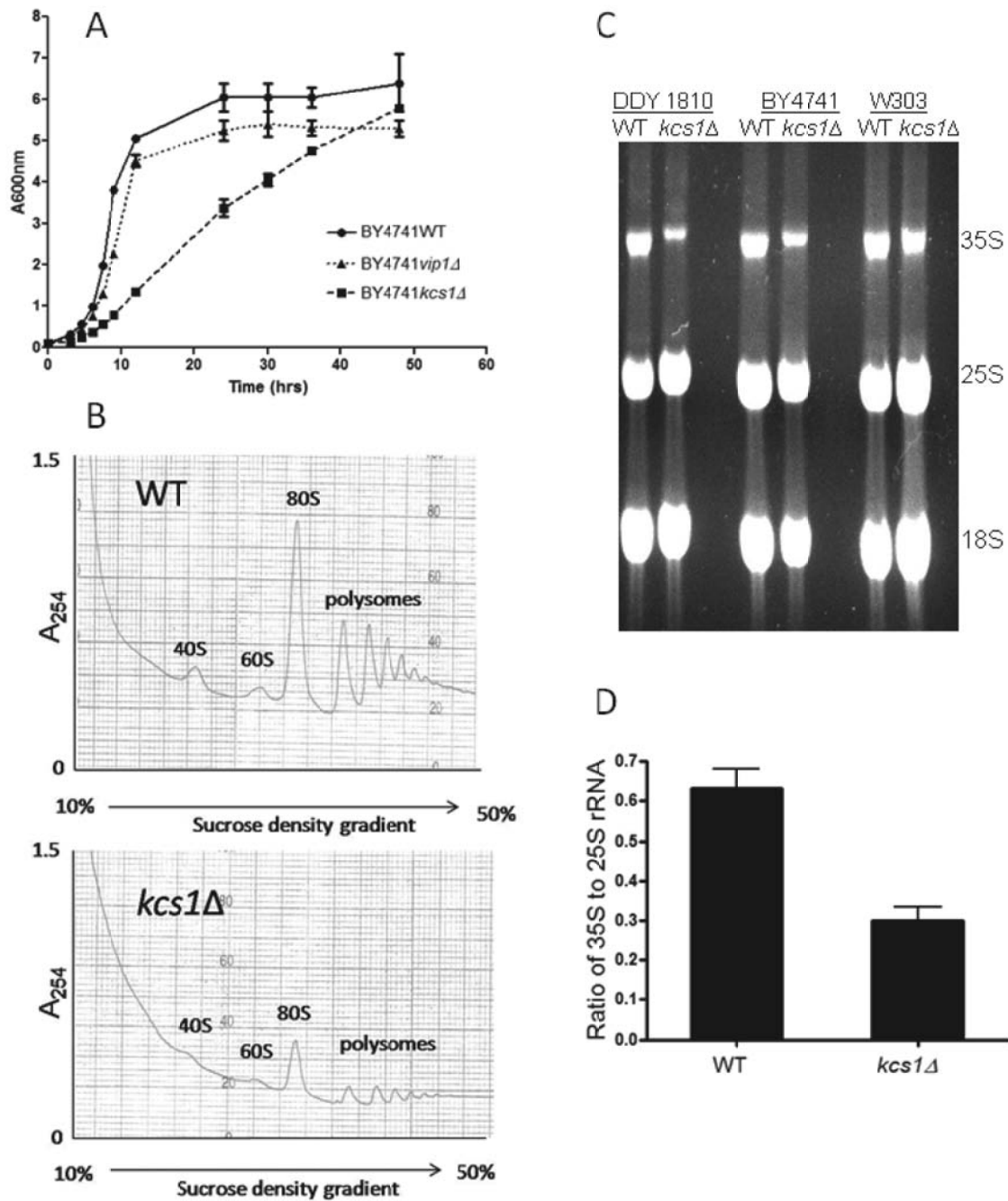
Our aim is to understand the biochemical link between protein pyrophosphorylation and cellular phenomena regulated by inositol pyrophosphates. We utilise *S. cerevisiae*, mammalian cell lines, and knockout mouse strains as model systems to investigate the signalling and metabolic pathways that are altered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

Since IP<sub>7</sub> pyrophosphorylates nucleolar proteins involved in ribosome biogenesis, we examined whether cells with altered IP<sub>7</sub> levels display defects in ribosome synthesis. We observed that *S. cerevisiae* strains lacking the IP<sub>6</sub> kinase *kcs1* display sensitivity towards antibiotics that inhibit ribosome function, and have reduced levels of ribosomes. This observation suggests that protein pyrophosphorylation by IP<sub>7</sub> may control ribosome biogenesis, and thereby regulate cell growth and proliferation.

### Details of progress made in the current reporting year (April 1, 2009 - March 31, 2010)

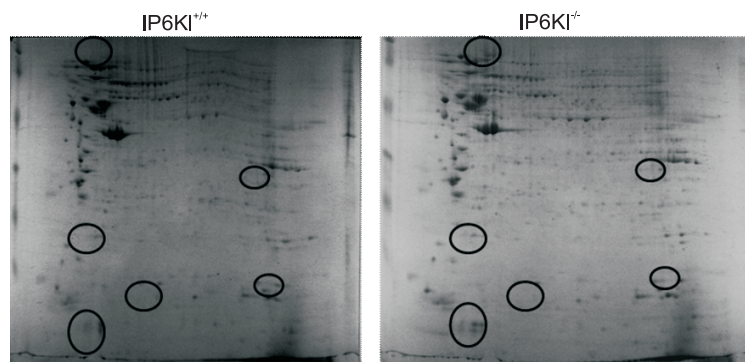
#### Project 1: Regulation of cell proliferation and ribosome biogenesis by IP<sub>7</sub>

In *S. cerevisiae*, IP<sub>6</sub> is converted to IP<sub>7</sub> by *Kcs1*, and the IP<sub>7</sub> kinase *Vip1* converts IP<sub>7</sub> to IP<sub>8</sub>. We carried out a growth rate analysis of wild type,



**Fig. 1:** *S. cerevisiae* lacking IP<sub>7</sub> display a defect in ribosome synthesis.

- A.** Cell growth was monitored by measuring absorbance at 600 nm over the indicated time, starting with a culture at A<sub>600</sub> = 0.1. The doubling time of the different strains calculated from the log phase of growth are wild type 1.7 h, *vip1Δ* 2.1 h and *kcs1Δ* 3 h.
- B.** Extracts from wild type and *kcs1Δ* strains containing equivalent absorbance units (A<sub>254</sub> nm = 10) were resolved on a sucrose density gradient and the relative levels of ribosome subunits, monosomes and polysomes were monitored.
- C.** Total RNA was prepared from wild type (WT) and *kcs1Δ* cells in three different strain backgrounds, and resolved on a 1% agarose gel.
- D.** The intensity of the 35S, 25S and 18S rRNA species was measured and the ratio of 35S to 25S rRNA was calculated. Data shown are the mean ± SEM for three different strains.



**Fig. 2:** Differences in the proteome of wild type and IP6K1 knockout cells. 2D gel electrophoresis of extracts prepared from wild type and IP6K1 knockout mouse embryonic fibroblasts show alteration in the levels of several proteins (marked by circles).

*kcs1Δ* and *vip1Δ* *S. cerevisiae* strains and observed that yeast lacking IP<sub>7</sub> take twice the time to divide compared with wild type yeast, whereas yeast lacking IP<sub>8</sub> show a close to normal growth curve (**Fig. 1A**). This defect in growth rate could be attributed to the lowered levels of ribosomes present in *kcs1Δ* cells (**Fig. 1B**). To further characterize the defect in ribosome levels observed in *kcs1Δ* cells, we are conducting a detailed analysis of the different stages of ribosome synthesis in *kcs1Δ* and wild type yeast. Our data show that the steady state levels of 35S rRNA are lowered by 50% in cells lacking IP<sub>7</sub>, and this defect is observed in three different strain backgrounds (**Fig. 1C, 1D**). Furthermore, our preliminary results show that the rate of incorporation of radiolabelled uracil into rRNA is substantially lowered in *kcs1Δ* cells.

#### Future directions

Our data suggest that RNA polymerase I mediated rDNA transcription is compromised in *kcs1Δ* yeast. We will verify this by measuring the rate of transcription using nuclear run-on assays. We will also examine whether transcription by RNA polymerases II and III is altered in cells lacking IP<sub>7</sub>. In addition, we will monitor the downstream stages of ribosome synthesis, such as rRNA modification and processing, ribosome subunit assembly and cytoplasmic export in *kcs1Δ* yeast.

#### Project 2: Cellular functions of mammalian IP6K1

Our goal is to utilise IP6K1 knockout (KO) mice, as well as mouse embryonic fibroblasts (MEFs) derived from these mice to understand the physiological role of inositol pyrophosphates in

mammals. We have carried out a gene expression microarray analysis of IP6K1 KO MEFs, comparing them with MEFs derived from wild type embryos. The expression of 379 genes is up regulated and 913 genes is down regulated in IP6K1 KO cells. We analysed this data using online pathway analysis tools designed to interpret gene expression microarray data and find that a significant number of genes encoding proteins involved in cell signalling pathways display altered expression in the IP6K1 knockout cells. We are currently conducting RT-PCR analyses to confirm the results of the gene expression microarray. In order to probe changes in protein levels that may be independent of alteration in transcript levels, we have carried out 2D gel analysis of extracts from WT and IP6K1 KO MEFs (**Fig. 2**), and observe a few proteins displaying altered levels in KO cells. These spots will be excised from the gels and the proteins will be identified by mass spectrometry.

We have established a colony of IP6K1 heterozygous mice and are breeding wild type and knockout litter mates for further analysis. Also, we have raised a rabbit polyclonal antibody that specifically recognises IP6K1, but not the other two isoforms IP6K2 and IP6K3.

#### Future directions

IP6K1 specific antibodies will be used to examine the tissue distribution of IP6K1 in mice and its subcellular localisation in MEFs, using tissues from IP6K1 knockout mice as a negative control. The IP<sub>7</sub> regulated signalling pathways uncovered by our gene expression microarray will be investigated in further detail using both MEFs and mice as model systems.

### Project 3: Generation of tools to detect protein pyrophosphorylation

Serine pyrophosphorylation by  $IP_7$  occurs on pre-phosphorylated serine residues present in acidic serine sequences, *i.e.* a stretch of two or more serine residues interspersed with Glu and/or Asp residues. Such sequences occur commonly throughout the proteome of all eukaryotic organisms. We have identified several candidate proteins that may be pyrophosphorylated by  $IP_7$ , but in order to investigate whether they are pyrophosphorylated *in vivo*, we require a reagent to detect pyrophosphoserine residues in cellular proteins. We have obtained synthetic pyrophosphoserine from our collaborator and are currently screening a DNA aptamer library to obtain specific aptamers that recognise pyrophosphoserine, but not phosphoserine.

#### Future directions

Once we obtain an aptamer that specifically recognises pyrophosphoserine, we will use it as a

tool to map the 'pyrophosphoproteome' in *S. cerevisiae* and mammalian cells, starting out by examining proteins known to participate in ribosome synthesis (see Project 1).

#### Publications

1. \*Basu N, Bhandari R, Natarajan VT and Visweswariah SS (2009) Cross talk between receptor guanylyl cyclase C and c-src tyrosine kinase regulates colon cancer cell cytoskeleton. ***Molecular and Cellular Biology*** 29: 5277-5289.
2. Werner JK Jr, Speed T and Bhandari R (2010) Protein pyrophosphorylation by diphosphoinositol pentakisphosphate (InsP7) in Inositol Phosphates and Lipids: Methods and Protocols, Barker CJ (ed.), ***Methods in Molecular Biology*** 645, Humana Press (In press).

*\*Work done elsewhere*



## Laboratory of Plant Microbe Interaction

### Understanding virulence mechanisms of *Xanthomonas* plant pathogens and interaction with host plants

<b>Principal Investigator</b>	Subhadeep Chatterjee	Staff Scientist
<b>Ph D Students</b>	Rikky Rai	Junior Research Fellow
	Sheo Shankar Pandey	Junior Research Fellow
<b>Other Members</b>	Binod Bihari Pradhan	Technical Officer
	Manish Ranjan	Junior Research Fellow (DBT Project)
<b>Collaborators</b>	Sunil K Manna, CDFD, Hyderabad	
	Nashreen S Islam, Tejpur University	

#### 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 role in virulence
4. Role of PAMP in pathogen recognition and plant defense response.

#### Summary of the work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)

*Xanthomonas* group of plant pathogens causes more than 350 different plant diseases. Several of the members infect commercially important plants like-rice, cabbage, citrus and tomato. 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).

Central to the virulence of *Xanthomonas* group of plant pathogen is Diffusible Signaling Factor (DSF), fatty acid like quorum sensing signaling molecule. DSF from different *Xanthomonas* regulates different virulence traits and therefore, these pathogens are able to fine tune virulence to suite different lifestyle. We have earlier made mutants of Xoo and Xcc, which are deficient in DSF production and virulence. We have also made 'Blind' mutants of Xcc, which are now proficient in making signal and overproduce DSF but are unable to sense DSF. These mutations are in the two-component system in the DSF regulon.

Similar to *Xanthomonas*, many animal and plant pathogenic bacteria make various kind of quorum sensing signals (Language), which regulates diverse phenotypes including, biofilm formation, attachment, regulation of production of virulence effectors. These signaling molecules are also involved in interspecies as well as inter strain communication in the environment. Study of the dynamics of cell-cell signaling will lead us to understand the regulatory mechanism of quorum sensing as well as biology of these pathogens.

To understand the role of novel virulence factors, we have earlier screened approximately 1600 transposon induced mutants of Xoo on rice leaves and isolated a mutant (SC2), which is proficient in all virulence associated functions so far reported in *Xanthomonas* group of plant pathogens. Mapping of the mutation in SC2 revealed that it is defective in a gene, which we named as *motA* (motilityA; annotated in the genome as hypothetical protein). *motA* mutants exhibited a hyper motility phenotype as compare to the wild type strain. Complementation of Sc2 mutant with the wild type gene restores motility similar to wild type.

#### Details of the progress made in the current reporting year (April 1, 2009 - March 31, 2010)

##### a) Extracellular cell-cell communication system in plant pathogenic bacteria

To study the dynamics of quorum sensing, we have made an Xcc biosensor in which an eGFP variant which has a short half-life has been cloned downstream from a DSF responsive endoglucanase gene promoter. Wild type Xcc cells containing the DSF biosensor exhibited increased GFP fluorescence as compared to the *rpfF* Xcc mutant (DSF synthase deficient mutant), which exhibited



reduced fluorescence (**Fig. 1A**). The wild type Xcc biosensor also exhibited a density dependent quorum phenotype as revealed by cell normalized fluorescence as compared to the DSF deficient mutant, 8523 (*rpfF* Xcc mutant, **Fig. 1C**).

We have also characterized a Acyl homoserine lactone (AHL) biosensor in the *Pseudomonas syringae* pv. *phaseoli* (B728a; a pathogen of bean which produces AHL signaling molecule). In B728a, the eGFP is placed downstream from the *ahlI ahlR* (AHL synthase and regulator) promoter and exhibited a density dependent GFP fluorescence (**Fig. 1B**) in the wild type background as compare to a *ahlI* mutant strain (BHSL; *ahlI* mutant).

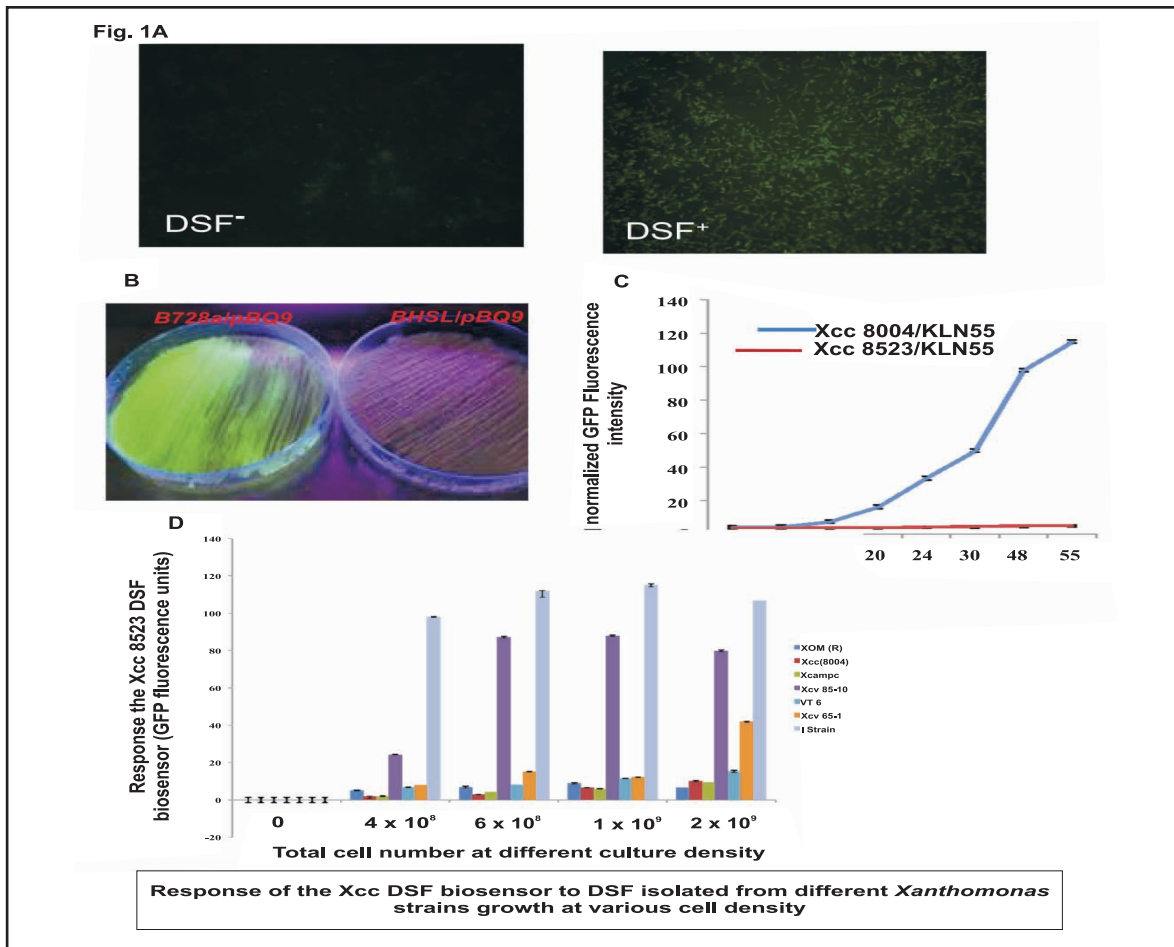
We have also developed a GUS (glucuronidase) based biosensor for detecting DSF production inside the host plant and will be of particularly helpful to see the dynamics of quorum sensing inside the plant host.

To understand the dynamics of cell-cell signaling at a population level, we are using FACS (Fluorescence Activated Cell Sorting). Comparison of quorum sensing in individual cells with respect

to the rest of the cells in the population will reveal whether quorum sensing is uniform and homogeneous at different density. According to the present knowledge in the field of quorum sensing, it has been proposed that quorum sensing is density dependent, as the density increases, which is dependent on growth time, all the cells in a fixed space will respond depending on different thresholds of quorum molecules in that space, which is mainly influenced by total number of cells at that particular growth stage. Higher density will result in production of more quorum molecule and therefore the intensity of the quorum response will be higher as compared to a low density culture. We propose to test this theory by using our biosensors, to see how single cells in a population behaves to quorum and whether the classical quorum sensing response seen (**Fig. 1C**) is also true in the single cell level in a constant volume or space by varying time.

#### b) Role of DSF in virulence of *Xanthomonas*

As *Xanthomonas* group of plant pathogens are very diverse in terms of colonization in different host, fine-tuning of virulence is required for the co-



ordination of virulence factor synthesis. To understand, how DSF can regulate different traits in *Xanthomonas*, we have used the Xcc DSF biosensor 8523 (which does not produce its own DSF but can sense any DSF like molecules). The Xcc DSF biosensor exhibited differential response with DSF isolated at various cell density (**Fig. 1D**) from different strains of *Xanthomonas*- *X. oryzae* pv. *oryzae* (Xom; Xoo), *X. oryzae* pv. *oryzicola* (YT6; Xcola); *X. campestris* pv. *campestris* (Xcc), *X. axonopodis* pv. *citri* (Xcampc); *X. campestris* pv. *vesicatoria* (Xcv85-10, Xcv65-1; pathogens of pepper and I strain, a pathogen of Tomato). Interestingly, the Xcc biosensor responded better with the Xcv DSF as compare to DSF from self or from other *Xanthomonas* strains. These results indicated that DSF from various *Xanthomonas* has different characteristics in terms of regulation of production of virulence associated functions.

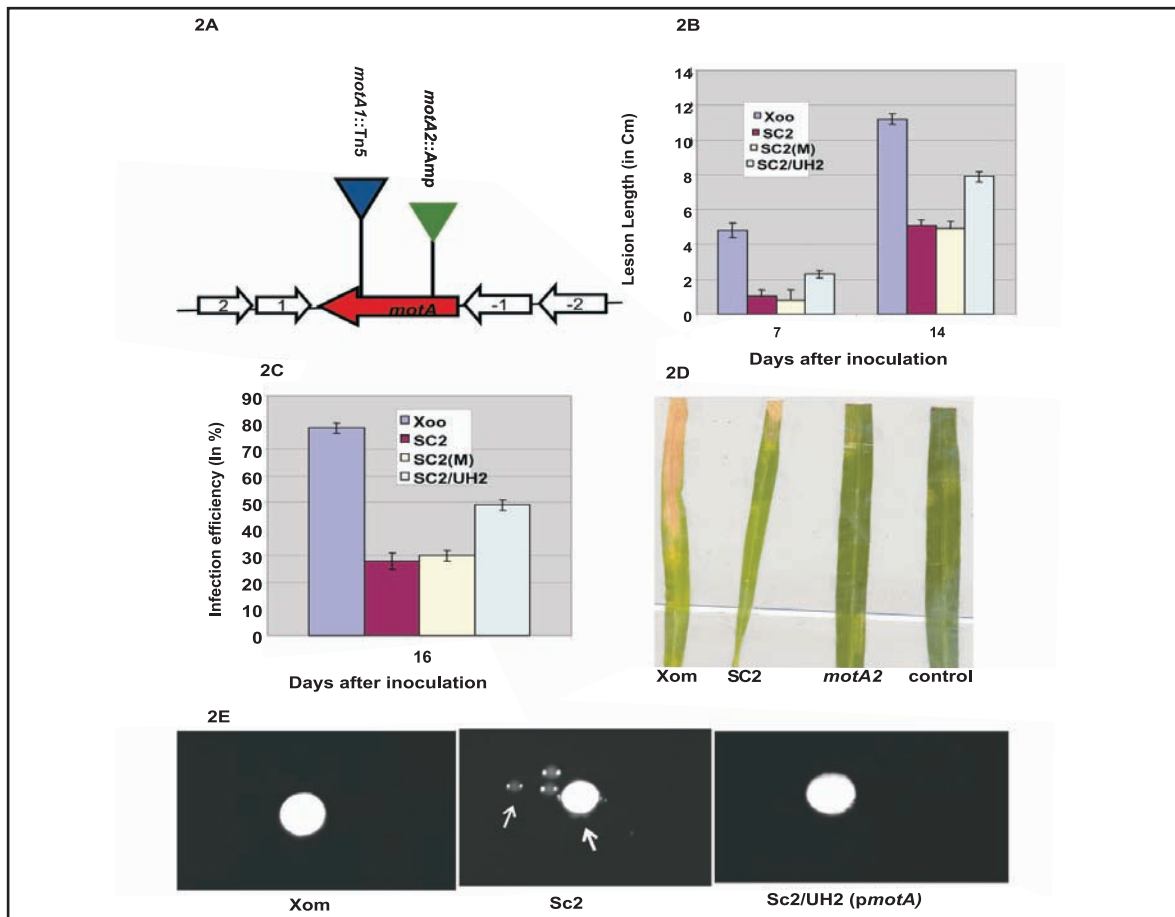
In future, we want to do phenocopy experiments with DSF switching, to see how DSF from various strains cross complements, which will elucidate aspects of inter species and inter strain

communication. We also wanted to do hetrologous genetic complementation tests, by expressing DSF synthase gene(s) in the DSF deficient mutants of these different *Xanthomonas* species.

We have also initiated functional genetic screens and micro array based approach to understand the DSF regulon in different *Xanthomonas* species.

### c) Understanding the mechanism of biofilm formation and motility and virulence

Biofilm formation and motility has been implicated in the virulence of *Xanthomonas* group of plant pathogens. Earlier, we have isolated a novel virulence deficient mutant named SC2. The mutation is in a gene which we have designated as *motA*. The MotA sequence does not exhibit any homology to known proteins in the database. Sequence analysis revealed that *motA* is located in the genomic region of Xoo which is rich in transposable elements (ORF1, 2, -1, -2; **Fig. 2A**). Presence of transposable elements flanking *motA*, indicates that it might be acquired by Xoo by horizontal gene transfer. The only sequence feature



which prompted us was the presence of RHS repeats. However, knockouts in other RHS homologs in Xcc, did not effect virulence or motility phenotype. Phenotypic analysis of separate insertions in the *motA* gene revealed that the virulence deficiency and the hyper motility phenotype is due to the transposon insertion and can be complemented by the wild type gene in trans (**Fig. 2A**). Virulence analysis by wound infection also indicated (**Fig. 2B and 2D**) that, *motA* is required for optimum virulence of Xoo. Epiphytic mode of infection (Natural mode of entry of the pathogen through pores called as hydathodes located at the tip of the leaves) indicated that, *motA* is required for natural mode of infection (**Fig. 2C**). These results and several plate phenotypes indicated that *motA* is a novel adhesin of *Xanthomonas* and hypermotility of the *motA* mutants is due to reduced stickiness on various surfaces. To see whether *motA* affects other forms of motility like twitching, which involves type IV pili, we did a twitching assay on filter disc. Formation of satellite colonies away from the solid disc

indicated bacterial migration from the solid support (**Fig. 2E**). These results indicated that *motA* affects not only flagella mediated swimming motility but also effects twitching motility.

This will be the first report of *motA* like gene as a virulence factor, which is involved in attachment and probably biofilm formation in any bacteria.

In future, we are going to study the localization and expression of MotA, as well as more detailed biofilm assays to see, at what stage, MotA is required for the biofilm formation.

### Publications

1. \*Chatterjee S, Killiny S, Almeida RPP and Lindow SE (2010) Role of cyclic di-GMP in *Xylella fastidiosa* biofilm formation, plant virulence and insect transmission. ***Molecular Plant Microbe Interactions*** (In press).

\*Work done elsewhere

# **Other Scientific Services / Facilities**



## Bioinformatics

<b>In-charge</b>	HA Nagarajaram	Staff Scientist (since Jan. 2010)
	M Kavita Rao	Staff Scientist (till Dec. 2009)
<b>Other Members</b>	M N Pavan	Technical Officer (till June 2009)
	R Chandra Mohan	Technical Officer
	Prashanthi Katta	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 develop computer applications for the automation of Institute activities
5. To coordinate the procurement process of workstations, PCs, laptops, printers, other peripheral devices and software required
6. To secure the CDFD network from security threats
7. To integrate Institute's network into National and International grid computing networks.

### Summary of work done until the beginning of this reporting year (April 1, 2008 - March 31, 2009)

- Data Center in the new campus was retrofitted with deployment of various services such as E-mail, internet, web. Internet bandwidth was upgraded to 4Mbps from existing 2Mbps. The network infrastructure was implemented in both Laboratory building and Administrative building and the two buildings were interconnected with 2Mbps point to point leased circuit.
- Activities related to installation, administration and maintenance of servers which provide various services, databases and computational jobs were undertaken. A comprehensive PC Annual maintenance contract was awarded to a private vendor.
- An online LAN based examination was facilitated for the posts of Research Scholars as well as for Project Staff.

### Details of progress made in the current reporting year (April 1, 2009 - March 31, 2010)

E-mail, Internet, web services have been provided with enhanced functionalities.

High-end PCs (40), workstations (10), laptops (5), scanner and printers were procured and installed. A comprehensive PC Annual Maintenance Contract awarded to a private vendor was also renewed.

Symantec Endpoint security 11.0 Antivirus - 100 licenses were procured in addition to the existing 150 licenses in order to secure the newly procured PCs and Firewall license is renewed.

There was a proposal from National Informatics Centre to implement National Knowledge Network (NKN) that connects several research and educational institutions across the country with a backbone of 10Gbps to enable sharing of knowledge, specialized resources and also to foster collaborations among research groups. The process of connecting CDFD network to NKN was initiated which involved proper planning for the network migration, physical installation and configuration of the router, setting up of a separate UPS. Physical cable connectivity was completed vide the MuX equipment, Battery bank and router to integrate institute's network into the prestigious National Knowledge Network. To implement smooth migration with minimum downtime, necessary precautionary measures were taken. These measures included configuring the proxy server, configuring and testing of NKN clients for various services such as mails, online library access etc., testing the connectivity between the two buildings for intranet services between the buildings such as online stores software and online salary package. With these ground preparations, CDFD was ready to migrate to NKN network.



## Instrumentation

<b>Head</b>	Raghavendrachar J	Staff Scientist
<b>Other Members</b>	R N Mishra	Technical Officer I
	S D Varalaxmi	Technical Officer I
	M Laxman	Technical Assistant
	Sathyanarayana	Technical Assistant
	N P Sharma	Junior Assistant II (till Jan.2010)
	Praneetha	Junior Assistant I

### Objectives

To maintain, repair and service all the equipment in CDFD. 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, 2008 - March 31, 2009)

We had performed over 37 new installations of various equipment, like CO<sub>2</sub> Incubators, Gel Documentation Systems, PCR Machines, Water Purification System, Nanodrop Spectrophotometers, Refrigerated Table Top Centrifuges, Shaking Water baths, Orbital Shaker, Tissue Homogenizer, -86°C Freezer, -20°C Freezers, Refrigerators, Micro centrifuges, Electrophoresis apparatus, etc.

We had also completed 246 work orders for repair and maintenance of various laboratory equipments. We were actively involved in un-installation, packing, un-packing and re-installation of equipments from Nacharam to Nampally Campus. We were involved in planning and setting up the laboratory and procurement of additional laboratory tables for Nampally campus.

### Details of progress made in the current reporting year (April 1, 2009 - March 31, 2010)

We have set up the facilities for major instruments like Bruker X-Ray Diffraction system, Bruker Maldi TOF/TOF MS, BD FACSVantage SE Flowcytometer, Carl Zeiss Confocal Microscope, installed the equipment and set up standard operating

procedures. We have set up the out sourcing facility, installed all the equipment like DNA Sequencers, RT-PCR, Biacore SPR System, dHPLC, HPLC, CD Spectro-polarimeter, Karyotyping System in Diagnostics, Genetic Analyzer and GC-MS. We have also installed various instruments like High Speed Centrifuges of Sorvall and Beckman Coulter, Ultra centrifuge of Beckman Coulter, Refrigerated Incubator Shakers, Gel Documentation Systems, set up Tissue Culture Facility and installed Laminar Flow hoods and CO<sub>2</sub> incubators. We have also set up H1N1 testing laboratory and have installed all microscopes, FPLCs, LPLCs, Nanodrop Spectrophotometers, etc. We are updating with newer technologies and helping the scientists in procuring better equipment at reasonable costs.

During the year 2009-10, we have installed 94 new equipments and completed 312 work orders for repair and maintenance of various laboratory equipments. In addition to shifting of equipments, we were involved in getting the laboratory tables dismantled at Nacharam and have installed few tables on I floor of Tuljaguda campus and got the rest stored at Gandipet.

In addition, we were involved in organizing the audio-visual requirements for presentations in various seminars, lectures and workshops, Foundation Day lectures, Distinguished Scientist Lectures held in CDFD both at Nampally and Gandipet auditorium. We were actively involved in conducting the CDFD-CCMB Retreat held for two days at Gandipet. We 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.

# **Publications**



## Research Papers Published in 2009

1. Achary MS and Nagarajaram HA (2009) Effects of Disease Causing Mutations on the essential Motions in proteins. ***Journal of Biomolecular Structure and Dynamics*** 26:609-624.
2. Angalena R, Chaudhary A, Bashyam MD and Dalal A (2009) Hemoglobin D (Iran) masquerading as hemoglobin E: An interesting case report. ***Newsletter of Genetics Chapter of Indian Academy of Pediatrics*** 2:11-12.
3. Arunkumar KP, Mita K and Nagaraju J (2009) Silkworm Z chromosome is enriched in testis-specific genes. ***Genetics*** 182: 493-501.
4. Ahmed N, Ehtesham NZ and Hasnain SE (2009) Ancestral *Mycobacterium tuberculosis* genotypes in India: implications for TB control programmes. ***Infection, Genetics and Evolution*** 9:142-146.
5. Bashyam MD (2009) Nonsense-mediated decay: linking a basic cellular process to human disease. ***Expert Review of Molecular Diagnostics*** 9:299-303.
6. Bashyam MD (2009) Studies on nonsense mediated decay reveal novel therapeutic options for genetic diseases. ***Recent Patents on DNA & Gene Sequences*** 3:7-15.
7. Basu D, Khare G, Singh S, Tyagi A, Khosla S and Mande SC (2009) A novel nucleoid-associated protein of *Mycobacterium tuberculosis* is a sequence homolog of GroEL. ***Nucleic Acids Research*** 37:4944-4954.
8. \*Basu N, Bhandari R, Natarajan VT and Visweswariah SS (2009) Cross talk between receptor guanylyl cyclase C and c-src tyrosine kinase regulates colon cancer cell cytoskeleton. ***Molecular and Cellular Biology*** 29: 5277-5289.
9. Beech CJ, Nagaraju J, Vasani SS, Rose RI, Othman RY, Pillai V and Saraswathy TS (on behalf of the working groups) (2009) Risk analysis of a hypothetical open field release of a self-limiting transgenic *Aedes aegypti* mosquito strain to combat dengue. ***Asia Pacific Journal of Molecular Biology and Biotechnology*** 17: 99-111.
10. Beech CJ, Vasani SS, Quinlan MM, Capurro ML, Alphey L, Bayard V, Bouari M, McLeod MC, Kittayapong P, Lavery JV, Lim HL, Marrelli MT, Nagaraju J, Ombongi K, Othman RY, Pillai V, Ramsey J, Reuben R, Rose RI, Tyagi BK and Mumford J (2009) Deployment of innovative genetic vector control strategies: Progress on regulatory and biosafety aspects, capacity building and development of best-practice guidance. ***Asia Pacific Journal of Molecular Biology and Biotechnology*** 17: 75-85.
11. Bhate RH and Ramasarma T (2009) Evidence for H<sub>2</sub>O<sub>2</sub> as the product of reduction of oxygen by alternative oxidase in mitochondria from potato tubers. ***Archives of Biochemistry and Biophysics*** 486: 165-169.
12. Bose JS, Gangan V, Jain SK and Manna SK (2009) Downregulation of inflammatory responses by novel caffeic acid ester derivative by inhibiting NF-kappaB. ***Journal of Clinical Immunology*** 29: 90-98.
13. Bose JS, Gangan V, Jain SK and Manna SK (2009) Novel caffeic acid ester derivative induces apoptosis by expressing FasL and downregulating NF-kappaB: Potentiation of cell death mediated by chemotherapeutic agents. ***Journal of Cellular Physiology*** 218:653-662.
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15. Dalal A and Mehrotra RN (2009) Hypertrichosis, hyperkeratosis and mental retardation syndrome: further delineation of phenotype. ***Clinical Dysmorphology*** 18: 83-84.
16. Dalal A (2009) Stem cell therapy: Current status. ***Newsletter of Genetics Chapter of Indian Academy of Pediatrics*** 2:5-7.
17. Dutta D, Bandyopadhyay K, Datta AB, Sardesai AA and Parrack P (2009) Properties of HflX, an enigmatic protein from *Escherichia coli*. ***Journal of Bacteriology*** 191: 2307-2314.
18. Gangadharan C, Thoh M and Manna SK (2009) Inhibition of constitutive activity of nuclear transcription factor kappaB sensitizes doxorubicin-resistant cells to apoptosis. ***Journal of Cellular Biochemistry*** 107: 203-213.
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24. Kumar MS, Ramachandran A, Hasnain SE and Bashyam MD (2009) Octamer and heat shock elements regulate transcription from the AcMNPV polyhedrin gene promoter. ***Archives of Virology*** 154: 445-456.
25. Kumar R, Tamhankar PM, Panigrahi I, Dalal A and Agarwal S (2009) A novel beta-globin mutation (HBB:c.107A>G; or codon 35 beta (A→G)) at alpha-beta chain interfaces. ***Annals of Hematology*** 88: 1269-1271.
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27. Kumar S, Farhana A and Hasnain SE (2009) In-vitro helix opening of *M. tuberculosis oriC* by DnaA occurs at precise location and is inhibited by IciA like protein. ***PLoS One***4(1): e4139.
28. \*Lee SJ, Trostel A, Le P, Harinarayanan R, Fitzgerald PC and Adhya S (2009) Cellular stress created by intermediary metabolite imbalances. ***Proceedings of the National Academy of Sciences of the USA*** 106: 19515-19520.
29. Manimaran P, Hegde SR and Mande SC (2009) Prediction of conditional gene essentiality through graph theoretical analysis of genome-wide functional linkages. ***Molecular Biosystems*** 5: 1936- 1942.
30. Manna SK and Gangadharan C (2009) Decrease in RelA phosphorylation by inhibiting protein kinase A induces cell death in NF-kappaB-expressing and drug-resistant tumor cells. ***Molecular Immunology*** 46: 1340-1350.
31. Mudunuri SB, Rao AP, Pallamsetty S, Mishra P and Nagarajaram HA (2009) VMD: Viral Microsatellite Database - A Comprehensive Resource for All Viral Microsatellites. ***Journal of Computer Science and Systems Biology*** 22: 283-000. doi:10.4172/jcsb.1000043: 001-004.
32. Nair S, Ramaswamy PA, Ghosh S, Joshi DC, Pathak N, Siddiqui I, Sharma P, Hasnain SE, Mande SC and Mukhopadhyay S (2009) The PPE18 of *Mycobacterium tuberculosis* interacts with TLR2 and activates IL-10 induction in macrophage. ***Journal of Immunology*** 183: 6269- 6281.
33. Nandineni MR and Vedanayagam JP (2009) Selective enrichment of human DNA from non-human DNAs for DNA typing of decomposed skeletal remains (2009) ***Forensic Science International: Genetics Supplement Series*** 2: 520-521.
34. Pani B, Ranjan A and Sen R (2009) Interaction surface of bacteriophage P4 protein Psi required for the complex formation with the transcription terminator Rho. ***Journal of Molecular Biology*** 389: 647-660.
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36. Raghavendra PB, Pathak N and Manna SK (2009) Novel role of thiazolidine derivatives in inducing cell death through Myc-Max, Akt, FKHR, and FasL pathway. ***Biochemical Pharmacology*** 78: 495-503.
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- \*Work done elsewhere.

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43. Gangadharan C, Thoh M and Manna SK (2010) Late phase activation of nuclear transcription factor kappaB by doxorubicin is mediated by interleukin-8 and induction of apoptosis via FasL. **Breast Cancer Research and Treatment** 120: 671-683.
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45. Khamurai S, Ranjan A, Pani B, Sen R and Sen U (2010) Crystallization and preliminary X-Ray analysis of Psu, an inhibitor of bacterial transcription terminator Rho. **Acta Crystallographica Section F Structural Biology and Crystallization Communication** 66: 204-206.
46. Kumar P, Joshi DC, Akif Mohd, Akhter Y, Hasnain SE and Mande SC (2010) Mapping conformational transitions in cyclic AMP receptor protein: crystal structure and normal-mode analysis of *Mycobacterium tuberculosis* apo-cAMP receptor protein. **Biophysical Journal** 98: 305- 314.
47. Mudunuri SB, Rao AP, Mishra P and Nagarajaram HA (2010) Comparative analysis of microsatellite detecting software: A significant variation in results and influence of parameters. **Proceedings of International Symposium on Biocomputing**, (ISB 2010), Kerala, February 15-17, 2010. (Link to ACM Digital Library)
48. Nisha CK, Ranjan A, Kalyani S, Wal M and Sen R (2010) A bacterial transcription terminator with inefficient molecular motor action but with a robust transcription termination function. **Journal of Molecular Biology** 395: 966-982.
49. Thoh M, Kumar P, Nagarajaram HA and Manna SK (2010) Azadirachtin interacts with the TNF binding domain of its receptors and inhibits TNF-induced biological responses. **Journal of Biological Chemistry** 285: 5888-5895.

### In Press (as on 31st March 2010)

50. Agarwal S, Tamhankar PM, Kumar R and Dalal A (2010) Clinical and haematological features in a compound heterozygote (HBB:c.92 + 5G > C/HBB:c.93-2A > C) case of thalassaemia major. **International Journal of Laboratory Hematology**.
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53. Bose S, Sakhuja P, Bezawada L, Agarwal AK, Kazim SN, Khan LA, Sarin SK and Ramakrishna G (2010) Hepatocellular carcinoma with persistent hepatitis B virus infection shows unusual downregulation of Ras expression and differential response to Ras mediated signaling. ***Journal of Gastroenterology and Hepatology***.
54. \*Chatterjee S, Killiny S, Almeida RPP and Lindow SE (2010) Role of cyclic di-GMP in *Xylella fastidiosa* biofilm formation, plant virulence and insect transmission. ***Molecular Plant Microbe Interactions***.
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62. Rajita P and Dalal A (2010) Partial monosomy 7q: case report. ***Indian Pediatrics***.
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\*Work done elsewhere

## Other Publications

1. Gowrishankar J (2009) Regulation of genetically modified organisms: has the time come to amend the law? ***Current Science*** 96: 1574.
2. Gowrishankar J (2009) Swine flu: perhaps to do nothing is the best strategy for India? ***The Hindu***, 2 July 2009.
3. Gowrishankar J (2009) H1N1: Option for India. ***Biotech News*** (2009) 4: 44-47.
4. Kaur R (2009) Review of: Lilavati's daughters: The women scientists of India. Rohini Godbole and Ram Ramaswamy (eds). ***Current Science*** 96: 1137-1138.
5. Gowrishankar J (2010) Extramural research funding by institutions that undertake intramural research. ***Current Science*** 98: 478.

## Patents (2009-10)

### A. Patents issued:

1. Hasnain S E *et al.* A method of diagnosing tuberculosis. European Patent 1779116, granted on 3 June, 2009.
2. Hasnain S E *et al.* A method of diagnosing tuberculosis. Indian Patent 234890, granted on 19 June, 2009.
3. Hasnain S E *et al.* A method of diagnosing tuberculosis. USA Patent 7575877 B2 18 August, 2009.

### B. Patent applications filed:

1. Nagarajaram HA and Shamim MTA. Fold-wise classification of proteins. USPTO Patent Application No. 20100057419.
2. Mukhopadhyay S, Bhat K. H and Khan N. Inhibitors of Rv0256c. USPTO Patent Application No. 20100129809.



# **Human Resource Development**



## **Ph.D. Program**

For our Ph.D. program we invite 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, we especially encourage 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 Ph.D. program of Manipal Academy of Higher Education or University of Hyderabad.

The eligibility for the program is a Masters degree in any branch of Science, Technology, Medicine or Agriculture. Candidates must have cleared the CSIR/UGC/ICMR/ICAR NET for JRF. Those who have appeared, 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.

Currently we have 73 Research Scholars working for their doctorates in different areas of research. In the reporting year 4 of our Research Scholars have completed Ph.D. and are pursuing careers in science elsewhere in India or abroad.

## **Postdoctoral Program**

In addition to our JRF program, we also carry 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**

In the past couple of years, CDFD has restricted admission to the summer training program only to those students who are supported either by the Indian Academy of Sciences, Bangalore or the Jawaharlal Nehru Centre for Advanced Scientific Research, Bangalore or the Kishore Vigyanic Protsahan Yojana, New Delhi. In the reporting year 27 students received their summer training at CDFD.

## **Training for students from BITS, Pilani**

CDFD has formalized 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 hand-on experience in modern biology. In the reporting year 4 students were given the opportunity to avail training under this programme.





# **Lectures, Meetings, Workshops and Important Events**



- ❖ **Dr Amit Singh**, University of Alabama at Birmingham, USA delivered a lecture on “*Mycobacterium tuberculosis* Redox Sensing Mechanisms: Linking Environmental Cues and Virulence Pathways” (06.04.2009)
- ❖ **Dr Alok Bhattacharya**, School of Life Sciences, JNU, New Delhi delivered a lecture on “Comparative Genomics of Mycobacteria and Development of Novel Algorithms for Identification Polymorphisms and Phylogeny” (06.05.2009)
- ❖ **Dr M.S.Reddy**, Yale University School of Medicine, New Haven, USA delivered a lecture on “Post-translational Modifications in the Control of Cell Cycle, Apoptosis and Cancer” (08.07.2010)
- ❖ **Dr Radha Chauhan**, The Rockefeller University, New York delivered a lecture on “The Central Channel of Nuclear Pore Complex” (20.08.09)
- ❖ **Dr Rohit Joshi**, Columbia University Medical Center, New York, USA delivered a lecture on “Molecular Basis of Hox Specificity” (09.09.2009)
- ❖ **Dr Sulagna Banerjee**, Madras Institute of Technology, Chennai delivered a lecture on “Genomics to Functional Glycomics: The Story of the Protists” (10.09.2009)
- ❖ **Hindi Day celebrations** were held at CDFD Tuljaguda Complex (14.09.2009)
- ❖ **Dr Marimuthu Krishnan**, Oak Ridge National Lab, USA delivered a lecture on “Unveiling Functional Protein Motions with Computer Simulations: An Atomic-level Understanding of Protein Functions” (16.09.2009)
- ❖ **Dr Raja Jothi**, National Institute of Health, USA delivered a lecture on “Systems Biology and Epigenetics of Gene Regulation” (22.10.2009)
- ❖ **Dr Manas Santra**, University of Massachusetts Medical School, USA delivered a lecture on “Identification of FBXO31 as a Novel G1/S Checkpoint Regulator in DNA Damage Pathway” (05.11.2009)
- ❖ **Dr Anindya Dutta**, University of Virginia Health Sciences Center, USA delivered a lecture on “Re-replication, Genomic Instability and Cancers” (06.11.2009)
- ❖ **Dr Kiran Kondabagil**, The Catholic University of America, Washington DC, USA delivered a lecture on “Viruses Start Your Engines! Phage T4 DNA Packaging Nanomotor: Structure, Function and Mechanism” (09.11.2009)
- ❖ **Dr V Sabareesh**, Jawaharlal Nehru Centre for Advanced Scientific Research, Bangalore delivered a lecture on “Mass Spectrometry for Peptidomics and Proteomics” (27.11.2009)
- ❖ A three member delegation from University of Nebraska Medical Centre visited CDFD and interacted with faculty (1.12.09)
- ❖ **Dr Sarath Chandra Janga**, Cambridge University, UK delivered a lecture on “Employing Network-based Approaches to Understand the Design Principles of Biological Systems” (03.12.2009)
- ❖ **Prof Daniel L Hartl**, Harvard University, USA delivered a lecture on “Selection without Adaptation: Finicky Proteins and Compensatory Mutations” (04.12.2009)
- ❖ **Prof Mike Turner**, University of Glasgow, UK delivered a lecture on “Variation Amongst Pathogen Drives Disease Outcome: A Case Study on African Trypanosomes” (07.12.2009)
- ❖ **Prof Max E Gottesman**, Institute of Cancer Research, Columbia University, USA delivered a lecture on “Regulation of Transcription Termination in *E. coli*” (15.12.2009)
- ❖ MoU signed between Life Science Incubator-IKP Knowledge Park (LSI-IKP), Hyderabad and CDFD for commercialization of technologies and products which have been developed in-house (16.12.09)
- ❖ **Dr Subhajyoti De**, Cambridge University, UK delivered a lecture on “The impact of Genomic Neighborhood on Transcriptome Evolution” (05.01.2010)
- ❖ **Prof Kazuei Mita**, National Institute of Agrobiological Sciences, Japan delivered a lecture on “Genome Analysis of Lepidopteran Model Insect, *Bombyx mori* and Full-length cDNA Information for Annotation of Silkworm Genome” (09.01.2010)
- ❖ **Dr Alexey Murzin**, MRC Lab of Molecular Biology, Cambridge, UK delivered a lecture on “Metamorphic Proteins” (15.01.2010)

- ❖ **Prof Charles J Dorman**, University of Dublin, Ireland delivered a lecture on “Local and Global Gene Regulatory Mechanisms in Gram-negative Bacteria” ( 20.01.2010)
- ❖ **Dr David Sherman**, Seattle Biomedical Research Institute, USA delivered a lecture on “Environmental Response in *M. tuberculosis*” (01.02. 2010)
- ❖ **Prof Nasreen S Islam**, Tejpur University, Assam delivered a lecture on “Polymer Anchored Peroxometallates as Bio-inspired Oxidation Catalysts and Biochemically Active Agents” (04.02.2010)
- ❖ A team of forty six Police Officers and experts from different countries visited the Centre as part of the training program conducted by National Crime Records Bureau, New Delhi (04.02.2010)
- ❖ **Dr Narottam Acharya**, University of Texas Medical Branch, Galveston, USA delivered a lecture on “Molecular Dissection of DNA Replication and Trans-lesion DNA Synthesis in Eukaryotes” (19.02.2010)
- ❖ An Academic Retreat Program was organized jointly between CCMB and CDFD at the CDFD, Gandipet campus (5.03.10 - 6.03.10)
- ❖ **Dr Akira Ishihama**, Hosei University, Japan delivered a lecture on “Prokaryotic Genome Regulation: Multi-factor Promoters, Multi-target Regulators and Multi-factor Networks” (16.03.2010)

# **Senior Staff and Officers of CDFD**





## **SCIENTIFIC GROUP LEADERS (FACULTY)**

Dr J Gowrishankar

Dr J Nagaraju

Dr Shekhar C Mande

Dr Murali D Bashyam

Dr Sunil Kumar Manna

Dr H A Nagarajaram

Dr Akash Ranjan

Dr Sangita Mukhopadhyay

Dr Gayatri Ramakrishna

Dr Sanjeev Khosla

Dr Ranjan Sen

Dr Rupinder Kaur

Dr Madhusudan R Nandineni

Dr Ashwin Dalal

Dr Abhijit A Sardesai

Dr Rashna Bhandari

Dr R Harinarayanan

Dr Subhadeep Chatterjee

## **ADJUNCT FACULTY**

Dr E A Siddiq

Prof T Ramasarma

Prof Anuradha Lohia

## **OTHER GROUP LEADERS**

Mr Raghavendrachar J

Dr P Janila (until Oct. 2009)

Ms M Kavita Rao

## **SENIOR ADMINISTRATIVE STAFF**

Mr K Ananda Rao

Mr J Sanjeev Rao



# **Deputations abroad of CDFD Personnel**



## SCIENTISTS AND STAFF

- ❖ **Dr M D Bashyam** (USA) attended the 100th annual meeting of the American Association for Cancer Research at Denver, Colorado, 13-25 April 2009
- ❖ **Dr J Gowrishankar** (United Kingdom and France) attended the meeting of Wellcome Trust-DBT Alliance in London, visited Wellcome Trust's Hinxton Campus in Cambridge and participated in the meeting of the Scientific Council of the Indo-French Council for Promotion of Advanced Research in Montpellier, 11-26 May 2009
- ❖ **Dr Rashna Bhandari** (United Kingdom) attended an interview for the Wellcome Trust-DBT Senior Research Fellowship and as a guest of Dr. Adolfo Saiardi, Collaborator at University College, London, 11-16 May 2009
- ❖ **Dr N Madhusudan Reddy** (Germany) availed the Max Planck India Fellowship to carry out research in Prof. Mark Stoneking's laboratory at the Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology, Leipzig, 15 June to 27 July 2009
- ❖ **Dr Ranjan Sen** (USA) attended the FASEB Summer Conference "Mechanism & Regulation of Prokaryotic Transcription" at Vermont, 20-27 June 2009
- ❖ **Dr M D Bashyam** (USA) attended the courses "The Principles and Practice of Cancer Prevention and Control Course" and "Molecular Prevention Course" at National Cancer Institute, Maryland, 6 July to 8 August 2009
- ❖ **Dr Shekhar C Mande** (Russia) visited collaborator Dr. Vsevolod J Makeev and attended the "Moscow Conference on Computational Molecular Biology 2009" at Moscow, 20 July to 6 August 2009
- ❖ **Ms. Muthu Lakshmi** (Japan) visited the laboratory of Prof. Toshiki Tamura, National Institute of Agrobiological Science for specialized training on "Microinjection of Silkworm Eggs to Construct Transgenic Strains" at Tsukuba, Ibaraki, 31 July to 31 October 2009
- ❖ **Dr J Gowrishankar** (USA) attended the Burgess Symposium and made a poster presentation on his group's research work in the "2009 Molecular Genetics of Bacteria and Phages Meeting" at University of Wisconsin, Madison, Wisconsin and carried out scientific discussions with the laboratory of Prof. Laszlo Csonka at Purdue University, West Lafayette, Indiana, 03-09 August 2009
- ❖ **Dr J Nagaraju** (Greece) attended the 8th International Workshop on "Molecular Biology and Genetics of the Lepidoptera" at Crete, 21-30 August 2009
- ❖ **Dr Rashna Bhandari** (France) attended the 34th European Symposium on "Hormones and Cell Regulation" at Obernai, Alsace, France, 13-19 September 2009
- ❖ **Dr N Madhusudan Reddy** (Argentina) attended the 23rd World Congress of the International Society for Forensic Genetics and presented a poster on his group's research work at Buenos Aires, 15-18 September 2009
- ❖ **Dr J Nagaraju** (China) attended the "International Symposium on *Bombyx mori* Functional Genomics and Modern Silk Road" at Chongqing, 17-27 October 2009
- ❖ **Dr Gayatri Ramakrishna** (Japan) attended the 3rd AIST-DBT Bilateral Workshop and discussed various aspects of the collaborative project with Dr. Renu Wadhwa, Leader of Cell Engineering Session at Tsukuba, 24-29 October 2009
- ❖ **Dr J Nagaraju** (Austria) participated in the 1st technical meeting on "Development and Evaluation of Improved Strains of Insect Pests of SIT" at Vienna, 14-21 November 2009



- ❖ **Dr J Gowrishankar** (Japan) visited the National Institute of Genetics, Mishima for discussions with the group of Prof. Nobuo Shimamoto, delivered an invited talk, and chaired the Indian delegation of the Bureau of Indian Standards in the second plenary meeting of ISO/TC 34/SC 16 “Horizontal methods of molecular biomarker analysis” at Tokyo. He also visited the Hosei University in Tokyo for discussions with the group of Prof. Akira Ishihama and delivered an invited lecture, 08-12 February 2010
- ❖ **Dr M D Bashyam** (Jordan) attended the 2<sup>nd</sup> Annual American Association for Cancer Research Dead Sea International Conference on “Advances in Cancer Research: From the Laboratory to the Clinic” at Dead Sea, 07-10 March 2010
- ❖ **Dr Rupinder Kaur** (USA) presented her work in the 10<sup>th</sup> American Society for Microbiology Conference on Candida and Candidiasis at Miami, Florida and visited Dr. Brendan Cormack’s laboratory at Johns Hopkins School of Medicine, Baltimore, 20-31 March 2010

## STUDENTS

- ❖ **Ms Shiny Nair** (Canada) attended the keynote symposia on “Pattern Recognition Molecules and Immune Sensors of Pathogens” at Fairmont Banff Springs, Banff, 29 March to 3 April 2009
- ❖ **Mr R Ratheesh** (USA) attended the 100<sup>th</sup> annual meeting of the American Association for Cancer Research at Denver, Colorado, and visited the laboratory of Dr Jonathan Pollack at Stanford University School of Medicine, Stanford, 13-25 April 2009
- ❖ **Mr Kaiser Alam** (Denmark) attended the international conference on “Prophylactic and Therapeutic Intervention in Host-Pathogen Interaction” at LO-Skolen, Helsingor, 5 May to 8 June 2009
- ❖ **Mr Atul Udgata** (Hong Kong) attended the workshop on “Mycobacterial Biosafety”, 3-7 August 2009
- ❖ **Ms Syeda Aisha Haneea** (USA) attended the Burgess Symposium and the “2009 Molecular Genetics of Bacteria and Phages Meeting” at University of Wisconsin, Madison, Wisconsin, 3-9 August 2009
- ❖ **Ms G Charitha** (USA) attended the “Cell Death Meeting” at New York, 6-10 October 2009
- ❖ **Mr M Thoh** (USA) attended the “Cell Death Meeting” at New York, 6-10 October 2009
- ❖ **Ms Shivalika Saxena** (France) worked in the LBPA (Laboratoire de Biotechnologie et de Pharmacologie Genetique Appliquee) ENS (Ecole Normale Superieure) within the ARCUS programme at Cachan, 6 November to 6 December 2009
- ❖ **Ms Jyoti Singh** (USA) attended the “RNA Silencing Conference” at Keystone, Colorado, 14-19 January 2010
- ❖ **Dr Shashi Kiran** (Japan) availed the fellowship awarded by National Institute of Advanced Industrial Science and Technology, Tsukuba, 10 October 2009 to 31 March 2010

# **Committees of the institute**

**(As on 31.03.2010)**



## MEMBERS OF CDFD SOCIETY

<b>Shri Prithviraj Chavan</b> Hon'ble Minister for S&T and Earth Sciences	-	President
<b>Prof M K Bhan</b> Secretary, DBT, New Delhi	-	Member
<b>Prof P Balaram</b> Director, IISc, Bangalore	-	Member
Director General, CSIR, New Delhi	-	Member
<b>Prof V S Chauhan</b> Director, ICGEB, New Delhi	-	Member
<b>Dr Siddhartha Roy</b> Director, IICB	-	Member
Joint Secretary (PM), MHA, New Delhi	-	Member
Joint Secretary & Legal Adviser, Ministry of Law, New Delhi	-	Member
Joint Secretary & Financial Advisor, DBT, New Delhi	-	Member
Director General, Bureau of Police Research & Development, New Delhi	-	Member
<b>Dr Alka Sharma</b> Jt. Director, DBT, New Delhi	-	Member
<b>Dr J Gowrishankar</b> Director, CDFD, Hyderabad	-	Member Secretary

## MEMBERS OF CDFD GOVERNING COUNCIL

<b>Prof M K Bhan</b> Secretary, DBT, New Delhi	-	Chairperson
Director General, CSIR, New Delhi	-	Member
<b>Prof V S Chauhan</b> Director, ICGEB, New Delhi	-	Member
<b>Prof P Balaram</b> Director, IISc, Bangalore	-	Member
<b>Dr Siddhartha Roy</b> Director, IICB, New Delhi	-	Member
Joint Secretary, Ministry of Law, New Delhi	-	Member
Joint Secretary (PM), MHA, New Delhi	-	Member
Joint Secretary & Financial Advisor, DBT, New Delhi	-	Member
Director General Bureau of Police Research & Development, New Delhi	-	Member
<b>Dr Alka Sharma</b> Jt. Director, DBT, New Delhi	-	Member
<b>Dr J Gowrishankar</b> Director, CDFD, Hyderabad	-	Member Secretary

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

<b>Prof P Balaram</b> Director, IISc., Bangalore	-	Chairman
<b>Dr Veena K Parnaik</b> (Nominee of CCMB) Scientist, CCMB, Hyderabad	-	Member
<b>Dr Siddhartha Roy</b> Director, IICB, Kolkata	-	Member
<b>Prof P P Majumder</b> Professor, ISI, Kolkata	-	Member
<b>Prof D Balasubramanian</b> Research Director, LVPEI, Hyderabad	-	Member
<b>Dr Indira Nath</b> Institute of Pathology (ICMR), New Delhi	-	Member
<b>Dr Sandhya S Visweswaraiah</b> Professor, IISc., Bangalore	-	Member
<b>Prof T D Dogra</b> Professor, AIIMS, New Delhi	-	Member
<b>Dr G C Mishra</b> Director, NCCS, Pune	-	Member
<b>Prof Manju Bansal</b> Professor, IISc., Bangalore	-	Member
<b>Dr Dinakar M Salunke</b> Executive Director, Regional Centre for Biotechnology, Gurgaon	-	Member
<b>Prof H Sharat Chandra</b> Director, Centre for Human Genetics, Bangalore	-	Member
<b>Dr Ch Mohan Rao</b> Director, CCMB, Hyderabad	-	Member

<b>Dr Samit Adhya</b> Scientist, IICB, Kolkata	-	Member
<b>Prof Umesh Varshney</b> Professor, IISc., Bangalore		Member
<b>Dr V M Katoch</b> Director General, ICMR, New Delhi	-	Member
<b>Dr Anil K Tyagi</b> Professor, University of Delhi, Delhi	-	Member
<b>Dr S S Agarwal</b> Director (Retd.), SGPGIMS, Lucknow	-	Member
<b>Director General</b> Indian Council of Agricultural Research, New Delhi	-	Member
<b>Home Secretary</b> Ministry of Home Affairs, GoI, New Delhi	-	Member



## MEMBERS OF CDFD ACADEMIC COMMITTEE

<b>Prof A S Raghavendra</b> Professor and Dean, School of Life Sciences University of Hyderabad	-	Chair
<b>Prof Anil K Tyagi</b> Professor, Delhi University	-	Member
<b>Dr K Satyamoorthy</b> Director, Manipal Life Sciences Centre Manipal University	-	Member
<b>Dr D P Kasbekar</b> Scientist, CCMB	-	Member
<b>Dr Ranjan Sen</b> Scientist, CDFD	-	Member
<b>Dr Shekhar C Mande</b> Staff Scientist and Dean, Academics, CDFD	-	Member Convenor

## MEMBERS OF CDFD FINANCE COMMITTEE

<b>Dr V S Chauhan</b> Director, ICGEB, New Delhi	-	Chairman
<b>Dr Siddhartha Roy</b> Director, IICB, Kolkata	-	Member
<b>Dr J Gowrishankar</b> Director, CDFD, Hyderabad	-	Member
<b>Ms Sheila Sangwan</b> Addl. Secretary & Financial Adviser DBT, New Delhi	-	Member
<b>Shri Virendra Kapoor</b> Director, DBT, New Delhi	-	Member
Joint Secretary, MHA, New Delhi	-	Member
<b>Shri E V Rao</b> Head, Finance & Accounts, CDFD, Hyderabad	-	Member Secretary

## MEMBERS OF CDFD BUILDING COMMITTEE

<b>Prof V S Chauhan</b> Director, ICGEB, New Delhi	-	Chairman
<b>Dr J Gowrishankar</b> Director, CDFD, Hyderabad	-	Member
Joint Secretary, DBT, New Delhi	-	Member
<b>Shri Virendra Kapoor</b> Director, DBT, New Delhi	-	Member
<b>Shri B Bose</b> Management Consultant & Former Sr. Manager, NII, New Delhi	-	Member
<b>Shri J Sanjeev Rao</b> Head, Administration, CDFD, Hyderabad	-	Member
<b>Shri E V Rao</b> Head, Finance & Accounts, CDFD, Hyderabad	-	Member
<b>Shri K Ananda Rao</b> Staff Scientist (Engg.), CDFD, Hyderabad	-	Member Convenor



# **Budget and Finance**



## CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS HYDERABAD

### Budget & Finance 2009-10

#### 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 (i) Research Grants provided by various National and International agencies, (ii) income from Services rendered by CDFD, and (iii) income from royalties, consultancies etc. 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 2009-10

Particulars	Amount in Lakhs	Percentage - %
Plan Grant in Aid	2437.00	73.62
Sponsored Projects	793.20	23.96
CDFD Services	27.21	0.82
Misc Receipts	53.07	1.60
<b>Total</b>	<b>3310.48</b>	<b>100.00</b>

#### I. Application of Funds during 2009-10 (Plan Grant in Aid)

S No	Particulars	Amount in Lakhs	Percentage- %
<b>1</b>	<b>Recurring</b>		
	Salaries & Wages	633.71	24.93
	Operating Exp	1061.27	41.75
	<b>Total</b>	<b>1694.98</b>	<b>66.68</b>
<b>2</b>	<b>Non-Recurring</b>		
	Equipments, Infrastructure & Furnishing	846.92	33.32
	<b>Total</b>	<b>846.92</b>	<b>33.32</b>
	<b>Grand Total</b>	<b>2541.90</b>	<b>100.00</b>

#### II. Application of Funds during 2009-10 (Extra Mural Projects)

S No	Particulars	Amount in Lakhs	Percentage- %
<b>1</b>	<b>Recurring</b>		
	Salaries & Wages	183.25	16.33
	Operating Exp	472.27	42.08
	<b>Total</b>	<b>655.52</b>	<b>58.41</b>
<b>2</b>	<b>Non-Recurring</b>		
	Equipments	466.72	41.59
	<b>Total</b>	<b>466.72</b>	<b>41.59</b>
	<b>Grand Total</b>	<b>1122.24</b>	<b>100.00</b>





# **Auditor's Report**



# BAPUJI & VENKAT

Chartered Accountants

## AUDITOR'S REPORT

Date: 20-08-2010

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 31<sup>st</sup> March 2010 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 in agreement with the books of account.
  - (a) The centre has maintained accounts on Cash 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 on adhoc basis 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.
4. 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 information required in the manner so required and give a true and fair view.
5. In so far it relates to the Balance sheet of the state of the organization as at 31<sup>st</sup> March 2010 and
6. In so far as it relates to the Income & Expenditure account of the surplus of the organization for the year ended on 31<sup>st</sup> March 2010.

for **BAPUJI & VENKAT**  
Chartered Accountants  
**[K VENKATACHARYULU]**

Place: Hyderabad

Date: 20/08/2010

**CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD**

BALANCE SHEET AS ON 31st MARCH, 2010

(Amount - Rs.)

	Schedule	Current Year	Previous Year
<b>CORPUS/CAPITAL FUND AND LIABILITIES</b>			
Corpus / Capital Fund	1	755462253.00	640497431.00
Reserves and Surplus	2	263489419.00	256900628.00
Earmarked / Endowment funds	3	18475777.00	51380091.00
Secured Loans & Borrowings	4	0.00	0.00
Unsecured Loans & Borrowings	5	0.00	0.00
Deferred Credit Liabilities	6	0.00	0.00
Current Liabilities and Provisions	7	72074128.00	56999369.00
<b>TOTAL</b>		<b>1109501577.00</b>	<b>1005777519.00</b>
<b>ASSETS</b>			
Fixed Assets	8	687939245.00	624411609.00
Investments - From Earmarked / Endowment Funds	9	80808000.00	97108000.00
Investments - Others	10	27346637.00	23241865.00
Current Assets, Loans, Advances etc.	11	311502191.00	259110542.00
Miscellaneous Expenditure		1905503.00	1905503.00
<b>Internal &amp; External Electrification</b>			
<b>TOTAL</b>		<b>1109501577.00</b>	<b>1005777519.00</b>
Significant Accounting Policies	24		
Contingent Liabilities and Notes on Accounts	25		
<b>DIRECTOR</b>			
CDFD			
		for BAPUJI & VENKAT CHARTERED ACCOUNTANTS [K VENKATACHARYULU] Partner	HEAD - FINANCE & ACCOUNTS CDFD

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>			
<b>INCOME AND EXPENDITURE ACCOUNT FOR THE YEAR ENDING 31st MARCH, 2010</b>			
			(Amount - Rs.)
<b>INCOME</b>	<b>Schedule</b>	<b>Current Year</b>	<b>Previous Year</b>
Income from Sales/Services	12	58500.00	2992427.00
Grants/Subsides	13	158700000.00	169000000.00
Fees/Subscriptions	14	0.00	0.00
Income from Investments	15	4816013.00	13862096.00
Income from Royalty, Publication etc.	16	0.00	0.00
Interest Earned	17	198597.00	388487.00
Other Income	18	963872.00	299173.50
Increase/(decrease) in stock of Finished goods and works-in-progress	19	0.00	0.00
<b>TOTAL (A)</b>		<b>164736982.00</b>	<b>186542183.50</b>
<b>EXPENDITURE</b>			
Establishment Expenses	20	63370989.00	50519191.00
Administrative Expenses etc.	21	94777202.00	86181557.50
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)			
<b>TOTAL (B)</b>		<b>158148191.00</b>	<b>136700748.50</b>
Balance being excess of income over Expenditure (A-B)		6588791.00	49841435.00
Transfer to Special Reserve (Specify each)			
Transfer to / from General Reserve			
<b>BALANCE BEING SURPLUS/(DEFICIT) CARRIED TO CORPUS/CAPITAL FUND</b>			
SIGNIFICANT ACCOUNTING POLICIES	24		
CONTINGENT LIABILITIES AND NOTES ON ACCOUNTS	25		
<b>DIRECTOR</b>			
CDFD			
		HEAD - FINANCE & ACCOUNTS	CDFD
			CDFD

**CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD**  
**RECEIPTS AND PAYMENTS ACCOUNT FOR THE YEAR ENDED 31st MARCH 2010**

(Amount - Rs.)

RECEIPTS	Current Year	Previous Year	PAYMENTS	Current Year	Previous Year
<b>1. Opening Balances</b>			<b>1. Expenses</b>		
a) Cash in hand	43969.00	76938.00	a) Establishment Expenses (corresponding to Schedule 20)	63370989.00	50519191.00
b) Bank Balances			b) Administrative Expenses (corresponding to Schedule 21)	94777202.00	86181557.50
i) In current accounts	50672076.25	20874371.25	c) Schedule 22	0.00	0.00
ii) In deposit accounts	0.00	0.00			
iii) Savings accounts	3826152.72	2342812.72	<b>II. Payments made against funds for various projects</b>		
<b>II. Grants Received</b>			(Name of the fund or project should be shown along with the particulars of payments made for each project)		
a) From Government of India			Projects (Annexure H)	112224334.00	65156569.00
b) From State Government	243700000.00	259000000.00	EMRC a/c (Stipend)	8374430.00	10523929.00
c) From other sources (details)	0.00	0.00	DBT A/c (Stipend)	2192064.00	2157724.00
(Grants for capital & revenue exp. To be shown separately)			IISc A/c (Stipend)	968125.00	681141.00
Research Associates - IISc (Stipend)	1613118.00	394423.00	UGC A/c (Stipend)	1670137.00	2039504.00
Research Associates - UGC (Stipend)	3455015.00	0.00	DBT-PDF A/c (Stipend)	0.00	0.00
Research Associates - DBT-JRF(Stipend)	213758.00	2181427.00	ICMR (Stipend)	637535.00	447328.00
Research Associates - EMRC (Stipend)	7969829.00	4194832.00			
Research Associates - DBT-PDF(Stipend)	0.00	0.00	<b>III. Investments and deposits made</b>		
Research Associates - ICMR (Stipend)	479627.00	335687.00	a) Out of Earmarked/Endowment funds	59500000.00	17200000.00
Projects (Annexure -D)	79320020.00	56892823.00	b) Out of Own Funds (Investments-others)	0.00	0.00
<b>III. Income on Investments from</b>			<b>IV. Expenditure on Fixed Assets &amp; Capital Work-in-Progress</b>		
a) Earmarked/Endow. Funds	4816013.00	13862096.00	a) Purchase of Fixed Assets :		
b) Own Funds (Oth. Investment)	0.00	0.00	Vehicles	56284.00	0.00
Investments cancelled	70000000.00	205159000.00	Books & Journals	692139.00	2869167.00
<b>IV. Interest Received</b>			Equipment - Lab / Office / Furniture	15598161.00	11191000.00
a) On Bank deposits	116256.00	159965.00	Non Consumables	0.00	9700.00
b) Loans, Advances etc	0.00	0.00	Expenditure on Capital Work-in-progress:		
Interest on HBA/ Vehicle advances	27927.00	24504.00	Building	17397329.00	84035581.00
Interest earned on LC	82341.00	285077.00	CMA fees	0.00	0.00

DIRECTOR  
CDFD

for BAPUJI & VENKAT  
CHARTERED ACCOUNTANTS  
[K VENKATACHARYULU]  
Partner

HEAD - FINANCE & ACCOUNTS  
CDFD



<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>					
<b>RECEIPTS AND PAYMENTS ACCOUNT FOR THE YEAR ENDED 31st MARCH 2010</b>					
(Amount - Rs.)					
RECEIPTS	Current Year	Previous Year	PAYMENTS	Current Year	Previous Year
<b>V. Other Income (Specify)</b>			<b>V. Refund of surplus money/Loans</b>		
Analysis Charges	0.00	3025783.00	a) To the Government of India	0.00	0.00
<b>VII. Any other receipts (give details)</b>			b) To the State Government	0.00	0.00
I- Remittances (Annexure -A)	6950973.00	8183546.00	c) To other provides of funds	0.00	0.00
TDS Recoveries (Annexure-B)	4510906.00	6505661.00	<b>VI. Finance Charges (Interest)</b>		
CPF -Sub, Arrears and adv. Refund	5752948.00	6652234.00			
Sundry receipts	744970.00	116324.50	<b>VII. Other Payments (Specify)</b>		
Sale of Tender forms	61500.00	60520.00	Advances (Annexure - E)	89613075.00	45376525.00
Application Fees	93700.00	72700.00	I-Remittances (Annexure - F)	7043784.00	7850109.00
Guest House receipts	23950.00	15050.00	TDS remitted (Annexure- G)	6026079.00	5253391.00
Hostel receipts	11825.00	10075.00	CPF A/c	5752974.00	6652234.00
Loans & Advances (Recovery)- (Annexure - C)	33594876.00	23592165.00	Life Membership fees	1510.00	0.00
Asset Transfer	16706823.00	0.00	other receipts - refund	0.00	0.00
CDFD Revolving Fund A/c	0.00	2615.00	Analysis Charges paid / refund	0.00	33356.00
Indo-Australian Biotech Conference A/c	8643.00	25000.00	Aluminium Partition Works	0.00	0.00
Sale of Vehicle	181099.00	74700.00	NIMS - Advance	0.00	10000000.00
DST Expert meeting	0.00	400000.00	CDFD Revolving Fund Expenses a/c	60000.00	150125.00
Indo - US workshop	0.00	3150000.00	Advance for Workshop	394494.00	0.00
Other receipts	600000.00	0.00	Workshop A/c expenses	56.00	0.00
Sale of Scrap	58500.00	0.00	Collaboration Expenses a/c	5800056.00	0.00
Collaboration A/c receipts	5827821.00	0.00	<b>VIII. Closing Balances</b>		
Workshop receipts	3711.00	0.00	a) Cash in hand	65550.00	43969.00
			b) Bank Balances		
			i) In current accounts	42391687.25	50672076.25
			ii) In deposit accounts	0.00	0.00
			iii) Savings accounts	6860352.72	3826152.72
<b>TOTAL</b>	541468346.97	617670329.47	<b>TOTAL</b>	541468346.97	617670329.47
<b>DIRECTOR</b> CDFD	for BAPUJI & VENKAT CHARTERED ACCOUNTANTS [K VENKATACHARYULU] Partner				HEAD - FINANCE & ACCOUNTS CDFD

<b>SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2010</b>		<b>(Amount - Rs.)</b>		
		<b>Current Year</b>		<b>Previous Year</b>
<b>SCHEDULE 1 - CORPUS/CAPITAL FUND :</b>				
Balance as at the beginning of the year				534208719.00
Add : Contribution towards Corpus/Capital Fund				
CDFD Core - Plan (Non-Recurring)		85000000.00	90000000.00	
Capitalised portion of fixed assets of projects		29964822.00	16288712.00	
Add : Balance of net income/(expenditure) transferred from the income and Expenditure Account				0.00
<b>BALANCE AS AT THE YEAR - END</b>		<b>755462253.00</b>		<b>640497431.00</b>

**CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD**

**SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2010**

(Amount - Rs.)

	Current Year		Previous Year	
<b>SCHEDULE 2 - RESERVES AND SURPLUSES :</b>				
1. Capital Reserve :				
As per last Account	256900628.00		207059193.00	
Addition during the year	6588791.00		49841435.00	
Less : Deductions during the year	0.00	263489419.00	0.00	256900628.00
2. Revaluation 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	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
<b>TOTAL</b>		<b>263489419.00</b>		<b>256900628.00</b>

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>			
<b>SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2010</b>			
<b>(Amount - Rs.)</b>			
<b>SCHEDULE 3 - EARMARKED/ENDOWMENT FUNDS</b>	<b>Current Year</b>		<b>Previous Year</b>
(Refer Annexures P 03-P 102, COE I & II & A to L)			
<b>(a) Opening balance of the funds</b>		<b>51380091.20</b>	59643837.20
<b>(b) Additions to the Funds :</b>			
i. Donations /grants	79320020.00		56892823.00
ii. Income from investments made on account of funds	0.00		0.00
iii. Other additions	0.00	79320020.00	56892823.00
<b>TOTAL (a+b)</b>		<b>130700111.20</b>	<b>1165366660.20</b>
<b>(c) Utilisation/Expenditure towards objective of funds</b>			
(i) Capital Expenditure (Refer Annexures I & II)			
- Fixed Assets	29964822.00		16288712.00
- Others	16706823.00	46671645.00	0.00
Total			16288712.00
(ii) Revenue Expenditure			
- Salaries, Wages and allowances etc.	18325596.00		13275703.00
- Rent	0.00		0.00
- Other Expenses	47227093.00	65552689.00	35592154.00
Total			48867857.00
<b>TOTAL (c)</b>		<b>112224334.00</b>	<b>65156569.00</b>
<b>NET BALANCE AS AT THE YEAR-END (a+b-c)</b>		<b>18475777.20</b>	<b>51380091.20</b>

**CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD**

**SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2010**

(Amount - Rs.)

	Current Year		Previous Year	
<b>SCHEDULE 4 - SECURED LOANS AND BORROWINGS:</b>				
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 accrued and due	0.00	0.00	0.00	0.00
4. Banks:				
(a) Term Loans	0.00		0.00	
- Interest accrued and due	0.00		0.00	
(b) Other Loans (specify)	0.00		0.00	
- Interest accrued 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
<b>TOTAL</b>		<b>0.00</b>		<b>0.00</b>
Note: Amount due within one year				

**CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD**  
**SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2010**

(Amount - Rs.)		Current Year		Previous Year	
<b>SCHEDULE 5 - UNSECURED LOANS AND BORROWINGS:</b>					
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
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
<b>TOTAL</b>			<b>0.00</b>		<b>0.00</b>
Note: Amounts due within one year					

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>		
<b>SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2010</b>		
<b>(Amount - Rs.)</b>		
	<b>Current Year</b>	<b>Previous Year</b>
<b>SCHEDULE 6 - DEFFERED CREDIT LIABILITIES:</b>		
(a) Acceptances secured by hypothecation of capital equipment and other assets	0.00	0.00
(b) Others	0.00	0.00
<b>TOTAL</b>	<b>0.00</b>	<b>0.00</b>
Note: Amount due within one year		



**CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD**

**SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2010**

(Amount - Rs.)

	Current Year		Previous Year	
<b>SCHEDULE 7 - CURRENT LIABILITIES AND PROVISIONS</b>				
<b>A. CURRENT LIABILITIES</b>				
1. Acceptances	0.00	0.00	0.00	0.00
2. Sundry Creditors:	0.00	0.00	0.00	0.00
3. Advances Received	0.00	0.00	0.00	0.00
4. Interest accrued but not due on:	0.00	0.00	0.00	0.00
5. Statutory Liabilities:	0.00	0.00	0.00	0.00
<b>6. Other current Liabilities</b>				
CDFD CP Fund A/c (Annexure - I)	27346637.32	23241865.32	17187979.00	805109.00
Collaboration a/c	11415744.00	17187979.00	805109.00	493868.00
Workshop a/c	808763.50	502511.00	2824290.00	0.00
Indo-Australian Biotech Conference A/c	502511.00	16706823.00	17691.00	500000.00
CDFD Revolving Fund A/c	2764290.00	500000.00	402040.00	1033066.00
Asset Transfer	16706823.00	258439.00	1773612.00	825.00
BOYSCOST Fellowship	17691.00	825.00	1301.00	706250.00
Amersham Biosciences (Maintenance)	500000.00	2051.00	2223361.00	3804648.00
Swarnajayanthi Fellowship meeting	402040.00	807750.00	2452934.00	365915.00
Grant Host Meetings refundable	1033066.00	1475975.00	192044.00	9914.00
T.D.S. Payable	258439.00	825041.00	72535.00	180048.00
Other Loans	825.00			
Profession tax	2051.00			
HSD , LSD & TSD	807750.00			
Security deposit/Retention money	1475975.00			
EMD / Margin money	2452934.00			
Works tax	192044.00			
GSLI	72535.00			
IISc Bangalore Stipend	825041.00			

**CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD**

**SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2010**

(Amount - Rs.)

	Current Year		Previous Year	
<b>SCHEDULE 7 - CURRENT LIABILITIES AND PROVISIONS</b>				
Vehicle Advance	57272.00		22604.00	
Income Tax	35167.00		17478.00	
Computer Advance	39900.00		14700.00	
Indo- US Workshop	1166374.00		1166374.00	
DST Expert Meeting	200431.00		200431.00	
Other receipts	600000.00		0.00	
HBA	78820.00		0.00	
Royalties & Consultancy	2305004.00		0.00	
PPF	6000.00	72074127.82	6000.00	56999369.32
<b>TOTAL (A)</b>		72074127.82		56999369.32
<b>B. PROVISIONS</b>				
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)	0.00	0.00	0.00	0.00
<b>TOTAL (B)</b>		0.00		0.00
<b>TOTAL (A+B)</b>		<b>72074127.82</b>		<b>56999369.32</b>

**CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD**  
**SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2010**

(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
<b>A. FIXED ASSETS:</b>										
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	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	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	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
not belongs to the entity										
3. PLANT MACHINERY & EQUIPMENT	254517722.05	55729286.00	10506041.00	299740947.05	0.00	0.00	0.00	0.00	299740947.05	254517722.05
4. VEHICLES	4261243.00	56284.00	181099.00	4136428.00	0.00	0.00	0.00	0.00	4136428.00	4261243.00
5. FURNITURE, FIXTURES	15299647.00	121600.00	0.00	15421247.00	0.00	0.00	0.00	0.00	15421247.00	15299647.00
6. OFFICE EQUIPMENT	10827320.00	218158.00	0.00	11045478.00	0.00	0.00	0.00	0.00	11045478.00	10827320.00
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	336985.00	0.00	0.00	336985.00	0.00	0.00	0.00	0.00	336985.00	336985.00
9. LIBRARY BOOKS	12350897.00	682139.00	0.00	13043036.00	0.00	0.00	0.00	0.00	13043036.00	12350897.00
10. TUBEWELLS & WATER SUPPLY	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
11. OTHER FIXED ASSETS										
Airconditioning works	5337154.00	0.00	0.00	5337154.00	0.00	0.00	0.00	0.00	5337154.00	5337154.00
Aluminium partition work	1213252.00	0.00	0.00	1213252.00	0.00	0.00	0.00	0.00	1213252.00	1213252.00
DG Set	1646305.00	0.00	0.00	1646305.00	0.00	0.00	0.00	0.00	1646305.00	1646305.00
Paintings	40000.00	0.00	0.00	40000.00	0.00	0.00	0.00	0.00	40000.00	40000.00
Typewriters	42450.00	0.00	0.00	42450.00	0.00	0.00	0.00	0.00	42450.00	42450.00
Miscellaneous non consumables	957984.50	0.00	0.00	957984.50	0.00	0.00	0.00	0.00	957984.50	957984.00
Other Assets	1018618.00	0.00	0.00	1018618.00	0.00	0.00	0.00	0.00	1018618.00	1018618.00
EMB Net	5229909.00	0.00	0.00	5229909.00	0.00	0.00	0.00	0.00	5229909.00	5229909.00
<b>TOTAL</b>	316979486.05	56817447.00	10687140.00	363109793.55	0.00	0.00	0.00	0.00	363109793.55	316979486.05
<b>B. CAPITAL WORK-IN-PROGRESS</b>	307432122.70	17397329.00	0.00	324829451.70	0.00	0.00	0.00	0.00	324829451.70	307432122.70
<b>TOTAL</b>	<b>624411608.75</b>	<b>74214776.00</b>	<b>10687140.00</b>	<b>687939245.25</b>	0.00	0.00	0.00	0.00	<b>687939245.25</b>	<b>624411608.75</b>

Note:- Out of the Total addition of Rs. 45223225/- the amount pertaining to Projects & Core Grants are as follows:-  
Projects - Equipment : 29964822.00  
CDFD Core Grant: 15258403.00

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>		
<b>SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2010</b>		
	<b>(Amount - Rs.)</b>	
	<b>Current Year</b>	<b>Previous Year</b>
<b>SCHEDULE 9 - INVESTMENTS FROM EARMARKED/ENDOWMENT FUNDS</b>		
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 - L)	80808000.00	97108000.00
<b>TOTAL</b>	<b>80808000.00</b>	<b>97108000.00</b>

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>		
<b>SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2010</b>		
	<b>(Amount - Rs.)</b>	
	<b>Current Year</b>	<b>Previous Year</b>
<b>SCHEDULE 10 - INVESTMENTS - OTHERS</b>		
<b>(Annexure - M)</b>		
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	936360.00	936360.00
5. Subsidiaries and Joint Ventures	0.00	0.00
6. Others (to be specified) - STDRs (CPF), CDFD CP FUND A/c	26410277.32	22305505.32
<b>TOTAL</b>	<b>27346637.32</b>	<b>23241865.32</b>

**CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD**

**SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2010**

(Amount - Rs.)

	Current Year		Previous Year	
<b>SCHEDULE 11 - CURRENT ASSETS, LOANS, ADVANCES ETC.</b>				
<b>A. CURRENT ASSETS:</b>				
<b>1. Inventors:</b>				
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
<b>2. Sundry Debtors:</b>				
a) Debts Outstanding for a period exceeding six months			0.00	
b) Others - Life Membership Fees	165935.00	165935.00	164425.00	164425.00
<b>3. Cash balances in hand (including cheques/drafts and imprest)</b>		65550.00		43969.00
<b>4. Bank Balances:</b>				
a) With Scheduled Banks:				
-On Current Accounts	42391687.25		50672076.25	
-On Deposit Accounts (includes margin money)	0.00		0.00	
-On Savings Accounts	6860352.72	49252039.97	3826152.72	54498228.97
b) With non-Scheduled 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
<b>5. Post Office-Savings Accounts</b>				
<b>TOTAL (A)</b>		<b>49483524.97</b>		<b>54706622.97</b>

**CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD**  
**SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MARCH 2010**

(Amount - Rs.)

SCHEDULE 11 - CURRENT ASSETS, LOANS, ADVANCES ETC. B. LOANS, ADVANCES AND OTHER ASSETS	Current Year		Previous Year	
<b>1. Loans:</b>				
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
<b>2. Advances and other amounts recoverable in cash or in kind or for value to be received</b>				
a) On Capital Account (Annexure - J)	245684551.51		186069805.51	
b) Prepayments - Deposits (Annexure- K)	16334115.00		18334113.00	
c) Others	0.00	262018666.51	0.00	204403918.51
<b>3. Income Accrued:</b>				
a) On Investments from Earmarked/Endowment 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
<b>4. Claims Receivable</b>				
<b>TOTAL (B)</b>		262018666.51		204403918.51
<b>TOTAL (A+B)</b>		<b>311502191.48</b>		<b>259110541.48</b>

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>		
<b>SCHEDULES FORMING PART OF INCOME &amp; EXPENDITURE AS AT 31st MARCH 2010</b>		
	<b>Current Year</b>	<b>Previous Year</b>
	<b>(Amount - Rs.)</b>	
<b>SCHEDULE 12 - INCOME FROM SALES/SERVICES</b>		
<b>1) Income from Sales</b>		
a) Sale of Finished Goods	0.00	0.00
b) Sale of Raw Material	0.00	0.00
c) Sale of Scraps	58500.00	0.00
<b>2) Income from Services</b>		
a) Labour and Processing Charges	0.00	0.00
b) Professional/Consultancy Services (Analysis Charges)	0.00	2992427.00
c) Agency Commission and Brokerage	0.00	0.00
d) Maintenance Services (Equipment/Property)	0.00	0.00
e) Others (Specify)	0.00	0.00
<b>TOTAL</b>	<b>58500.00</b>	<b>2992427.00</b>
<b>SCHEDULE 13 - GRANTS/SUBSIDIES</b>		
<b>(Irrevocable Grants &amp; Subsidies Received)</b>		
1) Central Government (DBT Plan Grant-in-Aid)	158700000.00	169000000.00
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
<b>TOTAL</b>	<b>158700000.00</b>	<b>169000000.00</b>

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>		
<b>SCHEDULES FORMING PART OF INCOME &amp; EXPENDITURE AS AT 31st MARCH 2010</b>		
(Amount - Rs.)		
<b>SCHEDULE 14 - FEES/SUBSCRIPTIONS</b>	<b>Current Year</b>	<b>Previous Year</b>
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
<b>TOTAL</b>	<b>0.00</b>	<b>0.00</b>

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>			
<b>SCHEDULES FORMING PART OF INCOME &amp; EXPENDITURE AS AT 31st MARCH 2010</b>			
(Amount - Rs.)			
<b>SCHEDULE 15 - INCOME FROM INVESTMENTS</b>	<b>Investment from Earmarked Fund</b>		<b>Investments - Others</b>
(Income on Invest from Earmarked/Endowment Funds transferred to Funds)	<b>Current Year</b>	<b>Previous Year</b>	<b>Current Year</b>
1) Interest	<b>Current Year</b>	<b>Previous Year</b>	<b>Previous Year</b>
a) On Govt. Securities	0.00		0.00
b) Other Bonds/Debentures	0.00	0.00	0.00
2) Dividends:			
a) On Shares	0.00	0.00	0.00
b) On Mutual Fund Securities	0.00	0.00	0.00
3) Rents			
<b>4) Others (Specify) STDRs</b>	<b>4816013.00</b>	<b>13862096.00</b>	<b>0.00</b>
<b>TOTAL</b>	<b>4816013.00</b>	<b>13862096.00</b>	<b>0.00</b>
<b>TRANSFERRED TO EARMARKED/ENDOWMENT FUNDS</b>			



<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>		
<b>SCHEDULES FORMING PART OF INCOME &amp; EXPENDITURE AS AT 31st MARCH 2010</b>		
	<b>Current Year</b>	<b>Previous Year</b>
	<b>(Amount - Rs.)</b>	
<b>SCHEDULE 16 - INCOME FROM ROYALTY, PUBLICATION ETC.</b>		
1) Income from Royalty	0.00	0.00
2) Income from Publications	0.00	0.00
3) Others (Specify)	0.00	0.00
<b>TOTAL</b>	<b>0.00</b>	<b>0.00</b>

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>		
<b>SCHEDULES FORMING PART OF INCOME &amp; EXPENDITURE AS AT 31st MARCH 2010</b>		
	<b>Current Year</b>	<b>Previous Year</b>
	<b>(Amount - Rs.)</b>	
<b>SCHEDULE 17 - INTEREST EARNED</b>		
<b>1) On Term Deposits</b>		
a) With Scheduled Banks	82341.00	285077.00
b) With Non-Scheduled Banks	0.00	0.00
c) With Institutions	0.00	0.00
d) Others	0.00	0.00
<b>2) On Savings Accounts</b>		
a) With Scheduled Banks	116256.00	103410.00
b) With Non-Scheduled Banks	0.00	0.00
c) Post Office Savings Accounts	0.00	0.00
d) Others	0.00	0.00
<b>3) On Loans</b>		
a) Employees/Staff	0.00	0.00
b) Others	0.00	0.00
<b>4) Interest on Debtors and Other Receivables</b>	<b>0.00</b>	<b>0.00</b>
<b>TOTAL</b>	<b>198597.00</b>	<b>388487.00</b>
Note - Tax deducted at source to be indicated		

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>		
<b>SCHEDULES FORMING PART OF INCOME &amp; EXPENDITURE AS AT 31st MARCH 2010</b>		
	<b>Current Year</b>	<b>Previous Year</b>
	<b>(Amount - Rs.)</b>	
<b>SCHEDULE 18 - OTHER INCOME</b>		
1) Profit on Sale/disposal of Assets:		
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 Income:		
Sundry receipts	744970.00	116324.50
Sale of Tender forms	61500.00	60520.00
Guest House receipts	23950.00	15050.00
Hostel receipts	11825.00	10075.00
Application Fees	93700.00	72700.00
Interest on HBA/Vehicle advance	27927.00	24504.00
<b>TOTAL</b>	<b>963872.00</b>	<b>299173.50</b>

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>		
<b>SCHEDULES FORMING PART OF INCOME &amp; EXPENDITURE AS AT 31st MARCH 2010</b>		
	<b>Current Year</b>	<b>Previous Year</b>
	<b>(Amount - Rs.)</b>	
<b>SCHEDULE 19 - INCREASE/(DECREASE) IN STOCK OF FINISHED GOODS &amp; WORK IN PROGRESS</b>		
a) Closing stock		
-Finished Goods	0.00	0.00
-Work-in-progress	0.00	0.00
<b>Total (a)</b>	<b>0.00</b>	<b>0.00</b>
b) Less: Opening Stock		
-Finished Goods	0.00	0.00
-Work-in-progress	0.00	0.00
<b>Total (b)</b>	<b>0.00</b>	<b>0.00</b>
<b>NET INCREASE/(DECREASE) [a-b]</b>	<b>0.00</b>	<b>0.00</b>

**CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD**

**SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MARCH 2010**

(Amount - Rs.)

<b>SCHEDULE 20 - ESTABLISHMENT EXPENSES</b>	<b>Current Year</b>	<b>Previous Year</b>
a) Salaries and Wages	58453457.00	45382721.00
b) Allowances and Bonus	240737.00	324379.00
c) Contribution to Provident Fund	2305393.00	4000185.00
d) Contribution to Other Fund (Specify)	0.00	0.00
e) Staff Welfare Expenses - Medical charges	1389524.00	726622.00
f) Expenses on Employees Retirement and Terminal Benefits	966386.00	0.00
g) Others (specify) - Staff leased House	15492.00	85284.00
<b>TOTAL</b>	<b>63370989.00</b>	<b>50519191.00</b>

**CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD**  
**SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MARCH 2010**

		(Amount - Rs.)	
<b>SCHEDULE 21 - OTHER ADMINISTRATIVE EXPENSES ETC.</b>		<b>Current Year</b>	<b>Previous Year</b>
1	Purchases (Consumables)	17188298.00	25060556.00
2	Labour and processing expenses	0.00	0.00
3	Cartage and Carriage Inwards	0.00	0.00
4	Electricity and power / Water Charges	10996083.00	8395610.00
5	Water charges	0.00	0.00
6	Insurance	0.00	0.00
7	Repairs and Maintenance	16227158.00	10694928.50
8	Excise Duty	0.00	0.00
9	Rent, Rates and Taxes	17343170.00	14217728.00
10	Vehicles Running and Maintenance	844972.00	924625.00
11	Postage, Telephone and Communication Charges	1597656.00	1749047.00
12	Printing and Stationary	838824.00	1061574.00
13	Travelling and Conveyance Expenses	6736314.00	7665012.00
14	Expenses on Seminar/Workshops	0.00	0.00
15	Subscription Expenses	23128.00	25164.00
16	Expenses on Fees (Membership Fees)	49160.00	37798.00
17	Auditors Remuneration	19854.00	20225.00
18	Hospitality Expenses (Meeting Expenses)	1623309.00	723271.00
19	Professional Charges (Legal Expenses incl. Patent charges)	4811881.00	2465067.00
20	Provision for Doubtful Debts/Advances - Workshop	0.00	0.00
21	Irrecoverable Balances Written-off	0.00	0.00
22	Packing Charges	0.00	0.00
23	Freight and Forwarding Expenses	0.00	0.00
24	Distribution Expenses	0.00	0.00
25	Advertisement and Publicity	4001687.00	3156743.00

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>			
<b>SCHEDULES FORMING PART OF INCOME &amp; EXPENDITURE AS AT 31st MARCH 2010</b>			
<b>(Amount - Rs.)</b>			
	<b>Current Year</b>	<b>Previous Year</b>	
<b>SCHEDULE 21 - OTHER ADMINISTRATIVE EXPENSES ETC.</b>			
26	Hindi / Foundation day expenses 44424.00	124382.00	
27	Bank charges 6830.00	170.00	
28	Security & Cleaning contract charges 10621730.00	7480979.00	
29	Internet leased line charges 1640095.00	1904816.00	
30	Training Course / Symposia 162629.00	473862.00	
	<b>TOTAL</b>	<b>94777202.00</b>	<b>86181557.50</b>

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>			
<b>SCHEDULES FORMING PART OF INCOME &amp; EXPENDITURE AS AT 31st MARCH 2010</b>			
<b>(Amount - Rs.)</b>			
	<b>Current Year</b>	<b>Previous Year</b>	
<b>SCHEDULE 22 - EXPENDITURE ON GRANTS, SUBSIDIES ETC.</b>			
	a) Grants given to Institutions/Organisations 0.00	0.00	
	b) Subsidies given to Institutions/Organisations 0.00	0.00	
	<b>TOTAL</b>	<b>0.00</b>	<b>0.00</b>

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>			
<b>SCHEDULES FORMING PART OF INCOME &amp; EXPENDITURE AS AT 31st MARCH 2010</b>			
<b>(Amount - Rs.)</b>			
	<b>Current Year</b>	<b>Previous Year</b>	
<b>SCHEDULE 23 - INTERST</b>			
	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	
	<b>TOTAL</b>	<b>0.00</b>	<b>0.00</b>

**Schedule 24: Significant Accounting Policies, and  
Schedule 25: Contingent Liabilities & Notes on Account  
for the period ended 31/03/10**

**1. Method of Accounting:**

- a. The accounting system adopted by the organization is on "Cash 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: No depreciation on the Fixed Assets is charged and as such no ageing of fixed assets are being done.
- (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 **Bapuji & Venkat**  
Chartered Accountants  
**[K VENKATACHARYULU]**

Place: Hyderabad

Date: 20/08/10

## **CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS HYDERABAD**

### **CLARIFICATION ON NOTES ON ACCOUNTS: 2009-10**

- ❖ Notes on Accounts 1 to 6 & 8: Method of Accounting/ Revenue recognition/Fixed Asset/Inventories/ Foreign Currency transactions/Investments:

These are all only informatory items.

- ❖ 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.

**E V RAO**

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 2010**

Amount in Rs.

Previous year	P No	Particulars	Current Year
-630047.00	P-03	"Transgenesis and Genetic basis of Pathogen Resistance in the Silkworm, Bombyx Mori	-630047.00
1000000.00	P-04	"Silkworm Breeding for Productivity improvement of silk	0.00
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
6737.00	P-13	"Programme to delineate gene functions in the post – genomics era by a systematic two gene knockout method"	6737.00
0.00	P-15	"The Helicobacter Pylori genome programme – Genome sequencing, functional analysis and comparative genomics of the strains obtained from Indian patients"	0.00
-687887.00	P-17	"Studies on inositol-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 parasite"	-274286.00
0.00	P-19	"Construction of Integrated RAPD, RFLP and Microsatellite linkage map of the Silkworm, Bombyx mori and its corelation with the Phenotypic linkage Map"	0.00
-1888111.00	P-20	"Genomic Micro array R&D Programmes on infectious diseases and Neurological Disorders"	-1888111.00
0.00	P-21	Development of Versatile, portable software for Bio-informatics	0.00
-79.50	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
2124902.00	P-30	"Transcription termination and anti termination in E. Coli"	2124902.00
827383.00	P-31	Role of K-ras in Lung type II epithelial cells	827383.00
-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 silkmths"	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"	-226058.00
1873605.00	P-41	"Construction, characterization and analysis of expressed sequences from silkworm "	1873605.00
-860386.00	P-42	"Structural and functional studies on Mycobacterium tuberculosis heat shock proteins".	-2219464.00
1092711.70	P-43	"A generalized mechanism of transcription termination in prokaryotes: a quest for mechanism based transcription inhibitors for microbial pathogens".	754048.70
-457538.00	P-44	"Understanding of role of Ras and NO / iNOS signalling in promotion of hepatocellular carcinomas with persistent HBV infection"	-457538.00
624070.00	P-45	Specialized chromatin structures as epigenetic imprints to distinguish parental alleles".	624070.00
339070.00	P-46	"Effect of reactive oxygen species (ROS) on immune response : Relevance in immunosuppression and Pathogenesis"	0.00
-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
0.00	P-49	"The Mycobacterium W genome program : Complete genome sequencing and comparative genomics"	0.00
627369.00	P-49A	Grant sanctioned by International Atomic Energy	470313.00
57663.00	P-50	"Cervical cancer prevention by multiple strategies in rural community in Andhra pradesh"	0.00
-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
-708289.00	P-53	Collaborative research project on molecular ecology and systematics	0.00
-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
3394100.00	P-57	Improved genome annotation through a combination of machine learning and experimental methods: Plasmodium falciparum as a case study.	0.00
267773.00	P-58	"Indo-Malaysian collaboration in Bioinformatics: Development and maintenance of a web-portal hosting databases and tools of common interest"	0.00
200000.00	P-58A	Functional Genomics on Rice	0.00
-2155484.00	P-59	"An integrated Approach towards understanding the biology of Mycobacterium tuberculosis: Genetic, biochemical, immunological and structural analyses."	-2215024.00
497609.00	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 nucleole protein H-NS"	-280000.00
-278928.00	P-62	"HIV – 1 Pathogenesis: Role of Integrate in Reverse Transcription and Nuclear Transport of Viral Genome"	-278928.00



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 2010**

Amount in Rs.

Previous year	P No	Particulars	Current Year
-837574.00	P-63	"Upgradation of the existing computing infrastructure at the Bioinformatics facility at CDFD"	-837574.00
-19755.00	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 Helicobacter pylori"	-582647.00
-8279524.00	P-65A	APEDA - CDFD Centre for Basmati DNA Analysis	7477508.00
-684722.00	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
-104487.00	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
-906808.00	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)	-159363.00
-497869.00	P-70	Identification of disease causing mutations in familial hypertrophic cardiomyopathy (FHC) patients from Andhra Pradesh	-21336.00
420845.00	P-71	Referral Centre for Genetic fidelity testing of tissue culture raised plants	-1615249.00
-1129718.00	P-72	Nuances of Non coding DNA near insulin-responsive genes	-1421653.00
-541887.00	P-73	Identification and characterization of pancreatic cancer genes located within novel localized copy number alterations	-857136.00
-168779.00	P-74	Molecular basic of insect plant interactions in rice under the national fund for basic and strategic research in agriculture	0.00
-10840.00	P-75	Preparing blueprint for the macromolecular crystallography beamline at Indus-II synchrotron source	-10840.00
-58267.00	P-76	A study of Molecular Markers in childhood Autism with special references to nuclear factors - APPA B"	-50234.00
-627570.00	P-77	Functional characterization of Mycobacterium tuberculosis PE/PPE proteins having SH3 binding domain: Understanding their role in modulating macrophage functions	126471.00
1304.00	P-78	Task Force - IMD Newborn Screening for Congenital Hypothyroidism & Congenital Adrenal Hyperplasia: A Multicentric Study"	1304.00
-1722377.00	P-79	Understanding the role of AGE proteins in inducing inflammatory responses and its regulation	-2636028.00
1108456.00	P-80	Referral Centre for Detection of Genetically Modified Foods employing DNA - based Markets	-28471.00
0.00	P-80A	Fluorescent amplified fragment length polymorphism analysis of different genomic species - development of species specific markers for the identification of Leptospirosis	0.00
38637629.00	COE-I	COE for Genetics and Genomics of silkworms	10330961.00
-141048.00	P-81	Reconstructing cellular Networks: Two-Component Regulatory Systems	-584848.00
0.00	P-81A	Financial Assistance for award of JC Bose Fellowship to Dr J Gowrishankar	0.00
795011.00	P-82	Functional Genomic Analysis of Candida Glabrata-macrophage	675598.00
-773176.00	P-83	Prokaryotic Transcription Termination Factor, Rho: Mechanism of Action and Biology	-1093034.00
-50383.00	P-83A	Understanding the mechanism of Azadirachtin-mediated cell signaling: role in anti-inflammation and anti-tumorigenesis	-86075.00
-1300000.00	P-84	Preparing for tuberculosis vaccine efficacy trials: Baseline epidemiology, improved diagnosis, markers of protection and phase I/II trials	-1150.00
1033462.00	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	655960.00
-275405.00	P-85	IdeR associated gene regulatory network in mycobacteria	-933501.00
334386.00	P-86	Evaluation of Mycobacterium W as an immunotherapeutic against paratuberculosis (John's Disease of cattle)	78291.00
-65698.00	P-87	Comparative genomic of wild silkworms under India-Japan Co-operative Science programme (IJCSP)	-65698.00
11800481.00	COE-II	DBT Centre of Excellence for Microbial Biology	-1454733.00
140000.00	P-88	Financial Assistance for award of TATA Innovation Fellowship to Dr J Nagaraju	282465.00
0.00	P-89	Characterization of Mycobacterium tuberculosis transcription machinery and Bacteriophage metagenomics	-300000.00
1057540.00	P-90	Role of Yapsins in the Pathobiology of Candida Glabrata	373213.00
1422879.00	P-91	DNMT3L: Epigenetic correlation with cancer	174154.00
9264550.00	P-92	Swarnajayanti Fellowship: Designing transcription anti-terminators: a novel approach for making new inhibitors of gene expression	-73314.00
4851300.00	P - 93	Virtual Centre of Excellence on multidisciplinary approaches aimed at interventions against tuberculosis	817860.00
-252909.00	P - 95	Construction of regulatory networks in prokaryotes through protein: Protein interaction predictions and transcription regulation predictions.	-121469.00
-1470450.00	P - 96	Molecular Characterization of sporadic colorectal cancer in the young from India	-1187015.00
0.00	P - 97	Proteome-wide Analysis of Serine pyrophosphorylation by inositol pyrophosphates	582700.00
0.00	P - 98	Role of cell - cell signaling mediated by Diffusible signaling factor (DSF) in Xanthomonas virulence	812907.00
0.00	P - 99	Role of inositol Pyrophosphates in eukaryotic cell growth, proliferation and ribosome biogenesis	1663500.00
0.00	P - 100	Effect of reactive oxygen species on T-Cell immune response: An approach to understand the molecular mechanism of immunosuppression during tuberculosis" - National Bioscience Award	0.00
0.00	P - 101	Role of inositol pyrophosphates in cell physiology: Investigating the biochemical significance of protein pyrophosphorylation - Senior Fellowship	15288801.00
0.00	P - 102	Understanding the role of Mycobacterium tuberculosis heat shock protein 60 as Th1/Th2 immunomodular	-483681.00
<b>51380091.20</b>		<b>Total</b>	<b>18475777.20</b>

Annexure - II  
**CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS**  
**Details of Fixed Assets Fund (Capitalised portion of Project Grants)**  
**for the year ended 31st March 2010**

Amount in Rs.

Previous year	P No	Particulars	Current Year
600000.00	P-03	"Transgenesis and Genetic basis of Pathogen Resistance in the Silkworm, Bombyx Mori	600000.00
329289.00	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"	329289.00
588400.00	P-09	"NMITLI Project on – Latent M.Tuberculosis: New targets, Drug delivery systems, Bio enhancers & Therapeutics"	588400.00
47400.00	P-10	"Role of upstream sequence elements in Hyper activation of transcription from Baculovirus polyhedrin gene promoter"	47400.00
529750.00	P-12	Molecular genetics and Functional genomics of M.Tuberculosis patient isolates in India	529750.00
1334600.00	P-13	"Programme to delineate gene functions in the post – genomics era by a systematic two gene knockout method"	1334600.00
5163243.00	P-14	"Comparative and functional genomics approaches for the identification and characterization of genes responsible for multi drug resistance of mycobacterium tuberculosis"	5163243.00
6000000.00	P-15	"The Helicobacter Pylori genome programme – Genome sequencing, functional analysis and comparative genomics of the strains obtained from Indian patients"	6000000.00
1814901.00	P-16	NMITLI Project on – Latent M.Tuberculosis: New targets, Drug delivery systems, Bio enhancers & Therapeutics	1814901.00
244400.00	P-17	"Studies on inositol-phosphate synthesis – a novel enzyme from Mycobacterium tuberculosis H37RV" – Transfer from IMTECH, Chandigarh	244400.00
344020.00	P-18	"Mapping of receptor binding site on the Eythrocyte binding of malaria parasite"	344020.00
7246511.00	P-19	"Construction of Integrated RAPD, RFLP and Microsatellite linkage map of the Silkworm, Bombyx mori and its corelation with the Phenotypic linkage Map"	7246511.00
27331134.00	P-20	"Genomic Micro array R&D Programmes on infectious diseases and Neurological Disorders"	27331134.00
5300000.00	P-21	Development of Versatile, portable software for Bio-informatics	5300000.00
603747.00	P-22	"Biotechnology for leather – towards cleaner processing"	603747.00
375999.00	P-23	"Development of PCR base assays for detection of GMO'S"	375999.00
600000.00	P-25	"Functional studies of Human Immuno - deficiency Virus Type– 2 (HIV-2) Viral protien X (VPX)"	600000.00
500000.00	P-26	Occurrence of Mutations in Non dividing cells of Escherichia Coli"	500000.00
260367.00	P-29	"Development of Hospital Surveillance system by advanced diagnostics method & Molecular DNA fingerprinting techniques"	260367.00
3746538.00	P-30	"Transcription termination and anti termination in E. Coli"	3746538.00
3131006.00	P-31	Role of K-ras in Lung type II epithelial cells	3131006.00
4857938.00	P-36	"Development of Artificial retina using Bacterio rhodospin and genetically engineered analogues "	4857938.00
358470.00	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"	358470.00
49738.00	P-40	"Antioxidants as a potential immuno adjuvant in anti tuberculosis immunotherapy"	49738.00
3894086.00	P-41	"Construction, characterization and analysis of expressed sequences from silkworm "	3894086.00
9500000.00	P-42	"Structural and functional studies on Mycobacterium tuberculosis heat shock proteins".	9500000.00
11644197.00	P-43	"A generalized mechanism of transcription termination in prokaryotes: a quest for mechanism based transcription inhibitors for microbial pathogens".	11970000.00
3313021.00	P-45	Specialized chromatin structures as epigenetic imprints to distinguish parental alleles".	3313021.00
416137.00	P-46	"Effect of reactive oxygen species (ROS) on immune response : Relevance in immunosuppression and Pathogenesis"	416137.00
377567.00	P-47	Research cum Training for DRDO Programme	377567.00
1413292.00	P-48	"Molecular characterization of human liver stem cells for use in the treatment of hepatic diseases".	1413292.00
198095.00	P-50	"Cervical cancer prevention by multiple strategies in rural community in Andhra pradesh"	198095.00
401738.00	P-51	"Understanding the mechanism of doxorubicin resistance in breast cancer celline MCF-7"	401738.00
1359129.00	P-52	"Nucleo Cytoplasmic transport of HIV – 1 Vpr"	1359129.00
1114495.00	P-53	Collaborative research project on molecular ecology and systematics	1114495.00
1163764.00	P-56	"Genetics of transcription-replication interplay and of stress adaptation in bacteria"	1163764.00
2131403.00	P-57	Improved genome annotation through a combination of machine learning and experimental methods: Plasmodium falciparum as a case study.	2131403.00
63000.00	P-58	"Indo-Malaysian collaboration in Bioinformatics: Development and maintenance of a web-portal hosting databases and tools of common interest"	63000.00
32924033.00	P-59	"An integrated Approach towards understanding the biology of Mycobacterium tuberculosis: Genetic, biochemical, immunological and structural analyses."	32974662.00
5720800.00	P-60	"National Database of Prevalent Genetic Disorders in India: Development, Curation and Services"	5720800.00
4308314.00	P-62	"HIV – 1 Pathogenesis: Role of Integrate in Reverse Transcription and Nuclear Transport of Viral Genome"	4308314.00
9637574.00	P-63	"Upgradation of the existing computing infrastructure at the Bioinformatics facility at CDFD"	9637574.00
600585.00	P-64	Biotechnology for Leather: Towards cleaner processing phase-II	600585.00
260000.00	P-65	"Molecular, genetic and functional analysis of the chromosomal plasticity region of the gastric pathogen Helicobater pylori"	260000.00

Annexure - II  
**CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS**  
**Details of Fixed Assets Fund (Capitalised portion of Project Grants)**  
**for the year ended 31st March 2010**

Amount in Rs.

Previous year	P No	Particulars	Current Year
16784524.00	P-65A	APEDA - CDFD Centre for Basmati DNA Analysis	16909024.00
267906.00	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	264430.00
622747.00	P-67	Identification of novel Esophageal Squamous cell carcinoma (ESCC) genes by using a combination of array-based CGH and gene expression micro arrays	622747.00
235593.00	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)	235593.00
1012807.00	P-70	Identification of disease causing mutations in familial hypertrophic cardiomyopathy (FHC) patients from Andhra Pradesh	1012807.00
1335675.00	P-71	Referral Centre for Genetic fidelity testing of tissue culture raised plants	1573795.00
45653.00	P-72	Nuances of Non coding DNA near insulin-responsive genes	45653.00
1000000.00	P-74	Molecular basic of insect plant interactions in rice under the national fund for basic and strategic research in agriculture	1000000.00
33672.00	P-75	Preparing blueprint for the macromolecular crystallography beamline at Indus-II synchrotron source	33672.00
253299.00	P-76	A study of Molecular Markers in childhood Autism with special references to nuclear factors - APPA B"	245266.00
1387301.00	P-77	Functional characterization of Mycobacterium tuberculosis PE/PPE proteins having SH3 binding domain: Understanding their role in modulating macrophage functions	1541411.00
356328.00	P-79	Understanding the role of AGE proteins in inducing inflammatory responses and its regulation	496826.00
4080575.00	P-80	Referral Centre for Detection of Genetically Modified Foods employing DNA - based Markets	4192480.00
0.00	P-81A	Financial Assistance for award of JC Bose Fellowship to Dr J Gowrishankar	77690.00
468000.00	P-82	Functional Genomic Analysis of Candida Glabrata-macrophage	1137050.00
912255.00	P-83	Prokaryotic Transcription Termination Factor, Rho: Mechanism of Action and Biology	912255.00
388583.00	P-83A	Understanding the mechanism of Azadirachtin-mediated cell signaling: role in anti-inflammation and anti-tumorigenesis	388583.00
44854.00	P-84	Preparing for tuberculosis vaccine efficacy trials: Baseline epidemiology, improved diagnosis, markers of protection and phase I/II trials	44854.00
431538.00	P-84A	Human epigenetic to the rescue of Human Identification process: Enriching human DNA from DNA mixture employing antibodiesdirected against 5-methylcytosine followed by whole genome amplification	1139040.00
300000.00	P-89	Characterization of Mycobacterium tuberculosis transcription machinery and Bacteriophage metagenomics	371200.00
734087.00	P-90	Role of Yapsins in the Pathobiology of Candida Glabrata	1003190.00
111600.00	P-91	DNMT3L: Epigenetic correlation with cancer	924523.00
486250.00	P-92	Swarnajayanti Fellowship: Designing transcription anti-terminators: a novel approach for making new inhibitors of gene expression	6505192.00
86300.00	P - 93	Virtual Centre of Excellence on multidisciplinary approaches aimed at interventions against tuberculosis	2104275.00
122909.00	P - 95	Construction of regulatory networks in prokaryotes through protein: Protein interaction predictions and transcription regulation predictions.	246320.00
0.00	P- 97	Proteome-wide Analysis of Serine pyrophosphorylation by inositol pyrophosphates	581900.00
0.00	P- 98	Role of cell - cell signaling mediated by Diffusible signaling factor (DSF) in Xanthomonas virulence	2159680.00
0.00	P- 99	Role of inositol Pyrophosphates in eukaryotic cell growth, proliferation and ribosomae biogenesis	1648300.00
0.00	P - 100	Effect of reactive oxygen species on T-Cell immune response: An approach to understand the molecular mechanism of immunosuppression during tuberculosis" - National Bioscience Award	17784.00
0.00	P-101	Role of inositol pyrophosphates in cell physiology: Investigating the biochemical significance of protein pyrophosphorylation - Senior Fellowship	1425442.00
0.00	P-102	Understanding the role of Mycobacterium tuberculosis heat shockprotein 60 as Th1/Th2 immuno modular	450000.00
2601795.00	COE-I	COE for Genetics and Genomics of silkmoths	8722699.00
2875676.00	COE-II	DBT Centre of Excellence for Microbial Biology	8534636.00
<b>198778608.00</b>		<b>Total</b>	<b>228743430.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS FOR THE YEAR ENDED 31st MARCH 2010 Annexure: A Forming part of Receipts & Payment a/c		
Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	<b>I-Remittances</b>	
214560.00	GSLI	265031.00
3771984.00	Income tax	4403709.00
582060.00	LIC	662389.00
3390.00	Other Loans	0.00
317924.00	Professional tax	388447.00
2623468.00	Works Tax	447534.00
163535.00	Service Tax	188478.00
367890.00	PPF	595385.00
138735.00	Donations	0.00
<b>8183546.00</b>		<b>6950973.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS FOR THE YEAR ENDED 31st MARCH 2010 Annexure: B Forming part of Receipts & Payment a/c		
Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	<b>T.D.S.Recoveries</b>	
555937.00	TDS on professional service	673378.00
3798894.00	TDS on Rent	2891099.00
2150830.00	TDS on works / Contractors	946429.00
<b>6505661.00</b>		<b>4510906.00</b>

**CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS  
FOR THE YEAR ENDED 31st MARCH 2010**

**Annexure: C Forming part of Receipts & Payment a/c**

Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	<b>Advance refunds/recovery/Adjst.</b>	
2697481.00	Advances for Consumables	3506494.00
1768637.00	Advances for Equipment	7755111.00
426160.00	Advances to staff for L.P	265561.00
9042083.00	Deposits - Customs duty	6044413.00
845400.00	EMD / Margin money	736700.00
45750.00	Festival Advances recovery	79350.00
29400.00	H B A	477703.00
203000.00	HSD, LSD & TSD	161500.00
420700.00	LTC Advances	694219.00
444804.00	Other Advances	684642.00
90461.00	Revolving Advances	173590.00
5600036.00	TA/DAAvances	3422034.00
28848.00	Vehicle / Conveyance advance	35268.00
0.00	Royalties & Consultancy	7250000.00
1934705.00	Security Deposit / Retension Money	195937.00
14700.00	Computer Advance	25200.00
0.00	Rent advance	2087154.00
<b>23592165.00</b>		<b>33594876.00</b>

**CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS  
FOR THE YEAR ENDED 31st MARCH 2010**

**Annexure: D Forming part of Receipts & Payment a/c**

Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	<b>Projects - Receipts</b>	
0.00	P - 22	327500.00
2090042.00	P - 45	0.00
0.00	P - 53	1904000.00
270000.00	P - 60	0.00
640000.00	P - 64	679000.00
581881.00	P - 65A	17028704.00
1469000.00	P - 67	0.00
0.00	P - 69	845840.00
616000.00	P - 70	628000.00
906000.00	P - 71	0.00
700000.00	P - 73	0.00
1726300.00	P - 74	666200.00
0.00	P- 77	2709000.00
0.00	P- 80	300000.00
300000.00	P- 80A	0.00
600000.00	P- 81A	800000.00
1265000.00	P- 82	1480000.00
0.00	P- 83	1170400.00
0.00	P- 83A	550000.00
0.00	P- 84	1298850.00
1265000.00	P- 84A	1480000.00
0.00	P- 85	400000.00
66000.00	P- 87	0.00
740000.00	P - 88	740000.00
300000.00	P - 89	0.00
2417000.00	P - 90	626000.00
2295000.00	P - 91	760000.00
10367600.00	P - 92	0.00
5281000.00	P - 93	0.00
0.00	P - 95	1006020.00
0.00	P - 96	1737438.00
0.00	P - 97	2027000.00
0.00	P - 98	3947000.00
0.00	P - 99	4225000.00
0.00	P - 100	300000.00
0.00	P - 101	18792749.00
0.00	P - 102	481319.00
3729000.00	COE- I	7821000.00
19268000.00	COE- II	4589000.00
<b>56892823.00</b>		<b>79320020.00</b>

**CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS  
FOR THE YEAR ENDED 31st MARCH 2010**

**Annexure: E Forming part of Receipts & Payment a/c**

Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	<b>Advances</b>	
317900.00	Advance to staff for Local purchases	238420.00
17755095.00	Advances for Consumables	13360502.00
7752682.00	Advances for Equipment	63536388.00
5013407.00	Deposits for Custom duty etc.,	4044415.00
130000.00	EMD / Margin money	2088414.00
73500.00	Festival advances paid	93000.00
153500.00	LSD , HSD & TSD	60000.00
475475.00	LTC Advance	1182112.00
1013884.00	Other Advances	1343177.00
117000.00	Revolving Advance	151000.00
6173439.00	TA/ DA Advance	2563966.00
3480000.00	Royalties & Consultancy	0.00
55947.00	Security Deposit / Retension Money	943323.00
681501.00	Indo-Japan Workshop	0.00
1983626.00	Indo-US Workshop	0.00
199569.00	DST Expert Meeting	0.00
0.00	HBA	7758.00
0.00	Vehicle Advance	600.00
<b>45376525.00</b>		<b>89613075.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS FOR THE YEAR ENDED 31st MARCH 2010 Annexure: F Forming part of Receipts & Payment a/c		
Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	<b>I-Remittances paid</b>	
213519.00	GSLI	202410.00
3752386.00	Income tax	4386020.00
582060.00	LIC	662389.00
3390.00	Other Loans	0.00
317314.00	Professional tax	387697.00
2317208.00	Works Tax	621405.00
163607.00	Service Tax	188478.00
361890.00	PPF	595385.00
138735.00	Donations	0.00
<b>7850109.00</b>		<b>7043784.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS FOR THE YEAR ENDED 31st MARCH 2010 Annexure: G Forming part of Receipts & Payment a/c		
Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	<b>TDS remitted in Central Govt. a/c</b>	
331512.00	TDS on professional service	812934.00
2746190.00	TDS on Rent	4202516.00
2175689.00	TDS on works / Contractors	1010629.00
<b>5253391.00</b>		<b>6026079.00</b>



**CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS  
FOR THE YEAR ENDED 31st MARCH 2010**

**Annexure: H Forming part of Receipts & Payment a/c**

Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	<b>Projects - Expenditure</b>	
0.00	P - 4	1000000.00
156069.00	P - 15	0.00
234582.00	P - 19	0.00
25160.00	P - 21	0.00
327500.00	P - 22	327420.00
4619074.00	P - 42	1359078.00
5072263.00	P - 43	338663.00
0.00	P - 46	339070.00
0.00	P - 47	0.00
289299.00	P - 49	0.00
248744.00	P - 49A	157056.00
0.00	P - 50	57663.00
755801.00	P - 53	1195711.00
0.00	P - 57	3394100.00
5172.00	P - 58	267773.00
400000.00	P - 58A	200000.00
1367133.00	P - 59	59540.00
207775.00	P - 60	15485.00
35761.00	P - 62	0.00
250985.00	P - 64	659403.00
540383.00	P - 65	0.00
3388111.00	P - 65A	1271672.00
342099.00	P - 66	-3476.00
1374240.00	P - 67	9058.00
175874.00	P - 68	0.00
786884.00	P - 69	98395.00
539080.00	P - 70	151467.00
1293773.00	P - 71	2036094.00
530000.00	P - 72	291935.00
1023420.00	P - 73	315249.00
2171981.00	P - 74	497421.00
254011.00	P - 75	0.00
428241.00	P - 76	-8033.00

**CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS  
FOR THE YEAR ENDED 31st MARCH 2010**

**Annexure: H Forming part of Receipts & Payment a/c**

Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	<b>Projects - Expenditure</b>	
2089814.00	P - 77	1954959.00
136730.00	P - 78	0.00
1369951.00	P - 79	913651.00
2683008.00	P - 80	1436927.00
300000.00	P - 80A	0.00
444190.00	P - 81	443800.00
800000.00	P - 81A	800000.00
1569989.00	P - 82	1599413.00
1910096.00	P - 83	1490258.00
763333.00	P - 83A	585692.00
845276.00	P - 84	0.00
1331538.00	P - 84A	1857502.00
955405.00	P - 85	1058096.00
257614.00	P - 86	256095.00
165756.00	P - 87	0.00
600000.00	P - 88	597535.00
300000.00	P - 89	300000.00
1359460.00	P - 90	1310327.00
872121.00	P - 91	2008725.00
1103050.00	P - 92	9337864.00
429700.00	P - 93	4033440.00
252909.00	P - 95	874580.00
1470450.00	P - 96	1454003.00
0.00	P - 97	1444300.00
0.00	P - 98	3134093.00
0.00	P - 99	2561500.00
0.00	P - 100	300000.00
0.00	P - 101	3503948.00
0.00	P - 102	965000.00
8835245.00	COE - I	36127668.00
7467519.00	COE - II	17844214.00
<b>65156569.00</b>		<b>112224334.00</b>

**CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS  
FOR THE YEAR ENDED 31st MARCH 2010**

**Annexure: I Forming part of Balance sheet**

Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	<b>CDFD C.P.FUND ACCOUNT</b>	
13943836.32	Opening Balance	23241865.32
	<b>Add:</b>	
6887209.00	Employees subscription / refunds	5812355.00
0.00	Transfer from other departments	
4501331.00	Institute contribution (incl. Projects staff)	2765162.00
31495.00	Interest received	133561.00
25363871.32		31952943.32
2122006.00	Less:Advances/withdrawals/Transfer/ Adjst	4606306.00
<b>23241865.32</b>		<b>27346637.32</b>

**CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS  
FOR THE YEAR ENDED 31st MARCH 2010**

**Annexure: J Forming part of Balance sheet**

Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	<b>LOANS AND ADVANCES</b>	
52614706.00	Advances for Consumables	62468714.00
98337165.45	Advances for Equipment	154118442.45
261721.50	Advances to staff for L.P	234580.50
4944996.00	Royalties & Consultancy	0.00
25512.00	DBT PDF (Stipend receivable)	25512.00
45150.00	Festival Advance	58800.00
4310.00	G.S.L.I Recovery	4310.00
907246.00	Grant receivable - Host meetings	907246.00
391125.00	H B A	0.00
94479.00	LTC Advance	582372.00
4272939.00	Other Advances	4931474.00
0.00	Income Tax	0.00
2327723.00	Rent advance	240569.00
156255.00	Revolving Advances	133665.00
1493299.56	TA/DA Advance & Recoupments	635231.56
0.00	Vehicle / Conveyance advance	0.00
3000000.00	CDFD Staff Reserve Fund	3000000.00
1639.00	DBT JRF A/c (Stipend receivable)	1979945.00
4383756.00	EMRC A/c (Stipend receivable)	4788357.00
91233.00	ICMR A/c (Stipend receivable)	249141.00
681501.00	Indo - Japan Workshop	681501.00
10000000.00	NIMS - Advance	10000000.00
72.00	Service Tax	72.00
2034977.00	UGC (Stipend receivable)	250099.00
0.00	Advance for workshop	394494.00
0.00	CPF Subscription	26.00
<b>186069805.51</b>		<b>245684551.51</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS FOR THE YEAR ENDED 31st MARCH 2010 Annexure: K Forming part of Balance sheet		
Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	<b>DEPOSITS</b>	
4317957.00	A.P.Transco	4317957.00
13713169.00	Balmer Lawrie - Customs duty	11713171.00
35900.00	Gas agencies	35900.00
15000.00	Internet	15000.00
185000.00	Telephones	185000.00
47680.00	APSRTC	47680.00
12000.00	University Filling Station	12000.00
7407.00	Others	7407.00
<b>18334113.00</b>		<b>16334115.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS FOR THE YEAR ENDED 31st MARCH 2010 Annexure: L Forming part of Balance sheet		
Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	<b>INVESTMENT A/C</b>	
12270000.00	Internal resources / Core	12270000.00
67738000.00	Project Funds	57238000.00
16400000.00	Collaboration Funds	10600000.00
700000.00	Workshop funds	700000.00
<b>97108000.00</b>		<b>80808000.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS FOR THE YEAR ENDED 31st MARCH 2010 Annexure: M Forming part of Balance sheet		
Previous Year Amount Rs.	Particulars	Current Year Amount Rs.
	<b>CDFD C.P.FUND INVESTMENT A/C</b>	
660170.00	60229.549 Units of UTI BOND FUND	660170.00
276190.00	21616.5080 Units of UTI BOND FUND	276190.00
16202519.00	Fixed deposits	22202519.00
6102986.32	CDFD C.P.FUND a/c	4207758.32
<b>23241865.32</b>		<b>27346637.32</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD						
P-03 : D.B.T Project on "TRANSGENESIS & GENETIC BASIS OF PATHOGEN RESISTANCE IN THE SILKWORM, BombyxMori"						
PI: Dr J NAGARAJU						
RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010						
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	Equipment	0.00	
			0.00	Salaries - Manpower	0.00	
			0.00	Consumables	0.00	
			0.00	Travel	0.00	
			0.00	Contingencies	0.00	
0.00		0.00	630047.00		630047.00	
630047.00	Excess of expenditure over income	630047.00				
<b>630047.00</b>		<b>630047.00</b>	<b>630047.00</b>		<b>630047.00</b>	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD						
P-04 : APSSRDI Project on "SILKWORM BREEDING FOR PRODUCTIVITY IMPROVEMENT OF SILK"						
PI: Dr J NAGARAJU						
RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010						
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs	
1000000.00	Opening Balance	1000000.00	0.00	Collaborative research cost	0.00	
0.00	Grant in aid	0.00	0.00	Technical expertise	1000000.00	
			0.00	Training cost	0.00	
1000000.00		1000000.00	0.00	Closing balance	1000000.00	
			1000000.00		0.00	
<b>1000000.00</b>		<b>1000000.00</b>	<b>1000000.00</b>		<b>1000000.00</b>	

<p align="center"><b>P-09 - "CSIR, NMITLI Project on - Latent M.Tuberculosis: New targets, Drug delivery systems, Bio enhancers &amp; Therapeutics"</b>  <b>PI.: Dr SEYEDE HASNAIN</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
244305.00	<b>Opening Balance</b>	244305.00	0.00	Salaries- Manpower	0.00
0.00	Grant in aid	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
244305.00		244305.00	0.00	Closing Balance	0.00
			244305.00		244305.00
<b>244305.00</b>		<b>244305.00</b>	<b>244305.00</b>		<b>244305.00</b>

<p align="center"><b>P-10 : DST Project on "ROLE OF UPSTREAM SEQUENCE ELEMENTS IN HYPERACTIVATION OF TRANSCRIPTION FROM BACULOVIRUS POLYHEDRIN GENE PROMOTER" -</b>  <b>PI : Dr M D BASHYAM</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
0.00	<b>Opening Balance</b>	0.00	28332.00	Opening Balance	28332.00
0.00	Grant in aid	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		0.00	28332.00		28332.00
28332.00	Excess of expenditure over income	28332.00			
<b>28332.00</b>		<b>28332.00</b>	<b>28332.00</b>		<b>28332.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD					
P-13 : DBT Project on "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 01.04.2009 TO 31.03.2010					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
6737.00	<b>Opening Balance</b>	6737.00	0.00	Salaries- Manpower	0.00
0.00	Grant in aid	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
6737.00		6737.00	0.00	Closing balance	0.00
<b>6737.00</b>		<b>6737.00</b>	<b>6737.00</b>		<b>6737.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD					
P-15 : DBT Project on "THE HELICOBACTER PYLORI GENOME PROGRAMME - GENOME SEQUENCING, FUNCTIONAL ANALYSIS AND COMPARITIVE GENOMICS OF THE STRAINS OBTAINED FROM INDIAN PATIENTS"					
P.I.: Dr NIYAZ AHMED					
RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
156069.00	<b>Opening Balance</b>	0.00	0.00	Salaries - Manpower	0.00
0.00	Grant in aid	0.00	0.00	Consumables	0.00
			0.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Equipment	0.00
			156069.00	Project funds refund	0.00
156069.00			156069.00	Closing balance	0.00
<b>156069.00</b>		<b>0.00</b>	<b>156069.00</b>		<b>0.00</b>



CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD					
P-17 : DST Project on "STUDIES ON INOSITAL - PHOSPHATE SYNTHESIS - A NOVEL ENZYME FROM MYCOBACTERIUM TUBERCULOSIS - H37RV"					
P.I : Dr SHEKHAR C MANDE					
RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010					
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount
0.00	Opening Balance Grant in aid	0.00	687887.00	Opening Balance	687887.00
0.00		0.00	0.00	Salaries- Manpower	0.00
				Consumables	0.00
				Contingencies	0.00
				Travel	0.00
				Over heads	0.00
				Equipment	0.00
0.00		0.00	687887.00		687887.00
687887.00	Excess of expenditure over income	687887.00			
<b>687887.00</b>		<b>687887.00</b>	<b>687887.00</b>		<b>687887.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD					
P-18 : DST Project on "MAPPING OF RECEPTOR BINDING SITE ON THE EYTHROCYTE BINDING OF MALARIA PARASITE"					
P.I : Dr AKASH RANJAN					
RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010					
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount
0.00	Opening Balance Grant in aid	0.00	274286.00	Opening balance	274286.00
0.00		0.00	0.00	Consumables	0.00
				Contingencies	0.00
				Travel	0.00
				Overheads	0.00
				Equipment	0.00
0.00		0.00	274286.00		274286.00
274286.00	Excess of expenditure over income	274286.00			
<b>274286.00</b>		<b>274286.00</b>	<b>274286.00</b>		<b>274286.00</b>

<p align="center"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-19 : DBT Project on "CONSTRUCTION OF INTEGRATED RAPD, RFLP AND MICROSATELLITE LINKAGE MAP OF THE SILKWORM, BOMBYX MORI AND ITS CORRELATION WITH THE PHENOTYPIC LINKAGE MAP"</b>  <b>PI: Dr J NAGARAJU</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>									
Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year Amount	Rs	Payments	Current Year Amount	Rs
234582.00		<b>Opening Balance</b>		0.00		0.00	Salaries- Manpower		0.00
0.00		Grant in aid		0.00		0.00	Consumables		0.00
						0.00	Contingencies		0.00
						0.00	Travel		0.00
						0.00	Equipment		0.00
234582.00					234582.00		Project funds refund		0.00
					234582.00		Closing balance		0.00
<b>234582.00</b>				<b>0.00</b>	<b>234582.00</b>				<b>0.00</b>

<p align="center"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P - 20 : DBT Project on "Genomic Micro array R&amp;D programmes on infectious diseases and Neurological Disorders"</b>  <b>PI: Dr M D BASHYAM</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>									
Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year Amount	Rs	Payments	Current Year Amount	Rs
0.00		<b>Opening Balance</b>		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					1888111.00		Closing balance		1888111.00
1888111.00		Excess of expenditure over income		1888111.00		0.00			0.00
<b>1888111.00</b>				<b>1888111.00</b>	<b>1888111.00</b>				<b>1888111.00</b>

<p style="text-align: center;"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-21 : CSIR Project on "Development of Versatile portable software for Bio informatics"</b>  <b>PI : Dr SHEKHAR C MANDE</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>						
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs	
25160.00	<b>Opening Balance</b>	0.00	0.00	Salaries-Manpower	0.00	
0.00	Grant in aid	0.00	0.00	Consumables	0.00	
			0.00	Contingencies	0.00	
			0.00	Travel	0.00	
			0.00	Equipment	0.00	
			25160.00	Project funds refund	0.00	
25160.00			25160.00		0.00	
			0.00	Closing balance	0.00	
<b>25160.00</b>		<b>0.00</b>	<b>25160.00</b>		<b>0.00</b>	

<p style="text-align: center;"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-22 : CSIR Project on "Biotechnology for Leather towards cleaner processing"</b>  <b>PI : Dr J GOWRISHANKAR</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>						
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs	
327420.50	<b>Opening Balance</b>		0.00	Opening balance	79.50	
0.00	Grant in aid	0.00	0.00	Salaries- Manpower	0.00	
	Cheque cancelled	327500.00	0.00	Consumables	0.00	
			0.00	Contingencies	0.00	
			0.00	Travel	0.00	
			0.00	Equipment	0.00	
			327500.00	Project funds refund	327420.00	
327420.50		327500.00	327500.00		327499.50	
79.50	Excess of expenditure over income	0.00	0.00	Closing balance	0.50	
<b>327500.00</b>		<b>327500.00</b>	<b>327500.00</b>		<b>327500.00</b>	

<p style="text-align: center;"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-23: DBT Project on "Development of PCR base assays for detection of GMO'S"</b>  <b>PI : Dr J NAGARAJU</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>						
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs	
0.00	<b>Opening Balance</b>		34495.00	Opening balance	34495.00	
0.00	Grant in aid	0.00	0.00	Salaries- Manpower	0.00	
		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	
34495.00	Excess of expenditure over income	0.00	34495.00	Closing balance	34495.00	
<b>34495.00</b>		<b>34495.00</b>	<b>34495.00</b>		<b>34495.00</b>	

<p style="text-align: center;"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-25 : DBT Project on "Functional studies of Human Immuno deficiency virus type-2(HIV-2), Viral protein X(VPX)"</b>  <b>PI : Dr S MAHALINGAM</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>						
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs	
0.00	<b>Opening Balance</b>		529111.00	Opening balance	529111.00	
0.00	Grant in aid	0.00	0.00	Salaries- Manpower	0.00	
		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	
529111.00	Excess of expenditure over income	0.00	529111.00		529111.00	
<b>529111.00</b>		<b>529111.00</b>	<b>529111.00</b>		<b>529111.00</b>	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD P-26 : IFCPAR Project on "Occurrence of Mutations in Non-dividing cells of Escherichia coli" Pi: Dr J GOWRISHANKAR RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010						
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs	
0.00	<b>Opening Balance</b>	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		0.00	79533.00		79533.00	
79533.00	Excess of expenditure over income	79533.00	79533.00		79533.00	
<b>79533.00</b>		<b>79533.00</b>	<b>79533.00</b>		<b>79533.00</b>	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD P-28 : IFCPAR Project on "Baculovirus - Resistance in transgenic silkworms" P.I : Dr J NAGARAJU RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010						
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs	
0.00	<b>Opening Balance</b>	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		0.00	37624.00		37624.00	
37624.00	Excess of expenditure over income	37624.00	37624.00		37624.00	
<b>37624.00</b>		<b>37624.00</b>	<b>37624.00</b>		<b>37624.00</b>	

<p style="text-align: center;"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-29 : DST Project on "Development of Hospital infection surveillance system by advanced diagnostics method &amp; Molecular DNA fingerprinting techniques"</b>  <b>PI : Dr K PRASHANTH</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
0.00	<b>Opening Balance</b> Grant in aid	0.00	310302.00	Opening balance	310302.00
0.00		0.00	0.00	Salaries- Manpower	0.00
				Consumables	0.00
				Contingencies	0.00
				Travel	0.00
				Overheads	0.00
				Equipment	0.00
0.00		0.00	310302.00		310302.00
310302.00	Excess of expenditure over income	310302.00			
<b>310302.00</b>		<b>310302.00</b>	<b>310302.00</b>		<b>310302.00</b>

<p style="text-align: center;"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-30 : NIH Project on "Transcription termination and anti termination in E. Coli"</b>  <b>PI : Dr RANJAN SEN</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
2124902.00	<b>Opening Balance</b> Grant in aid	2124902.00	0.00	Salaries-Manpower	0.00
0.00		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
2124902.00		2124902.00	0.00		0.00
			2124902.00	Closing balance	2124902.00
<b>2124902.00</b>		<b>2124902.00</b>	<b>2124902.00</b>		<b>2124902.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD P-31 : NIH Project on "Functioning of K-ras in lung type II epithelial cells" P.I : Dr GAYATRI RAMAKRISHNA RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
827383.00	<b>Opening Balance</b>	827383.00	0.00	Salaries- Manpower	0.00
0.00	Grant in aid	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
827383.00		827383.00	0.00		0.00
<b>827383.00</b>		<b>827383.00</b>	827383.00	Closing balance	827383.00
			<b>827383.00</b>		<b>827383.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD P-33: DBT Project on "Molecular and Epidemiological characterisation of cryptosporidium - An enteric protozoon parasite" P.I : Dr A RADHA RAMA DEVI RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
0.00	<b>Opening Balance</b>	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		0.00	234000.00		234000.00
234000.00	Excess of expenditure over income	234000.00	234000.00		
<b>234000.00</b>		<b>234000.00</b>	<b>234000.00</b>		<b>234000.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD						
P-34 : DBT Project on "Molecular analysis of lepidopteran - specific immune proteins from silkworms"						
PI: Dr J NAGARAJU						
RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010						
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount	Rs
26334.00	<b>Opening Balance</b>	26334.00	0.00	Salaries- Manpower		0.00
0.00	Grant in aid	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
26334.00		26334.00	0.00			0.00
<b>26334.00</b>		<b>26334.00</b>	26334.00	Closing balance		26334.00
			<b>26334.00</b>			<b>26334.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD						
P-35 : DST Project on "Identification, Characterization and physical mapping of Z-chromosome linked genes of the silkworm, Bombyx mori"						
PI: Dr J NAGARAJU						
RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010						
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount	Rs
0.00	<b>Opening Balance</b>	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		0.00	0.00			0.00
283883.00	Excess of expenditure over income	283883.00	0.00			0.00
<b>283883.00</b>		<b>283883.00</b>	<b>283883.00</b>			<b>283883.00</b>



<b>P-36 : DBT Multicentric project on "Development of artificial retina using Bacteriorhodospin and genetically engineered analogues" at CDFD &amp; MRC - P.J : Dr SHEKAR C MANDE</b> <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b>						
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount	Current Year Rs
2073896.00	<b>Opening Balance</b>	2073896.00	0.00	Salaries- Manpower		0.00
0.00	Grant in aid	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
2073896.00		2073896.00	0.00			0.00
			2073896.00	Closing balance		2073896.00
<b>2073896.00</b>		<b>2073896.00</b>	<b>2073896.00</b>			<b>2073896.00</b>

<b>P-40 : DST Project on "Antioxidants as a potential immuno-adjutant in anti-tuberculosis immunotherapy"</b> <b>P.I : Dr SANGITA MUKHOPADHYAY</b> <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b>						
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount	Current Year Rs
0.00	<b>Opening Balance</b>	0.00	226058.00	Opening balance		226058.00
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		0.00	226058.00			226058.00
226058.00	Excess of expenditure over income	226058.00	226058.00			226058.00
<b>226058.00</b>		<b>226058.00</b>	<b>226058.00</b>			<b>226058.00</b>

<p align="center"><b>P-41 : DBT Project on "Construction and characterization and analysis of expressed sequences from silkworm"</b>  <b>PI : Dr J NAGARAJU</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>						
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs	
1873605.00	<b>Opening Balance</b>	1873605.00	0.00	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	
1873605.00		1873605.00	0.00		0.00	
0.00	Excess of expenditure over income	0.00	1873605.00	Closing balance	1873605.00	
<b>1873605.00</b>		<b>1873605.00</b>	<b>1873605.00</b>		<b>1873605.00</b>	

<p align="center"><b>P-42 : The Wellcome Trust, UK Project on "Structural and functional studies on Mycobacterium tuberculosis heat shock proteins"</b>  <b>PI : Dr SHEKAR C MANDE</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>						
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs	
3758688.00	<b>Opening Balance</b>	0.00	0.00	Opening balance	860386.00	
0.00	Grant in aid	0.00	748306.00	Salaries- Manpower	60228.00	
			3200000.00	Consumables	0.00	
			0.00	Contingencies	0.00	
			170768.00	Travel	0.00	
			500000.00	Overheads	0.00	
			0.00	Equipment	0.00	
			0.00	Funds transferred to P-84	1298850.00	
3758688.00		0.00	4619074.00		2219464.00	
860386.00	Excess of expenditure over income	2219464.00	0.00	Closing balance	0.00	
<b>4619074.00</b>		<b>2219464.00</b>	<b>4619074.00</b>		<b>2219464.00</b>	

<p align="center"><b>P-43 : The Wellcome Trust, UK Project on "A generalised mechanism of transcription termination in prokaryotes: A quest for mechanism based transcription inhibitors for microbial pathogens"</b>  <b>PI: Dr.RANJAN SEN</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
6164974.70	<b>Opening Balance</b>	1092711.70	526666.00	Salaries- Manpower	12860.00
0.00	Grant in aid	0.00	3000000.00	Consumables	0.00
			500000.00	Contingencies	0.00
			160338.00	Travel	0.00
			0.00	Overheads	0.00
			885259.00	Equipment	325803.00
6164974.70		1092711.70	5072263.00		338663.00
			1092711.70	Closing balance	754048.70
<b>6164974.70</b>		<b>1092711.70</b>	<b>6164974.70</b>		<b>1092711.70</b>

<p align="center"><b>P-44 : DBT Project on "Understanding the role of Ras and NO /INOS signalling in promotion of hepatocellular carcinomas with persistent HBV infection"</b>  <b>PI : Dr GAYATRI RAMAKRISHNA</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
0.00	<b>Opening Balance</b>	0.00	447412.00	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
			10126.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
0.00		0.00	457538.00		457538.00
457538.00	Excess of expenditure over income	457538.00			
<b>457538.00</b>		<b>457538.00</b>	<b>457538.00</b>		<b>457538.00</b>

<p align="center"><b>P-45 : The Wellcome Trust, UK Project on "Specialised chromatin structures as epigenetic imprints to distinguish parental alleles"</b>  <b>PI: Dr SANJEEV KHOSLA</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
0.00	<b>Opening Balance</b>	624070.00	1465972.00	Opening balance	0.00
2090042.00	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
2090042.00		624070.00	1465972.00		0.00
0.00	Excess of expenditure over income		624070.00	Closing Balance	624070.00
<b>2090042.00</b>		<b>624070.00</b>	<b>2090042.00</b>		<b>624070.00</b>

<p align="center"><b>P-46 : DBT Project on "Effect of reactive oxygen species (ROS) on immune response: Relevance in Immunosuppression and Pathogenesis"</b>  <b>PI: Dr SANGITA MUKHOPADHYAY</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
339070.00	<b>Opening Balance</b>	339070.00	0.00	Salaries- Manpower	0.00
0.00	Grant in aid	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	Funds refund	339070.00
339070.00		339070.00	0.00		339070.00
			339070.00	Closing balance	0.00
<b>339070.00</b>		<b>339070.00</b>	<b>339070.00</b>		<b>339070.00</b>

<p style="text-align: center;"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-47 DRDO - DBT Project on " Research Cum Training for DRDO Programme"</b>  <b>PI : Dr J GOWRISHANKAR, Dr S MAHALINGAM, Dr SHEKAR C MANDE, Dr J NAGARAJU &amp; Dr NIYAZ AHMED</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>						
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount	
0.00	<b>Opening Balance</b>	0.00	1586965.00	Opening balance	1586965.00	
0.00	Grant in aid	0.00	0.00	Salaries- Manpower	0.00	
				Consumables	0.00	
				Contingencies	0.00	
				Travel	0.00	
				Overheads	0.00	
				Equipment	0.00	
1586965.00	Excess of expenditure over income	1586965.00	1586965.00			
<b>1586965.00</b>		<b>1586965.00</b>	<b>1586965.00</b>		<b>1586965.00</b>	

<p style="text-align: center;"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-48 DBT Project on " Molecular Characterization of human liver stem cells for use in the treatment of hepatic diseases"</b>  <b>PI: Dr SANJEEV KHOSLA</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>						
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount	
151826.00	<b>Opening Balance</b>	151826.00	0.00	Salaries- Manpower	0.00	
0.00	Grant in aid	0.00	0.00	Consumables	0.00	
				Contingencies	0.00	
				Travel	0.00	
				Overheads	0.00	
				Equipment	0.00	
151826.00		151826.00	0.00			
			151826.00	Closing balance	151826.00	
<b>151826.00</b>		<b>151826.00</b>	<b>151826.00</b>		<b>151826.00</b>	

<p align="center"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-49 : DBT Project on "The Mycobacterium W genome program: Complete genome sequencing and comparative genomics"</b>  <b>PI: Dr SEYEDE HASNAIN</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>						
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount	Rs
289299.00	<b>Opening Balance</b>		1597401.00	Opening Balance		0.00
0.00	Grant in aid	0.00	0.00	Opening Balance		0.00
		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	Equipment		0.00
			289299.00	Project funds refund		0.00
289299.00		0.00	289299.00			0.00
0.00	Excess of expenditure over income	0.00	0.00	Closing balance		0.00
<b>289299.00</b>		<b>0.00</b>	<b>289299.00</b>			<b>0.00</b>

<p align="center"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-49 A: "Grant sanctioned by International Atomic Energy"</b>  <b>PI: Dr J NAGARAJU</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>						
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount	Rs
876113.00	<b>Opening Balance</b>	627369.00	0.00	Salaries- Manpower		0.00
0.00	Grant in aid	0.00	0.00	Consumables		0.00
			0.00	Contingencies		0.00
			248744.00	Travel		157056.00
			0.00	Overheads		0.00
			0.00	Equipment		0.00
			248744.00			157056.00
876113.00		627369.00	627369.00	Closing balance		470313.00
<b>876113.00</b>		<b>627369.00</b>	<b>876113.00</b>			<b>627369.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD						
P-50: DBT Project on " Cervical Cancer prevention by multiple strategies in rural community in Andhra Pradesh"						
PI: Dr GAYATHRI RAMAKRISHNA						
RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010						
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount	Rs
57663.00	<b>Opening Balance</b>	57663.00	0.00	Salaries- Manpower		0.00
0.00	Grant in aid	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	Funds refund		57663.00
57663.00		57663.00	0.00	Closing balance		57663.00
<b>57663.00</b>		<b>57663.00</b>	<b>57663.00</b>			<b>57663.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD						
P-51: DST Project on " Understanding the mechanism of doxorubicin resistance in breast cancer celline MCF - 7						
- PI : Dr SUNIL KUMAR MANNA						
RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010						
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount	Rs
0.00	<b>Opening Balance</b>	0.00	284065.00	Opening Balance	284065.00	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		0.00	284065.00			284065.00
284065.00	Excess of expenditure over income	284065.00				
<b>284065.00</b>		<b>284065.00</b>	<b>284065.00</b>			<b>284065.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD						
P-52: DBT Project on " Nucleo Cytoplasmic transport of HIV - 1 Vpr"						
P.I. Dr S MAHALINGAM & Dr SUNIL KUMAR MANNA						
RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010						
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs	
0.00	<b>Opening Balance</b>	0.00	1231118.00	Opening Balance	1231118.00	
0.00	Grant in aid	0.00		Salaries- Manpower	0.00	
				Consumables	0.00	
				Contingencies	0.00	
				Travel	0.00	
				Overheads	0.00	
				Equipment	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	
<b>1231118.00</b>		<b>1231118.00</b>	<b>1231118.00</b>		<b>1231118.00</b>	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD						
P-53: DBT Project on " Collaborative Research Project on Molecular Ecology and Systematics"						
P.I: Dr J NAGARAJU						
RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010						
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs	
47512.00	<b>Opening Balance</b>	0.00	0.00	Opening Balance	708289.00	
0.00	Grant in aid	0.00	161633.00	Salaries- Manpower	477437.00	
		1904000.00	500000.00	Consumables	500000.00	
			50000.00	Contingencies	0.00	
			44168.00	Travel	12768.00	
			0.00	Workshop / Training	205506.00	
			0.00	Overheads	0.00	
			0.00	Equipment	0.00	
47512.00		1904000.00	755801.00		1904000.00	
708289.00	Excess of expenditure over income	0.00	0.00	Closing balance	0.00	
<b>755801.00</b>		<b>1904000.00</b>	<b>755801.00</b>		<b>1904000.00</b>	



CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD					
P-54: ICMR Project on "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 01.04.2009 TO 31.03.2010					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
0.00	<b>Opening Balance</b>	0.00	37877.00	Opening balance	37877.00
0.00	Grant in aid	0.00	0.00	Salaries- Manpower	0.00
		0.00	0.00	Consumables	0.00
		0.00	0.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	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
<b>37877.00</b>		<b>37877.00</b>	<b>37877.00</b>		<b>37877.00</b>

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CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD					
P-55: DBT Project on " Identification of DNA Markers for baculovirus resistance in silkworm, Bombyx mori"					
P.I. Dr J NAGARAJU					
RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
224.00	<b>Opening Balance</b>	224.00	0.00	Salaries- Manpower	0.00
0.00	Grant in aid	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
224.00		224.00	0.00		0.00
			224.00	Closing Balance	224.00
<b>224.00</b>		<b>224.00</b>	<b>224.00</b>		<b>224.00</b>

<p style="text-align: center;"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-56: DBT Project on " Genetics of transcription - replication interplay and of stress adaptation in bacteria"</b>  <b>PI: Dr J GOWRISHANKAR</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>						
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount	
0.00	<b>Opening Balance</b>	0.00	1231164.00	Opening Balance	1231164.00	
0.00	Grant in aid	0.00	0.00	Salaries- Manpower	0.00	
				Consumables	0.00	
				Contingencies	0.00	
				Travel	0.00	
				Overheads	0.00	
				Equipment	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	
<b>1231164.00</b>		<b>1231164.00</b>	<b>1231164.00</b>		<b>1231164.00</b>	

<p style="text-align: center;"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-57: NMITLI Project on " Improved Genome Annotation through a combination of machine learning and experimental methods"</b>  <b>PI: Dr AKASH RANJAN</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>						
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount	
3394100.00	<b>Opening Balance</b>	3394100.00	0.00	Salaries- Manpower	59532.00	
0.00	Grant in aid	0.00	0.00	Consumables	0.00	
				Contingencies	0.00	
				Travel	0.00	
				Overheads	0.00	
				Equipment	0.00	
				Funds transferred/ refund	3334568.00	
3394100.00		3394100.00	3394100.00	Closing Balance	3394100.00	
<b>3394100.00</b>		<b>3394100.00</b>	<b>3394100.00</b>		<b>3394100.00</b>	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD P-58: DBT Project on "Indo-Malaysian Collaboration in Bioinformatics: Development and maintenance of a web-portal hosting databases and tools of common interest" P.I. : Dr H A NAGARAJRAM RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010						
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs	
272945.00	<b>Opening Balance</b>	267773.00	5172.00	Salaries- Manpower	0.00	
0.00	Grant in aid	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	Funds refund	267773.00	
272945.00		267773.00	5172.00	Closing Balance	267773.00	
<b>272945.00</b>		<b>267773.00</b>	<b>272945.00</b>		<b>267773.00</b>	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD P-58A: DRR Project on "Functional Genomics on Rice" P.I. : Dr J NAGARAJU RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010						
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs	
600000.00	<b>Opening Balance</b>	200000.00	0.00	Salaries- Manpower	0.00	
0.00	Grant in aid	0.00	200000.00	Consumables	200000.00	
			0.00	Contingencies	0.00	
			0.00	Travel	0.00	
			0.00	Overheads	0.00	
			0.00	Equipment	0.00	
			200000.00	Transfer to Core	00.00	
600000.00		200000.00	400000.00	Closing Balance	200000.00	
0.00	Excess of expenditure over income	0.00	200000.00		0.00	
<b>600000.00</b>		<b>200000.00</b>	<b>600000.00</b>		<b>200000.00</b>	

<p style="text-align: center;"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-59: DBT Project on "An integrated Approach towards understanding the biology of Mycobacterium tuberculosis: Genetic, biochemical, immunological and structural analyses"</b>  <b>PI. - Dr SE HASNAIN, Dr J GOWRISHANKAR, Dr SHEKHAR C MANDE &amp; Dr RANJAN SEN</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>					
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount
0.00	<b>Opening Balance</b>	0.00	788351.00	Opening Balance	2155484.00
0.00	Grant in aid	0.00	217133.00	Salaries- Manpower	8911.00
			1000000.00	Consumables	0.00
			1500000.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	50629.00
0.00		0.00	2155484.00	Closing Balance	2215024.00
2155484.00	Excess of expenditure over income	2215024.00	0.00		0.00
<b>2155484.00</b>		<b>2215024.00</b>	<b>2155484.00</b>		<b>2215024.00</b>

<p style="text-align: center;"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-60: DBT Project on "National Database of Prevalent Genetic Disorders in India: Development, Curation and Services"</b>  <b>PI: Dr H A NAGARAJARAM</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>					
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount
435384.00	<b>Opening Balance</b>	497609.00	152775.00	Salaries- Manpower	15485.00
270000.00	Grant in aid	0.00	0.00	Consumables	0.00
			20000.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			35000.00	Equipment	0.00
705384.00		497609.00	207775.00	Closing Balance	15485.00
<b>705384.00</b>		<b>497609.00</b>	<b>705384.00</b>		<b>497609.00</b>

<p align="center"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-61: DST Project on "Dissection of a novel phenotype of lethal accumulation of potassium in Escherichia coli mutants defective in thioredoxin / thioredoxin reductase and nucleoid protein H-NS"</b>  <b>PI: ABHIJIT A SARDESAI</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>									
Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year Amount	Rs	Payments	Current Year Amount	Rs
0.00		<b>Opening Balance</b>			280000.00		Opening balance	280000.00	
0.00		Grant in aid		0.00	0.00		Salaries- Manpower	0.00	
				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				0.00	280000.00			280000.00	
280000.00		Excess of expenditure over income		280000.00					
<b>280000.00</b>				<b>280000.00</b>				<b>280000.00</b>	

<p align="center"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-62: DBT Project on "HIV-1 Pathogenesis: Role of Integrate in Reverse Transcription and Nuclear Transport of Viral Genome"</b>  <b>PI: Dr S MAHALINGAM</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>									
Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year Amount	Rs	Payments	Current Year Amount	Rs
0.00		<b>Opening Balance</b>			243167.00		Opening Balance	278928.00	
0.00		Grant in aid		0.00	6903.00		Salaries- Manpower	0.00	
				0.00	0.00		Consumables	0.00	
					1491.00		Contingencies	0.00	
					27367.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	0.00	
0.00				0.00	278928.00			278928.00	
278928.00		Excess of expenditure over income		278928.00			Closing Balance		0.00
<b>278928.00</b>				<b>278928.00</b>				<b>278928.00</b>	

<p align="center"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-63: DBT Project on "Upgradation of the existing computing infrastructure at the Bioinformatics facility at CDFD"</b>  <b>PI: Dr. SEYED E HASNAIN</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
0.00	<b>Opening Balance</b>	0.00	837574.00	Opening balance	837574.00
0.00	Grant in aid	0.00		Salaries-Manpower	0.00
				Consumables	0.00
				Contingencies	0.00
				Travel	0.00
				Overheads	0.00
				Equipment	0.00
0.00		0.00	837574.00		837574.00
837574.00	Excess of expenditure over income	837574.00			
<b>837574.00</b>		<b>837574.00</b>	<b>837574.00</b>		<b>837574.00</b>

<p align="center"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-64: NMITLI Project on "Biotechnology for Leather: Towards cleaner processing phase - II"</b>  <b>PI: Dr J GOWRISHANKAR</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
0.00	<b>Opening Balance</b>	0.00	408770.00	Opening Balance	19755.00
640000.00	Grant in aid	679000.00		Salaries- Manpower	171000.00
				Consumables	300000.00
				Contingencies	50000.00
				Travel	26403.00
				Overheads	112000.00
				Equipment	0.00
640000.00		679000.00	659755.00		679158.00
19755.00	Excess of expenditure over income	158.00			
<b>659755.00</b>		<b>679158.00</b>	<b>659755.00</b>		<b>679158.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD P-65: DST Project on "Molecular, genetic and functional analysis of the chromosomal plasticity region of the gastric pathogen Helicobacter pylori" P.I. Dr AYESHA ALVI RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	<b>Opening Balance</b>	0.00	42264.00	Opening balance	582647.00
0.00	Grant in aid	0.00	248226.00	Salaries- Manpower	0.00
			0.00	Consumables	0.00
			10000.00	Contingencies	0.00
			2157.00	Travel	0.00
			20000.00	Overheads	0.00
			260000.00	Equipment	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
<b>582647.00</b>		<b>582647.00</b>	<b>582647.00</b>		<b>582647.00</b>

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 01.04.2009 TO 31.03.2010					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	<b>Opening Balance</b>	0.00	5473294.00	Opening Balance	8279524.00
0.00	Grant in aid	15110300.00	375175.00	Salaries- Manpower	687372.00
581881.00	Basmati Analysis Charges	1918404.00	169000.00	Consumables	0.00
			3200.00	Contingencies	9800.00
			53051.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Consultancy & Knowledge fee	450000.00
			884250.00	Vehicle	0.00
			1903435.00	Equipment	124500.00
581881.00		17028704.00	8861405.00		9551196.00
8279524.00	Excess of expenditure over income		0.00	Closing Balance	7477508.00
<b>8861405.00</b>		<b>17028704.00</b>	<b>8861405.00</b>		<b>17028704.00</b>

<p align="center"><b>P-66: DBT Project on "Human Epigenome Variation: Analysis of CpG island methylation in chromosomes 18 and Y, and in some Hox, Insulin signaling and chromatin reprogramming genes"</b>  <b>PI: Dr SANJEEV KHOSLA</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
0.00	<b>Opening Balance</b>	0.00	342623.00	Opening Balance	684722.00
0.00	Grant in aid	0.00	2099.00	Salaries- Manpower	0.00
			300000.00	Consumables	0.00
			40000.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	-3476.00
684722.00	Excess of expenditure over income	681246.00	684722.00	Closing Balance	681246.00
<b>684722.00</b>		<b>681246.00</b>	<b>684722.00</b>		<b>681246.00</b>

<p align="center"><b>P-67: DBT Project on "Identification of novel Esophageal Squamous Cell Carcinoma (ESCC) genes by using a combination of array-based CGH and gene expression microarrays"</b>  <b>PI: Dr M D BASHYAM</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
0.00	<b>Opening Balance</b>	0.00	199247.00	Opening Balance	104487.00
1469000.00	Grant in aid	0.00	135200.00	Salaries- Manpower	9058.00
			1200000.00	Consumables	0.00
			13000.00	Contingencies	0.00
			26040.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
1469000.00	Excess of expenditure over income	0.00	1573487.00		113545.00
104487.00		113545.00			
<b>1573487.00</b>		<b>113545.00</b>	<b>1573487.00</b>		<b>113545.00</b>



CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD P-68: DST Project on "Identification of High Risk Individual with Precancerous States of Esophageal Cancer" PI: Dr GAYATRI RAMAKRISHNA RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
116000.00	<b>Opening Balance</b>	0.00	0.00	Opening Balance	59874.00
0.00	Grant in aid	0.00	0.00	Salaries- Manpower	0.00
		0.00	100000.00	Consumables	0.00
			20000.00	Contingencies	0.00
			7874.00	Travel	0.00
			48000.00	Overheads	0.00
			0.00	Equipment	0.00
116000.00		0.00	175874.00		59874.00
59874.00	Excess of expenditure over income	59874.00	0.00	Closing Balance	0.00
<b>175874.00</b>		<b>59874.00</b>	<b>175874.00</b>		<b>59874.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD P-69: ICMR Project on "Understanding the role of PE/PE family of M.tuberculosis in the activation of HIV Virus type I long terminal repeat (HIV-ILTP)" PI, Dr SANGITA MUKHOPADHYAY RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
0.00	<b>Opening Balance</b>	0.00	119924.00	Opening Balance	906808.00
0.00	Grant in aid	845840.00	315584.00	Salaries- Manpower	98395.00
			440000.00	Consumables	0.00
			15000.00	Contingencies	0.00
			0.00	Travel	0.00
			0.00	Overheads	0.00
			16300.00	Equipment	0.00
0.00		845840.00	906808.00		1005203.00
906808.00	Excess of expenditure over income	159363.00	0.00	Closing Balance	0.00
<b>906808.00</b>		<b>1005203.00</b>	<b>906808.00</b>		<b>1005203.00</b>

<b>P-70: DBT Project on "Identification of disease causing mutations in familial Hypertrophic Cardiomyopathy (FHC) patients from Andhra Pradesh" -            CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD            P.I : Dr M D BASHYAM            RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b>					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
0.00	<b>Opening Balance</b>	0.00	574789.00	Opening Balance	497869.00
616000.00	Grant in aid	628000.00	96000.00	Salaries- Manpower	51467.00
			400000.00	Consumables	100000.00
			20000.00	Contingencies	0.00
			8380.00	Travel	0.00
			0.00	Overheads	0.00
			14700.00	Equipment	0.00
616000.00		628000.00	1113869.00		649336.00
497869.00	Excess of expenditure over income	21336.00	0.00	Closing Balance	0.00
<b>1113869.00</b>		<b>649336.00</b>	<b>1113869.00</b>		<b>649336.00</b>

<b>P-71: DBT Project on "Referral Centre for Genetic Fidelity Testing of Tissue Culture Raised Plants"            CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD            P.I: DR N MADHUSUDAN REDDY            RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b>					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year. Amount Rs	Payments	Current Year Amount Rs
808618.00	<b>Opening Balance</b>	420845.00	219940.00	Salaries- Manpower	294400.00
906000.00	Grant in aid	0.00	500000.00	Consumables	1400000.00
			175000.00	Contingencies	75000.00
			12664.00	Travel	28574.00
			0.00	Overheads	0.00
			386169.00	Equipment	238120.00
1714618.00		420845.00	1293773.00		2036094.00
	Excess of expenditure over income	1615249.00	420845.00	Closing Balance	0.00
<b>1714618.00</b>		<b>2036094.00</b>	<b>1714618.00</b>		<b>2036094.00</b>

<p style="text-align: center;"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-72: DST Project on "Nuances of Non-coding DNA near insulin-responsive genes"</b>  <b>P.I. Dr NIRMALA YABALURI</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>						
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs	
0.00	<b>Opening Balance</b>	0.00	240000.00	Salaries- Manpower	141935.00	
0.00	Grant in aid	0.00	100000.00	Consumables	34000.00	
			40000.00	Contingencies	20000.00	
			0.00	Travel	0.00	
			150000.00	Overheads	96000.00	
			0.00	Equipment	0.00	
1129718.00	Excess of expenditure over income	1421653.00	1129718.00		1421653.00	
<b>1129718.00</b>		<b>1421653.00</b>	<b>1129718.00</b>		<b>1421653.00</b>	

<p style="text-align: center;"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-73: DST Project on "Identification and characterization of pancreatic cancer genes located within novel localized cpy number alternations"</b>  <b>- P.I: Dr M D BASHYAM</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>						
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs	
700000.00	<b>Opening Balance</b>	0.00	218467.00	Opening Balance	541887.00	
	Grant in aid		101400.00	Salaries- Manpower	67600.00	
			600000.00	Consumables	200000.00	
			100000.00	Contingencies	0.00	
			22020.00	Travel	47649.00	
			200000.00	Overheads	0.00	
			0.00	Equipment	0.00	
700000.00	Excess of expenditure over income	857136.00	1241887.00		857136.00	
541887.00		<b>857136.00</b>	<b>1241887.00</b>		<b>857136.00</b>	
<b>1241887.00</b>		<b>857136.00</b>	<b>1241887.00</b>		<b>857136.00</b>	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD P-74: ICAR Project on "Molecular Basic of Insect-Plant Interactions in Rice" P.I. Dr J NAGARAJU RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010						
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs	
276902.00	<b>Opening Balance</b>	0.00	0.00	Opening Balance	168779.00	
1726300.00	Grant in aid	666200.00	249935.00	Salaries- Manpower	345133.00	
			800000.00	Consumables	152288.00	
			0.00	Contingencies	0.00	
			16246.00	Travel	0.00	
			55800.00	Overheads	0.00	
			50000.00	Workshop/Seminar Exp	0.00	
			1000000.00	Equipment	0.00	
2003202.00		666200.00	2171981.00		666200.00	
168779.00	Excess of expenditure over income	0.00	0.00	Closing Balance	0.00	
<b>2171981.00</b>		<b>666200.00</b>	<b>2171981.00</b>		<b>666200.00</b>	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD P-75: DST Project on "Preparing blueprint for the macromolecular crystallography beamline at Indus-II synchrotron source" P.I: Dr SHEKAR C MANDE RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010						
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs	
243171.00	<b>Opening Balance</b>	0.00	0.00	Opening Balance	10840.00	
0.00	Grant in aid	0.00	0.00	Salaries- Manpower	0.00	
			50000.00	Consumables	0.00	
			20000.00	Contingencies	0.00	
			104011.00	Travel	0.00	
			80000.00	Overheads	0.00	
			0.00	Equipment	0.00	
243171.00		0.00	254011.00		10840.00	
10840.00	Excess of expenditure over income	10840.00	0.00	Closing Balance	0.00	
<b>254011.00</b>		<b>10840.00</b>	<b>254011.00</b>		<b>10840.00</b>	

<p align="center"><b>P-76: DBT project on "A study of Molecular Markers in childhood Autism with special references to nuclear factors - KAPPA B"</b>  <b>PI: Dr SUNIL KUMAR MANNA</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>									
Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year Amount	Rs	Payments	Current Year Amount	Rs
369974.00		<b>Opening Balance</b>		0.00		0.00	Opening Balance	58267.00	
0.00		Grant in aid		0.00		0.00	Salaries- Manpower	0.00	
				0.00	200000.00		Consumables	0.00	
					300000.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					198241.00		Equipment	-8033.00	
369974.00				0.00	428241.00			50234.00	
58267.00		Excess of expenditure over income		50234.00		0.00	Closing Balance		0.00
<b>428241.00</b>				<b>50234.00</b>		<b>428241.00</b>		<b>50234.00</b>	

<p align="center"><b>P-77 : DBT project on "Functional characterization of Mycobacterium tuberculosis PE/PPE proteins having SH3 binding domain: Understanding their role in modulating macrophage functions"</b>  <b>PI: Dr SANGITA MUKHOPADHYAY</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>									
Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year Amount	Rs	Payments	Current Year Amount	Rs
1462244.00		<b>Opening Balance</b>		0.00		0.00	Opening Balance	627570.00	
0.00		Grant in aid		0.00	202012.00		Salaries- Manpower	442779.00	
				2709000.00	1200000.00		Consumables	1300000.00	
					50000.00		Contingencies	30000.00	
					17566.00		Travel	28070.00	
					0.00		Overheads	0.00	
					620236.00		Equipment	154110.00	
1462244.00				2709000.00	2089814.00			2582529.00	
627570.00		Excess of expenditure over income		0.00		0.00	Closing Balance	126471.00	
<b>2089814.00</b>				<b>2709000.00</b>		<b>2089814.00</b>		<b>2709000.00</b>	

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b> <b>P-78: ICMR project on "Task Force - IMD Newborn Screening for Congenital Hypothyroidism &amp; Congenital Adrenal Hyperplasia: A Multicentric Study"</b> <b>PI: Dr A RADHA RAMA DEVI</b> <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b>					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
138034.00	<b>Opening Balance</b>	1304.00	35246.00	Opening Balance	1722377.00
0.00	Grant in aid	0.00	112865.00	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
138034.00		1304.00	23865.00	Project funds refund	0.00
			136730.00		
<b>138034.00</b>		<b>1304.00</b>	<b>138034.00</b>	Closing Balance	1304.00

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b> <b>P-79: DRDO project on "Understanding the role of AGE proteins in inducing inflammatory responses and its regulation"</b> <b>PI: Dr SUNIL KUMAR MANNA</b> <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b>					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
0.00	<b>Opening Balance</b>	0.00	352426.00	Opening Balance	1722377.00
0.00	Grant in aid	0.00	151191.00	Salaries- Manpower	202422.00
			700000.00	Consumables	450000.00
			50000.00	Contingencies	25000.00
			12432.00	Travel	25444.00
			100000.00	Overheads	70287.00
			356328.00	Equipment	140498.00
0.00		0.00	1722377.00		2636028.00
1722377.00	Excess of expenditure over income	2636028.00	0.00	Closing Balance	0.00
<b>1722377.00</b>		<b>2636028.00</b>	<b>1722377.00</b>		<b>2636028.00</b>

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b> <b>P-80: DBT Project on "Referral Centre for Detection of Genetically Modified Foods employing DNA - based Markets"</b> <b>P.I. Dr N MADHUSUDAN REDDY</b> <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b>					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
3791464.00	<b>Opening Balance</b>	1108456.00	546490.00	Salaries- Manpower	401120.00
0.00	Grant in aid	3000000.00	3000000.00	Consumables	900000.00
			37500.00	Contingencies	0.00
			12071.00	Travel	23902.00
			0.00	Overheads	0.00
			1786947.00	Equipment	111905.00
3791464.00		1408456.00	2683008.00		1436927.00
0.00	Excess of expenditure over income	28471.00	1108456.00	Closing Balance	0.00
<b>3791464.00</b>		<b>1436927.00</b>	<b>3791464.00</b>		<b>1436927.00</b>

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b> <b>P-80A: RMRC Project on "Fluorescent Amplified Fragment Length Polymorphism Analysis of different genomic species- Development of species specific markers for identification of Leptospirosis"</b> <b>P.I. Dr NIYAZ AHMED</b> <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b>					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
0.00	<b>Opening Balance</b>	0.00	0.00	Salaries- Manpower	0.00
3000000.00	Grant in aid	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
			3000000.00	Project funds refund	0.00
3000000.00		0.00	3000000.00		0.00
			0.00	Closing Balance	0.00
<b>3000000.00</b>		<b>0.00</b>	<b>3000000.00</b>		<b>0.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD					
P-81: DBT project on "Reconstructing cellular Networks: Two-Component Regulatory Systems"					
P.I.: Dr SHEKAR C MANDE					
RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
303142.00	<b>Opening Balance</b>	0.00	0.00	Opening Balance	141048.00
0.00	Grant in aid	0.00	233336.00	Salaries- Manpower	293800.00
			200000.00	Consumables	150000.00
			0.00	Contingencies	0.00
			10854.00	Travel	0.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
303142.00		0.00	444190.00		584848.00
141048.00	Excess of expenditure over income	584848.00	0.00	Closing Balance	0.00
<b>444190.00</b>		<b>584848.00</b>	<b>444190.00</b>		<b>584848.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD					
P-81A: Financial Assistance for award of JC Bose Fellowship to					
Dr J GOWRISHANKAR					
RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
200000.00	<b>Opening Balance</b>	200000.00	240000.00	Salaries- Manpower	240000.00
600000.00	Grant in aid	600000.00	202849.00	Consumables	138225.00
			0.00	Contingencies	0.00
			297151.00	Travel	284085.00
			0.00	Overheads	60000.00
			0.00	Equipment	77690.00
800000.00		800000.00	800000.00		800000.00
<b>800000.00</b>		<b>800000.00</b>	0.00	Closing Balance	0.00
			<b>800000.00</b>		<b>800000.00</b>



CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD						
P-82: DBT project on "Functional Genomic Analysis of Candida Glabrata-macrophage"						
P.I.: Dr RUPINDER KAUR						
RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010						
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount	Current Year Rs
1100000.00	<b>Opening Balance</b>	795011.00	0.00	Salaries- Manpower	66929.00	66929.00
1265000.00	Grant in aid	1480000.00	800000.00	Consumables	650000.00	650000.00
			0.00	Contingencies	0.00	0.00
			1989.00	Travel	13434.00	13434.00
			300000.00	Overheads	200000.00	200000.00
			468000.00	Equipment	669050.00	669050.00
2365000.00		2275011.00	1569989.00		1599413.00	1599413.00
0.00	Excess of expenditure over income	0.00	795011.00	Closing Balance	675598.00	675598.00
<b>2365000.00</b>		<b>2275011.00</b>	<b>2365000.00</b>		<b>2275011.00</b>	<b>2275011.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD						
P-83: DBT project on "Prokaryotic Transcription Termination Factor, Rho: Mechanism of Action and Biology"						
P.I.: Dr RANJAN SEN						
RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010						
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount	Current Year Rs
1136920.00	<b>Opening Balance</b>	0.00	0.00	Opening Balance	773176.00	773176.00
0.00	Grant in aid	1170400.00	80426.00	Salaries- Manpower	100893.00	100893.00
			1500000.00	Consumables	1300000.00	1300000.00
			60000.00	Contingencies	30000.00	30000.00
			18515.00	Travel	59365.00	59365.00
			0.00	Overheads	0.00	0.00
			251155.00	Equipment	0.00	0.00
1136920.00		1170400.00	1910096.00		2263434.00	2263434.00
773176.00	Excess of expenditure over income	1093034.00	0.00	Closing Balance	0.00	0.00
<b>1910096.00</b>		<b>2263434.00</b>	<b>1910096.00</b>		<b>2263434.00</b>	<b>2263434.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD						
P-83A: DST project on "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 01.04.2009 TO 31.03.2010						
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs	
712950.00	<b>Opening Balance</b>	0.00	0.00	Opening Balance	50383.00	
0.00	Grant in aid	550000.00	36800.00	Salaries- Manpower	110400.00	
			225000.00	Consumables	335000.00	
			60000.00	Contingencies	29000.00	
			0.00	Travel	11292.00	
			200000.00	Overheads	100000.00	
			241533.00	Equipment	0.00	
712950.00		550000.00	763333.00	Closing Balance	636075.00	
50383.00	Excess of expenditure over income	86075.00	0.00		0.00	
<b>763333.00</b>		<b>636075.00</b>	<b>763333.00</b>		<b>636075.00</b>	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD						
P-84: Norway project on "Preparing for tuberculosis 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 01.04.2009 TO 31.03.2010						
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs	
0.00	<b>Opening Balance</b>	0.00	454724.00	Opening Balance	1300000.00	
0.00	Grant in aid (Transfer from P-42)	1298850.00	345327.00	Salaries- Manpower	0.00	
			472412.00	Consumables	0.00	
			0.00	Contingencies	0.00	
			27537.00	Travel	0.00	
			0.00	Overheads	0.00	
			0.00	Equipment	0.00	
0.00		1298850.00	1300000.00	Closing Balance	1300000.00	
1300000.00	Excess of expenditure over income	1150.00	0.00		0.00	
<b>1300000.00</b>		<b>1300000.00</b>	<b>1300000.00</b>		<b>1300000.00</b>	

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b> <b>P-84A: DBT project on "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"</b> <b>PI.: Dr MADHUSUDANREDDY</b> <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b>					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
1100000.00	<b>Opening Balance</b>	1033462.00	0.00	Salaries- Manpower	0.00
1265000.00	Grant in aid	1480000.00	600000.00	Consumables	950000.00
			0.00	Contingencies	0.00
			0.00	Travel	0.00
			300000.00	Overheads	200000.00
			431538.00	Equipment	707502.00
2365000.00		2513462.00	1331538.00		1857502.00
0.00	Excess of expenditure over income	0.00	1033462.00	Closing Balance	655960.00
<b>2365000.00</b>		<b>2513462.00</b>	<b>2365000.00</b>		<b>2513462.00</b>

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b> <b>P-85: DBT project on "IdeR associated gene regulatory network in mycobacteria"</b> <b>PI.: Dr AKASH RANJAN</b> <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b>					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
680000.00	<b>Opening Balance</b>	0.00	0.00	Opening Balance	275405.00
0.00	Grant in aid	400000.00	339559.00	Salaries- Manpower	348699.00
			500000.00	Consumables	600000.00
			60000.00	Contingencies	30000.00
			55846.00	Travel	79397.00
			0.00	Overheads	0.00
			0.00	Equipment	0.00
680000.00		400000.00	955405.00		1333501.00
275405.00	Excess of expenditure over income	933501.00	0.00	Closing Balance	0.00
<b>955405.00</b>		<b>1333501.00</b>	<b>955405.00</b>		<b>1333501.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD						
P-86: DBT project on "Evaluation of Mycobacterium W as an immunotherapeutic against paratuberculosis (John's Disease of cattle)"						
P.I.: Dr NIYAZ AHMED						
RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010						
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount	Rs
592000.00	<b>Opening Balance</b>	334386.00	207614.00	Salaries- Manpower		0.00
0.00	Grant in aid	0.00	0.00	Consumables		0.00
			50000.00	Contingencies		0.00
			0.00	Travel		0.00
			0.00	Overheads		0.00
			0.00	Equipment		0.00
			0.00	Project funds refund		256095.00
592000.00	Excess of expenditure over income	334386.00	257614.00			256095.00
0.00		0.00	334386.00	Closing Balance		78291.00
<b>592000.00</b>		<b>334386.00</b>	<b>592000.00</b>			<b>334386.00</b>

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD						
P-87: DST project on "Comparative genomic of wild silkmoths under India-Japan Co-operative Science programme (IJCSP)"						
P.I.: Dr J NAGARAJU & Dr TORU SHIMADA						
RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010						
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount	Rs
34058.00	<b>Opening Balance</b>	0.00	0.00	Opening Balance		65698.00
66000.00	Grant in aid	0.00	0.00	Salaries- Manpower		0.00
			0.00	Consumables		0.00
			0.00	Contingencies		0.00
			165756.00	Travel		0.00
			0.00	Overheads		0.00
			0.00	Equipment		0.00
100058.00	Excess of expenditure over income	0.00	165756.00			65698.00
65698.00		65698.00	0.00	Closing Balance		0.00
<b>165756.00</b>		<b>65698.00</b>	<b>165756.00</b>			<b>65698.00</b>

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b> <b>P-88: DBT Project on Introduction of anti-baculoviral property in commercial silkworm strains by expression of multiple of RNAi viral targets”</b> <b>PI.: Dr J NAGARAJU</b> <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b>						
Previous Year Amount	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs	
0.00	<b>Opening Balance</b>	140000.00	300000.00	Salaries- Manpower	240000.00	
740000.00	Grant in aid	740000.00	300000.00	Consumables	0.00	
			0.00	Contingencies	0.00	
			0.00	Travel	357535.00	
			0.00	Overheads	0.00	
			0.00	Equipment	0.00	
740000.00		880000.00	600000.00		597535.00	
0.00	Excess of expenditure over income	0.00	140000.00	Closing Balance	282465.00	
<b>740000.00</b>		<b>880000.00</b>	<b>740000.00</b>		<b>880000.00</b>	

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b> <b>P-89: DBT Project on “Characterization of Mycobacterium tuberculosis transcription machinery and Bacteriophage metagenomics”</b> <b>PI.: Dr RANJAN SEN</b> <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b>						
Previous Year Amount	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs	
0.00	<b>Opening Balance</b>	0.00	0.00	Salaries- Manpower	38400.00	
300000.00	Grant in aid	0.00	0.00	Consumables	190400.00	
			0.00	Contingencies	0.00	
			0.00	Travel	0.00	
			0.00	Overheads	0.00	
			300000.00	Equipment	71200.00	
300000.00		0.00	300000.00		300000.00	
0.00	Excess of expenditure over income	300000.00	0.00	Closing Balance	0.00	
<b>300000.00</b>		<b>300000.00</b>	<b>300000.00</b>		<b>300000.00</b>	

<p style="text-align: center;"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-90: DBT Project on "Role of Yapsins in the Pathobiology of Candida Glabrata"</b>  <b>PI.: Dr RUPINDER KAUR</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>						
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount	
0.00	<b>Opening Balance</b>	1057540.00	95373.00	Salaries- Manpower	204844.00	
2417000.00	Grant in aid	626000.00	500000.00	Consumables	800000.00	
			30000.00	Contingencies	30000.00	
			0.00	Travel	6380.00	
			0.00	Overheads	0.00	
2417000.00		1683540.00	734087.00	Equipment	269103.00	
0.00	Excess of expenditure over income	0.00	1359460.00		1310327.00	
<b>2417000.00</b>		<b>1683540.00</b>	1057540.00	Closing Balance	373213.00	
			<b>2417000.00</b>		<b>1683540.00</b>	

<p style="text-align: center;"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-91: DBT Project on "DNMT3L: Epigenetic correlation with cancer"</b>  <b>PI.: Dr SANJEEV KHOSLA &amp; Dr GAYATRI RAMAKRISHNA</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>						
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount	
0.00	<b>Opening Balance</b>	1422879.00	94219.00	Salaries- Manpower	216000.00	
2295000.00	Grant in aid	760000.00	600000.00	Consumables	900000.00	
			50000.00	Contingencies	50000.00	
			16302.00	Travel	29802.00	
			0.00	Overheads	0.00	
			111600.00	Equipment	812923.00	
2295000.00		2182879.00	872121.00		2008725.00	
0.00	Excess of expenditure over income	0.00	1422879.00	Closing Balance	174154.00	
<b>2295000.00</b>		<b>2182879.00</b>	<b>2295000.00</b>		<b>2182879.00</b>	

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b> <b>P-92 : DST project on "Swarnajayanti Fellowship: Designing transcription anti-terminators: a novel approach for making new inhibitors of gene expression"</b> <b>PI.: Dr RANJAN SEN</b> <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b>					
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount
0.00	<b>Opening Balance</b>	9264550.00	196800.00	Salaries- Manpower	675348.00
10367600.00	Grant in aid	0.00	400000.00	Consumables	2500000.00
			20000.00	Contingencies	30000.00
			0.00	Travel	13574.00
			0.00	Overheads	100000.00
			486250.00	Equipment	6018942.00
10367600.00	Excess of expenditure over income	9264550.00	1103050.00	Closing Balance	9337864.00
<b>10367600.00</b>		<b>9337864.00</b>	<b>10367600.00</b>		<b>9337864.00</b>

<b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b> <b>P-93: DBT Project on "Virtual Centre of Excellence on multidisciplinary approaches aimed at interventions against tuberculosis"</b> <b>PI.: Dr SHEKAR C MANDE &amp; Dr SANGITA MUKHOPADHYAY</b> <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b>					
Previous Year Amount	Receipts	Current Year Amount	Previous Year Amount	Payments	Current Year Amount
0.00	<b>Opening Balance</b>	4851300.00	0.00	Salaries- Manpower	212693.00
5281000.00	Grant in aid	0.00	250000.00	Consumables	1600000.00
			20000.00	Contingencies	160000.00
			73400.00	Travel	42772.00
			0.00	Overheads	0.00
			86300.00	Equipment	2017975.00
5281000.00	Excess of expenditure over income	4851300.00	429700.00	Closing Balance	4033440.00
<b>5281000.00</b>		<b>4851300.00</b>	<b>5281000.00</b>		<b>4851300.00</b>

<p style="text-align: center;"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-95: DST Project on "Construction of regulatory networks in prokaryotes through protein: Protein interaction predictions and transcription regulation predictions."</b>  <b>PI.: Dr SHEKAR C MANDE</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
0.00	<b>Opening Balance</b>	0.00	0.00	Opening balance	252909.00
0.00	Grant in aid	1006020.00	100000.00	Salaries- Manpower	151975.00
			10000.00	Consumables	400000.00
			0.00	Contingencies	40000.00
			20000.00	Travel	81815.00
			122909.00	Overheads	77379.00
			252909.00	Equipment	123411.00
252909.00	Excess of expenditure over income	121469.00	0.00	Closing Balance	1127489.00
<b>252909.00</b>		<b>1127489.00</b>	<b>252909.00</b>		<b>1127489.00</b>

<p style="text-align: center;"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-96 : NIH / FIRCA Project on "Molecular Characterization of sporadic colorectal cancer in the young from India"</b>  <b>PI.: Dr M D BASHYAM</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
0.00	<b>Opening Balance</b>	0.00	0.00	Opening Balance	1470450.00
0.00	Grant in aid	1737438.00	150000.00	Salaries- Manpower	257400.00
			1115600.00	Consumables	823636.00
			25576.00	Contingencies	120497.00
			69274.00	Travel	130317.00
			110000.00	Overheads	122153.00
			0.00	Equipment	0.00
0.00	Excess of expenditure over income	1737438.00	1470450.00	Closing Balance	2924453.00
1470450.00		1187015.00	0.00		0.00
<b>1470450.00</b>		<b>2924453.00</b>	<b>1470450.00</b>		<b>2924453.00</b>



<p style="text-align: center;"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-97 : DBT Project on "Proteome-wide Analysis of Serine pyrophosphorylation by inositol pyrophosphates"</b>  <b>PI.: Dr RASHNA BHANDARI</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>						
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs	
0.00	<b>Opening Balance</b>	0.00	0.00	Salaries- Manpower	62400.00	
0.00	Grant in aid	2027000.00	0.00	Consumables	591256.00	
			0.00	Contingencies	0.00	
			0.00	Travel	8744.00	
			0.00	Overheads	200000.00	
			0.00	Equipment	581900.00	
0.00		2027000.00	0.00		1444300.00	
0.00			0.00	Closing Balance	582700.00	
<b>0.00</b>		<b>2027000.00</b>	<b>0.00</b>		<b>2027000.00</b>	

<p style="text-align: center;"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-98 : DBT Project on "Role of cell - cell signaling mediated by Diffusible signaling factor (DSF) in Xanthomonas virulence"</b>  <b>PI.: Dr SUBHADEEP CHATTERJEE</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>						
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs	
0.00	<b>Opening Balance</b>	0.00	0.00	Salaries- Manpower	64413.00	
0.00	Grant in aid	3947000.00	0.00	Consumables	900000.00	
			0.00	Contingencies	10000.00	
			0.00	Travel	0.00	
			0.00	Overheads	0.00	
			0.00	Equipment	2159680.00	
0.00		3947000.00	0.00		3134093.00	
0.00			0.00	Closing Balance	812907.00	
<b>0.00</b>		<b>3947000.00</b>	<b>0.00</b>		<b>3947000.00</b>	

<p align="center"><b>P-99 : DBT Project on "Role of inositol Pyrophosphates in eukaryotic cell growth, proliferation and ribosome biogenesis"</b>  <b>PI.: Dr RASHNA BHANDARI</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>									
Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year Amount	Rs	Payments	Current Year Amount	Rs
0.00		<b>Opening Balance</b>	0.00		0.00		Salaries- Manpower	83200.00	
0.00		Grant in aid	4225000.00		0.00		Consumables	800000.00	
					0.00		Contingencies	300000.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	1648300.00	
0.00			4225000.00		0.00		Closing Balance	2561500.00	
0.00			<b>4225000.00</b>		0.00			<b>1663500.00</b>	
<b>0.00</b>					<b>0.00</b>			<b>4225000.00</b>	

<p align="center"><b>P-100: DBT Project on "Effect of reactive oxygen species on T-Cell immune response: An approach to understand the molecular mechanism of immunosuppression during tuberculosis" - National Bioscience Award"</b>  <b>PI.: Dr SANGITA MUKHOPADHAYAY</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>									
Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year Amount	Rs	Payments	Current Year Amount	Rs
0.00		<b>Opening Balance</b>	0.00		0.00		Salaries- Manpower	72950.00	
0.00		Grant in aid	3000000.00		0.00		Consumables	209266.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	0.00	
					0.00		Equipment	17784.00	
0.00			3000000.00		0.00		Closing Balance	300000.00	
0.00			<b>3000000.00</b>		0.00			<b>0.00</b>	
<b>0.00</b>					<b>0.00</b>			<b>300000.00</b>	

<p align="center"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-101 : WT-DBT Alliance Project on "Role of Inositol pyrophosphates in cell physiology: Investigating the biochemical significance of protein pyrophosphorylation - Senior Fellowship"</b>  <b>PI.: Dr RASHNA BHANDARI</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>									
Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year Amount	Rs	Payments	Current Year Amount	Rs
0.00		<b>Opening Balance</b>	0.00		0.00		Salaries- Manpower	459965.00	
0.00		Grant in aid	18792749.00		0.00		Consumables	1300000.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	318541.00	
					0.00		Equipment	1425442.00	
0.00			18792749.00		0.00		Closing Balance	3503948.00	
0.00					0.00			15288801.00	
<b>0.00</b>			<b>18792749.00</b>		<b>0.00</b>			<b>18792749.00</b>	

<p align="center"><b>CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD</b>  <b>P-102 : ICMR Project on "Understanding the role of Mycobacterium tuberculosis heat shockprotein 60 as Th1/Th2 immuno modular"</b>  <b>PI.: Dr SANGITA MUKHOPADHYAY</b>  <b>RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010</b></p>									
Previous Year Amount	Rs	Receipts	Current Year Amount	Rs.	Previous Year Amount	Rs	Payments	Current Year Amount	Rs
0.00		<b>Opening Balance</b>	0.00		0.00		Salaries- Manpower	0.00	
0.00		Grant in aid	481319.00		0.00		Consumables	500000.00	
					0.00		Contingencies	0.00	
					0.00		Travel	0.00	
					0.00		Overheads	15000.00	
					0.00		Equipment	450000.00	
0.00			481319.00		0.00		Closing Balance	965000.00	
0.00		Excess of expenditure over income	483681.00		0.00			0.00	
<b>0.00</b>			<b>965000.00</b>		<b>0.00</b>			<b>965000.00</b>	

CENTRE FOR DNA FINGERPRINTING AND DIAGNOSTICS, HYDERABAD COE on Genetics and Genomic of Silkworms P.I. Dr J NAGARAJU RECEIPTS AND PAYMENTS ACCOUNT FROM 01.04.2009 TO 31.03.2010					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
43743874.00	Opening Balance Grant in aid	38637629.00	3901735.00	Salaries- Manpower	5621624.00
3729000.00		7821000.00	1700000.00	Consumables	7000000.00
			560000.00	Contingencies	280000.00
			71715.00	Travel	398317.00
			0.00	Overheads	0.00
47472874.00		46458629.00	2601795.00	Equipment	22827727.00
			8835245.00	Closing Balance	36127668.00
<b>47472874.00</b>		<b>46458629.00</b>	<b>47472874.00</b>		<b>10330961.00</b>
					<b>46458629.00</b>

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 01.04.2008 TO 31.03.2009					
Previous Year Amount Rs	Receipts	Current Year Amount Rs.	Previous Year Amount Rs	Payments	Current Year Amount Rs
0.00	Opening Balance Grant in aid	11800481.00	2239809.00	Salaries- Manpower	5256529.00
19268000.00		4589000.00	1800000.00	Consumables	5900000.00
			330000.00	Contingencies	710000.00
			222034.00	Travel	318725.00
			0.00	Overheads	0.00
19268000.00		16389481.00	2875676.00	Equipment	5658960.00
0.00	Excess of expenditure over income	1454733.00	7467519.00	Closing Balance	17844214.00
<b>19268000.00</b>		<b>17844214.00</b>	<b>19268000.00</b>		<b>0.00</b>
					<b>17844214.00</b>



# Photo Gallery



Dr J Gowrishankar and CDFD officials saluting the national flag on Independence Day, 2009



Dr J Nagaraju receiving 'Biotech Product and Process Development and Commercialisation Award 2009' from Dr A P J Abdul Kalam in the august presence of Shri Prithviraj Chavan, Hon'ble Minister of Science & Technology and Earth Sciences

Dr J Gowrishankar, Director, CDFD and Dr Deepanwita Chatopadhyay, MD & CEO, LSI-IKP Knowledge Park, signing MoU for Technology Commercialisation Program, 16th December, 2009



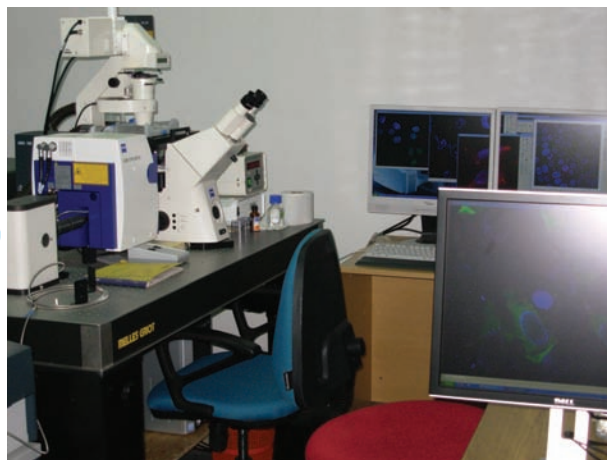




← CDFD-CCMB scientific staff & students at the joint academic retreat program at CDFD Gandipet campus, 5-6 March, 2010

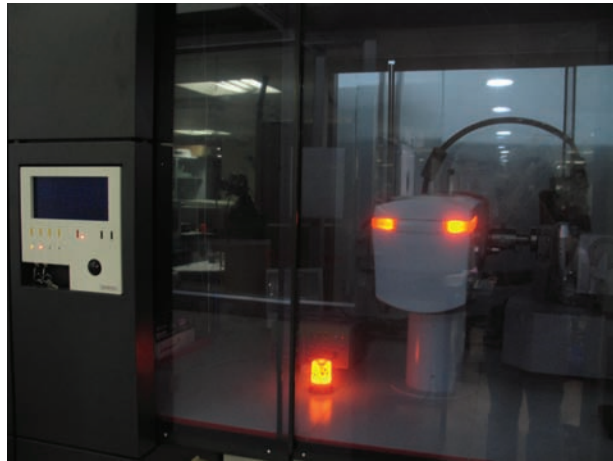
### *New installations at our laboratories*

Confocal Microscope →



← Maldi TOF TOF Mass Spectrometer

X-ray Crystallography facility



DNA Sequencer

Fluorescence Activated Cell Sorter





A few of the senior scholars @ CDFD