NIAB

National Institute of Animal Biotechnology

वार्षिक प्रतिवेदन

2016 - 17

राष्ट्रीय पशु जैव प्रौद्योगिकी संस्थान

National Institute of Animal Biotechnology

(An Autonomous Institute of the Department of Biotechnology, Ministry of Science & Technology, Government of India)

D.No: 1-121/1, 4th & 5th Floors, Axis Clinicals Building, Miyapur, Hyderabad - 500049.

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Mission

Development of sustainable and globally competitive livestock based economy through innovative science & technology development and entrepreneurship promotion.

Vision

To demonstrate excellence in science; develop technology and solutions in animal biotechnology leading to eventual commercialization.

Objectives:

1. To undertake directed, basic and applied research towards technology and product innovation. Characterization of breeds and selective breeding to enhance productivity; develop technologies for multiplication of elite genotypes. Development of transgenic animals for producing molecules of pharmaceutical value. Enrichment of crop residues into high value products. Development of new generation vaccines, diagnostics and drugs.

2. To develop human resource across the value chain, primarily for translational research, industrial R&D; facilitate introduction of short term advanced training, new courses like MSc/MVSc-PhD and Ph.D. degree with a focus on interdisciplinary science, innovation and the science of manufacturing.

3. To contribute to national policy formulation related to animal biotechnology, animal bio-safety issues and ethical issues.

4. To promote intellectual property protection, business development, technology transfer, and academia-industry partnerships.

5. To develop collaborative programmes with national and international partners with focus on translational research and product development.

6. To provide incubation facilities for entrepreneurs/startup companies.

7. To create (i) extramural centers with emphasis on product innovation and translational research (ii) 'not for profit' companies; and (iii) facilitate the creation of 'for profit' companies.

From the Desk of Director

From the Desk of Director

It gives me immense pleasure to present the 2016-2017 Annual Report of the National Institute of Animal Biotechnology (NIAB), an autonomous Institute under administrative control of the Department of Biotechnology (DBT), Ministry of Science & Technology, Government of India.

NIAB aims to harness novel and emerging biotechnologies and take up research in the cutting edge areas for improving animal health and productivity. The Institute's focus of research is on Animal Genetics and Genomics, Transgenic Technology, Reproductive Biotechnology, Animal Diseases, Bioinformatics and Nutrition Enrichment. The institute focuses on basic research which would lead to the development of novel vaccines, diagnostics and improved therapeutic molecules for farm animals.

There is a steady increase in the number of scientists and students at NIAB. New faculty have joined during the last quarter of the reporting period. The institute is operating from a rented premises with state of the art facilities for research activities. The ongoing research projects in the area of infectious diseases include those on brucellosis, leptospirosis, staphylococcosis, Newcastle disease, Peste des petits ruminants (PPR), babesiosis, theileriosis and toxoplasmosis. Host-pathogen interactions, virulence mechanisms, and molecular pathogenesis are being studied with the ultimate objective of technology and product innovation for development of efficient diagnostic tools and novel vaccines. In the area of animal reproduction, NIAB is focusing on addressing the problem of infertility in livestock. With the joining of new faculty, the institute has started research activities towards gene and protein engineering, functional genomics, transgenic animals, immunological memory and immunity and applied animal nutrition.The various projects are being ably supported by the bioinformatics team,especially for genomic studies.

In order to strengthen the national and international research activities, NIAB has signed MoUs with (i) Cornell University for purpose of research and (ii) Indian Veterinary Research Institute (IVRI) for jointly undertaking teaching and research in Animal Biotechnology and allied subjects.

Academic programmes of the institute include “Research Scholar Programme” where NIAB has MoU with Manipal University and the University of Hyderabad for PhD registrations of the Research Scholars. NIAB has also partnered with the Pirbright Institute and Roslin Institute (both in the UK) in the Newton Fund PhD programme, with students being jointly mentored by faculty from all the partner institutions.

NIAB had organized a brainstorming meeting on livestock genomics and on strategies for developing appropriate animal models to establish safety and toxicity of stem cells for diseases. NIAB is working with keen interest in connecting the lab with the students of local schools and colleges. Under this programme,

scientists visited schools for teaching, and students visited NIAB labs for getting first hand information of scientific work.

I also wish to report on the development of NIAB's permanent campus, which is under construction on 100 acres of land alienated to NIAB by the State Government, adjacent to the campus of the University of Hyderabad. All the necessary permissions have been obtained from the pertinent agencies and construction is going on in full swing. We are hopeful of shifting to our permanent campus in reasonably short period of time during this year.

I sincerely acknowledge the support and encouragement received from the Department of Biotechnology, the distinguished members of the NIAB Society, Governing Body, Scientific Advisory Committee, Finance Committee and Building Committee. We also acknowledge the support received from local institutions such as CDFD, CCMB and University of Hyderabad, TS Veterinary University and others.

I also acknowledge the contributions of highly dedicated scientific, technical and administrative staff of NIAB for their untiring efforts in meeting the challenges with limited resources. We encourage them for using Rajbhasha in daily communication. In this connection, my expression in Hindi may be seen on last page of this report. I sincerely hope and wish for the continued support and encouragement of all in the years to come in achieving excellence in all our endeavors.

31 March 2017

Dr Subeer S Majumdar

Research Projects

Animal Health

Bacterial Diseases

Laboratory of Immunology and Microbial Pathogenesis

Understanding the Virulence Mechanisms of the Zoonotic Pathogen *Brucella,* and Development of Novel Vaccines and Diagnostic Assays for Animal and Human Brucellosis.

Principal Investigator	Girish K Radhakrishnan	Scientist D
PhD Students	Padmaja Jakka	DST-INSPIRE Fellow (since July 2015)
	Mega Shravani	Newton Fund PhD student (since Jan 2016)
	Prachita Nandini	CSIR-JRF (since July 2016)
Research Fellows	Swapna Namani	Research Fellow (since Sep 2015)
	Varadendra BMr	Research Fellow (since Sep 2016)
	Komala Yedlla	Research Fellow (until March 2017)
	Nivedita Rai	Research Fellow (until October 2016)
	Subathra Murugan	Research Associate
Collaborators	Prof. Satya Parida	The Pirbright Institute, UK
	Dr. Dhinkar Raj	TRPVB, TANUVAS, Chennai

Objectives

Brucellosis is an infectious disease caused by bacteria of the genus *Brucella* that affects humans as well as domestic and wild animals, leading to significant impact on public health and livestock industry. *Brucellosis is endemic in India and the disease has been reported in cattle, buffaloes, sheep, goats, pigs, dogs and humans.* Brucellosis in livestock and its impact on public health causes an annual loss of US $ 3.4 billion (Rs. 22,800 crore) in India. Antibiotic treatment of brucellosis remains complex, requiring prolonged administration of more than one antibiotic and the efficacy of treatment is often reduced due to frequent treatment failures and relapses. There is no human vaccine available for brucellosis and the existing animal vaccines have several disadvantages. Minimal information is available on the basis of *Brucella* host specificity and the virulence factors that enable *Brucella* to survive and replicate in the host. Given the limitations of current vaccines and therapies for brucellosis, novel therapeutic and preventive strategies are needed, however, the progress has been hampered by a lack of knowledge in the essential mechanisms and virulence factors enabling Brucella to survive and replicate in the host. Overall objectives of my research projects are as follows:-

1) To develop novel vaccines and diagnostic assays for animal and human brucellosis.

2) To understand the mechanisms by which *Brucella* subvert the host immune responses.

3) To characterize the host factors that support the invasion and intracellular multiplication of *Brucella.*

Summary of work done until the beginning of this reporting year (up to March 31, 2016)

To develop novel sero-diagnostic assays for animal and human brucellosis, a high throughput immunoprobing of a

Brucella protein microarray was performed with serum samples of *Brucella*-infected animals and humans. The analysis identified several putative immunodominant antigens. Towards understanding the mechanisms by which *Brucella* subvert the host innate immune responses, detailed characterization of *Brucella effector* protein, TcpB, which inhibits TLR2 and 4 signaling, has been carried out. A high throughput yeast two-hybrid screening identified a positive interaction between TcpB and the microtubule tip binding protein CLIP170. Subsequent studies revealed that CLIP170 suppresses LPS-induced pro-inflammatory signaling in macrophages and mice. Peste des petits ruminants (PPR) is a contagious viral disease of sheep and goats. TLR7 plays essential role in innate immune responses against viral infections. Nectin-4 has been identified as the receptor for PPRV entry to the cells. We analyzed the expression levels of Nectin-4 and TLR7 genes in various goat breeds to examine the association between gene expression levels and disease resistance or susceptibility. The analysis revealed a significantly low level of Nectin-4 expression and an enhanced level of TLR7 expression in Kanni breed, which is resistant to PPRV infection.

Details of progress made in the current reporting year (April 1, 2016 - March 31, 2017)

Project 1: Characterization of immunodominant antigens of ***Brucella.***

Diagnosis of *Brucella* by culture is difficult because of its fastidious nature, slow growth and potential hazard to the laboratory personnel. Existing sero-diagnostic assays for brucellosis have many disadvantages such as poor sensitivity, cross-reactivity and lack of "Differentiating Infected from Vaccinated Animals" (DIVA) capability. Therefore, identification of novel sero-diagnostic antigens are essential for developing reliable and more specific diagnostic assays for animal and human brucellosis. Towards this objective, we performed a high throughput immunoprofiling of *Brucella* antigens with the serum samples from *Brucella*-infected cattle (naturally infected as well as S19 vaccinated), goats, dogs and humans. The analysis identified various immunodominant antigens that were shared or uniquely present in various hosts. Subsequently, we cloned and overexpressed 10 high ranking immunodominant antigens followed by their purification. The purified *Brucella* proteins were immunoprobed with the infected serum from both animals and humans. Two of the purified proteins (BM-5 and BM-7) reacted with serum samples from animals and humans but not with serum from S19 vaccinated cattle. This indicates that BM-5 and BM-7 antigens can differentiate vaccinated from naturally infected cattle (i.e. DIVA capability). Next, we developed a prototype Lateral Flow Assay (LFA)-based brucellosis diagnosis device with DIVA capability using the BM-5 antigen.

Project 2: To understand the mechanisms by which Brucella effector protein, TcpB suppresses host innate immune responses.

Brucella secretes a TIR domain-containing protein (TcpB), which suppresses host innate immune responses by inhibiting the signaling through TLR2 and 4 receptors. However, the mechanism by which TcpB suppresses TLR2/4 signaling remains obscure. We performed a high throughput yeast-two hybrid screening that identified a positive interaction between TcpB and the microtubule tip binding protein CLIP170. Subsequent studies revealed that CLIP170 suppresses TLR-2/4 mediated pro-inflammatory responses in macrophages and mouse. Further, we identified that CLIP170 interacts with the TLR-2/4 adaptor protein TIRAP and promotes its degradation (Fig. 1). Selective protein degradation in eukaryotic cells is achieved by ubiquitination of target proteins and their degradation by 20S proteasome complex. Therefore, we examined whether CLIP170 induces ubiquitination of TIRAP. *In vivo* ubiquitination assays indicated that CLIP170 induces enhanced ubiquitination of TIRAP (Fig. 2). Our

experimental data suggest that targeted ubiquitination and degradation of TIRAP leads to attenuation of LPS-induced TLR-2/4 signaling. It appears that TcpB recruits CLIP170 for targeted elimination of TIRAP to subvert the TLR2/4-mediated innate immune responses. Next, we examined whether TcpB could inhibit intracellular LPS-mediated cell death and pro-inflammatory cytokine expression in macrophages. Our preliminary studies revealed that the recombinant TcpB protein could efficiently suppress LPS-induced LDH release and secretion of IL-1 β in macrophages (Fig. 3). Experiments are in progress to understand the mechanism by which TcpB attenuates intracellular LPS-induced innate immune responses.

Project 4: Molecular characterization of V and C genes of PPRV

Viruses employ various strategies to subvert the host immune responses, including the induction of immunosuppression. Peste des petits ruminants (PPR) is an acute and highly contagious viral disease of small ruminants including sheep and goats. Like other Morbilliviruses, PPRV induces host immune suppression during the acute infection, favoring viral pathogenesis and secondary infections. Studies have established that V and C proteins of Morbilliviruses interfere with different steps in the IFN-I transduction pathway. Towards understanding the role of V and C genes of PPRV in modulation of host immune responses, we amplified and cloned V and C genes from PPRV followed by their expression in a eukaryotic expression vector with HA or c-Myc tag. Studies are in progress to examine the immune modulatory properties of V and C genes of PPRV.

Summary

Detailed characterization of identified immunodominant antigens of *Brucella* has been performed, which led to the identification of *Brucella* protein antigens with DIVA capability. A prototype LFA-based brucellosis diagnostic device was developed based on the BM-5 antigen. Studies on the mammalian protein, CLIP170 that interacts with the *Brucella* effector protein, TcpB revealed that CLIP170 acts as an intrinsic negative regulator of TLR2/4 signaling. CLIP170 promotes enhanced ubiquitination and degradation of the TLR adaptor protein, TIRAP. Our preliminary studies indicate that TcpB is capable of attenuating intracellular LPS-mediated innate immune responses in macrophages. We have achieved cloning and expression of V and C genes of PPRV towards understanding their role in host immune modulation.

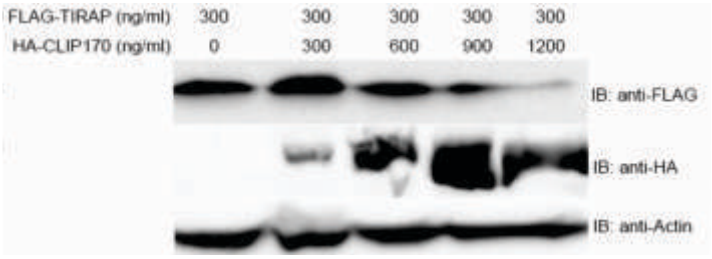

Figure 1. CLIP170 promotes degradation of TIRAP. HEK293T cells were co-transfected with FLAG-TIRAP and increasing amounts of HA-CLIP170 plasmids. 24 hours post-transfection, cells were lysed and subjected to immunoblotting. The blot was probed with anti-FLAG and anti-HA antibodies to detect FLAG-TIRAP and HA-CLIP170, respectively. Actin served as the loading control.

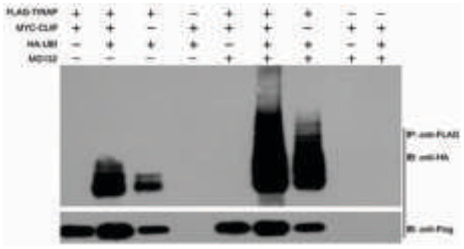

Figure 2. CLIP170 induces ubiquitination of TIRAP. HEK293T cells were co-transfected with various combinations of FLAG-TIRAP, MYC-CLIP170 and HA-Ubiquitin plasmid as indicated. 24 hours post-transfection, cells were treated with 20 µm MG132 for 4 hours as indicated in the figure. Cells were then lysed and FLAG-TIRAP was immunoprecipitated followed by immunoblotting. The blot was probed with anti-HA antibody to detect the HA-Ubiquitin-conjugated FLAG-TIRAP.

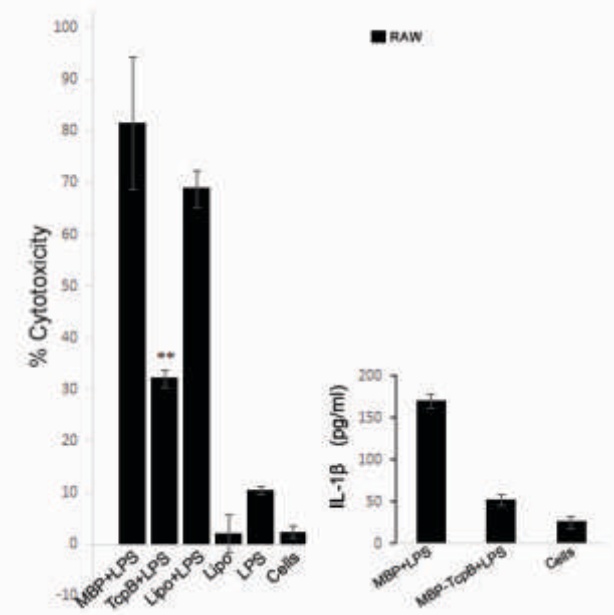

Fig 3. TcpB suppresses pyroptotic cell death and IL-1β secretion induced by intracellular delivery of LPS. RAW264 cells were primed with Pam3CSK4 to induce the signaling cascade followed by treatment with recombinant TcpB fused with Maltose Binding Protein (MBP) or MBP alone. Cells were then transfected with LPS followed by quantification of LDH and IL-1β released in the media. MBP served as the negative control.

Publication

Sarwar A, Rao SB, Jakka P, Rao VN,Bhargavi B, Gupta VK and **Radhakrishnan G**(2016) Genetic characterization and comparative genome analysis of *Brucella melitensis* isolates from India. *International Journal of Genomics.*Article ID 3034756. doi:10.1155/2016/3034756.

Laboratory of Immunomodulation and Drug Delivery

Understanding the Host Response and Molecular Pathogenesis of *Leptospira* Infection

Principal Investigator	Syed Faisal	Scientist D and Ramalingaswami Fellow
Lab members	Vivek Varma	Senior Research Fellow
	Anil Sunkara	Project Fellow
	Ajay Kumar	PhD student (since August 2016)
Collaborators	Prof. Yung-Fu Chang, Cornell University, USA	
	Prof. Avery August, Cornell University, USA	
	Prof. Dhinakar Raj, TRPVB, Chennai, India	
	Dr. Mirza Saquib Baig, IIT, Indore, India	
	Dr. Ramu Sridhar, HCU, Hyderabad, India	
	Dr. Mohd Akif, HCU, Hyderabad, India	
	Mr. Sarwar Azam, NIAB, Hyderabad	

Objectives

Leptospirosis, a zoonotic disease caused by a Gram negative bacterium, *Leptospira interrogans,* is widespread globally. It causes fatal infection in farm and domestic animals as well as in humans. The disease is highly prevalent in India and it is of significant importance as the country has a fast growing livestock sector and huge production of animal products. Current vaccines provide limited protection and are unable to prevent the shedding of bacteria in the urine of infected animals.

Recent research has shown that *Leptospira* disrupts Toll-like receptor (TLR) signalling by varying Lipopolysaccharide (LPS) expression or down-regulating expression of surface proteins to evade host immune attack and quickly disseminate and establish infection in various organs. The main focus of my research group is to understand how *Leptospira* modulates the host immune response via TLRs by exploiting its surface proteins, thereby establishing infection. Our research is focused on the following objectives.

1. To determine whether targeting TLR2/4 via surface proteins leads to activation of innate response.
2. To identify the pathways involved in the associated inflammatory response.
3. To analyze the TLR-dependent immune response and identify the best candidate for development of subunit vaccines for Leptospirosis.

Summary of work done until the beginning of this reporting year (up to March 31, 2016)

To understand the role of outer membrane/surface proteins in modulating the host innate immune response, we cloned, expressed and attempted to purify some more outer membrane proteins of *Leptospira* viz.LipL32, Lsa21 and LigA. Of these proteins, Lsa21 induced strong TLR activity as confirmed by luciferase assay and induction of IL-8 by HEK293 cells transfected with TLR2/4 plasmids. We then confirmed the TLR2 and TLR4 activity of Lsa21 on RAW264.7 mouse macrophage cell lines. Our result showed that TLR2/4 activity of Lsa21 was dramatically reduced when TLR receptors were blocked with monoclonal antibodies as revealed by reduced production of pro-inflammatory cytokines, IL-6 and TNFα. Confocal microscopy and protein docking studies showed strong binding of Lsa21 with TLR2. The activation of innate response was dependent on activation of

mitogen activated protein kinases (MAPKs) by stimulating the rapid phosphorylation of p38 and JNK. These results indicate that Lsa21 is a potent TLR2 and TLR4 agonist.

Details of progress made in the current reporting year (April 1, 2016 - March 31, 2017)

Project 1: Testing of TLR activity of various surface proteins of *Leptospira*

We cloned, expressed and purified various surface proteins of *Leptospira,* however, most of these proteins were insoluble and segregated into inclusion bodies (Fig.1). We were able to successfully purify *Leptospira* immunoglobulin like proteins LigA and LigB in soluble form as truncated fragments (conserved and variable regions). Three fragments were able to induce production of pro-inflammatory cytokines IL-6, TNFα and IL-1β by RAW 264.7 cells (Fig.2). We are in the process of analyzing the mechanism of activation of innate response by this protein in various knock-out macrophage cell lines.

Project 2: Creating *Leptospira* mutants: To identify novel virulence factor and vaccine candidates

In the proposed research, our objective is to create *Leptospira* mutants by both random and targeted mutagenesis and characterize these mutants in order to understand molecular pathogenesis, identify novel virulence factors and test their efficacy as live attenuated vaccines. We standardized the technique of introducing plasmid in *Leptospira* to create mutants. We successfully obtained a single random mutant that grows faster than the wild type. We are in the process of analyzing this mutant. We are also standardizing the technique for creating targeted mutants through CRISPR/Cas9.

Project 3: Understanding the mechanism of Mangiferin from *Peureria tuberosa*in reducing inflammation

In collaboration with Dr. Muralidhara Rao from Krishnadevraya University, Anantapur, we studied the anti-inflammatory mechanism of Mangiferin from *Peureria tuberosa.* In mouse air pouch model of inflammation, we successfully proved that Mangiferin was more effective in reducing carrageenan-induced inflammation than standard anti-inflammatory drug Celecoxib. This reduction in inflammation was mainly due to inactivation of NLRP3 inflammosome (Fig. 3).

Project 4: Evaluation of various adjuvants and drug/gene delivery systems for veterinary applications

Our research effort is also focused on the development of vaccine adjuvants/drug delivery systems for veterinary applications. In this direction, we standardized the preparation of a few vaccine adjuvants/delivery systems like liposomes, microparticles, nanoparticles, ISCOMs, oil adjuvants which can be used in animal vaccines. We have also started testing the potency of some oil-based adjuvants that can be used for animal vaccines.

Summary

We have analysed the mechanism of activation of innate response by *Leptospira* surface adhesin (Lsa21) through TLR2 and TLR4. The data was published recently in *Scientific Reports*. We are purifying more proteins and screening for TLR activity and found the *Leptospira* immunoglobulin like proteins LigA and LigB induced production of pro-inflammtory cytokines. We standardized technique for generating random mutants of *Leptospira* (attenuated in virulence) for developing live attenuated vaccine. We determined anti-inflammatory mechanism of Mangiferin isolated from *Peureria tuberosa.* The data was published recently in *Scientific Reports.* We are also developing various adjuvants/ drug delivery systems for veterinary applications.

Publications

Ramakrishna Bulugonda, Kotha Anil Kumar, Gangappa D, Muralidhara Rao*and **Syed M. Faisal*** (2017)Mangiferin

from *Pueraria tuberosa* reduces inflammation via inactivation of NLRP3 inflammasome. *Scientific Reports*7: 42683(*corresponding author).

Faisal SM*, Verma V, Subathra M, Sunkara AK, Azam S, Akif M, Baig MS and Chang YF (2016) *Leptospira* surface protein Lsa21 induces proiflammatory cytokines by Toll like receptor 2 and 4 mediated signaling pathways. *Scientific Reports*6: 39530(*corresponding author).

Roy A, Srivastava M, Saqib U, Liu D, **Faisal SM** and Baig MS (2016) Potential therapeutic targets for inflammation in toll-like receptor 4 (TLR4)-mediated signaling pathways. *International Immunopharmacology* 40:79-89.

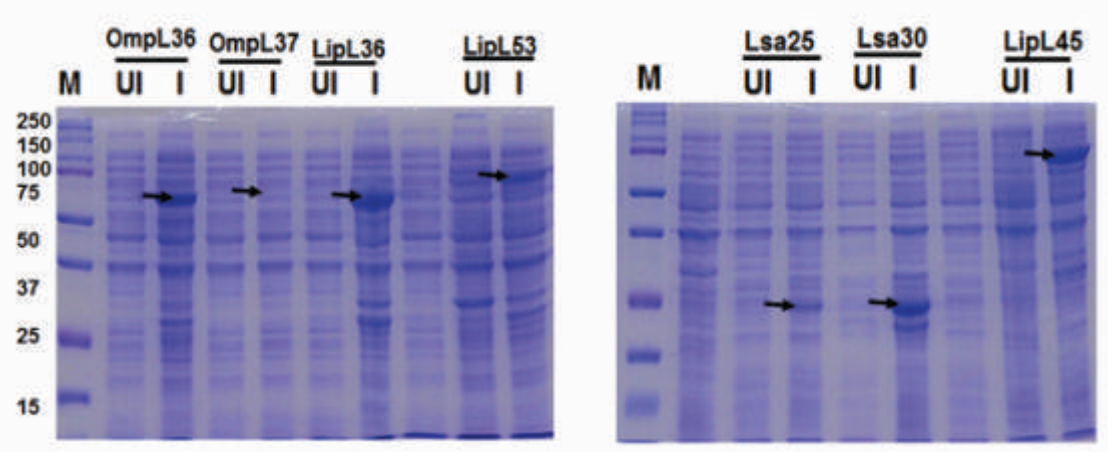

Figure 1. Expression of GST fused outer membrane proteins/surface proteins of *Leptospira.* OMPs genes coding for OmpL36, OmpL37, LipL36, LipL53, Lsa25, Lsa30 and LipL45 were cloned in pGEX4T2 vector and expressed in *E. coli*. The expression was checked following induction with 1 mM IPTG. M indicates Molecular weight marker. UI indicates un-induced cultures whereas I indicates culture induced with IPTG. Arrow indicates expected band

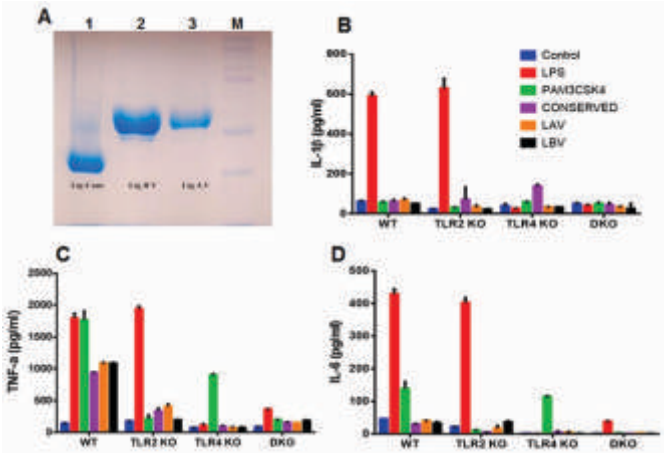

Figure 2. Production of pro-inflammatory cytokines by mouse macrophages upon stimulation with *Leptospira* immunoglobulin like proteins LigA and LigB. (A)Purified fragments of Lig proteins. Lane 1: Conserved region of Lig (Ligcon); lane 2: Variable region of LigA; lane C: Variable region of LigB as analyzed by SDS-PAGE. Analysis of various cytokines viz. IL-1β (B), TNFα (C), IL-6(D) in culture supernatant of mouse macrophages stimulated with Lig proteins. PAM3CSK4 and LPS were used as positive controls for TLR2 and TLR4 stimulations, respectively. 'Conserved' indicates conserved region of Lig protein, LAV indicates LigA variable protein, and LBV indicates LigB variable protein.

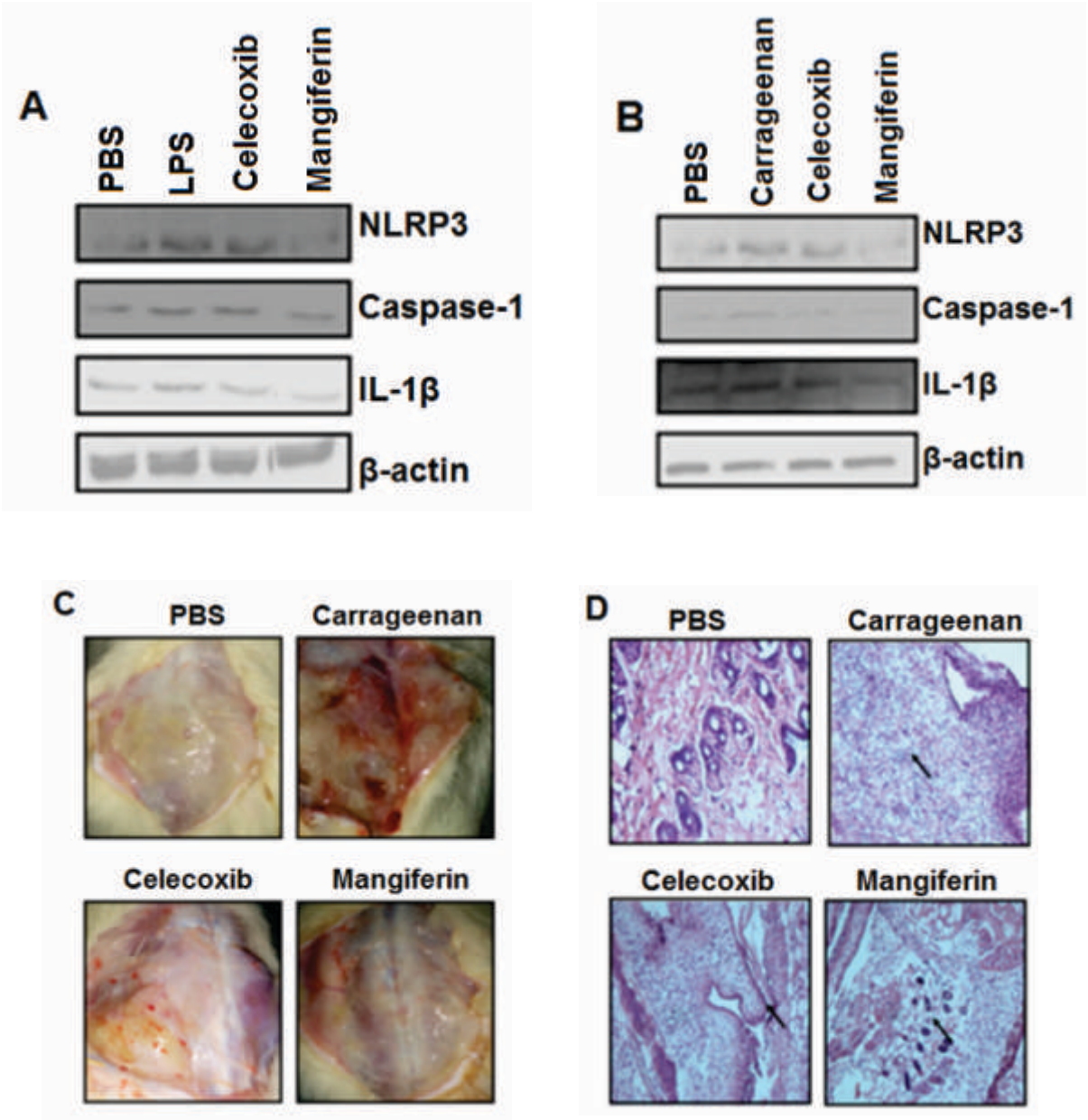

Figure 3. Mangiferin reduces inflammation via inactivation of NLRP3 inflammosomes. (A)Western blot analysis showing reduced levels of NLRP3, caspase-1 and IL-1β in mouse macrophages after treatment with Mangiferin. (B) Western blot analysis showing reduced levels of NLRP3, caspase-1 and IL-1β in mouse air pouch tissue after treatment with Mangiferin. (C) Mangiferin significantly reduced inflammation in mouse air pouch tissue as revealed in pictures taken 24h after treatment. (D) Photo micrographs of histopathological analysis of the same.

Laboratory of Antimicrobial Resistance

Surveillance of Antibiotic Susceptibility and Mechanism of Antimicrobial Resistance

Principal Investigator Vasundhra Bhandari DST-INSPIRE Faculty (Since Dec 2016)

Objectives:

Emergence of antimicrobial resistant pathogens has threatened us to reach the post-antibiotic era. Antimicrobial resistance (AMR) is globally recognized as a huge problem resulting in mortality, economic loss, increased medical cost and prolonged treatment duration. The other major challenge associated with AMR is potential transmission of resistant microbes between animals and humans, or *vice versa,* by direct contact, consumption, or through environment. This makes AMR a problem affecting multiple sectors of life and requires a coordinated, "One Health" approach. Therefore, the tripartite organizations, viz. WHO, FAO and OIE, have decided to jointly address the problem of AMR at the animal-human-ecosystems interface.

Methicillin Resistant *Staphylococcus aureus* (MRSA) is one such deadly pathogen, which is resistant towards major classes of antibiotics and has been kept on high priority list by WHO for developing new treatment options. MRSA infects humans and animals, resulting in mild to severe infections and can be fatal. Reports of potential zoonotic transmission have further impeded the problem. In order to tackle the AMR problem, the foremost requirement is surveillance of antimicrobial susceptibility in clinical isolates of microbes to keep a check on the emerging resistance in the field. Further, understanding the underlying AMR functioning in the animal and human origin strains will lead us to design better treatment options and identify drug targets for controlling the disease.

Project 1: To investigate the resistance mechanism of Oxacillin susceptible *mec*A positive *Staphylococcus aureus*(OS-MRSA): a new type of MRSA

MRSA isolates have been defined as isolates carrying the methicillin resistant determinant gene, *mecA*, which produces an additional protein PBP2A and exhibit oxacillin minimum inhibitory concentration (MIC) of ≥4mg/L. However, we have found isolates, which were *mecA* positive and susceptible to oxacillin (MICs 0.25mg/L to 1mg/L) and are referred as OS-MRSA isolates. These OS-MRSA isolates were found in human and animal origin *S. aureus* infections. Reports of OS-MRSA that surfaced globally are considered as pre-MRSA strains. There are limited reports on their resistance mechanism. Therefore, studies are underway to determine the resistance mechanism operative in the clinical isolates of *S. aureus* from animals and humans in our lab.

Project 2: Characterization of Vancomycin Resistant *Staphylococcus aureus*(VRSA)

Vancomycin is considered as a drug of last resort for the treatment of MRSA infections. Vancomycin Resistant *S. aureus* (VRSA) have been reportedacross the globe. Earlier, reports of VRSA described the transfer of plasmid borne *vanA* gene from *Enterococcus faecium* to *S. aureus* responsible for imparting high resistance towards vancomycin. However, there are reports of VRSA strains which do not contain the *vanA* gene. There are limited studies on VRSA strains and their mechanism of resistance; however, development of thick cell wall as a characteristic feature has been reported. Therefore, we aim to understand the phenotypic changes and mechanism of VRSA resistance operative in the clinical isolates.

Until now, after screening the staphylococcal strains of animal and human origin, we could not find any VRSA strains (MIC>8µg/ml). However, we found a few strains with reduced vancomycin susceptibility (RVS, MIC≤2µg/ml). Further, we observed a thick cell wall of RVS strains as compared to sensitive strains. Therefore, we are now targeting the membrane transglycosylases involved in peptidoglycan biosynthesis to see their effect on vancomycin resistance.

Viral Diseases

Laboratory of Animal Virology

Host Pathogen Interaction Studies on Animal and Avian Viruses

Principal Investigator	Madhuri Subbiah	Scientist C
Lab Members	Saraswathy Iyer	Project Fellow
	Soumya Nair	Project Fellow (Until Nov 2016)
	Venkateswaran Ganesan	Project Fellow
	Nagarjuna Yegavinti	JRF (Since June 2016)
	B. Nagaraj Nayak	Research Scholar (Since July 2016)
	Sunny Deval	Research Scholar (Since Mar 2017)
Collaborators	Prof. Vengupal Nair, The Pirbright Institute, UK	
	Dr. Suresh Kuchipudi, Penn State University, USA	
	Dr. Piruthiviraj, Globion Pvt. Ltd, Hyderabad, India	
	Dr. TR Kannaki, ICAR-Directorate of Poultry Research, India	
	Dr. Tridib Rajkhowa, Central Agricultural University, India	

Objectives

Avian Paramyxoviruses (APMV) are a group of 13 avian viruses in the genus *Avulavirus* within the family *Paramyxoviridae.* The prototype APMV, APMV serotype 1 or Newcastle disease virus (NDV) causes a highly contagious respiratory, neurological, or enteric disease in chickens. The genome of NDV consists of single stranded negative sense RNA genome of ~ 15 kb with six genes in tandem that code for six proteins: nucleocapsid protein (NP), phosphoprotein (P), matrix protein (M), fusion protein (F), hemagglutinin-neuraminidase protein (HN) and the large (L) polymerase (3'-NP-P-M-F-HN-L- 5'). NDV expresses two non-structural proteins (V and W) from P gene by RNA editing mechanism. Both V and W proteins are expressed in minute quantities only during viral infection and are not packaged into the virion. Researchers have shown that NDV mutants lacking both V and W proteins or lacking only the carboxyl terminal of V protein yielded less progeny viruses in cell culture, failed to propagate in 9 - 10 day-old embryonated chicken eggs and were highly attenuated in vivo. These results have demonstrated the role of V protein only (in anti-interferon activity, viral replication and virulence). We are currently studying the function of W protein of NDV. The rationale behind this study is to understand the specific role played by W protein in NDV life cycle. Furthermore, the virulence determining factors in NDV are not explicit and it is essential to identify the functions of every viral protein to completely understand the viral life cycle.

The second project in the lab is focused on sialic acid receptors in Emus. Influenza viruses (IAVs) are a great threat not only to human health but also to animal health. Influenza viruses are enveloped, contain 8 segments of single stranded, negative sense RNA genomes and belong to the family *Orthomyxoviridae.* IAVs have a wide host range with clinical outcomes ranging from mild inapparent infections to severe fatal disease depending on the host and the virus strain involved. Though wild aquatic birds are considered as the natural reservoirs for influenza viruses, several terrestrial birds such as chickens, turkeys and quails can act as intermediate hosts and can transmit IAVs to other species. Ratites (ostrich, emu and rheas) that are either in wild or farmed in open areas have a high

chance of getting exposed to avian influenza viruses (AIVs) from wild birds. Emus *(Dromaius novaehollandiae),* second-largest living birds in the world by height after Ostriches, were once commonly found on the east coast of Australia. In the last decade, emu farming has become a popular and lucrative business and continues to grow especially in developing countries such as India and China. There are several reports of isolation of low pathogenic avian influenza virus(LPAIV) subtypes namely H9N2, H5N2, H10N7 and H7N1, as well as highly pathogenic avian influenza virus(HPAIV) subtypes, e.g. H5N1, from emus from different parts of the world. Understanding the 'emu-influenza virus interaction' is of great importance considering their exposure to wild birds and close proximity to other terrestrial birds and farm workers.

The entry of the influenza virus into the host is facilitated by binding of viral hemagglutinin (HA) protein to the host sialic acid (SA) receptors. Since there was no information on the SA receptors in emu, we undertook a study on the expression and distribution of SA receptors in emu tissues by lectin histochemistry.

Summary of work done until the beginning of this reporting year (upto March 31, 2016)

Project 1: Understanding the role of non-structural viral protein (W) of NDV

NDV expresses two NS proteins, V and W, by co-transcriptional (mRNA) editing of P gene by polymerase stuttering mechanism. These two NS proteins share common N-terminal region with P protein and vary at their C-terminal ends. These NS proteins are not packaged in the virion but are expressed only when the virus is actively replicating in the host cell. Our current study is attempted to answer the following questions: Why does NDV express W protein only during viral infection, could W mRNA and/or W protein be a key factor for the viral replication and transcription, to evade host immune response or for pathogenesis? We are studying the effect of over expression of W protein on viral growth kinetics. We are also in the process of rescue of recombinant (r) NDV lacking W and rNDV carrying W mutations to understand the function of W protein with respect to viral biology.

Project 2: Co-expression of sialic acid receptors compatible with avian and human influenza virus binding in emus *(Dromaius novaehollandiae)*

The entry of the influenza virus into the host is facilitated by binding of viral haemagglutinin (HA) protein to the host sialic acid (SA) receptors. The receptor binding specificity is influenced by the amino acid sequence of HA protein. The type of SA receptors expressed on the host cell surface determines the host's susceptibility, viral tissue tropism, pathogenesis and transmission of influenza A viruses. Until now, there is no information on the SA receptor profile in emu and our study is the first report on the expression and distribution of the avian type (α2,3-SA) and the human type (α2,6-SA) receptors in various tissues of emu. The distribution and expression of SA receptors was planned to be studied by lectin histochemistry using receptor specific lectins. The lectins *Maackia amurensis* agglutinin II (MAAII) is specific for α2,3-SA receptors and *Sambucus nigra* agglutinin (SNA) is specific for α2,6-SA receptors. The knowledge of the SA receptor distribution and expression is important to understand the host's susceptibility/resistance to influenza virus infections, the role of the host species in the transmission of the viruses, viral pathogenesis and tissue tropism, emergence of novel genetic variants of viruses, and finally the information can help in effective control of transmission of avian and human influenza viruses.

Details of progress made in the current reporting year (April 1, 2016 - March 31, 2017)

Project 1: Understanding the role of non-structural viral protein (W) of NDV

Our preliminary bioinformatics analysis predicted W protein to localize in the nucleus. The sequence analyses of C terminal domain of W protein revealed a stretch of basic amino acid residues indicating probable nuclear localizing signal. W protein is predicted to have protein-protein interaction sites and protein-nucleic acid interaction sites. Further the ontology studies indicate possible role of W protein in antiviral response by host

immune system. We have studied the nuclear localization signal of W protein using plasmid based system. Currently, work is ongoing to understand the effect of over expression of W protein on virus growth and experiments will be designed next to understand if W has any role in immune evasion. Further, cloning work is ongoing to rescue W mutant and W null recombinant NDVs. These viruses will be characterized to understand the W protein function.

Project 2: Co-expression of sialic acid receptors compatible with avian and human influenza virus binding in emus *(Dromaius novaehollandiae)*

Influenza A viruses (IAV) continue to threaten animal and human health with constant emergence of novel variants. Aquatic birds are considered as important reservoirs of most IAVs. Since 2006, several reports of IAV isolations from emus have surfaced and it is now known that IAV infection of emus can lead to the selection of PB2-E627K and PB2-D701N mutants. However, the potential of emus to be co-infected with avian and mammalian IAVs is not yet understood. As a first step, we investigated sialic acid (SA) receptor distribution across major organs and body systems of Emu and found a widespread co-expression of both avian (α-2,3) and mammalian (α-2,6) SA receptors in various tissues (Fig. 1-3). Our results suggest that emus could play an important role in the ecology and evolution of IAVs.

Summary

We have shown by confocal studies for the first time that the W protein of NDV, a non-structural viral protein expressed by co-transcriptional editing, translocates into nucleus. We have identified the nuclear localization signal of W protein by mutation studies. We are currently investigating the functional role of nuclear localization of W protein. In addition, we are in the process of cloning full lengths of W mutant and W null clones for the rescue of recombinant NDVs to understand the W protein's function.

In our second project, we studied the sialic acid receptor in Emu for the first time. We have observed that the respiratory system of emu had abundant co-expression of both α 2,3-SA and α 2,6-SA receptors similar to pigs, pheasants and quails. The epithelial lining of small and large intestinal mucosa of emu expressed predominantly human type (α2,6-SA) receptors and avian type (α2,3-SA) receptors, respectively, with a gradual increase in the avian type (α2,3-SA) receptors from duodenum to colon unlike in chickens and ducks that predominantly express avian type receptors throughout the alimentary tract. The other internal organs of emu expressed both avian and human type receptors similar to that of chickens. These results suggest that emu is susceptible to both avian and human influenza viral infections. Hence, emu can be a potential 'mixing vessel' for influenza viruses, and can lead to generation of pandemic reassortant strains.

Publications

Gujjar N, Chothe SK, Gawai S, Nissly R, Bhushan G, Kanagaraj V, Jayarao BM, Kathaperumal K, Subbiah M* and Kuchipudi SV* (2017) Co-expression of sialic acid receptors compatible with avian and human influenza virus binding in emus (Dromaius novaehollandiae). Virology 500: 14-121 (*Corresponding authors)

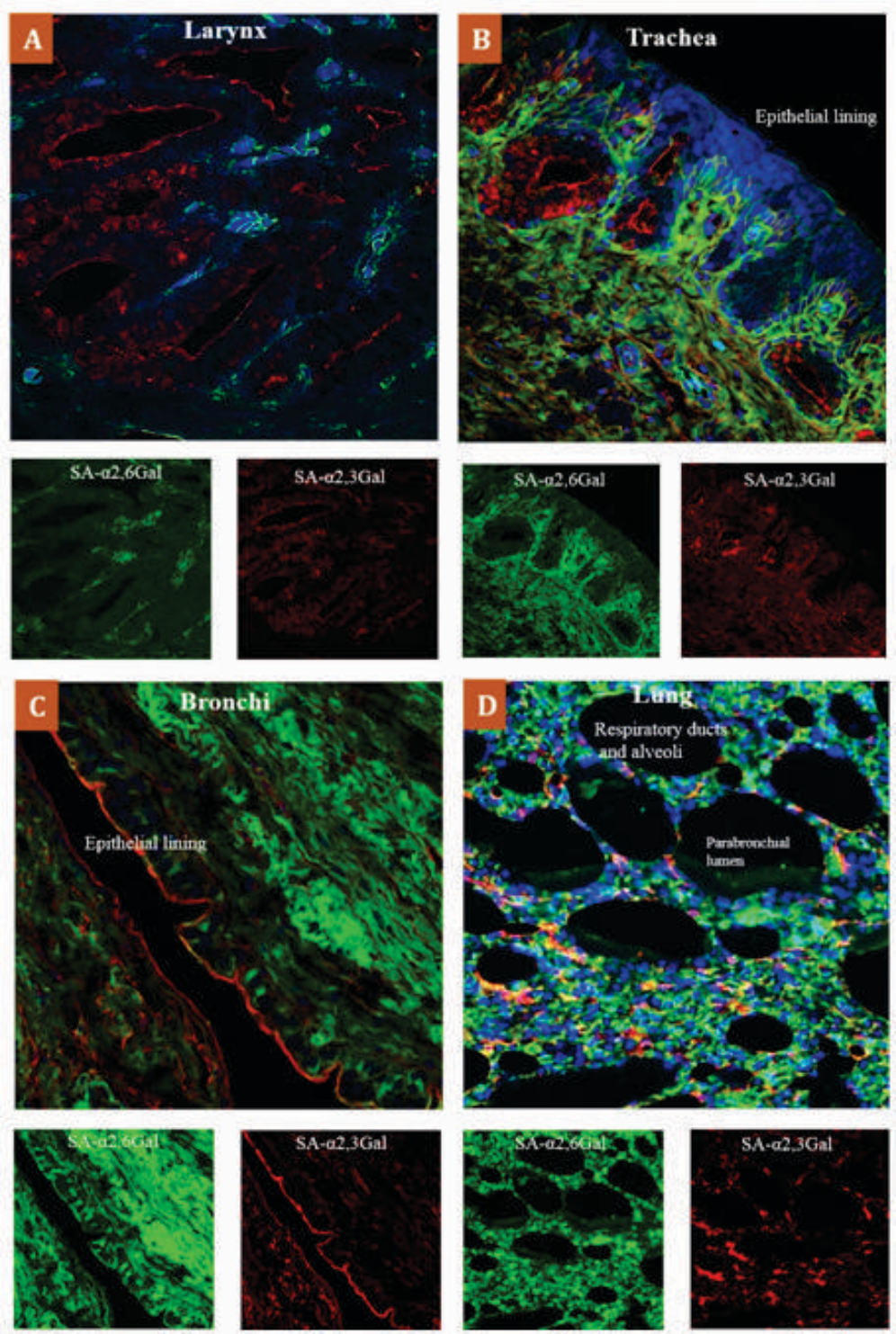

Figure 1. Co-expression of SAα2,6-Gal and SAα2,3-Gal receptors in emu respiratory tract: Composite confocal images show abundant co-expression of SAα2,6-Gal receptors (green) and SAα2,3-Gal receptors (red) throughout emu respiratory tract. Comparable expression of SAα2,3Gal and SAα2,6Gal was observed in the ciliated epithelial cells, goblet cells and non-ciliated epithelial cells of (A) larynx, (B) trachea, (C) bronchi and (D) alveoli of lungs. Tissue sections were stained with biotinylated MAAII (red-specific for SAα2,3-Gal) and FITC labelled SNA (green-specific for SAα2,6-Gal) lectins, and nuclear staining with DAPI (blue).

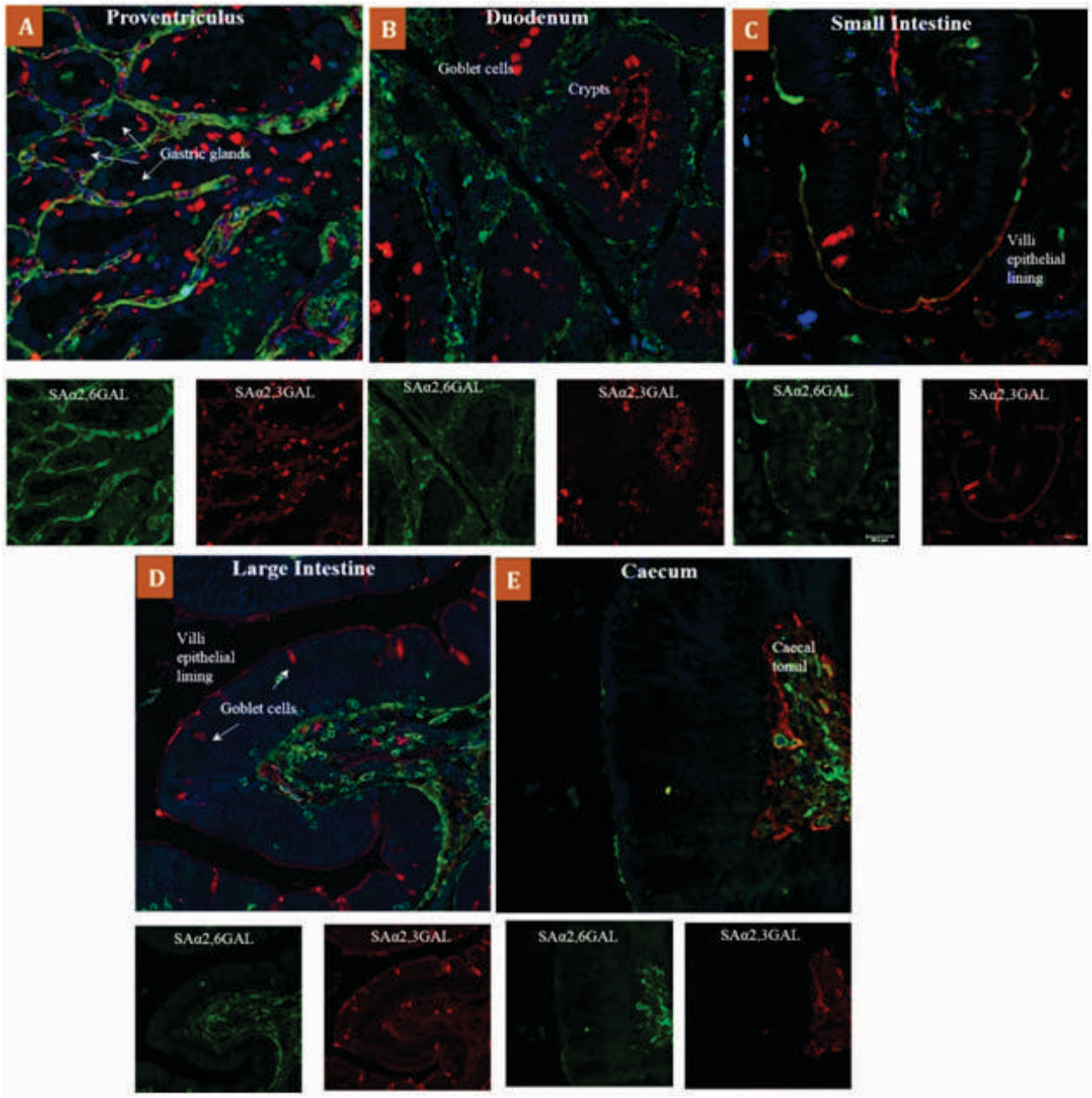

Figure 2. Co-expression of SAα2,6-Gal and SAα2,3-Gal receptors in emu digestive tract: Composite confocal images show abundant co-expression of SAα2,6-Gal receptors (green) and SAα2,3-Gal receptors (red) in (A) proventriculus, (B) duodenum, (C) small intestine, (D) large intestine and (E) caecum of emu. Expression of both receptors was observed throughout the digestive tract with a gradual increase in the expression of α2,3-SA receptor from duodenum to colon. Tissue sections were stained with biotinylated MAAII (red-specific for SAα2,3-Gal) and FITC labelled SNA (green-specific for SAα2,6-Gal) lectins, and nuclear staining with DAPI (blue).

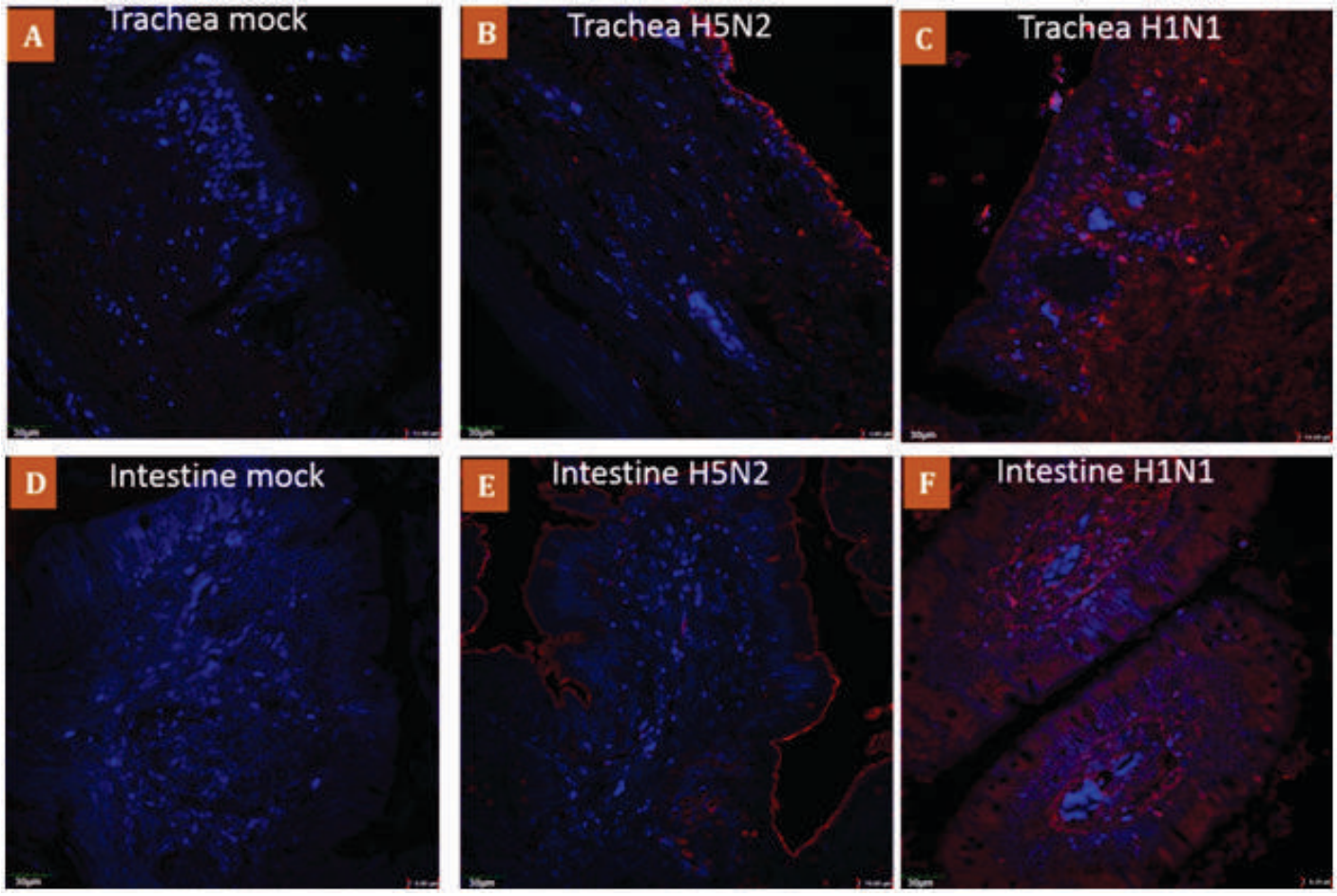

Figure 3. Virus binding assays of human H1N1 and avian H5N2 viruses on emu tissues expressing SAα2,3-Gal and SAα2,6-Gal receptors. SAα2,3-Gal and SAα2,6-Gal receptors in emu were compatible with binding of avian and human influenza viruses respectively. Virus binding assays with human H1N1 and avian H5N2 viruses on emu tissues are consistent with virus affinity for particular host receptor type. The presence of both SAα2,6-Gal and SAα2,3-Gal receptors in trachea is mirrored by a similar binding pattern of (B) avian H5N2 virus and (C) human H1N1 virus. Similarly extensive binding of (E) avian H5N2 and (F) human H1N1 viruses to intestine was found. Virus binding assays were performed with human pandemic H1N1 virus (A/H1N1/Virginia/2009), or low pathogenic avian influenza H5N2 virus (A/chicken/PA/7659/85). (A &D) Mock controls performed with no virus treatment show absence of fluorescence.

Protozoal Diseases

Laboratory of Molecular Interactions

Understanding Host-Parasite-Vector Interactions at Molecular Level

Principal Investigator	Anand Srivastava	Scientist C
Lab Members	Prasanna Babu Araveti	JRF (Since Sep 2015)
	Rolly Kumari	Project JRF (Apr 16-Mar 17)

Objectives

My research group works on "Ticks and Tick Borne diseases" (TTBDs) that are responsible for the high economic losses in livestock sector especially in developing countries like India. Ticks, apart from sucking blood, act as carriers for various disease causing bacteria, viruses and parasites. In the context of India, the important parasites which are transmitted by ticks are *Theileria* and *Babesia*. These parasites have complex interactions with the host(s) and the vector (tick). Molecular understanding of these interactions will provide key information about important pathways for the survival of both parasites and vector. Furthermore, disruption of these important interactions will be lethal for parasites and vectors.

My research interests are to understand molecular interactions involved in host-parasite-vector cross talk and to identify potential targets for development of vaccine(s) and diagnostics, especially for theileriosis.

Theileria spp. infect ruminants, including cattle and sheep, and cause theileriosis. The *theileria* parasites are obligate intracellular apicomplexan haemoprotozoans. In India, bovine theileriosis is mainly caused by *Theileria annulata* and the disease is known as "bovine tropical theileriosis". This disease is highly common in exotic breeds, their cross breeds and young indigenous calves.

Our aim is to understand the basic metabolic pathway(s) important for survival for parasites and vector. We utilize tools of molecular biology, imaging, *in vitro* parasite culture techniques, etc to investigate the basic metabolic pathway. Furthermore, we perform epidemiological studies to understand disease burden at the farm level. In particular, we have been focusing on the following objectives:

1) To understand the molecular mechanism(s) involved in transformation of host cell by *Theileria* parasite.

2) To understand haemoglobin uptake by tick during blood meal.

Summary of work done until the beginning of this reporting year (up to March 31, 2016)

Previously, we successfully adopted *Theileria* infected lymphocytes, isolated from the field, to laboratory conditions. The presence of *Theileria* was detected using PCR for *Theileria* specific genes. We also started epidemiological studies to find out the presence of *Theileria* infections at the farm level. In random sampling, we estimated approximately 12% infection of *Theileria* in the field. Further, we have been working towards understanding the role of *Theileria* parasite molecules in transformation of host cells. Using bioinformatic approaches, we identified many potential molecules for transformation of host cell. One of them was prohibitin and the gene was recombinantly expressed, however, the efforts to produce soluble recombinant prohibitin protein have not been fruitful till date. Antibodies against synthetic peptide of this protein were raised. We have also started work to understand molecular mechanisms involved in the digestion of blood by the ticks.

Details of progress made in the current reporting year (April 1, 2016 - March 31, 2017)

Project 1: Effect of curcumin on *Theileria* infected cattle lymphocytes.

Curcumin, a natural polyphenolic compound, is isolated from the rhizome of Curcuma *longa*. Various reports have shown anticancer activity of curcumin. In the present study, we have reported for the first time the effect of curcumin on *Theileria* infected cattle lymphocytes. To confirm the anti-proliferation effect of curcumin on *Theileria* infected cell lines we performed the cellular viability and proliferation assay by trypan blue exclusion assay and MTT assay, respectively. *Theileria* infected cattle lymphocytes were treated with different concentration of curcumin (1mM, 2.5mM, 5 mM, 10mM, 20mM) for different time (0, 12, 24, 36 hrs) and the rate of proliferation was estimated. The curcumin exerted concentration and time dependent inhibition in proliferation (Fig. 1A).

DNA fragmentation by endogenous nucleases is one of the important event during apoptosis. The fragmented DNA carries 3' hydroxyl group which can be detected by fluorescein-dUTP using Tunnel assay. Treatment with curcumin for 24hrs at different concentration was analyzed for DNA fragmentation analysis using FACS. The analysis showed that curcumin induces DNA fragmentation (Fig 1B). Further to confirm apoptosis annexin V staining was performed. After treatment with 20µM curcumin the infected lymphocytes showed increase in apoptosis (Fig. 1C). In addition, curcumin treatment showed no cytotoxic effects upon PBMCs. Furthermore, western blotting with caspase 3 and caspase 8 showed the activation of apoptosis pathway (Fig. 2A) which was further shown to be blocked by inhibitor of caspase 3 and 8 (Fig. 2B). We also found that autophagy marker (LC3b) is also being upregulated in the curcumin treated cells (data not shown). Efforts are ongoing to understand the complete pathway by which curcumin induces apoptosis in the *Theileria* infected cattle lymphocytes.

Our studies demonstrate that curcumin treatment induces apoptosis in *Theileria* infected cattle lymphocytes. Together, these data suggest that curcumin exerts anti-theilerial effects. Further we are conducting experiments for identification of molecules in upstream of the apoptosis pathway and their link to the autophagy pathway.

Significance

Curcumin could provide cost effective method for treatment of Theileriosis. It may help in reduction of doses of commonly used drugs for treatment of Theileriosis.

Summary

We showed that curcumin has anti-theilerial effect on *Theileria* infected cells. We demonstrated that curcumin treatment led to upregulation of apoptotic pathway in *Theileria* infected cells.

Publications

Anilkumar K, Reddy GV, Azad R, Yarla NS, Dharmapuri G, Srivastava A, Kamal MA and Pallu R (2017) Evaluation of anti-inflammatory properties of isoorientin isolated from tubers of *Pueraria tuberosa.Oxidative Medicine and Cellular Longevity* Article ID 5498054. doi:10.1155/2017/5498054.

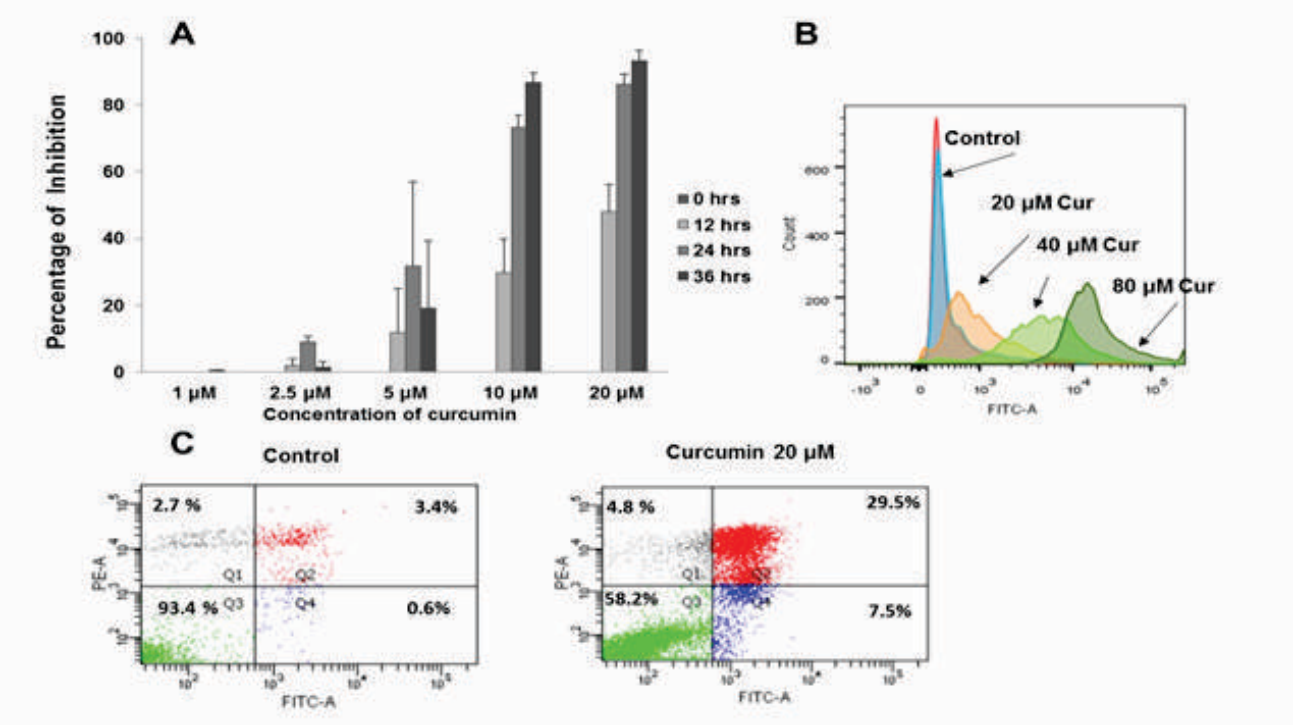

Figure 1.Effect of curcumin on *Theileria* infected cattle lymphocytes. A. Effect of curcumin on cell proliferation. Increasing concentration of curcumin showed increase in cell death in dose and time dependent manner, B. Tunnel assay showing increasing level of fragmentation with increasing concentration of curcumin, C. Annexin V assay showing increase in apoptotic cells with 2µM curcumin.

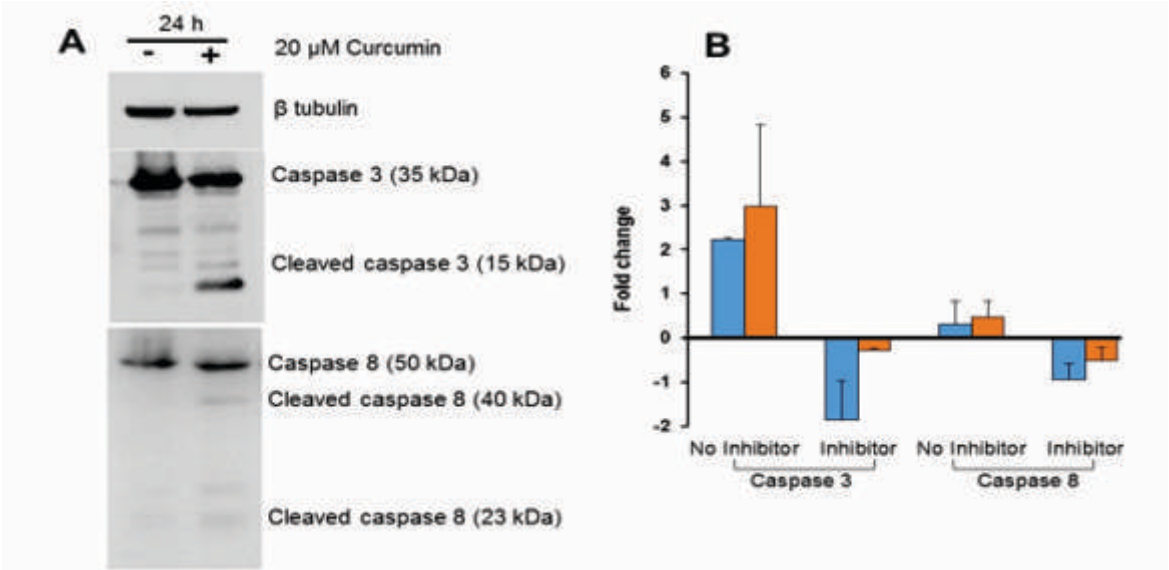

Figure 2.Induction of apoptosis in *Theileria* infected cattle lymphocytes upon treatment of curcumin A. Curcumin treatment of infected cells lead to increase in cleavage of caspase 3 and caspase 8, B. Activity of caspase 3 and 8 was inhibited by specific inhibitor.

Laboratory of Pathogen Biology

Study of Virulence mechanism and Pathogenesis during Intracellular Pathogen infections

Principal Investigator	Paresh Sharma	Scientist C
PhD Students	Sonti Roy	JRF (From July 2016)
	Debabrata Dandasena	JRF (From Feb 2017)
Hiral Mistry	JRF (Until Jan 2017)	
Other Members	Shweta Noori	Project SRF (From Aug 2016)
	Shalini Chakraborty	Project JRF (From Sep 2016)
Umarani Brahma	Project JRF (From Mar 2017)	
	Kumar Reddy	Project SRF
Collaborators	Prof. P. Reddanna, University of Hyderabad, Hyderabad	
	Dr. Vasundhra Bhandari, NIAB, Hyderabad	
	Dr. Anand Kumar, SV University, Proddatur	

Project 1: Identification of genetic and antigenic variations in Haemoprotozoan parasites causing livestock infections

Objectives

Haemoprotozoan parasites like *Theileria*, *Anaplasma, Babesia* and *Trypanosoma* have a major impact on the health and productivity of the livestock. Lack of proper diagnosis and treatment results in huge economic loss to livestock industry. At NIAB, we are routinely helping farmers and veterinarians by active surveillance of these haemoprotozoan infections in livestock, especially cattle. Understanding the mechanism of virulence and genetic diversity of the prevalent parasites can be helpful in designing new tools for controlling these pathogens.

Summary of work done until the beginning of this reporting year (upto March 31, 2016)

Molecular and Phylogenetic analysis was done for identifying prevalent genotypes of *Theileria* from the southern states (Telangana and Andhra Pradesh) of India. We have reported new genotypes of *T. annulata* and *T. orientalis* parasites from India. The emergence of these new genotypes could be an explanation for the frequent outbreaks of bovine theileriosis (Neena et al, 2015).

Details of progress made in the current reporting year (April 1, 2016 - March 31, 2017)

Recently, we have characterized *Anaplasma marginale* strains from India (Andhra Pradesh and Telangana) using parasite specific major surface protein 4 gene (*msp4*). Phylogenetic association analysis revealed that most of the strains showed close proximity with strains from Mexico and other strains showed closeness to strains reported from countries like Brazil, Zimbabwe, Puerto Rico and Hungary (Fig. 1). This is the first report from India identifying heterogeneous population of *A. marginale* strains causing anaplasmosis (George et al, 2017). We have developed a prototype Lateral Flow Assay (LFA) using *T. annulata* and *T. orientalis* specific antigens for point of care diagnosis of bovine theileriosis in the field and it needs to be validated. Further, looking into the need of the hour, we intend to develop a single multiplex kit that detects major blood borne pathogens of livestock.

Project 2: Identification of virulence genes in *S. aureus* clinically isolated from bovine mastitis

Objectives

The project is aimed at characterizing *S. aureus* strains that cause bovine mastitis in India using genomic and proteomic tools. This will help in the understanding of disease pathogenesis and, therefore, it can be of a great help to the livestock industry.

Summary of work done until the beginning of this reporting year (upto 31st Mar, 2016)

We have collected milk samples from cattle, buffalo and goat showing subclinical and clinical forms of mastitis from different districts of Andhra Pradesh, Telangana and Tamil Nadu. *S. aureus* clinical isolates (39) were checked for the presence of virulence genes (such as *pvl* gene) and they were typed using *agr* gene and *Staphylococcus* protein A (*spa*) gene.

Details of progress made in the current reporting year (April 1, 2016 - March 31, 2017)

Around 50 strains were genotypically and phenotypically characterized as *S. aureus*. Molecular characterization based on multilocus sequence typing (MLST), *spa* typing, *agr* typing and SCC*mec* classification revealed strains belonging to different groups. Moreover, strains showed *spa* types (t2526, t9602) and MLST sequence types, ST-72, ST-88 and ST-239 which have been earlier reported in human infections. A novel sequence type, ST-1687 was also found among the strains from Telangana and Tamil Nadu. Increased genotypic variability with strain related to human infections and PVL positive isolates indicates a worrisome situation with the possibility of bilateral transfer (Mistry et al., 2016).

Project 3: Identification of virulence mechanisms involved in host pathogenesis during *T. annulata* infection:

Objectives

T. annulata causes immense loss to the livestock industry and therefore, eradication and control strategies are needed for the control of the disease. Our focus is on identifying the mechanisms of virulence or disease pathogenesis during *T. annulata* infections. Identifying genes involved in virulence/host parasite interaction and disease resistance could lead to development of new drugs/diagnostic tools/strategies to reduce infection and control the disease in livestock.

D**etails of progress made in the current reporting year (April 1, 2016 - March 31, 2017)**

In vitro culture of the *T. annulata* strains isolated from the clinically infected animals have been established. Studies are on-going for identification of genes involved during parasite infection. In another project, we are trying to understand the genetic basis of disease resistance by conducting genome wide association study (GWAS) among *T. annulata* susceptible and resistant animals. For the GWAS study, we have collected 550 blood samples of suspected disease susceptible and resistant animals from four different states namely Telangana (n=200), Andhra Pradesh (n=118), Punjab (n=100) and Haryana (n=132). Samples were collected from areas with suspected cases of *Theileria* based on clinical symptoms and also blood samples from the neighboring healthy animals were collected which showed no clinical symptoms of any disease. Genomic DNA were isolated from all the animals and microscopy was done to observe the blood smear for *Theileria* piroplasm. Animals reported without any clinical symptoms and negative for both microscopy and PCR assays were treated as disease resistant animals, however, animals with clinical symptoms and positive for both diagnostic approaches were classified as disease susceptible animals (Fig. 2). Until now, out of 550 samples screened, 181 have been designated as susceptible based on microscopic and PCR based assay whereas 369 are disease resistant animals. Ongoing studies are aimed to identify

targets that could lead to development of new drugs/diagnostic tools/strategies to reduce infection and control disease in livestock.

Publications

George N,Bhandari V andSharma P(2017) Phylogenetic relationship and genotypic variability in *Anaplasma marginale* strains causing anaplasmosis in India. *Infection Genetics and Evolution* 48:71-75.

Mistry H*, Sharma P*, Mahato S, Saravanan R, Kumar PA, Bhandari V(2016) Prevalence and Characterization of Oxacillin susceptible mecA - positiveclinical isolates of *Staphylococcus aureus* causing bovine mastitis in India. PLOSONE11:e0162256. doi: 10.1371/journal.pone.0162256.

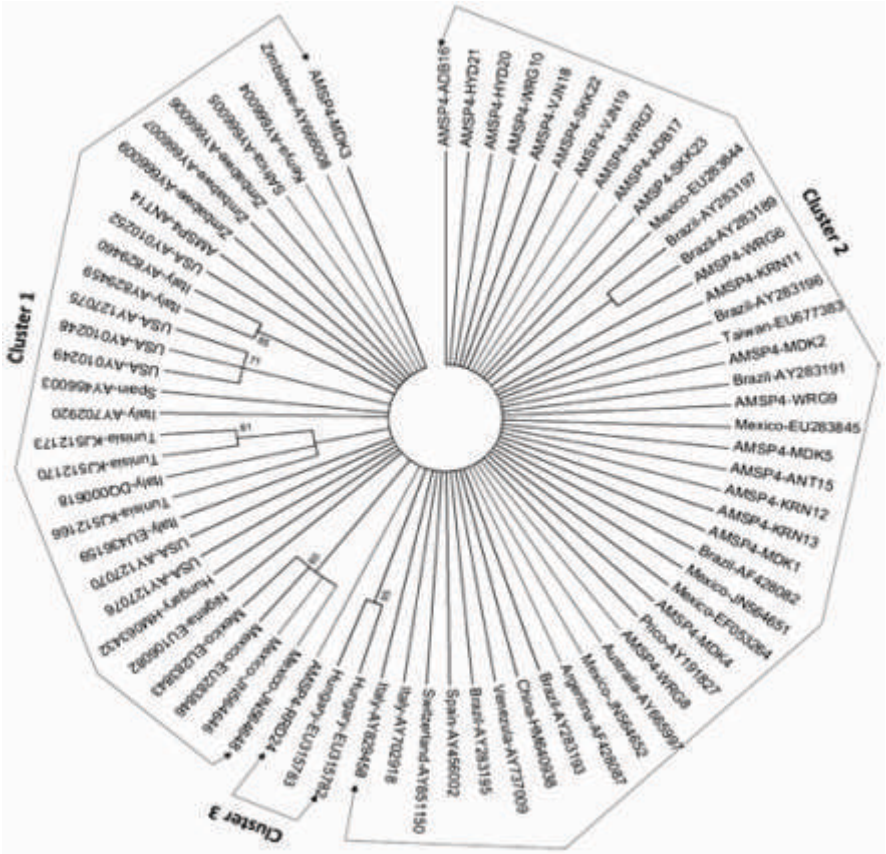

Figure 1: Phylogenetic relationship tree using the Maximum Likelihood method. The evolutionary history was inferred based on the Kimura 2-parameter model. Phylogenetic relationship among the nucleotide sequences of msp4 gene of samples collected from Andhra Pradesh and Telangana states, with published sequences available at NCBI database. Cloned sequences from Medak were designated as AMSP4-MDK 1–5 [GenBank: KX989510, KX989511, KX989531, KX989512, KX989513], Warangal: AMSP4-WRG 6–10 [GenBank: KX989514, KX989515, KX989516, KX989517, KX989533] ; Karimnagar: AMSP4-KRN 11–13 [GenBank: KX989518, KX989519, KX989520]; Anantpur: AMSP4-ANT 14, 15 [GenBank: KX989521, KX989530]; Adilabad: AMSP4-ADB 16, 17 [GenBank: KX989522, KX989523]: Vijayanagram; AMSP4-VJN 18, 19 [GenBank: KX989524, KX989525]: Hyderabad: AMSP4-HYD 20, 21[GenBank: KX989526, KX989532]; Srikakulam: AMSP4-SKK 22, 23 [GenBank: KX989527, KX989528] and Rangareddy: AMSP4-RRD 24 [GenBank: KX989529].

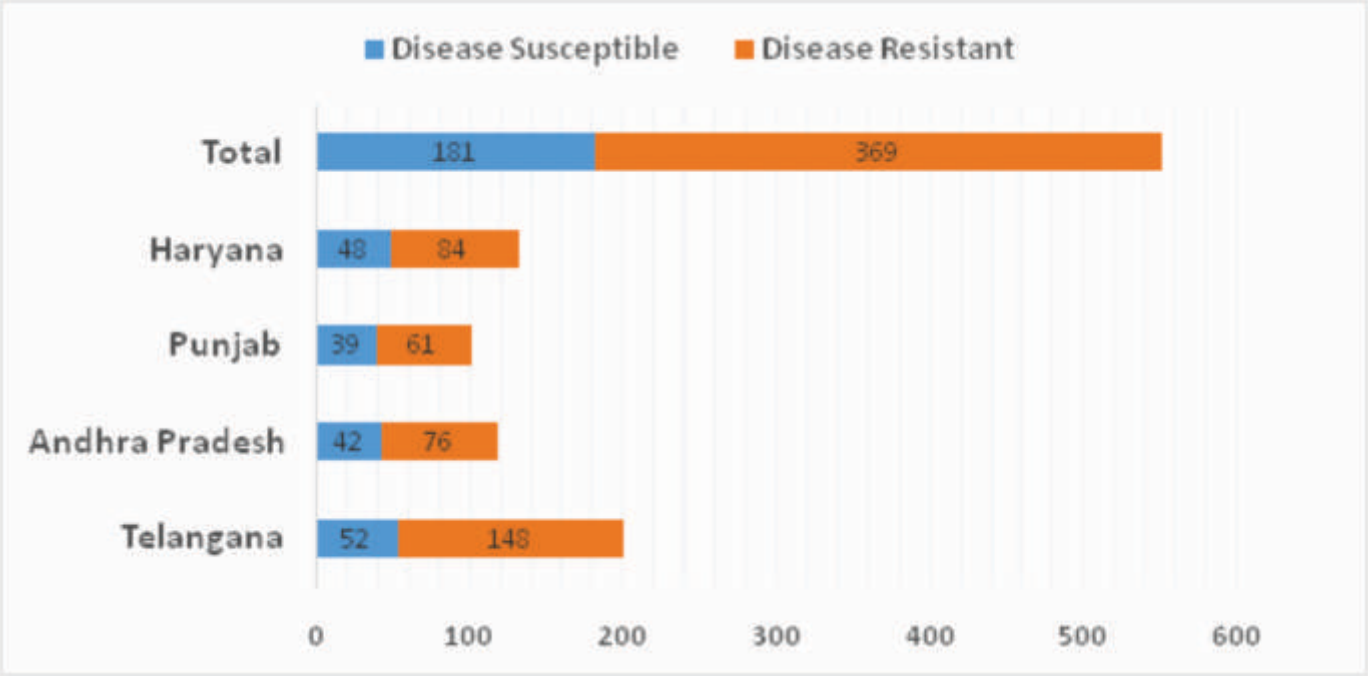

Figure 2. Total cases of disease susceptible and resistant animals screened from Telangana, Andhra Pradesh, Punjab and Haryana. The bar represents the disease susceptible and resistant animals out of the total number of samples collected from an area.

Laboratory of Molecular Parasitology

Studies on the Role of *Toxoplasma gondii* Novel Cell Cycle Regulators in RNAPII Mediated Transcription

Principal Investigator	Abhijit S. Deshmukh	Scientist C& DST-INSPIRE Faculty
PhD student	Ashok K. Kolagani	JRF (since July 2016)
Other member	Rajkumar Gurupwar	Project Assistant (until March 2017)
Collaborators	Dr. Arun Kumar Kota, HCU, Hyderabad	
	Dr. Pallabi Mitra, DST/INSPIRE Faculty, HCU, Hyderabad	
	Dr. Dhanasekaran Shanmugam, NCL, Pune	

Objectives

Toxoplasma gondii is an obligate intracellular protozoan parasite responsible for abortion, stillbirth and neonatal mortality in livestock. *T. gondii tachyzoites* (highly replicating parasite stage) replication cycle differs from the classical animal cell cycle as they divide using a three-phase cycle i.e. G1, S and M phases pointing to potentially novel mechanisms of control over their complex cell cycles. In metazoans, both cell cycle and RNA Pol II (RNAPII) mediated transcription are regulated by variety of cyclin and cyclin-dependent kinases (CDK) pairs. The existence of such CDK and their cognate partner cylcin has not been investigated in the parasites. In our recently published work, we identified Cdk7 based ternary complex and showed its role in RNAPII mediated transcription initiation in *Toxoplasma*. In the follow-up studies, we are identifying and investigating the role of cyclins and CDKs in RNAPII mediated transcription elongation using bioinformatics and biochemical approaches. In particular, we focus on the following objectives.

I. Identify and functionally characterize *T. gondii* cyclin and CDK involved in transcription

ii. Understand the role of the identified cyclin-CDK pair in RNAPII mediated transcription elongation

Summary of work done until the beginning of this reporting year (upto March 31, 2016)

Cyclin-dependent kinase 7 (Cdk7), in conjunction with CyclinH and Mat1, activates cell cycle CDKs and is a part of the general transcription factor TFIIH. Role of Cdk7 is well characterized in model eukaryotes, however, its relevance in protozoan parasites has not been investigated. This important regulator of key processes warrants closer examination, particularly in this parasite, given its unique cell cycle progression and flexible mode of replication. We report functional characterization of TgCdk7 and its partners TgCyclinH and TgMat1. Recombinant Cdk7 displays kinase activity upon binding its cyclin partner and this activity is further enhanced in the presence of Mat1. The activated kinase phosphorylates C-terminal domain (CTD) of TgRPB1 suggesting its role in parasite transcription. Therefore, the function of Cdk7 in CTD phosphorylation and RPB1 mediated transcription was investigated using Cdk7 inhibitor. Unphosphorylated CTD binds promoter DNA while phosphorylation by Cdk7 triggers its dissociation from DNA with implications for transcription initiation. Inhibition of Cdk7 in the parasite led to strong reduction in serine 5 phosphorylation of TgRPB1-CTD at the promoters of constitutively expressed actin1 and sag1 genes with concomitant reduction of both nascent RNA synthesis and 5'-capped transcripts. Therefore, we provide compelling evidence for crucial role of TgCdk7 kinase activity in mRNA synthesis.

Details of the progress made in the current reporting year (April 1, 2016- March 31, 2017)

Project: Identification of *Toxoplasma* cyclins and CDKs involved in transcription elongation

Data mining using *Toxoplasma* genome suggests a general conservation of basal eukaryotic transcriptional machinery, however, the functional identity of proteins involved as well as the mechanisms underlying the regulation of transcription have not been addressed. To fully understand and appreciate the biology of these parasites, it is important to identify and establish the key regulators of this fundamental process which currently poses a substantial knowledge gap. The process of mRNA synthesis by the transcription machinery is a complex multi-step event which comprises of pre-initiation, initiation, promoter clearance, elongation and termination. All of these processes are coordinated by several proteins which form dynamic complexes interacting with DNA and pre-mRNAs. Phosphorylation plays a key role in mechanistic regulation of these complexes. In model eukaryotes, several protein kinases have been identified that are capable of phosphorylating proteins involved in mRNA production.

In the recent study, we systematically identified and functionally characterized Cdk7 and associated proteins CyclinH and Mat1. Importantly, we elucidated their central role in the parasite transcription initiation whereby phosphorylation of RNAPII CTD at crucial serine residue by Cdk7 aids in nascent RNA synthesis and subsequent maturation by recruitment of capping enzymes. In metazoans, transcription elongation is positively regulated by the positive transcription elongation factor b (P-TEFb), consisting of CDK9 and cyclin T1. P-TEFb enables transition from abortive to productive transcription elongation by phosphorylating CTD in RNAPII and negative transcription elongation factors. In the follow-up study, we would like to identify the existence of P-TEFb like complex and understand its role in transcription elongation of *T. gondii*.

In silico identification of *T. gondii* Cdk9 and Cyclin T

We performed BLASTP searches of the *Toxoplasma gondii* genome database (http://www.toxodb.org/) as queries of Cdk9 and cyclin T sequences from yeast and human. This enabled us to identify TGME49_281450 and TGME49_264690, homologs of the *H. sapiens* Cdk9 and cyclin T proteins respectively, which we call TgCdk9 and TgCyclin T. The predicted proteins (Cdk9 and Cyclin T) show overall 30 to 40 % 30 to 40% identity with the human and yeast proteins. In addition, TgCdk9 possesses two ATP binding domain (86–94aa and 179-181aa) and the T-loop (241–262 aa) (Fig. 1A). TgCyclin T protein contains conserved cyclin box (1-311aa), a region responsible for Cdk binding (Fig. 1B). Along with cyclin box, TgCyclin T also contains nuclear localization signal (570–573aa), in addition to unique C-terminal extension (Fig. 1B).

The TgCdk9 and TgCyclin T share low sequence identity with other eukaryotic counterparts, therefore, it is important to evaluate the structural conservation of these proteins. Crystal structures of human Cyclin T and Cdk9 are available. With the aid of HsCdk9 and HsCyclin T crystal structures as templates, we attempted homology modelling of TgCdk9 and cyclin box of TgCyclin T and superimposed them with their counterparts. The superimposed protein models of TgCdk9 and cyclin box of TgCyclin T with their human counterparts show overall similar structures (Fig. 1C-F). TgCdk9 and TgCyclin T protein models were validated using Ramachandran plot data and G-factors.

T. gondii Cdk9 and Cyclin T functionally complement *S. cerevisiae Bur1 and Bur2* genes respectively

To investigate whether *Toxoplasma* Cdk9, and Cyclin T are P-TEFb homologs, we performed a functional complementation assay. For complementation studies, yeast mutant strains with a deletion of chromosomal copy of *Bur1 and Bur2* and bearing the wild-type copy of the respective gene in a plasmid containing an ura3 marker were transformed with plasmids for expressing *Sccdk9, Sccyclin* T and pYES3/CT (empty vector), or *T. gondii cdk9*

and *cyclin T genes* under a galactose-inducible promoter with a tryptophan marker. Following transformation, the transformants were grown either in the absence or presence of 5-fluoroorotic acid (5-FOA) for the selection of viable yeast cells in minimal medium lacking tryptophan with or without FOA. The results revealed that mutant cells expressing TgCdk9 or TgCyclin T were proficient for growth on SD-Trp+ FOA much like the situation with self-complemented strain, whereas those mutant cells transformed with pYES3/CT empty vector failed to grow on SD-Trp+ FOA (Fig. 1G-H). This result clearly showed that TgCdk9 and TgCyclin T were capable of fully functionally complementing the function of *Bur1 and Bur2*respectively within the yeast mutant strains. The results establish that the TgP-TEFb related proteins Cdk9 and Cyclin T are true functional counterparts of ScBur1 and ScBur2 respectively.

T. gondii cdk9 and cyclin T genes express in the parasite

To determine the endogenous expression of *T. gondii* P-TEFb related components in the parasites, full length Cdk9$^{175\text{-}454,}$ Cyclin T$^{1\text{-}634}$ were amplified from *T. gondii* cDNA. The amplicons for Cdk9 and Cyclin T were cloned in to the pET-21a vector introducing a C-terminal histidine fusion and expressed in *E. coli.* TgCdk9 was expressed as soluble proteins and TgCyclin T protein was expressed as a part of inclusion bodies. Recombinant proteins were purified using affinity chromatography. Each of the recombinant purified protein was used as antigen to raise specific polyclonal antibodies in mice and rabbits. The Cdk9 antiserum recognized the recombinant protein (~45 kDa) and a band of expected size at about 45 kDa (excluding signal peptide) in the parasite lysate (Fig. 2A). Similarly, the TgCyclin T anti-serum recognized the recombinant protein (~70 kDa) and a predicted size band at about 70 kDa in the parasite lysate (Fig. 2B). All the three polyclonal antibodies did not showcross-reactivity with HFF proteins.

Given that the *T. gondii* P-TEFb like components (Cdk9 and Cyclin T) functionally complemented *S. cerevisiae* mutant strains, we would like to explore the possibility of complex formation (Cdk9-CyclinT) like their counterparts in yeast. Further to examine the role of TgCdk9 in TgRPB1-driven transcription, we would like to check kinase activity of the TgCdk9 and investigate the role of active kinase in mRNA synthesis of the highly expressed candidate genes of *T. gondii* using Cdk9 specific kinase inhibitor.

Summary

Using Bioinformatics analysis, we identified putative P-TEFb subunits namely Cdk9 and Cyclin T in the *T. gondii* genome. Full length Cdk9 (excluding signal peptide) and cyclin T were expressed in *E. coli* as recombinant proteins. Polyclonal antibodies raised against respective proteins recognised native protein in parasite lysate indicating Cdk9 and cyclin T are expressed in *T. gondii.*

Publication

Deshmukh A S, Mitra P and Maruthi M (2016) Cdk7 mediates RPB1-driven mRNA synthesis in *Toxoplasma gondii.* Scientific Reports19;6:35288.

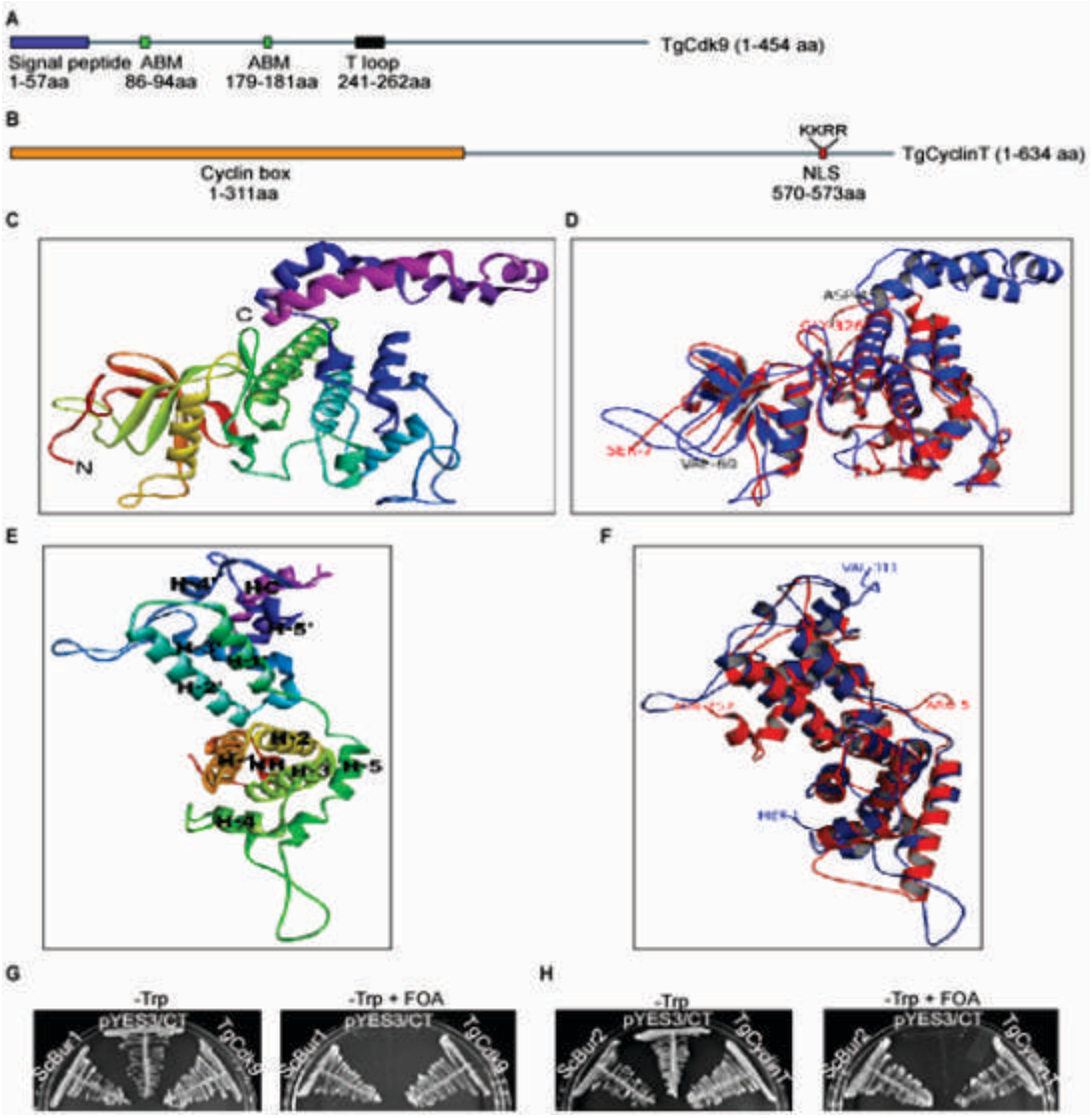

Figure 1. T. gondii cdk9 and cyclin T genes share functional homology with *S. cerevisiae bur1 and bur2 genes respectively.* (A) Schematic diagrams of full length *T. gondii* Cdk9 and Cyclin T. TgCdk9: two ATP binding domain and T-loop domain are shown. (B) TgCyclin T: cyclin box, nuclear localization signal are shown. (C-F) The homology modelling and superimposed structures of TgCdk9 and cyclin box of TgCyclin using HsCdk9 and cyclin box of HsCyclin T as a template. (G) *S. cerevisiae* strains with chromosomal copy deletion of *bur1and bur2* genes were transformed with yeast expression vector (pYES3/CT) carrying trp selection marker and the coding regions of respective *S. cerevisiae* wild type genes and *T. gondii cdk9* and *cyclin T genes.* Transformant were selected for tryptophan prototrophy by growing on medium lacking tryptophan. Selected colonies were streaked on to tryptophan-dropout medium with or without 1 mg/ml FOA. ScBur1, ScBur2 along with TgCdk9, TgCyclin T could rescue the growth of *bur1, bur2* mutant yeast strains respectively, in the presence of FOA, whereas empty vector could not support the genetic complementation of the strains under the same experimental conditions.

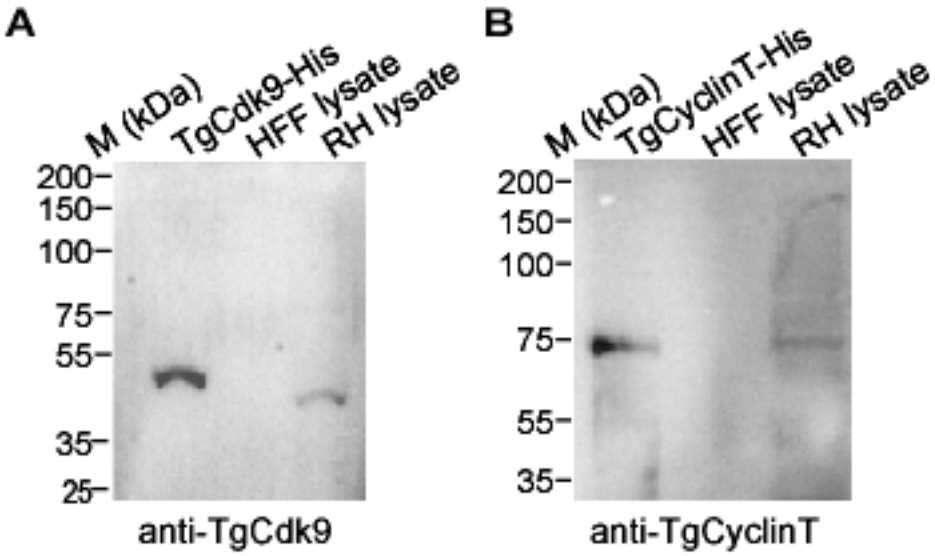

Figure 2. Characterization of polyclonal antibodies against TgCdk9 and TgCyclin T. (A) Polyclonal antibodies raised against TgCdk9 were specific aswestern blot analysis with immune sera recognized the band of expected size (~45 kDa) in the native parasite lysate. The antibodies also recognized TgCdk9-His recombinant protein (~45 kDa). (B) Similarly polyclonal antibodies recognized TgCyclin T native (~70 kDa) and recombinant proteins (~70 kDa). Raised antibodies did not cross-react with HFF proteins.

Animal Reproduction

Laboratory of Molecular Reproduction

Investigating the Role of Kisspeptin in Female Reproduction

Principal Investigator	Sathya Velmurugan	Scientist C
Lab Members	Meenal P Ullewar	Project Fellow (Until Sep'16)
	Sri Ravali S	Project Fellow (Until Mar'17)
	Srinivas S	JRF (Until May'16)
	Kiran Avula	JRF (Since June'16)
	Neelam Topno	Research Scholar (Apr'16 – Mar'17)
	Dr. MPS Magamage	DST-ISRF (Nov'16 - Mar'17)
Collaborators	Dr. G. Arunakumari, College of Veterinary Science, Korutla.	

Objectives

Neuroendocrine control of Gonadotropin Releasing Hormone (GnRH) neurons by kisspeptin orchestrates the sequences that take place during the oestrous cycle. Understanding kisspeptin regulation of reproductive axis might potentially revolutionize treatment strategies for infertility disorders in livestock. The objective of our studies is to understand the regulation of female reproduction by kisspeptin.

Summary of work done until the beginning of this reporting year (up to March 31, 2016)

Preliminary studies on effect of chronic kisspeptin (Kp-10) on puberty and expression of kisspeptin and its receptor during pregnancy in rats were carried out. Experiments to study endocrine profile and follicular dynamics in pre-pubertal buffaloes upon administration of Kp-10 were initiated.

Details of progress made in the current reporting year (April 1, 2016 - March 31, 2017)

Project 1: Effect of kisspeptin on plasma endocrine profile and follicular dynamics in buffaloes

Pre-pubertal and adult cycling buffaloes were treated with either Kp-10 (natural decapeptide) or Buserelin acetate (GnRH analogue) and endocrine profile and follicular dynamics were studied. These studies were carried out at Institutional Livestock Farm Complex (ILFC), College of Veterinary Science, Rajendranagar, Hyderabad.

Kisspeptin (IM and IV) dose dependently elevated plasma Luteinizing Hormone (LH) levels in pre-pubertal buffaloes (Fig. 1). However, the LH level reached basal values by 2 hrs. Upon administration of Buserelin (IM and IV), there was a gradual and sustained release of LH. Follicle Stimulating Hormone (FSH) was not significantly elevated upon kisspeptin, while Buserelin increased FSH in a slow and sustained manner similar to that of LH response. Repeated administration of kisspeptin (10 µg/kg BW) elevated LH in a sustained manner (Fig. 2). LH levels upon repeated kisspeptin administration were more than that following Buserelin injection. This study, hence, warrants the development of kisspeptin analogues with prolonged half-life.

In adult cycling animals, Kp-10 was administered IV at 10 µg/kg body weight on day 10 of oestrous cycle. Though Kp-10 significantly elevated LH level, it was four times lesser than that of Buserelin (Fig. 3).

The pre-pubertal buffalo heifers were monitored for their follicular growth on alternate days by ultrasound examination. The total number of follicles in a wave and the number of follicles at wave emergence were significantly more in Buserelin group compared to initial control period and Kp-10 group. Kp-10 IM at 5 µg/kg body weight significantly increased the growth rate of dominant follicles compared to all other doses of Kp-10 and of

Buserelin.

Project 2: Effect of kisspeptin on caprine primordial follicle development *in vitro*

The aims of the study were (1) to examine, in goat ovaries, the effect of Kp-10 on the development of primordial follicles *in vitro*, and (2)to study the expression of Vascular Endothelial Growth Factor (VEGF) and its modulation by Kp-10. Funding was partially supported by DST-ISRF Fellowship to Dr. Manjula PS Magamage, Sabaragamuwa University, Sri Lanka.

Ovarian cortical strips, dissected from slaughter house goat ovaries, were cultured for 7 days. Saline or Kp-10 (1, 10 or 100 ng/ml) was added on day 1. In the histological sections obtained thereafter, the follicles were classified into four categories according to the number and morphology of granulosa cell layers: (1) primordial follicles with single layer of flattened granulosa cells surrounding the oocyte, (2) intermediate follicles with a single layer containing a mixture of flat and cuboidal granulosa cells, (3) primary follicles with a single layer of cuboidal granulosa cells, and (4) secondary follicles with oocytes surrounded by two or more layers of cuboidal granulosa cells. Kp-10 treatment induced development of primordial follicles into primary and secondary follicles upon culture (Fig. 4). The mRNA expression of *VEGF165a* and *VEGF transcript variant 2* was basal on day 0 and drastically increased upon culture irrespective of Kp-10 treatment (Fig. 5).

Summary

(1) Kp-10 induced LH release is short-lived. Synthetic kisspeptin analogues with prolonged half-life may have greater impact on reproduction compared to natural decapeptide. Further studies are warranted on the mechanism of Kp-10 action in regulating follicular growth. (2) Kp-10 promotes development of primordial follicles into primary and secondary follicles independent of *VEGF.*

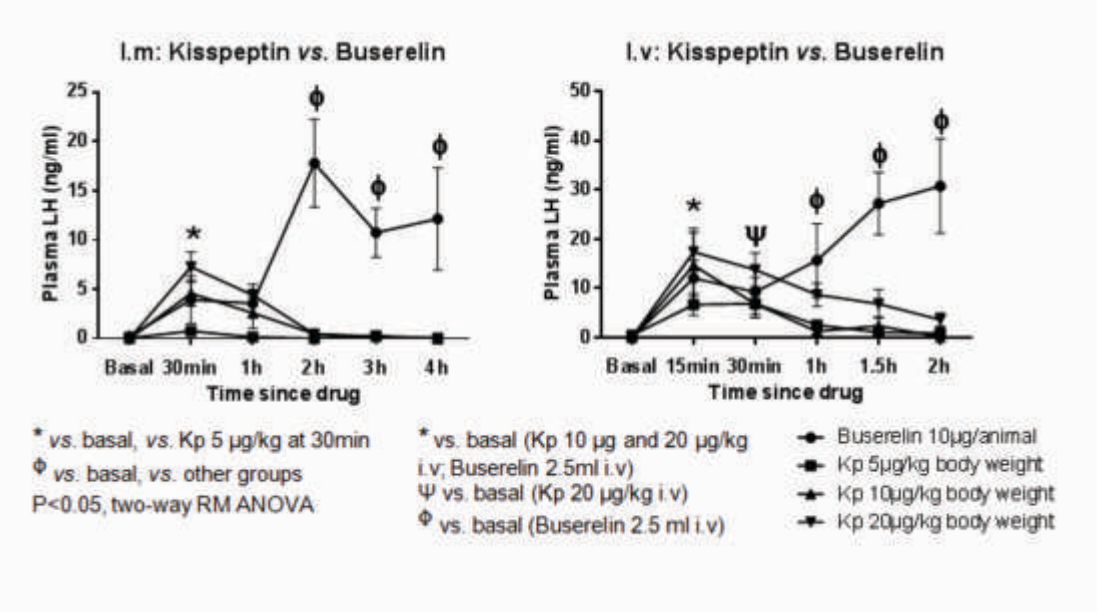

Figure 1. Changes in plasma LH concentration upon Kp-10 administration (IM or IV) in comparison with GnRH analogue. While Kp-10 dose dependently increases LH concentration for a short duration Buserelin administration results in sustained release of LH (P<0.05, two-way RM ANOVA followed by multiple comparisons).

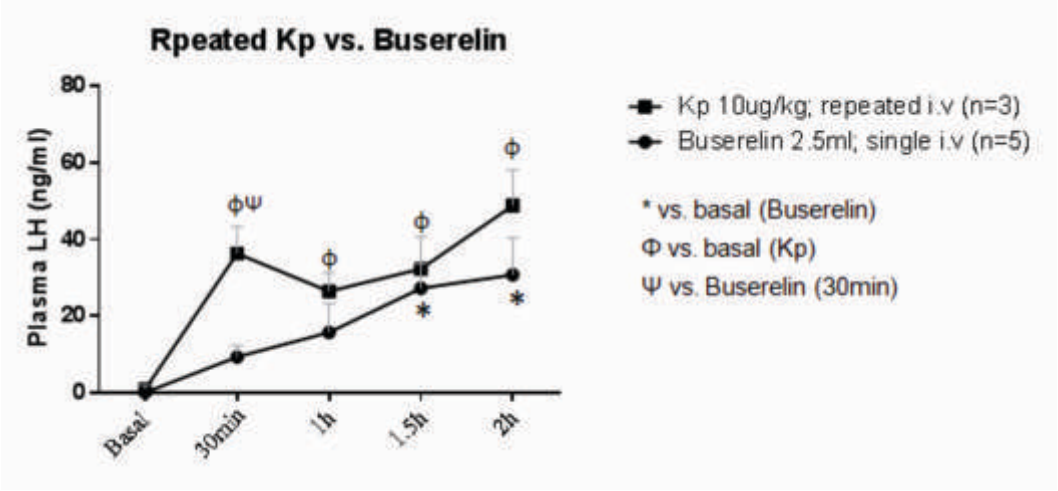

Figure 2. Change in plasma LH concentration upon repeated administration of Kp-10 vs. single dose of Buserelin. Repeated administration of Kp-10 resulted in a sustained increase in LH level, more than that by a single Buserelin injection (P<0.05, two-way RM ANOVA followed by multiple comparisons).

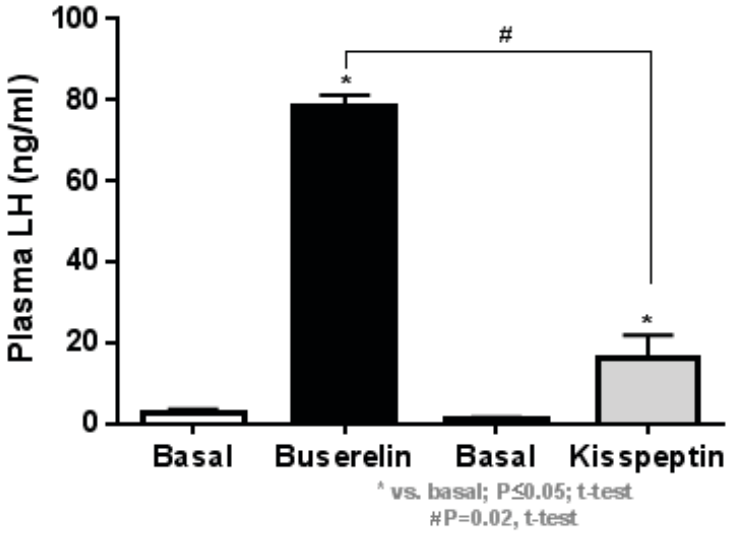

Figure 3. Change in plasma LH concentration upon Kp-10 or Buserelin injection on day 10 of oestrous cycle in adult cycling buffaloes. The increase in LH upon Buserelin was four fold higher than that upon Kp-10 (P=0.02, t-test).

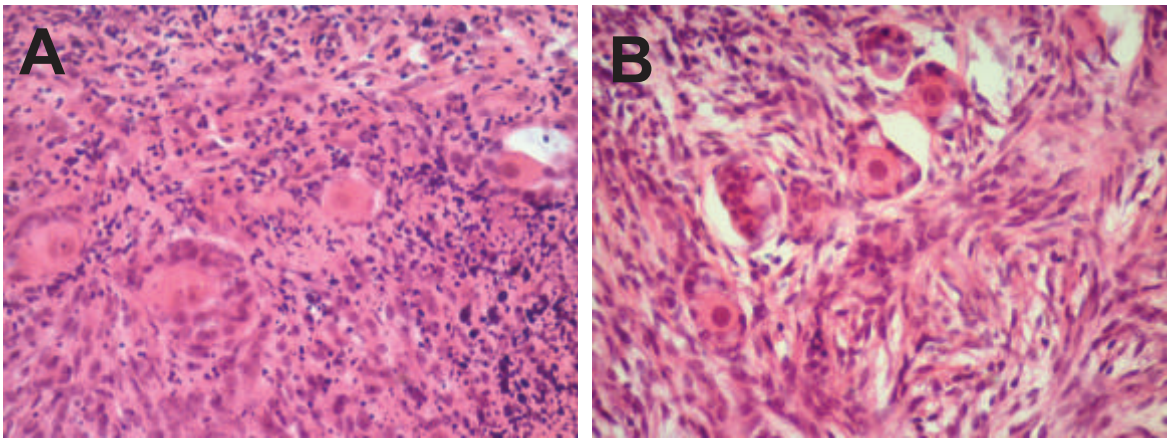

Figure 4: Histological sections of goat ovarian cortical strips cultured *in vitro* for 7 days with/without Kp-10. A. Day 7 cultured control without Kp-10. B. Day 7 cultured strips with Kp-10 (10 ng/ml). Magnification: 40X. While primordial follicles (with flat granulosa cells indistinct from ovarian stroma) are prominent in control strips, primary follicles (with cuboidal granulosa cells visible around the oocyte) are more in treated strips.

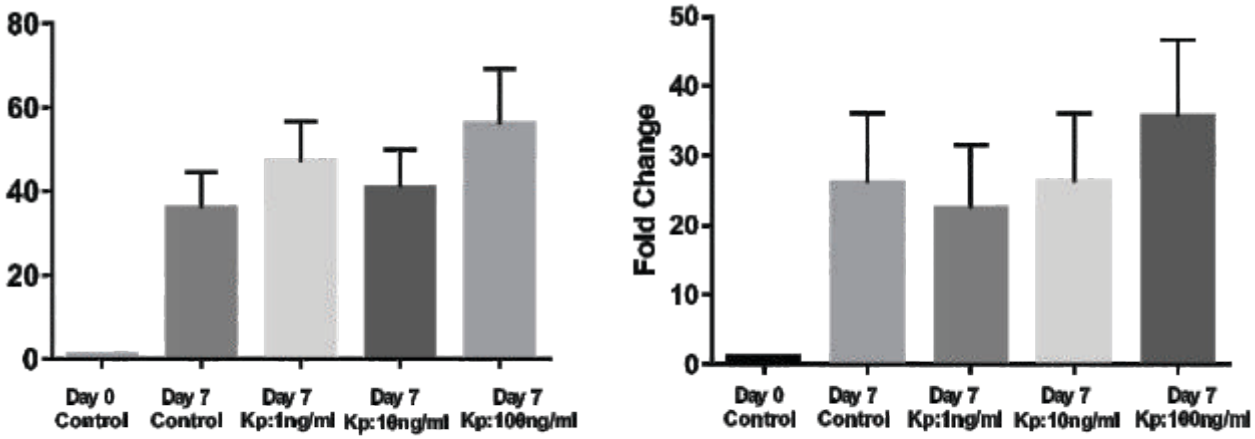

Figure 5: Expression profiles of *VEGF* and *VEGF Transcript variant 2* mRNA in cortical strips upon *in vitro* culture. The drastic increase in the expression profile upon culture ($P<0.0001$, one-way ANOVA) is independent of Kp-10 treatment.

Bioinformatics

Genomics and Computational Biology Laboratory

Analysing Sequence Data for Marker Discovery and Comparative Genomics

Principal Investigator	Sarwar Azam	Scientist B
Members	Veera Narasimha Rao	Project fellow (Until Dec 2016)
Collaborators	Prof S. Dayananada, University of Hyderabad.	
	Dr. Syed Faisal, NIAB, Hyderabad	

Project 1: Development of genome comparison tool (GCT)

Objectives

The objective of this study was to develop a tool so as to provide a platform for comparison between any two prokaryotic genomes for visualizing synteny, large indels and rearrangements. This allows users to compare any two prokaryotic genomes and display results rapidly.

Details of progress made in the current reporting year (April 1, 2016 - March 31, 2017)

Genome comparison tool (GCT) (Fig.1) provides option to customize three main parameters: the minimum percent identity (%), merge threshold (bp) and link threshold (bp). User can aptly choose parameters depending on the evolutionary closeness between the two genomes. One genome will act as subject while the other genome will act as query and thus query genome will be compared to subject genome. User has to specify the query and subjects provided on interface of the tool accordingly. To find the differences between two evolutionarily close genomes such as genome of two bacterial strain from the same species, user can increase the specificity by increasing the percent identity and decreasing merge threshold. On the other hand, to compare the two genomes from different species or from different genera, the minimum percent identity (%) needs to be decreased and merge threshold (bp) needs to be increased.However, default value of tool for percent identity is 95 and link threshold is 1000bp. Default values are more suitable to compare between strains of the same species of bacteria. A representative output of GCT of the two strains of the same species of bacteria on default values are shown in Figure 2.

Workflow and Architecture

Users are required to submit both the genome sequences in Fasta format. GCT cross checks the format of sequences and aligns both the sequences using NUCmer from the MUMmer package. Further, pipeline processes the NUCmer output and generates various required files such as karyptype file, configuration file, etc., for CIRCOS, which is the main tool for generating the circular display. The circular display is very useful to visualize the similarities and differences between genome and very helpful to catch the large scale indels and chromosomal rearrangements between the genomes. The final output will be automatically displayed on the page where user can download the image either in PNG and SVG format. However, as the whole analysis is executed rapidly, it may take some time to produce results. We have also integrated email features for users. Once the job is finished, Users will be notified via an email and links will be provided to download the resultant display. Users can use that link to download the image any time upto seven days after which server will automatically flush that link. The backbone scripts of pipeline are written in Perl. The graphical user interface (GUI) has been developed in JSP, Jquery and CSS. The Apache web server is used to deploy this web application.

Comparison with other tool

The genome comparison tool has been inspired with PGC tool integrated with Helicobase. However, PGC tool allows the user only to submit query genome and thus limits the functionality of the tool as subject genome is always that of *Helicobacter pylori.* Apart from limited function of PGC tool, we use different backbone to integrate NUCmer and Circos tools. In addition, GCT provides email feature and images in SVG and PNG, and is more user friendly than any other tools. Besides PGC, the Circoletto and RCircos areother tools with similar functions. These tools are not so user friendly as GCT and require knowledge of R programming. It was observed that GCT is that most user friendly tool and do not require any sort of installation at user end for comparing any two genome.

Availability:

GCT tool will be linked with NIAB web site and may be available on "http://192.168.138.94:7575/GCT/GCT.html". Currently, the tool is in testing phase and has not been released for public use.

Project 2:Characterization of organophosphate (OP) compound degrading bacteria *Sphingobium fuliginis*

Objectives

Organophosphate (OP) compounds are highly persistent and toxic. They are mainly present in pesticides and insecticides, which are causing bio-magnification, and effect different forms of life. These compounds affect the general health of animals especially those which are living in the surrounding and consumingpolluted water contaminated with insecticides and pesticides. Most affected animals are from the regions where manufacturing units of such OP compounds exist. One of the bacteria, namely*Flavobacterium* sp. ATCC 27551, isolated from diazinon contaminated agricultural soils, is a prominent OP degrading microorganism. However, it has recently been reclassified as *Sphingobium fuliginis* ATCC 27551. It is known that this bacteria contains one chromosome and four plasmids. Of these four plasmids, the *opd* containing pPDL2 has already been sequenced and has been shown to be a mobilizable plasmid within which the *opd* region has unique organizational features. However, to characterize other plasmids and the whole genome of bacteria with a focus to elucidate OP degrading pathways, complete genome sequencing will be done in this project. This will also help in verifying taxonomy and comparison with other OP degrading bacteria.

Summary of the work done until the beginning of this reporting year:

In continuation of the project "Characterization of Organophosphate (OP) compound degrading bacteria", we sequenced and characterized the genome of *Brevundimonas diminuta. B. dimiunta* were placed taxonomically in *Sphingopyxis* genus on the basis of whole genome rather than *Brevundimonas.* Thus, this bacteria was further renamed as *Sphingopyxis wildii.* The assembled genome was characterized for OP degradation genes and pathways. However, many outcomes and predictions in the study have provided bases to design wet-lab experiments to verify the same.

Details of progress made in the current reporting year (April 1, 2016 - March 31, 2017)

Genome sequencing, assembly and annotation:

S. fuliginis was sequenced using GAII, Ion Torrent platform, Hiseq 2000 and Miseq platform of Illumina. All data were assembled using SPAdes V3.1.0., SSPACE-BASIC V2.0 and Gapcloser program. Totally, 46 contigs were generated and further merged to 7 scaffolds of which many scaffolds showed more than expected plasmid size. This may be due to incorrectly merging of denovo assembled contigs. Thus, assembly was not convincing and ledus to sequence the bacteria again with third generation sequencing platform i.e. Pacbio. Total of 796 Mbp data were generated from one SMRT cell of Pacbio. The sequence data was assembled using Canu assembler and further

assembled sequences were circularised using Circulator.Finally, we assembled two chromosomes of *S. fuliginis* of size 3.8Mbp and 1.2Mbp and four plasmids. As both of the chromosomes were circularized, *S. fuliginis* genome was completely assembled and a finished reference genome was achieved. Ourfinding that *S. fuligins* has two chromosomes, in contrast to the earlier belief that it has only one chromosome, is novel. These two chromosomes harbour 5100 protein coding genes, 9 rRNA and 55 tRNA genes (Table1). On the other hand, all four plasmids were successfully assembled, of which three were successfully circularized, and show completeness. The detailed features of all the plasmid sequences are provided in Table 2.

Project 3: Testing of TLR activity of various surface proteins of Leptospira

This is a collaborative project with Dr. Syed Faisal, NIAB, and his report may be referred for details of the project. In this project, a heat map was generated to compare the fold change of different selected genes involved in TLR signaling in mouse macrophages (Fig. 3).

Summary

A tool was developed to compare between any two prokaryotic genomes for visualizing synteny, large indels and rearrangements. The tool, named as Genome Comparison Tool (GCT), is a web server and is user friendly. In another project, the genome of S. fuliginis, OP compound degrading bacteria, was sequenced using second and third generation sequencing. Finally, a gold standard finished reference genome was achieved using pacbio data. The genome was characterized with two chromosome harbouring 5100 protein coding genes, 9 rRNA and 55 tRNA genes. All four plasmids were also assembled successfully.

Publications

Parthasarathy* S, Azam* S, Lakshman Sagar A, Narasimha Rao, et al (2017) Genome-guided insights reveal organophosphate-degrading *Brevundimonas diminuta as Sphingopyxis wildii* and define its versatile metabolic capabilities and environmental adaptations. Genome biology and evolution 9(1): 77-81.

Faisal SM, Varma VP, Subathra M, Azam S, et al (2016) Leptospira surface adhesin (Lsa21) induces Toll like receptor 2 and 4 mediated inflammatory responses in macrophages. ***Scientific Reports*** 6:39530. doi: 10.1038/srep39530.

Azam S, Rao SB, Jakka P, NarasimhaRao V, Bhargavi B, Gupta VK and Radhakrishnan G (2016) Genetic characterization and comparative genome analysis of Brucella melitensis isolates from India. ***International Journal of Genomicsvol.*** 2016, Article ID 3034756, 13 pages, 2016. doi:10.1155/2016/3034756.

Table1: Structural annotations of *S. fuliginis* genome

Features	Total	Chromosome I	Chromosome II
Genome size (bp)	5058599	3844607	1213992
DNA coding region (bp)	4387135 (86.72%)	3312537 (86.16%)	1074598 (88.51%)
DNA G+C content (bp)	3265031 (64.54%)	2472960 (64.32%)	792071 (65.24%)
Total genes	5164	4030	1134
RNA genes	64	54	10
Protein coding genes	5100	3976	1124
Hypothetical genes	1438	1139	299
rRNA genes	9	3	6
tRNA genes	55	51	4

Table2: Structural annotations of plasmids of *S. fuliginis*

Features	Plasmid1	Plasmid2	Plasmid3	Plasmid4
Genome size (bp)	224736	60848	43234	27207
DNA coding region (bp)	190953 (84.96%)	50873 (83.60%)	35186 (81.38%)	22202 (81.60%)
DNA G+C content (bp)	140540 (62.53%)	37225 (61.17%)	26993 (62.43%)	17188 (63.17%)
Total genes	239	66	51	37
Hypothetical genes	89	19	20	10

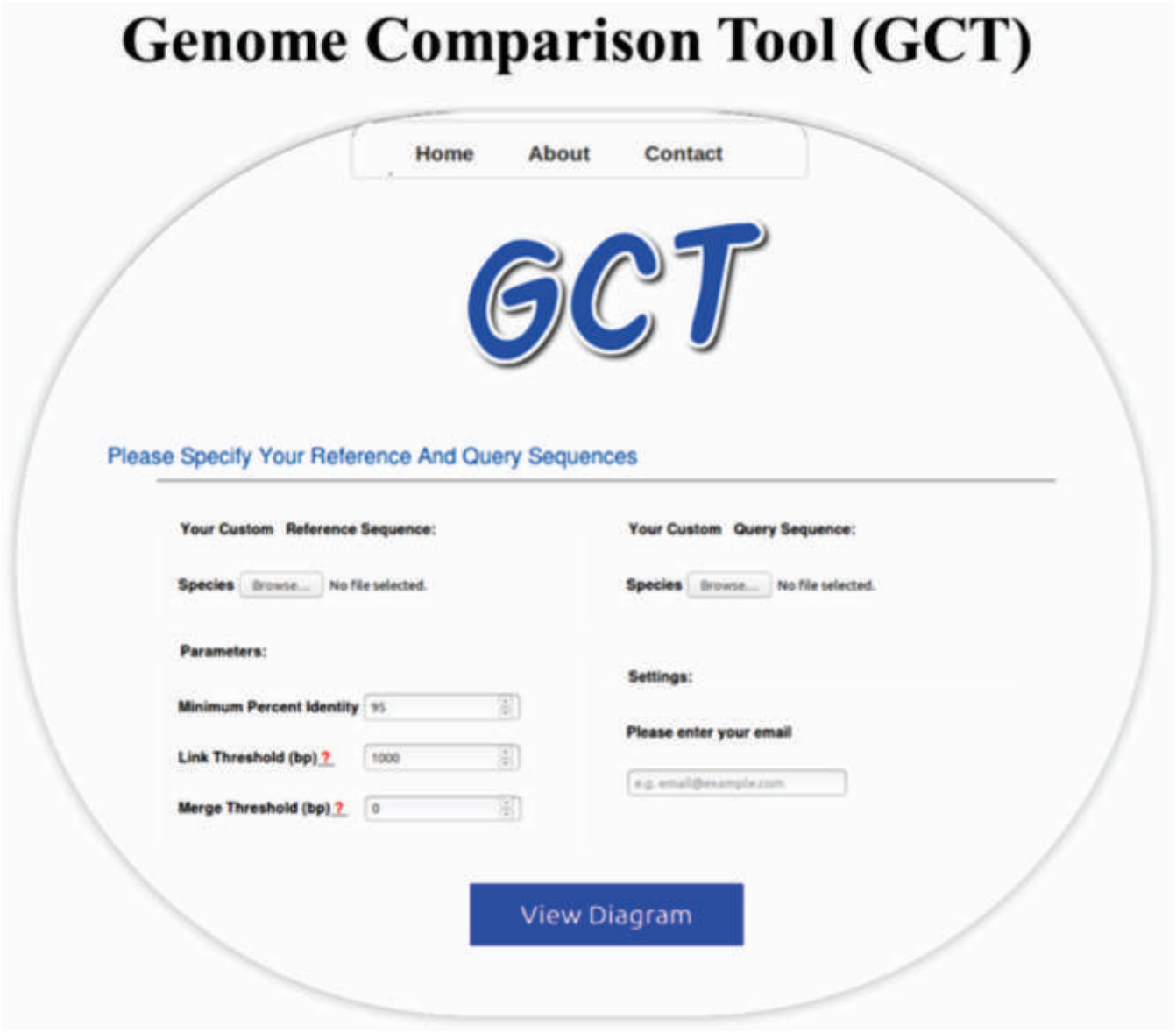

Figure1. Screenshot of web interface of Genome Comparison Tool (GCT) developed at NIAB.

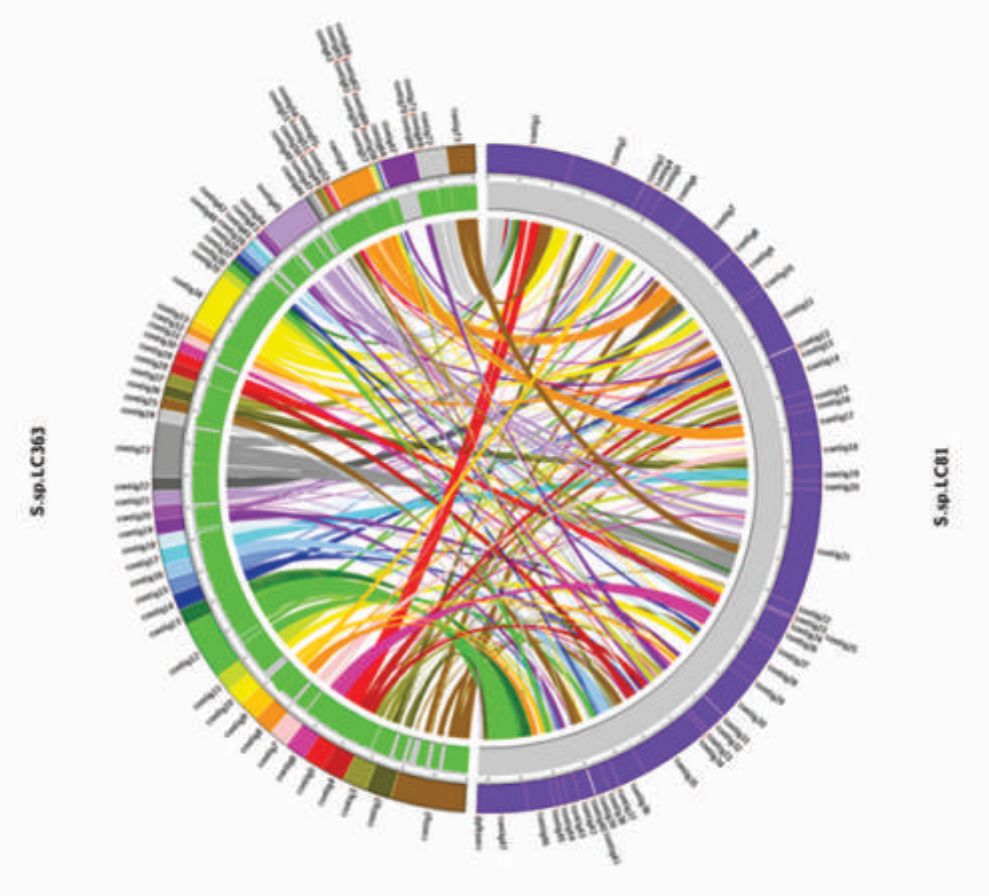

Figure2. Display of genomic similarity of the two strains of *Sphingopyxis* i.e. *Sphingopyxis LC81* and *Sphingopyxis LC363* are produced using default value of parameters by GCT. Colour of the ribbon is the colour of contig of query genome.

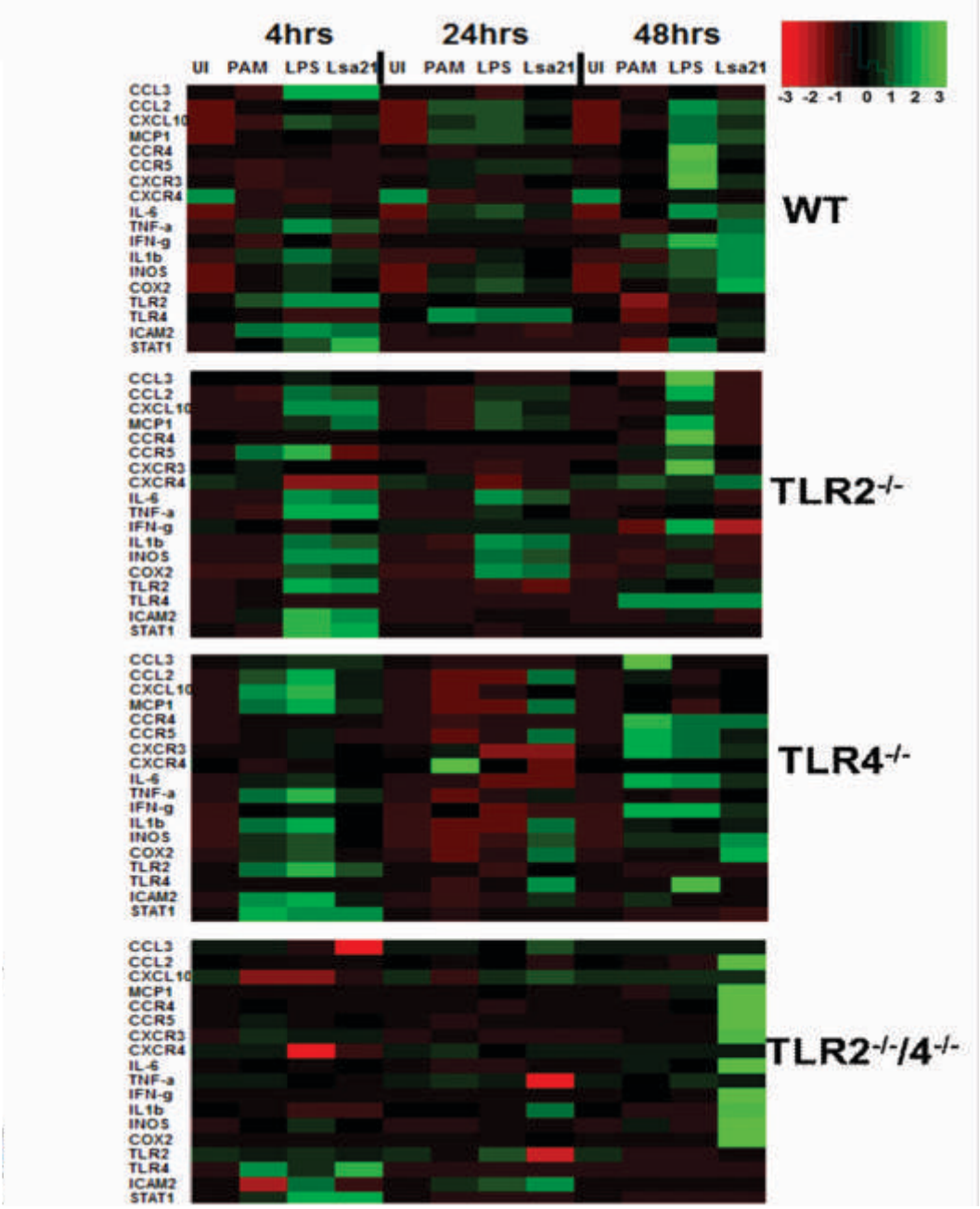

Figure 3. *Lsa21* induced gene expression profiling in mouse macrophages. WT, TLR2-/-, TLR4-/- and TLR2-/-/4-/- mouse macrophage cell lines were treated with rLsa21 (2 µg/ml), LPS (500ng/ml) or Pam3CSK4 (20ng/ml). The expression data was analysed at different time points (4h, 24h and 48h). The experimental data were presented as fold changes of gene expression of stimulated cells at various time points relative to control. mRNA levels of the analyzed genes were normalized to the amount of β-actin present in each sample. UI indicates un-induced or unstimulated cells, PAM indicates PAM3CSK (20ng/ml) and LPS is E.coli Lipopolysaccharide (500ng/ml).

Inflammation Biology

Laboratory of Eicosanoids and Inflammation

Role of Gamma Delta (γδ) T Cells in Inflammation

Principal Investigator Aparna Rachamallu DST-Women Scientist

Mentors Prof.P.Reddanna, HCU, Hyderabad (Sep 2014 – Feb 2016)

Dr.Sathya Velmurugan, NIAB, Hyderabad (Since Feb 2016)

Collaborators Dr. Rajagopal Subramanyam, HCU, Hyderabad

Objectives

Inflammation is a key component in host's defense mechanisms against pathogen's invasion, however, uncontrolled inflammation is attributed to cardiovascular, respiratory, and neurological and many lifestyle diseases. The inflammatory diseases in livestock include bovine respiratory disease (BRD), endotoxaemia due to infection of mammary gland (mastitis), uterus (metritis), lung (pneumonitis), etc. Bioactive lipids, such as eicosanoids, are one of the several important factors that mediate inflammation.

Eicosanoids, the oxygenated metabolites of polyunsaturated fatty acids (PUFAs) such as arachidonic acid, play a key role in physiological (i.e. reproduction) and pathological (i.e. inflammatory diseases) processes. At cellular level, arachidonic acid released from the membrane phospholipids is oxygenated via the cyclooxygenase (COX) and lipoxygenase (LOX) pathways, leading to the formation of eicosanoids such as prostaglandins and leukotrienes.

It is widely accepted that alterations in COX-2 expression and abundance of its enzymatic product, prostaglandin E2 (PGE2), play key roles in influencing development of various inflammatory diseases and cancers. Under normal conditions, acute inflammation is a tightly controlled self-limiting response to an offending stimulus. This involves integration of multiple cell types of vascular and immune systems so as to target, capture, degrade, and remove offending agents from tissues under attack. Concurrent with acute inflammation, COX-2 expression and PGE2 production by endothelial cells, epithelial cells, stromal cells, monocytes, and lymphocytes increase up to 100-fold compared to basal levels. Both COX isoforms play critical, but distinct roles, in T cell development and maturation. PGs influence cytokineproduction of both dendritic cells and T cells to regulate the differentiation of naïve T cells to Th1, Th2 and Th17 phenotypes. γδ T cells are early proliferative cells and COX-2 is an early immediate gene in various infections. Currently, little information is available on the role of COX-2 in γδ T cells mediated diseases.

It is critical to know how COX-2 plays a role in the modulation of innate immune system, specifically in the modulation of cytotoxic properties of γδ T cells. The present study is focused on understanding the role of COX-2 on modulation of γδ T cells with the following objectives:

1. To study the fate of naïve mouse γδ T cells upon in vitro model of inflammation.
2. To study the role of COXand PGE2 on mouse γδ T cells activation and immunological response.
3. To test the role of various novel natural COX-2 inhibitors on mouse γδ T cells activation and anti-inflammatory properties.
4. To decipher the regulatory pathways that are responsible for γδ T cells and COX2 mediated inflammation and infection.

Summary of work done until the beginning of this reporting year (up to March 31, 2016)

- Isolation and characterisation of γδ T cells by magnetically labelled beads with positive selection; purity was checked by flow cytometry using - PE antibody.
- Preliminary studies on induction of inflammatory response in naïve and CD3 activated γδ T cells by LPS.
- Growth kinetics studies of γδ T cells upon LPS treatment by CFSE labelling.
- Gene expression analysis of inflammatory gene like Cox-2 and its receptors EP1, EP2, EP3 & EP4 by Q-PCR in naïve and CD3 activated γδ T cells upon LPS treatment.
- Quantification of PGE2, a downstream regulator of COX-2, by ELISA in naïve and CD3 activated γδ T cells upon LPS treatment.

Details of progress made in the current reporting year (April 1, 2016 - March 31, 2017)

For localization of COX-2 expression in naïve and CD3 activated splenic γδT cells, the cells were cultured with or without CD3 and stained with PE conjugated γδ antibody (surface staining) and FITC conjugated COX-2 antibody (intracellular staining after permeabilization), respectively. Confocal images on localization of CD3 and COX-2 confirmed induction of COX-2 upon CD3 activation (Fig. 1).

Three animal models were used to study the role of γδ T cells in in vivo inflammatory conditions. Cells collected from these models were double stained for COX-2 producing cells using PE conjugated γδ antibody and FITC conjugated COX-2 antibody and subjected to flow cytometry analysis. The animal models are: (1) Intraperitoneal (IP) model using LPS: Saline or LPS (1 and 5 mg/kg; n=5 each) was administered IP and γδ T-cells were collected 24 h post-injection. (2) Air pouch model using carrageenan (Fig. 2):Saline, carrageenan (1% w/v) or carrageenan + celecoxib (5 mg/kg), a COX-2 inhibitor, was administered in the air pouch 6 days after creating the air pouch. γδ T-cells were collected from the infiltrate of air pouch 24 h post-injection. (3) Caecum Ligation and Puncture (CLP) model:The three experimental groups in this model were: sham-operated, CLP control and CLP + celecoxib (5 mg/kg; 1 h post-surgery; n=5 each).γδ T-cells were collected from the peritoneal fluid 24 h post-surgery.

IP administration of LPS did not increase the COX-2 expression by γδ T cells. Carrageenan administration into the air pouch induced inflammation compared to normal saline control animals and celecoxib inhibited the carrageenan induced inflammatory response at the site and is correlated with the total number of cells infiltrated at the site. Infiltrated γδ T cells in carrageenan induced group showed significantly higher expression of COX-2 (15%) compared to control (3.5%) and celecoxib group (8.6%). This indicated that carrageenan induced inflammation is associated with infiltration of COX-2 expressing γδ T cells (Fig. 3).

To decipher the exact role of γδ T cells and COX-2 in combating inflammation and immunity, CLP, a poly-microbial sepsis-induced inflammatory model, was used. CLP induced significant inflammationcompared with sham controls, whereas celecoxib treated group showed inhibition of CLP induced inflammatory response (Fig. 4). However, infiltration of total number of γδ T cells into the peritoneum was much higher in CLP-celecoxib (38%) group compared to CLP alone (9.8 %) and sham group (3%). This data infers that COX-2 inhibition increased the infiltration of γδ T cells in CLP induced peritoneum. When we examined the expression of COX-2 by FACS analysis, we found that more number of γδ T cells in celecoxib-CLP group were negative for COX-2 expression (15%) compared with CLP alone (5%) and sham group (2%) (Fig. 5). Hence, it appears that celecoxib, on one hand, increases the infiltration of γδ T cells, but on the other hand reduces COX-2 expression, both of which might aim to curtail inflammation. These results, from the above in vivo models, suggest that there might be qualitative and quantitative differences in γδ-T cell responses depending upon differences in the infectious and inflammatory conditions.

Summary

The contribution of γδ-T lymphocytes in inflammation and infection is not well characterized compared to the other immune cells, while the cellular composition of each organ, its micro-environment, and nature of the immune cell recruitment, has been known to influence local inflammation and tissue injury. Results from our studies highlight the distinct characteristics of γδ T cells response towards inflammation (i.e. LPS and carrageenan models) vs. infection (CLP model). In particular, differential expression of COX-2 in γδ T cells emphasizes the role of their metabolites, such as PGE2, and specific expression of EP4 receptors on γδ T cells, and finally the delicate functional balance of γδ T cells in immune modulation. Further studies in this line are imperative to understand the mechanisms involved in such processes, specifically the role of COX-2 positive and negative γδ T cells, and their critical responses in bridging innate and adaptive immune responses.

Publications

Yeggoni DP, Rachamallu A, Dubey S, Mitra A and Subramanyam R (2017) Probing the interaction mechanism of menthol with blood plasma proteins and its cytotoxicity activities. J Biomol Struct Dyn1-10. doi: 10.1080/07391102.2017.1286264

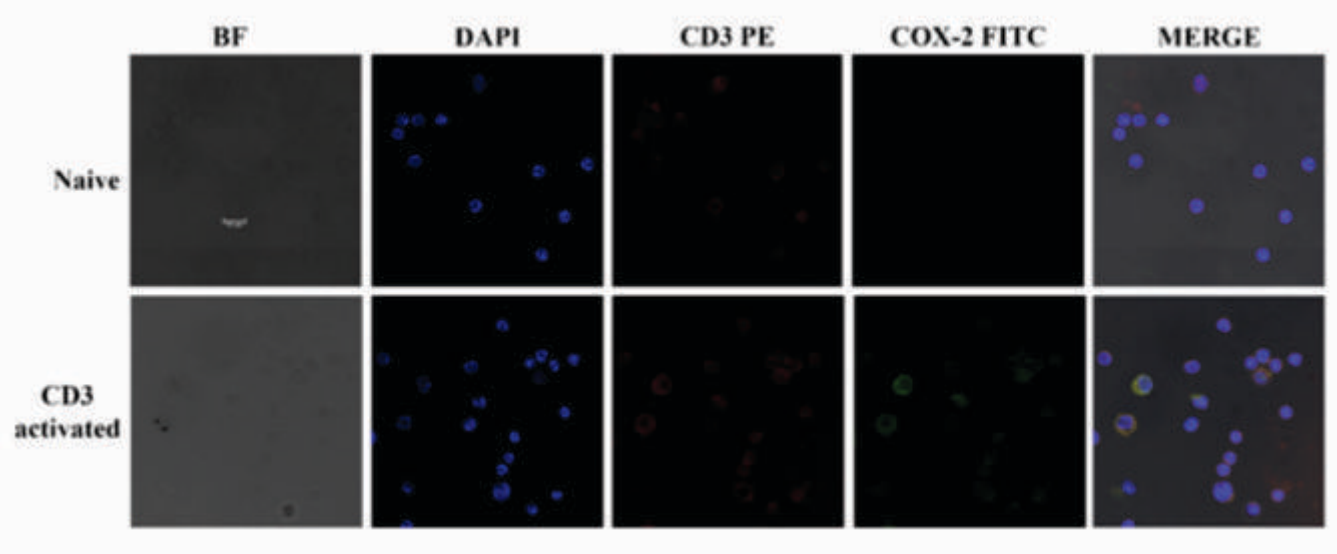

Figure 1.Localization of COX-2 expression in CD3 activated splenic γδT cells. Purified γδ T cells were treated with CD3 (1µg/mL) for 24h and subjected to confocal analysis after immunofluorescence staining with anti-COX-2 (FITC conjugated - green), anti-γδ (PE conjugated - red) antibodies and DAPI (nuclear staining - Blue). The presence of green fluorescence in CD3 activated cells confirm induction of COX-2 upon CD3 activation and presence of the same around the nucleus confirms the cytoplasmic localization of COX-2.

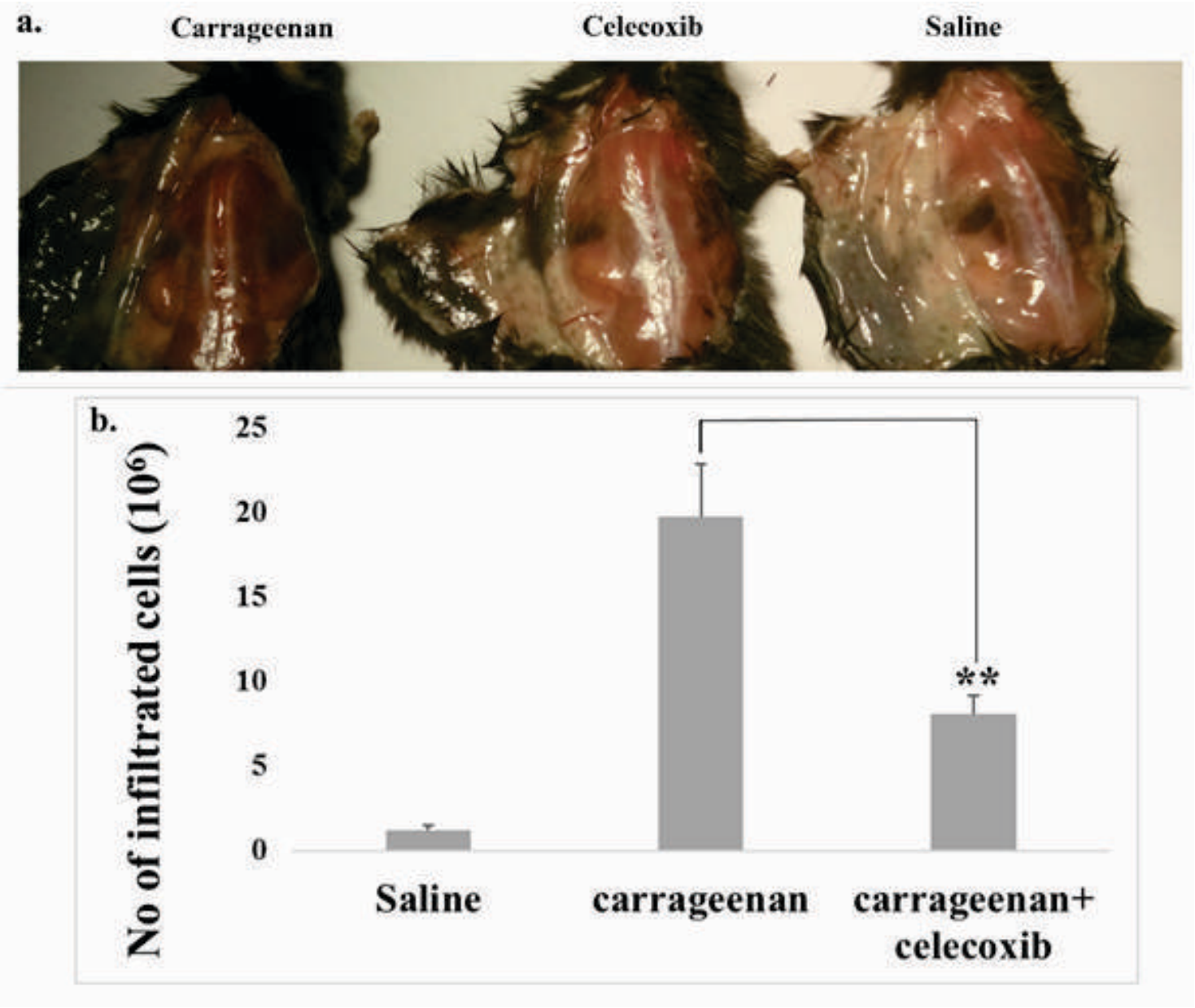

Figure 2.Mouse air pouch model of Inflammation. A. Signs of inflammation such as redness, angiogenesis, and hyperplasia of air pouch tissue and infiltration of fluid into the air pouch were compared among control (saline), carrageenan and carrageenan + celecoxib groups. B. Infiltration of cells into inflammatory sites in air-pouch. All the cells that infiltrated into the inflammatory site in the mouse air pouch model were collected and counted using Trypan Blue exclusion method. Carrageenan injection significantly increased the total number of cells infiltrated into the site while celecoxib treatment reduced the same.

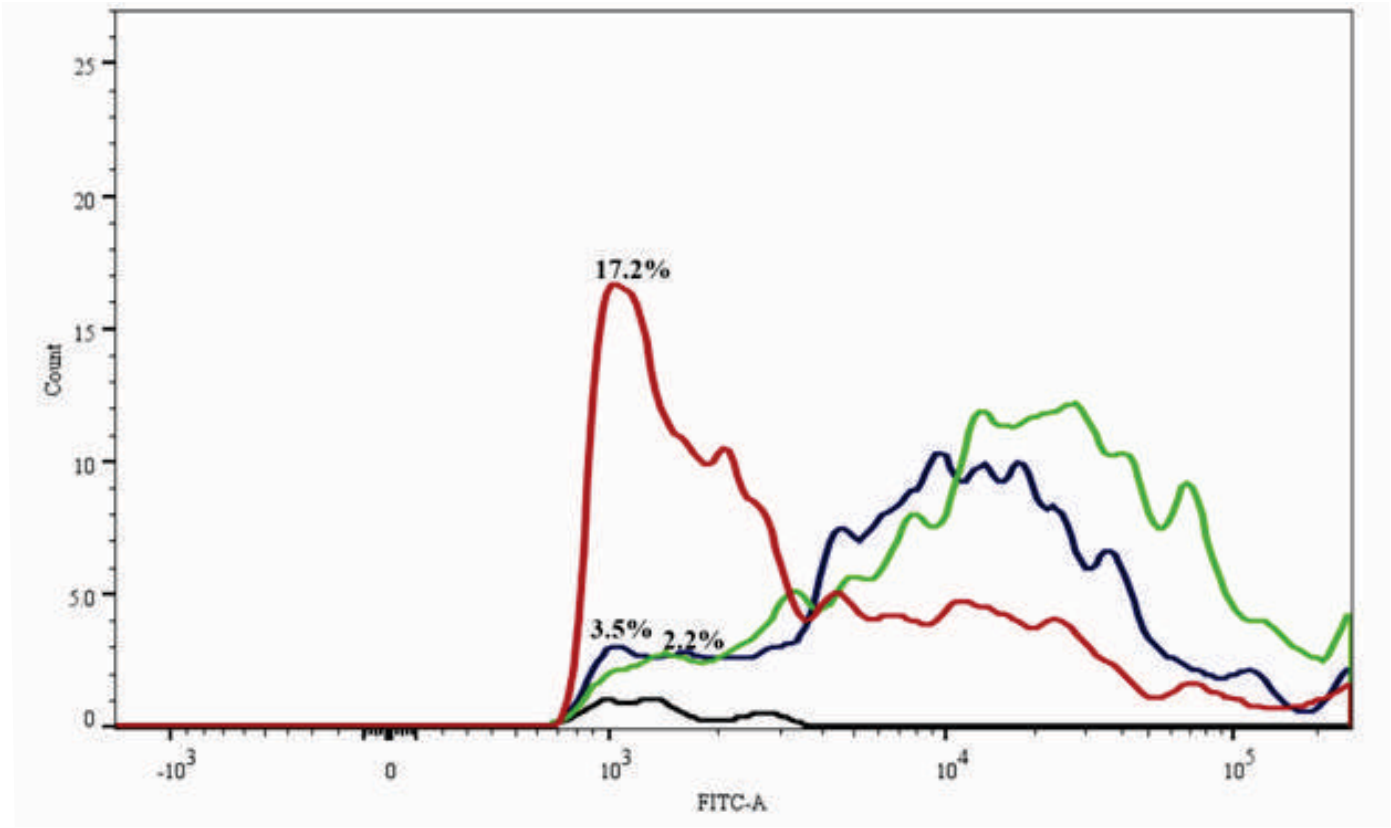

Figure 3.Percent of COX-2 producing γδT cells that infiltrated into the inflammatory fluid in mouse carrageenan model. Allcells that infiltrated into the mouse air pouch were collected after 24h of treatment. Cells were stained with γδT –PE and COX-2 –FITC antibodies and were analyzed by flow cytometry. Black: unstained. Blue: Saline group, Red: Carrageenan, and Green: Carrageenan with Celecoxib.

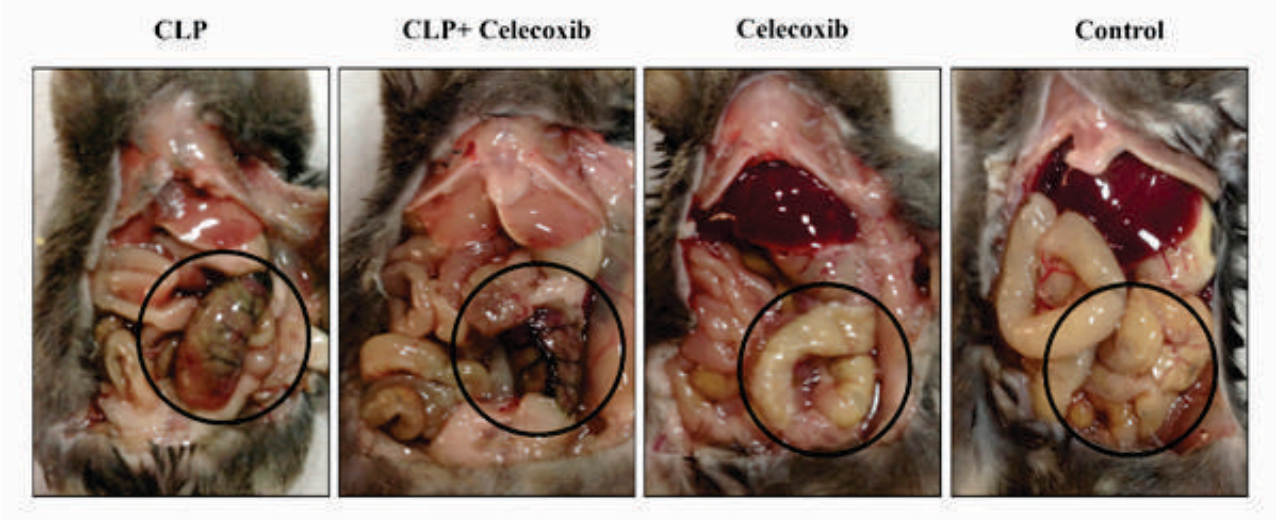

Figure 4:Caecum Ligation and Puncture (CLP) model of infection. After 24h of CLP, mice were sacrificed and wound was assessed for severity of inflammation. Images were taken immediately after opening of wound. Region showing ligation and inflammation are circled.

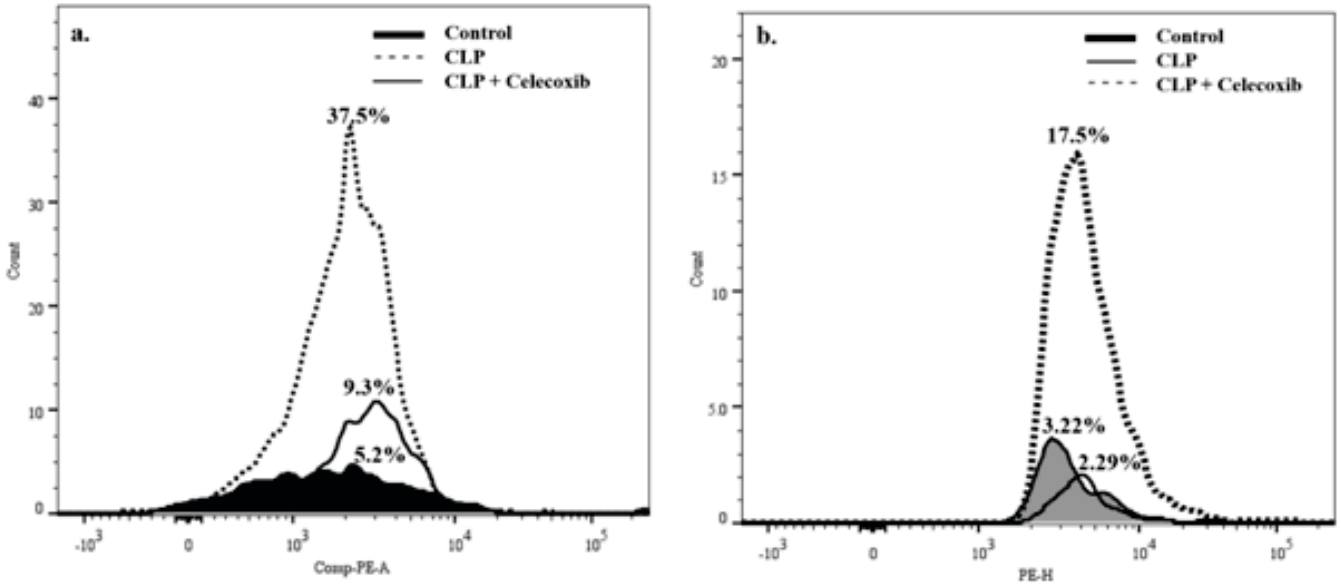

Figure 5. Percent of γδ-T cells in the peritoneal fluid of CLP model.A. Total cells were collected from peritoneal fluid after treatment and cells were stained for γδ-T cells with γδ-PE antibody. Cells were analyzed by flow cytometer. B. Percent of COX-2 negative or non COX-2 producing γδ-T cells in peritoneal fluid of CLP model. Cells were stained with γδ –PE and COX-2 –FITC antibodies and were analyzed by flow cytometer for COX-2 negative γδ-T cells in CLP model.

Publications

Publications with NIAB affiliation during the period 1st April 2016 – 31st March 2017:

Anilkumar K, Reddy GV, Azad R, Yarla NS, Dharmapuri G, Srivastava A, Kamal MA and Pallu R (2017) Evaluation of anti-inflammatory properties of isoorientin isolated from tubers of Pueraria tuberosa.Oxidative Medicine and Cellular LongevityArticle ID 5498054. doi:10.1155/2017/5498054.

Bulugonda R, Kumar KA, Gangappa D, Rao M* and Faisal SM* (2017) Mangiferin from Pueraria tuberosa reduces inflammation via inactivation of NLRP3 inflammasome. Scientific Reports7: 42683 (*corresponding author).

Deshmukh AS, Mitra P and Maruthi M (2016) Cdk7 mediates RPB1-driven mRNA synthesis in Toxoplasma gondii. Scientific Reports 6:35288.

Faisal SM*, Verma V, Subathra M, Sunkara AK, Azam S, Akif M, Baig MS and Chang YF (2016) Leptospira surface protein Lsa21 induces proiflammatory cytokines by Toll like receptor 2 and 4 mediated signaling pathways. Scientific Reports6: 39530(*corresponding author).

Ganguli N, Wadhwa N, Usmani A, Kunj N, Ganguli N, Sarkar RK, Ghorai SM and Majumdar SS (2016) An efficient method for generating a germ cell depleted animal model for studies related to spermatogonial stem cell transplantation. Stem Cell Research and Therapy 7(1): 142.

George N,Bhandari V andSharma P(2017)Phylogeneticrelationship and genotypic variability in Anaplasmamarginalestrainscausinganaplasmosisin India. Infection Genetics and Evolution48: 71-75.

Gujjar N, Chothe SK, Gawai S, Nissly R, Bhushan G, Kanagaraj V, Jayarao BM, Kathaperumal K, Subbiah M* and Kuchipudi SV* (2017) Co-expression of sialic acid receptors compatible with avian and human influenza virus binding in emus (Dromaius novaehollandiae). Virology 500: 14-121 (* Corresponding authors)

Mandal K, Bader SL, Kumar P, Malakar D, Campbell DS, Pradhan BS, Sarkar RK, Wadhwa N, Sensharma S, Jain V, Moritz RL and Majumdar SS (2017) An integrated transcriptomics-guided genome-wide promoter analysis and next-generation proteomics approach to mine factor(s) regulating cellular differentiation. DNA Research pii: dsw057. doi: 10.1093/dnares/dsw057.

Parthasarathy* S, Azam S*, Lakshman Sagar A, Rao N, et al (2017) Genome-guided insights reveal organophosphate-degrading Brevundimonas diminuta as Sphingopyxis wildii and define its versatile metabolic capabilities and environmental adaptations. Genome biology and evolution 9(1): 77-81.

Roy A, Srivastava M, Saqib U, Liu D, FaisalSM and Baig MS (2016) Potential therapeutic targets for inflammation in toll-like receptor 4 (TLR4)-mediated signaling pathways. International Immunopharmacology 40:79-89.

Sarwar A, Rao SB, Jakka P, Rao VN,Bhargavi B, Gupta VK and Radhakrishnan G(2016) Genetic characterization and comparative genome analysis of Brucella melitensis isolates from India. International Journal of Genomic.Article ID 3034756. doi:10.1155/2016/3034756.

Usmani A, Ganguli N, Jain SK, Ganguli N, Sarkar RK, Choubey M, Shukla M, Sarkar H and Majumdar SS (2016) Robust generation of transgenic mice by simple hypotonic solution mediated delivery of transgene in testicular germ cells. Molecular Therapy - Methods and Clinical Development 3:16076.

Yeggoni DP, Rachamallu A, Dubey S, Mitra A and Subramanyam R (2017) Probing the interaction mechanism of menthol with blood plasma proteins and its cytotoxicity activities. Journal of Biomolecular Structure and Dynamics 1-10. doi: 10.1080/07391102.2017.1286264.

Profiles of New Faculty

Name: **Subeer S. Majumdar**

Designation: **Director**

Areas of Specialization: **Gene and protein Engineering, Genomics, Functional Genomics, Transgenic animals**

Education and training:

Dr. Subeer S. Majumdar has done his M.Sc. from Nagpur University and did his Ph.D. work at National Institute of Health & Family Welfare, New Delhi, India. He did his Postdoctoral Research at School of Medicine, Southern Illinois University, USA, and at Department of Cell Biology and Physiology, University of Pittsburgh, USA. He was working at National Institute of Immunology, New Delhi prior to assuming this responsibility.

Research experience and contributions:

Dr. Majumdar's lab works in the field of animal biotechnology, genomics and animal reproduction. His present research focus lies in the following fields:

1. Production of therapeutic proteins for animal and human in milk of farmed animals.
2. Generation of bulls with X chromosome bearing sperm only to increase production of female offspring (cow).
3. Transgenesis for biomedical research and production of transgenic cattle, goat and buffalo, so as to increase the quality of herd with more disease resistant and high yielding animals.
4. Livestock genomics.
5. Alternative methods for gene knock out e.g. utilizing shRNA to generate transgenic animals.

Selected awards, honours and fellowships:

Fellowships of Science Academics:

- Fellow: The National Academy of Sciences, 2009
- Fellow: Indian National Science Academy, 2009
- Fellow: Indian Academy of Sciences, 2014

Membership of Professional Societies:

- Member, the Endocrine Society, USA
- Member, Society for the Study of Reproduction, USA

Selected publications:

1. Souvik Sen Sharma, Subeer S. Majumdar. Transcriptional co-activator YAP regulates cAMP signaling in Sertoli cells. Molecular and Cellular Endocrinology, 2017. Volume 450, 15 July 2017, Pages 64–73, https://doi.org/10.1016/j.mce.2017.04.017.

2. Kamal Mandal, Samue L. Bader, Pankaj Kumar, Dipankar Malakar, David S. Campbel, Bhola Shankar Pradhan, Rajesh K. Sarkar, Neerja Wadhwa, Souvik Sensharma, Vaibhav Jain, Robert L. Moritz, and Subeer S. Majumdar. An integrated transcriptomics-guided genomewide promoter analysis and next-generation proteomics approach to mine factor(s) regulating cellular differentiation. DNA Research, 2017, 0(0), 1–15 doi: 10.1093/dnares/dsw057.

3. Suveera Dhup and Subeer S. Majumdar. Transgenesis via permanent integration of genes in repopulating spermatogonial cells in vivo. Nature Methods, 2008 5(7):601-603.

4. Abul Usmani*, Nirmalya Ganguli*, Subodh K Jain, Nilanjana Ganguli, Rajesh Kumar Sarkar, Mayank Choubey, Mansi Shukla, Hironmoy Sarkar and Subeer S Majumdar. Robust generation of transgenic mice by simple hypotonic solution mediated delivery of transgene in testicular germ cells. Molecular Therapy- Methods & Clinical Development, 2016, 3, 16076; doi:10.1038/mtm. 2016.76

5. Abul Usmani, Nirmalya Ganguli, Hironmoy Sarkar, Suveera Dhup, Suryaprakash R. Batta, Manoj Vimal, Nilanjana Ganguli, Sayon Basu, P. Nagarajan and Subeer S. Majumdar. A non-surgical approach for male germ cell mediated gene transmission through transgenesis. Scientific Reports, 2013, 3, Article number: 3430 doi: 10.1038/srep03430.

6. Subeer S. Majumdar, Suveera Dhup and Abu-ul Usmani. Deathless transgenesis: A new spermatogonia mediated in vivo approach for generation of transgenic mice. Nature Protocols, 2008, DOI: 10.1038/nprot.2008.124.

7. Nirmalya Ganguli, Neerja Wadhwa, Abul Usmani, Neetu Kunj, Nilanjana Ganguli, Rajesh Kumar Sarkar, Soma M Ghorai, Subeer S Majumdar. An efficient method for generating a germ cell depleted animal model for studies related to spermatogonial stem cell transplantation. Stem Cell Research and Therapy, 2016, 7: 142. doi:10.1186/s13287-016-0405-1.

8. Neerja Wadhwa, Neetu Kunj, Shuchita Tiwari, Megha Saraiya, and Subeer S. Majumdar. Optimization of Embryo Culture Conditions for Increasing Efficiency of Cloning in Buffalo (Bubalus bubalis) and Generation of Transgenic Embryos via Cloning. Cloning and Stem cells. September 2009, 11(3): 387-395.

9. Nirmalya Ganguli, Nilanjana Ganguli, Abul Usmani and Subeer S. Majumdar. Isolation and functional characterization of buffalo (Bubalus bubalis) β-casein promoter for driving mammary epithelial cell-specific gene expression. Journal of Biotechnology, 2015, 198, 53-59.

10. Durba Pal, Suman Dasgupta, Rakesh Kundu, Sudipta Maitra, Gobardhan Das, Satinath Mukhopadhyay, Sukanta Ray, Subeer S Majumdar & Samir Bhattacharya. Fetuin-A acts as an endogenous ligand of TLR4 to promote lipid-induced insulin resistance. Nature Medicine, 2012 18(8):1279-1285.

Name: **Nagendra R. Hegde**

Designation: **Scientist-G**

Areas of Specialization: **Disease epidemiology, Host-pathogen interaction, Molecular pathogenesis, Virulence determinants, Vaccines, Diagnostics**

Education and training:

Dr. Nagendra R. Hegde completed B.V.Sc. (1989) and M.V.Sc. (1992; Veterinary Microbiology and Public Health – Virology) from the University of Agricultural Sciences, Bangalore, India, and Ph.D. (1998; Veterinary & Biomedical Sciences – Immunology) from the University of Nebraska, U.S.A. He then worked as a Post-doctoral Fellow (Aug 1998 to Mar 2004) and then as a Research Assistant Professor (Apr 2004 to May 2006) at the Oregon Health & Science University, U.S.A. Before joining NIAB on 30-03-2017, he was a Group Leader (Aug 2006 to Mar 2014) and then the Associate Director (Apr 2014 to Mar 2017) at Ella Foundation, Hyderabad, India.

Research experience and interests:

Dr. Hegde's research experience spans veterinary virology, immunology and microbiology. His major contribution has been in virology, where he has worked on epidemiology, genomics, diagnosis and prevention as well as interaction with host cells of animal (as well as human) DNA and RNA viruses. In immunology, he has worked on bovine major histocompatibility complex (MHC) and cell-mediated immunity (CMI). In microbiology, he has worked on epidemiology, diagnosis and preventive measures for bovine mastitis-causing pathogens. His research interests are to understand the epidemiology, genomics, and biology of important livestock diseases, to devise protective measures for these diseases, and to elucidate fundamentals of immunological responses.

Selected awards, honours and fellowships:

1. Academic Editor, PLoS ONE; Editorial Board, Clinical and Vaccine Immunology; Reviewer, several journals
2. Member, National Advisory Committee, Veterinary Virology Section, ViroCon 2016; International Conference on Global Perspectives in Virus Disease Management, Bengaluru, India, 2016
3. Chairman, Organizing Committee (Veterinary), National Conference on Emerging and Re-emerging Viral Outbreaks in India – Clinical Challenges and Management, Hyderabad, India, 2015
4. Contributed to the development of the World Health Organization's draft guidelines on the quality, safety and efficacy of Ebola vaccines, 2015

Selected publications:

1. D Hemadri, S Maan, MM Chanda, PP Rao, K Putty, Y Krishnajyothi, GH Reddy, V Kumar, K Batra, YV Reddy, NS Maan, YN Reddy, KP Singh, SB Shivachandra, NR Hegde, H Rahman, PPC Mertens. 2017. Dual infection with bluetongue virus serotypes and first time isolation of serotype 5 in India, Transboundary and Emerging Diseases, Epub ahead of print, 2016 Dec 21.

2. J Gogoi-Tiwari, V Williams, CB Waryah, P Costantino, H Al-Salami, S Mathavan, K Wells, HK Tiwari, N Hegde, S Isloor, H Al-Sallami, T Mukkur. 2017. Mammary gland pathology subsequent to acute infection with strong versus weak biofilm forming *Staphylococcus aureus* bovine mastitis isolates: a pilot study using non-invasive mouse mastitis model. PLoS ONE 12(1):e0170668.

3. YV Reddy, Y Krishnajyothi, B Susmitha, BV Devi, Y Brundavanam, SR Gollapalli, N Karunasri, B Sonali, K Kavitha, SR Patil, G Sunitha, K Putty, GH Reddy, YN Reddy, NR Hegde, PP Rao. 2016. Molecular typing of bluetongue viruses isolated over a decade in South India. Transboundary and Emerging Diseases 63(5):e412-8.

4. Y Krishnajyothi, S Maan, K Kandimalla, NS Maan, RB Tutika, YV Reddy, A Kumar, N Mrunalini, GH Reddy, K Putty, SM Ahmed, YN Reddy, D Hemadri, KP Singh, PPC Mertens, NR Hegde, PP Rao. 2016. Isolation of bluetongue virus 24 from India – an exotic serotype to Australasia. Transboundary and Emerging Diseases 63(4):360-4.

5. PL Preethirani, S Isloor, S Sundareshan, V Nuthanalakshmi, K Deepthikiran, AY Sinha, D Rathnamma, K Nithin Prabhu, R Sharada, TK Mukkur, NR Hegde. 2015. Isolation, biochemical and molecular identification, and *in-vitro* antimicrobial resistance patterns of bacteria isolated from bubaline subclinical mastitis in South India. PLoS ONE 10(11):e0142717.

6. PP Rao, YV Reddy, NR Hegde. 2015. Isolation and complete genome sequencing of bluetongue virus serotype 12 from India. Transboundary and Emerging Diseases 62(5):e52-9.

7. J Gogoi-Tiwari, CB Waryah, R Sunagar, HB Veeresh, V Nuthanalakshmi, PL Preethirani, R Sharada, A Bhat, S Isloor, H Al-Salami, NR Hegde, TK Mukkur. Typing of *Staphylococcus aureus* isolated from bovine mastitis cases in Australia and India. Australian Veterinary Journal 3(8):278-82.

8. S Manjunath, PG Kulkarni, K Nagavelu, RJ Samuel, S Srinivasan, N Ramasamy, NR Hegde, RS Gudde. 2015. Sero-prevalence of rodent pathogens in India. PLoS ONE 10(7):e0131706.

9. S Maan, NS Maan, M Belaganahalli, PP Rao, KP Singh, D Hemadri, K Putty, A Kumar, K Batra, Y Krishnajyothi, BS Chandel, GH Reddy, K Nomikou, YN Reddy, H Attoui, NR Hegde, PP Mertens. 2015. Full genome sequencing as a basis for molecular epidemiology of bluetongue virus in India. PLoS ONE 10(6):e0131257.

10. J Gogoi-Tiwari, CB Waryah, KY Eto, M Tau, K Wells, P Costantino, HK Tiwari, S Isloor, N Hegde, TK Mukkur. 2015. Relative distribution of virulence-associated factors among Australian bovine *Staphylococcus aureus* isolates: potential relevance to development of an effective bovine mastitis vaccine. Virulence 6(5):419-23.

Name: **Shailesh Sharma**

Designation: **Scientist D**

Areas of Specialization: **Bioinformatics**

Education and training:

Dr Shailesh Sharma completed B.Sc. (Biology) in 2002 from Maharshi Dayanand Saraswati University, Rajasthan, and M.Sc. (Bioinformatics) in 2004 from the University of Allahabad. He then completed the First Level Masters Program in Bioinformatics in 2006 from University of Torino, Italy, through an India-Italy joint education programme, followed by Ph.D. in Structural Biology in 2010 at the Magnetic Resonance Centre, CERM, University of Florence, Italy. He obtained further training as a post-doctoral fellow at the International Centre for Genetic Engineering and Biotechnology (ICGEB) through an Indo-US joint research programme. He was working as a Project Scientist from January 2012 to December 2016 at the National Agri-Food Biotechnology Institute (NABI), Mohali, India, before joining NIAB in February 2017.

Research experience and interests:

Dr. Sharma's research experience span bioinformatics and structural biology, including application of data mining, application of bioinformatics tools, computational biology, and structure-activity relationships. His earlier work included investigations into structural, functional and dynamic properties of metalloproteins. His research at NIAB will involve genome annotation, protein structure, target identification, and molecular dynamics simulations.

Selected awards, honours and fellowships:

1. Session Chairman and Invited Speaker, Seminar and Training Workshop on 'Molecular modelling, protein-protein interactions and computer-aided drug design', University of Allahabad, India, 2010.
2. Italian Government Scholarship in Biotechnology (processed by the Ministry Human Recourse and Development, Government of India), University of Turin, Italy, 2005-2006.
3. Training, National High Field NMR facility, Department of Chemical Sciences, Tata Institute of Fundamental Research, Mumbai, India, 2004.
4. Post-doctoral Fellow, US-India Joint Research Training Program, funded by Fogarty International Centre of the National Institute of Health, USA, 2010-11.

Selected publications:

1. S Angmo, N Tripathi, S Abbat, S Sharma, SS Singh, A Halder, K Yadav, G Shukla, R Sandhir, V Rishi, PV Bharatam, H Yadav, NK Singhal. 2017. Identification of Guanosine 5’-diphosphate as potential iron mobilizer: preventing the hepcidin-ferroportin interaction and modulating the interleukin-6/Stat-3 pathway. Scientific Reports 7:40097
2. Shumayla, S Sharma, AK Pandey, K Singh, SK Upadhyay. 2016. Molecular characterization and global expression

analysis of lectin receptor kinases in bread wheat (Triticum aestivum). PLoS ONE 11(4):e0153925

3. M Taneja, S Tyagi, S Sharma, SK Upadhyay. 2016. Ca2+ / cation antiporters (CaCA): identification, characterization and expression profiling in bread wheat (Triticum aestivum L.). Frontiers in Plant Science 7:1775
4. Shumayla, S Sharma, R Kumar, V Mendu, K Singh, SK Upadhyay. 2016 Genomic dissection and expression profiling revealed functional divergence in Triticum aestivum Leucine Rich Repeat Receptor Like Kinases (TaLRRKs). Frontiers in Plant Science 7:1374
5. SK Upadhyay, S Sharma, H Singh, S Dixit, J Kumar, PC Verma, K Chandrashekar. Whitefly genome expression reveals host symbiont interaction in amino acid biosynthesis. PLoS ONE 10(5):e0153925
6. K Upadhyay, S Sharma. 2014. SSFinder: High-throughput CRISPR-Cas target sites prediction tool. BioMed Research International 2014:742482
7. SK Upadhyay, S Dixit, S Sharma, H Singh, J Kumar, PC Verma, K Chandrashekar. 2013. siRNA machinery in whitefly (Bemisia tabaci). PLoS ONE 8(12):e83692
8. S Sharma, G Cavallaro, A Rosato. 2010. A systematic investigation of multiheme c-type cytochromes in prokaryotes. Journal of Biological Inorganic Chemistry 15:559-71
9. S Sharma, A Rosato A. 2009. Role of the N-terminal tail of metal-transporting P(1B)-type ATPases from genome-wide analysis and molecular dynamics simulations. Journal of Chemical Information and Modeling 49:76-83

Name: **Nirmalya Ganguli**

Designation: **Scientist C**

Areas of Specialization: **Transgenesis, Animal Bioreactor, Direct Mammary Gland Transfection, Protein Engineering**

Dr. Nirmalya Ganguli received his PhD (2015) in the field of Animal Biotechnology from Department of Biochemistry, University of Delhi - South Campus, Delhi. He did his Research Associateship on development of methods for testicular transgenesis and development of animal bioreactor at National Institute of Immunology (NII), New Delhi, from 2015 until he joined the National Institute of Animal Biotechnology in February 2017.

Research experience and contributions:

Dr. Ganguli has experience in the generation of transgenic mice, generation of gene knockdown mice using shRNA, production of therapeutic protein in milk, and testicular germ cell depletion & stem cell transplantation work.His current research interests include development of easy method of transgenesis of farmed animals. This will help in generation of farm animal models of diseases and development of disease resistance and/or high yielding animal herd. He is working on development of non-GMO animal bioreactor by directly transfecting the epithelial cells of udder gland for production of animal/human therapeutic proteins in milk. He is standardising the testicular germ cell depletion and spermatogonial stem cell transplantation study in farm animals to aid in utilisation of non-productive bull for production of elite bull sperm. This will also help in production of transgenic sperm by specific and precise genomic modification (site specific integration or deletion). Along with this he also intends to investigate the genomic basis of udder gland development in farm animals.

Selected publications:

1. A Usmani*, N Ganguli, SK Jain, N Ganguli, RK Sarkar, M Choubey, M Shukla, H Sarkar, SS Majumdar. 2016. Robust generation of transgenic mice by simple hypotonic solution mediated delivery of transgene in testicular germ cells. Molecular Therapy - Methods & Clinical Development 3:16076
2. N Ganguli, N Wadhwa, A Usmani, N Kunj, N Ganguli, RK Sarkar, SM Ghorai, SS Majumdar. 2016. An efficient method for generating a germ cell depleted animal model for studies related to spermatogonial stem cell transplantation. Stem Cell Research and Therapy 7:142
3. N Ganguli, N Ganguli, A Usmani, SS Majumdar. 2015. Isolation and functional characterization of buffalo (Bubalus bubalis) β-casein promoter for driving mammary epithelial cell-specific gene expression. Journal of Biotechnology53-9
4. A Usmani, N Ganguli, H Sarkar, S Dhup, SR Batta, M Vimal, N Ganguli, S Basu, P Nagarajan, SS Majumdar. 2013. A non-surgical approach for male germ cell mediated gene transmission through transgenesis. Scientific Reports 3:3430

Name: **Pankaj Suman**

Designation: **Scientist C**

Areas of Specialization: **Aptamer based diagnostics for animal diseases; Immunological memory and Immunity; Applied animal nutrition**

Education and training:

Dr. Pankaj Suman completed B.V.Sc. (2004) from Maharashtra Animal and Fishery Sciences University, Nagpur, M.Sc. (2006; Biotechnology) from Indian Institute of Technology, Roorkee, and Ph.D. (2011; Immunology) from the National Institute of Immunology (NII), New Delhi. He also worked as visiting scholar at the Friedrich-Schiller University, Jena, Germany (2007-2010). Later, he worked as a post-doctoral Fellow (2011-2013) at NII, New Delhi, and then as Assistant Professor (2013-2014) at Amity University, Noida, Uttar Pradesh. Before joining NIAB in 2017, he was associated with the Animal Husbandry and Fishery Resources Department, Govt. of Bihar, as a Veterinary Clinician.

Research experience and interests:

Dr. Suman's experience spans reproductive biology, immunology and veterinary clinical medicine. In the past, he has made significant contribution in understanding the molecular mechanisms behind the immunological basis of pregnancy. His laboratory at NIAB is dedicated to address the clinical problems in veterinary medicine through developing affordable diagnostics, designer probiotics and improving innate & adaptive immunity.

Selected awards, honours and fellowships:

1. Prof. G. P. Talwar Young Scientist Award for outstanding contribution in research in reproductive health(2014)
2. Travel Grants: United States Department of Agriculture (USDA) (2010); Department of Science and Technology (DST), Govt. of India (2010)
3. Best discussant Award, EMBIC summer School, Jena, Germany (2007)
4. CSIR-Junior Research Fellowship-NET (2006)
5. Dr. B. L. Purohit medal in Veterinary Pathology, MAFSU (2004)

Selected publications:

1. Godbole G*, Suman P*, Malik A*, Galvankar M, Joshi N, Fazleabas A, Gupta SK, Modi D. 2017. Decrease in Expression of HOXA10 in the Decidua after Embryo Implantation Promotes Trophoblast Invasion. Endocrinology 158(8):2618-33. *Equal contribution
2. Suman P*, Gandhi S, Kumar P, Garg K. 2017. Prospects of electrochemical immunosensors for early diagnosis of preeclampsia. American Journal of Reproductive Immunology 77 (1):e12584. *Corresponding Author
3. Malhotra SS, Suman P, Gupta SK. 2015. Alpha or beta human chorionic gonadotropin knockdown decrease BeWo cell fusion by down-regulating PKA and CREB activation. Scientific Reports 5:11210.

4. Suman P, Gupta SK. 2014. STAT3 and ERK1/2 cross-talk in leukaemia inhibitory factor mediated trophoblastic JEG-3 cell invasion and expression of mucin 1 and Fos. American Journal of Reproductive Immunology 72(1):65-74.
5. Suman P, Shembekar N, Gupta SK. 2013. LIF increases the invasiveness of trophoblastic cells through integrated increase in the expression of adhesion molecules and pappalysin 1 with a concomitant decrease in the expression of TIMPs. Fertility and Sterility 99(2):533-42.
6. Suman P, Gupta SK. 2012. Comparative analysis of the invasion-associated genes expression pattern in first trimester trophoblastic (HTR-8/SVneo) and JEG-3 choriocarcinoma cells. Placenta 33(10):874-877.
7. Suman P, Godbole G, Thakur R, Morales-Prieto DM, Modi DN, Markert UR, Gupta SK. 2012. AP-1 transcription factors, mucin-type molecules and MMPs regulate the IL-11 mediated invasiveness of JEG-3 and HTR-8/SVneo trophoblastic cells. PLoS One 7: e29745.
8. Godbole G, Suman P, Gupta SK, Modi D (2011) Decidualized endometrial stromal cell derived factors promote trophoblast invasion. Fertility and Sterility 95(4):1278-1283.
9. Suman P, Poehlmann TG, Prakash GJ, Markert UR, Gupta SK (2009) Interleukin-11 increases invasiveness of JEG-3 choriocarcinoma cells by modulating STAT3 expression. Journal of Reproductive Immunology 82(1):1-11.
10. Choudhury S, Kakkar V, Suman P, Chakrabarti K, Vrati S, Gupta SK. 2009. Immunogenicity of zona pellucida glycoprotein-3 and spermatozoa YLP(12) peptides presented on Johnson grass mosaic virus-like particles. Vaccine 27(22):2948-2953.

Name: **Satya Pal Arya**

Designation: **Scientist B**

Areas of Specialization: **Genetics and Genomics, Genome Editing, Sexed Semen Production**

Education and training:

Dr. Satya Pal Arya completed B.Sc. (2008) and M.Sc. Genetics (2010); from the University of Delhi South Campus, New Delhi, and Ph.D. (2016) from the National Institute of Immunology, New Delhi. After completing PhD, he joined as scientist B at NIAB in 2017.

Research experience and interests:

Dr. Arya's research experience spans microRNA biology, spermatogenesis and genome editing. His major area of work has been in gene expression studies, where he has worked on idiopathic infertility. His research interest includes gene expression and genetic variations to understand the genetic basis of economically important traits in livestock and poultry. He is interested in using gene editing tools such as Crispr/Cas-9 and Zinc Finger Nuclease to improve economically important traits in livestock and poultry. He is also interested in developing alternative approaches for producing sexed semen in livestock.

Selected awards, honours and fellowships:

- Awarded Dina Nath-Savitri Devi Gold Medal in BSc (H) at Delhi University (2008)
- Awarded CSIR Junior Research Fellowship in Life Sciences (2010)
- Qualified ICAR-NET (2015)

Selected publications:

1. H Sarkar, S Arya, U. Rai, SS Majumdar, 2016. A study of differential expression of testicular genes in various reproductive phases of Hemidactylus flaviviridis (wall lizard) to derive their association with onset of spermatogenesis and its relevance to mammals. PLoS ONE 11(3):e0151150
2. M Gautam, I Bhattacharya, Y. Devi, S Arya, SS Majumdar. 2016. Hormone responsiveness of cultured Sertoli cells obtained from adult rats after their rapid isolation under less harsh condition. Andrology 4(3):509-19
3. A Misra, S Iyer, P Baligar, S Arya, S Arindkar, A Kesarwani, PK Upadhayay, SS Majumdar, P Nagarajan. 2016. Role of antigen presenting cell invariant chain in the development of hepatic steatosis in mouse model. Experimental Cell Research 346(2):188-97

MEMORANDA OF UNDERSTANDING

The details of MoU signed during the period from 1st April 2016 to 31st March 2017 by NIAB is given below:

S.No.	MoU with	Signed by	Date of Signing
1.	Indian Veterinary Research Institute (IVRI), Bareilly	Dr Subeer Majumdar Director	19th Jan 2017
2.	Cornell University, USA	Dr Subeer Majumdar Director	24th Mar 2017

IMPLEMENTATION OF THE RIGHT TO INFORMATION (RTI) ACT, 2005

Appellate Authority : Dr. Girish K Radhakrishnan
Central Public Information Officer : Mr Harjit Singh
Details about the RTI applications and appeals received in NIAB

As received under RTI Act 2005	Opening Balance as on 1.4.2016	Received during the year 2016-17			Disposed of during the year 2016-17				
		Received directly	Received as transfer from other Public Authorities [u/s 6(3) of Act]	Total	Decisions where applications accepted / appeals upheld	Decisions where applications/ appeals rejected	Transferred to other Public Authorities [u/s 6(3) of Act]	Total	Closing Balance as on 31-3-2017
Applications	0	5	25	30	30	0	0	30	0
Appeals	0	2	Not applicable	0	0	2	Not applicable	0	0

Brainstorming meeting on Livestock Genomics held on 3rd Sep. 2016

Brainstorming Meeting : Strategy for developing appropriate animal models to establish safety and toxicity of stem cells for human diseases held on 28 Mar 2017

DISTINGUISHED VISITORS AND LECTURES

Distinguished lecture by Prof. Samir Bhattacharya, Emeritus Professor, School of Life Science, Visva Bharati (Central University), West Bengal and Mission Director, NEEP Project, North-East Institute of Science & Technology (A CSIR Institute), Assam on " How to make Research Better : Indian Scenario " on 17th Oct. 2016

Distinguished lecture by Dr Satish Kumar Gupta, Emeritus Scientist, JC Bose Fellow and former Deputy Director and Chief of Reproductive Cell Biology Laboratory, National Institute of Immunology, New Delhi on 9th Feb. 2017

Organisational Structure of NIAB

NIAB SOCIETY

Dr. Harsh Vardhan Hon'ble Minister of S & T and Earth Sciences	President
Prof. K VijayRaghavan Secretary, DBT, New Delhi	Member
Shri C P Goyal Joint Secretary, DBT	Member
Mrs Gargi Kaul JS & FA, DBT, New Delhi	Member
Dr. Trilochan Mohapatra Secretary, DARE, New Delhi	Member
Dr. A K Rawat Director, DBT, New Delhi	Member
Prof. Suresh S Honnappagol Commissioner, AH, New Delhi	Member
Prof. Appa Rao Podile Vice Chancellor,UOH, Hyderabad	Member
Dr. VA Srinivasan Indian Immunologicals, Hyderabad	Member
Dr. SK Bandyopadhyay Member, ASRB, New Delhi	Member
Dr. Shahid Jameel Welcome Trust, Hyderabad	Member
Dr. RNK Bamezai JNU, New Delhi	Member
Dr. AK Srivastava NDRI, Karnal	Member

NIAB SOCIETY

Dr. KT Sampath, Ex-Director NIANP, Bengaluru	Member
Dr. (Ms) Anuradha Acharya Oscimum Bio Solutions, Hyderabad	Member
Dr. Suresh Poosala BMS Preclinical R&D, Bengaluru	Member
Dr. Girish K Radhakrishnan Scientist D, NIAB, Hyderabad	Member
Dr.Subeer S. Majumdar **Director, NIAB**	Member Secretary

NIAB GOVERNING BODY

Prof K. VijayRaghavan Secretary, DBT, New Delhi	Chairman
Shri C P Goyal Joint Secretary, DBT, New Delhi	Member
Mrs Gargi Kaul JS & FA, DBT, New Delhi	Member
Dr. Trilochan Mohapatra Secretary, DARE, New Delhi	Member
Dr. A K Rawat Director, DBT, New Delhi	Member
Prof. Suresh S Honnappagol Commissioner, AH, New Delhi	Member
Prof. Appa Rao Podile Vice Chancellor,UOH, Hyderabad	Member
Dr. VA Srinivasan Indian Immunologicals, Hyderabad	Member
Dr. SK Bandyopadhyay Member, ASRB, New Delhi	Member
Dr. Shahid Jameel Welcome Trust, Hyderabad	Member
Dr. RNK Bamezai JNU, New Delhi	Member
Dr. AK Srivastava NDRI, Karnal	Member
Dr. KT Sampath, Ex-Director NIANP, Bengaluru	Member

NIAB GOVERNING BODY

Dr. (Ms) Anuradha Acharya Oscimum Bio Solutions, Hyderabad	Member
Dr. Suresh Poosala BMS Preclinical R&D, Bengaluru	Member
Dr. Girish K Radhakrishnan Scientist D, NIAB, Hyderabad	Member
Dr.Subeer S. Majumdar Director, NIAB	Member Secretary

NIAB SCIENTIFIC ADVISORY COMMITTEE (SAC)

Dr. Lalji Singh Ex-Director, CCMB & Ex- VC, BHU	Chairman
Dr. A K Rawat Director DBT, New Delhi	Member
Deputy Director General (Animal Science), Division of Animal Science, ICAR, New Delhi	Member
Dr.Subeer S. Majumdar Director, NIAB	Member Secretary
Prof. Lothar H Wieler Institut fur Mikrobiologie und Tierseuchen, Berlin, Germany	Member
Prof. Ramaswamy S C-CAMP, Bengaluru	Member
Dr. S N Singh Biovet, Bengaluru	Member
Prof. R Medhamurthy IISC, Bengaluru	Member
Mr Deepak Kapur Indovax, Gurgaon	Member
Prof. G Dhinakar Raj TANUVAS, Chennai	Member
Dr. B P Mishra IVRI, Izatnagar	Member

NIAB FINANCE COMMITTEE (FC)

Prof. K VijayRaghavan Secretary, DBT, New Delhi	Chairman
Mrs Gargi Kaul JS & FA, DBT, New Delhi	Member
Dr. A K Rawat Director, DBT, New Delhi	Member
Dr. J Gowrishankar CDFD, Hyderabad	Member
Dr. Durgadas P Kasbekar CDFD, Hyderabad	Member
Prof. Appa Rao Podile Vice Chancellor,UOH, Hyderabad	Member
Dr. A K Srivastava NDRI, Karnal	Member
Dr. (Ms) Anuradha Acharya Oscimum Bio Solutions, Hyderabad	Member
Dr. Subeer S Majumdar Director, NIAB	Member Secretary

NIAB BUILDING COMMITTEE (BC)

Dr. J Gowrishankar Former Director, CDFD	Chairman
Dr. A K Rawat Director, DBT	Member
Shri Roshan Lal Dy Secretary, DBT	Member
Shri B L N Reddy Superintending Engineer, HMDA, Hyderabad	Member
Dr. G Sundararajan Director, International Advanced Research Centre for Powder Metallurgy and new Materials(ARCI), Hyderabad	Member
Dr.Subeer S Majumdar Director, NIAB	Member
Shri S Ayub Basha Staff Scientist-V (Engineering), CDFD	Member
Shri Harjit Singh Senior Manager, NIAB	Member Convenor

COMPLAINT COMMITTEE FOR THE PREVENTION AND PROHIBITION OF SEXUAL HARASSMENT

The following internal complaint committee has been constituted for the prevention and prohibition of sexual harassment in accordance with Sexual Harassment of Women at Workplace (Prevention, Prohibition and Redressal) Act 2013:

Dr. Madhuri Subbiah, Scientist	-	Chairperson
Dr. Sathya Velmurugan, Scientist	-	Member
Smt. Sobha Krishna, Legal Expert	-	Member
Shri. Harjit Singh, Senior Manager	-	Member
Shri. Santosh Mhadeshwar, Manager S&P	-	Member
Smt. Krishna Priya, PA to Director	-	Member Secretary

NIAB Staff

Scientific

1.	Dr Subeer S Majumdar, PhD	Director (w.e.f 1 Aug. 2016)
2.	Dr Nagendra R Hegde, PhD	Scientist - G
3.	Dr Girish K Radhakrishnan,PhD	Scientist - D
4.	Dr Shailesh Sharma, PhD	Scientist - D
5.	Dr Syed Mohd Faisal, PhD	Scientist - D
6.	Dr Madhuri Subbiah, PhD	Scientist - C
7.	Dr Anand Srivastava,PhD	Scientist - C
8.	Dr Paresh Sharma,PhD	Scientist - C
9.	Dr Sathya Velmurugan,PhD	Scientist - C
10.	Dr Abhijit S Deshmukh,PhD	Scientist - C
11.	Dr Nirmalya Ganguli, PhD	Scientist - C
12.	Dr Pankaj Suman, PhD	Scientist - C
13.	Mr Sarwar Azam	Scientist - B
14.	Dr Satya Pal Arya, PhD	Scientist - B
15.	Prof Satya Parida, PhD	Visiting Faculty
16.	Dr Aparna Rachamallu,PhD	DST Women Scientist
17.	Dr Vasundhra Bhandari,PhD	DST Inspire Faculty(w.e.f 1 Dec 2016)

Administrative and Support Staff

1.	Mr Harjit Singh	Senior Manager
2.	Mr I Jagadeesh	Manager Office (Accounts)
3.	Mr Santosh N Mhadeshwar	Manager (Stores & Purchase)
4.	Mr V Ramesh Babu	Service & Maintenance Engineer
5.	Ms Krishna Priya	PA to Director
6.	Mr Mohammed Zaheeruddin	Junior Office Assistant
7.	Mr P S G S Pavan Kumar	Junior Office Assistant
8.	Mr Ratnesh Chandra	Junior Office Assistant
9.	Mr D Nagesh	Office Attendant
10.	Mr P Ramesh	Office Attendant
11.	Mr Jahid Hussain	Driver

Technical

1.	Mrs G. Rama Devi	Technical Officer
2.	Mr Shashikant D Gawai	Technical Officer
3.	Mr A Harikrishna	Technical Officer
4.	Mr Praveen Kumar Poosarla	Technical Officer

Consultants

1.	Mr B.J Acharyulu	Consultant (Finance & Accounts)

Picture Gallery

Dr. Subeer S Majumdar took over the charge as Director, NIAB on 1st Aug 2016

Picture Gallery

Independence Day Celebration at NIAB Site

Tree plantation Drive at NIAB Site

Picture Gallery

Signing of MoU with *Cornell University, USA*

Signing of MoU with *Indian Veterinary Research Institute (IVRI), Bareilly*

Hindi Pakhwara – 2016

Connecting Lab with Students

Dr Syed Faisal, Scientist-D of NIAB at Jawahar Navodaya Vidyalaya, Gopanpally, Hyderabad under High School teaching programme (Shiksha Setu)

Drs Madhuri Subbiah and Abhijit Deshmukh interacting with students at Pragati Junior and Women's degree college at Kukatpally, Hyderabad

Science Day 2017

Students from different schools participating in painting competition during Science day celebrations

Group picture of all Participants

NIAB organized a DBT Pavilion at "Pride of India" Expo of Indian Science Congress 2017 held at SV University, Tirupati from 03.01.2017-07.01.2017

NIAB organized a DBT stall at Bio Asia 2017 held at Hitex, Hyderabad from 06.02.2017-08.02.2017

Aerial view of main lab building

Aerial view of small animal house facility

Aerial view of Animal farms

Hostel Block

NIAB

National Institute of Animal Biotechnology

Audited Statements Of Accounts 2016 - 17

Auditor's Report

11th May 2017

The Director
National Institute of Animal Biotechnology
D.No. 1-121/1, 4th & 5th Floors, Axis Clinicals Building
Miyapur, Hyderabad – 500 049

We have audited the attached Balance Sheet of **NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY,** Hyderabad, as at 31st March 2017 and also the Income & Expenditure Account for the year ended on that date annexed there to. These financial statements are the responsibility of the organization management. Our responsibility is to express an opinion on these financial statements based on our audit.

We report that:

1. We have obtained all the information and explanations, which are to the best of our knowledge and belief, were necessary for the purpose of our audit.
2. In our opinion, the organization has kept proper books of account as required by law so far, as appears from our examination of those books.
3. The Balance sheet and Income & Expenditure account dealt with by this report is in agreement with the books of accounts.
4. The Institute has maintained accounts on Accrual basis.
5. In our opinion and to the best of our information and according to the explanations given to us, the said Balance sheet and the Income & Expenditure account read together with the notes thereon gives the required information in the manner so required and give a true and fair view.
    a) In so far it relates to the Balance sheet as at 31st March 2017 and
    b) In so far as it relates to the Income & Expenditure account excess of income over expenditure for the year ended on 31st March 2017.

For B Purushottam & Co
Chartered Accountants
Reg.No. 002808S

Place: Hyderabad
Date: 11/05/2017

(Ch.Satyanarayana)
Partner M.No.019092

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY, HYDERABAD

BALANCE SHEET AS ON 31st MARCH 2017

(Amount in Rs)

Particulars	Schedule	Current Year	Previous Year
CORPUS/CAPITAL FUND AND LIABILITIES			
Corpus / Capital Fund	1	819,811,531.00	566,716,104.00
Reserves and Surplus	2	25,062,633.51	19,169,158.21
Earmarked / Endowment funds	3	10,228,085.00	5,934,234.00
Secured Loans & Borrowings	4	-	-
Unsecured Loans & Borrowings	5	-	-
Deferred Credit Liabilities	6	-	-
Current Liabilities and Provisions	7	2,645,073.00	2,405,291.00
TOTAL		**857,747,322.51**	**594,224,787.21**
ASSETS			
Fixed Assets	8	817,384,125.00	564,218,609.00
Investments- From Earmarked / Endowment Funds	9	-	-
Investments - Others	10	-	-
Current Assets, Loans, Advances etc.	11	40,363,197.51	30,006,178.21
Miscellaneous Expenditure			
TOTAL		**857,747,322.51**	**594,224,787.21**
Significant Accounting Policies	24		
Contingent Liabilities and Notes on Accounts	25		

For B.Purushottam & Co.
CHARTERED ACCOUNTANTS
Reg.No. 002808S

Director	(Ch. Satyanarayana)	Finance Officer	Manager Office (Accounts)
NIAB	Partner M.No. 019092	NIAB	NIAB

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY,HYDERABAD

Income And Expenditure Statement for the year ended 31st MARCH 2017

(Amount in Rs)

Particulars	Schedule	Current Year		Previous Year	
INCOME					
Income from Sales/Services	12		-		-
Grants/Subsides	13		82,800,000.00		89,187,800.00
Fees/Subscriptions	14		-		-
Income from Investments	15		-		-
Income from Royalty, Publications etc.	16		-		-
Interest Earned	17		1,610,602.62		1,535,476.00
Other Income	18		699,230.00		505,250.82
Increase/(decrease) in stock of Finished goods and works-in-progress	19		-		-
TOTAL (A)			**85,109,832.62**		**91,228,526.82**
EXPENDITURE					
Establishment Expenses	20		20,777,403.00		18,478,142.00
Administrative Expenses etc.	21		58,174,156.32		71,344,091.13
Expenditure on Grants, Subsides etc.	22		-		-
Interest	23		-		-
Depreciation (Net Total at the year-end - corresponding to Schedule 8)		17,214,614.00		20,434,481.00	
Less: Transferred to Grants-in-Aid		17,214,614.00	-	20,434,481.00	
Provision For Salaries and other Expenses (Annexure-J)			264,798.00		747,641.00
TOTAL (B)			**79,216,357.32**		**90,569,874.13**
Balance being excess of Income over Expenditure (A-B)			**5,893,475.30**		**658,652.69**
Transfer to Special Reserve (Specify each)					
Transfer to/from General Reserve					
Balance being SURPLUS/(DEFICIT) carried to CORPUS/CAPITAL FUND					
Significant Accounting Policies	24				
Contingent Liabilities and Notes on Accounts	25				

For B Purushottam & Co.
CHARTERED ACCOUNTANTS
Reg.No. 002808S

Director	(Ch.Satyanarayana)	Finance Officer	Manager Office (Accounts)
NIAB	Partner M.No.019092	NIAB	NIAB

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY,HYDERABAD
RECEIPTS AND PAYMENTS ACCOUNT FOR THE YEAR ENDED 31st MAR 2017

(Amount - Rs.)

RECEIPTS	Current Year	Previous Year	PAYMENTS	Current Year	Previous Year
1.Opening Balances			1. Expenses		
a) Cash in hand	-	-	a) Establishment Expenses (corresponding to Schedule 20)	20,777,403.00	18,478,142.00
b) Bank Balances			b) Administrative Expenses (corresponding to Schedule 21)	58,174,156.32	71,344,091.13
i) In current accounts	-	-			
ii) In deposit accounts	-	-			
iii) Savings accounts	16,858,926.21	3,227,520.52			
2. Grants Received			2. Payments made against funds for various projects		
a) From Government of India	352,800,000.00	307,011,800.00	(Name of the fund or project should be shown along with		
b) From State government	-	-	the particulars of payments made for each project)		
c) From other sources (details)	-	-	Projects (Annexure F)	16,875,657.00	11,036,489.00
(Grants for capital & revenue					
exp. To be shown separately)			3. Investments and deposits made		
			a) Out of Earmarked/Endowment funds	-	-
d) Projects (Annexure - C)	21,169,508.00	14,841,868.00	b) Out of Own Funds (Investments-Others)	122,500,000.00	138,000,000.00
3. Income on Investments from			4. Expenditure on Fixed Assets & Capital Work-in-Progress		
a) Earmarked/Endow. Funds	-	-	a) Purchases of Fixed Assets:		
b) Own Funds (Oth. Investment)	-	-	Books & Journals	10,618.00	17,846.00
c) Investments Encashed	122,500,000.00	138,000,000.00	Equipment -Lab/Office/Furniture	1,036,751.00	8,166,423.00
			b) Expenditure on Capital Work-in-Progress	269,022,720.00	215,596,000.00
4. Interest Received					
a) On Bank deposits	1,195,442.00	1,036,623.00	5. Refund of surplus money/Loans		
b) Loans, Advances etc.	-	-	a) To the Government of India	-	-
c) on savings accounts	409,578.00	493,205.00	b) To the State Government	-	-
d) Interest on LC	5,582.62	5,648.00	c) To other providers of funds	-	-
5. Other Income(Specify)					
a) Analysis Charges	-	-	6. Finance Charges (Interest)	-	-
6. Amount Borrowed	-	-			
7. Any Other Receipts(Give Details)			7. Other Payments (Specify)		
I-Remittances (Annexure-A)	4,657,194.00	3,411,652.00	Advances (Annexure-D)	26,472,328.11	8,893,239.00
			I-Remittances (Annexure-E)	4,657,194.00	3,411,652.00
CPF-SUB, Arrears and adv. Refund/GPF	350,000.00	-	CPF A/c / GPF A/c	350,000.00	-
Sundry Receipts	531,730.00	237,250.82	New Pension Scheme	1,084,878.00	851,858.00
Application Fee	121,500.00	-			
Provident Fund Salvage	-	-	8. Closing Balances		
Free Gifts - Donations	-	-	a) Cash in hand	-	-
Sale of Tender Forms	46,000.00	268,000.00	b) Bank Balances		
Leave Salary-Pension Contribution	-	-	i) In current accounts	-	-
License Fee	-	-	ii) In deposit accounts	-	-
Welfare Fund	-	-	iii) Savings accounts	17,566,320.40	16,858,926.21
NPS	1,084,878.00	851,858.00			
Advance/Refunds/Recovery/					
Adj(Annexure-B)	16,797,687.00	23,269,241.00			
TOTAL	**538,528,025.83**	**492,654,666.34**	**TOTAL**	**538,528,025.83**	**492,654,666.34**

For B Purushottam & Co.
CHARTERED ACCOUNTANTS
Reg.No. 002808S

(Ch.Satyanarayana)
Partner M.No.019092

Director
NIAB

Finance Officer
NIAB

Manager Office (Accounts)
NIAB

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MAR 2017

(Amount - Rs.)

Particulars	Current Year		Previous Year	
SCHEDULE 1 - CORPUS/CAPITAL FUND :				
Balance as at the beginning of the year		566,716,104.00		368,887,939.00
Add : Contribution towards Corpus/Capital Fund				
NIAB Core - Plan (Non-Recurring)	270,000,000.00		217,824,000.00	
Capitalised portion of Capital Expenditure of projects	310,041.00		438,646.00	
Others (A.P. Govt. allotted 100 Acres land at free of Cost)	-	270,310,041.00	-	218,262,646.00
Less : Lump Sum Depreciation				
Less : Depreciation For the Year 2016-2017	17,214,614.00	17,214,614.00	20,434,481.00	20,434,481.00
Add : Balance of net income/(Expenditure) transferred from the income and Expenditure Account				
BALANCE AS AT THE YEAR - END		**819,811,531.00**		**566,716,104.00**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MAR 2017

(Amount - Rs.)

Particulars	Current Year		Previous Year	
SCHEDULE 2 -RESERVES AND SURPLUS :				
1. Capital Reserve :				
As per last Account	-		-	
Addition during the year	-		-	
Less : Deductions during the year	-	-	-	-
2. Revolution Reserve :				
As per last Account	-		-	
Addition during the year	-		-	
Less : Deductions during the year	-	-	-	-
3. Special Reserves :				
As per last Account	-		-	
Addition during the year	-		-	
Less : Deductions during the year	-	-	-	-
4. General Reserve :				
As per last Account	19,169,158.21		18,510,505.52	
Addition during the year	5,893,475.30		658,652.69	
Less : Deductions during the year	-	25,062,633.51	-	19,169,158.21
Total	**25,062,633.51**		**19,169,158.21**	

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MAR 2017

(Amount - Rs.)

Particulars	Current Year		Previous Year	
SCHEDULE 3 - EARMARKED/ENDOWMENT FUNDS :				
(Refer Annexures)				
(a) Opening balance of the Funds		5,934,234.00		2,128,855.00
(b) Additions to the Funds :				
i. Donations /grants	21,169,508.00		14,841,868.00	
ii. Income from investments made on account of funds	-		-	
iii. Other additions	-	21,169,508.00	-	14,841,868.00
TOTAL (a+b)		**27,103,742.00**		**16,970,723.00**
(c) Utilisation/Expenditure towards objective of funds				
(i) Capital Expenditure (Refer Annexures I & II)				
- Fixed Assets	310,041.00		438,646.00	
- Others	-		-	
- Total		310,041.00		438,646.00
(ii) Revenue Expenditure (Refer Annexures I & II)				
- Salaries, Wages and allowances etc.				
- Rent	-		-	
- Other Expenses	16,565,616.00		10,597,843.00	
Total		16,565,616.00		10,597,843.00
TOTAL (c)		**16,875,657.00**		**11,036,489.00**
NET BALANCE AS AT THE YEAR-END [(a + b)-c]		**10,228,085.00**		**5,934,234.00**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MAR 2017

(Amount - Rs.)

Particulars	Current Year		Previous Year	
SCHEDULE 4 - SECURED LOANS AND BORROWINGS :				
1. Central Government		-		-
2. State Government (Specify)		-		-
3. Financial Institutions				
a) Term Loans	-		-	
b) Interest accrued and due	-	-	-	-
4. Banks :				
a) Terms Loans	-		-	
- Interest accrued and due	-		-	
b) Other Loans	-		-	
- Interest accrued and due	-	-	-	-
5. Other Institutions and Agencies		-		-
6. Debentures and Bonds		-		-
7. Others (Specify)		-		-
TOTAL		**-**		**-**
Note: Amount due within one year				

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MAR 2017

(Amount - Rs.)

Particulars	Current Year		Previous Year	
SCHEDULE 5 - UNSECURED LOANS AND BORROWINGS :				
1. Central Government		-		-
2. State Government (Specify)		-		-
3. Financial Institutions		-		-
4. Banks :				
a) Terms Loans	-		-	
b) Other Loans	-	-	-	-
5. Other Institutions and Agencies		-		-
6. Debentures and Bonds		-		-
7. Fixed Deposits		-		-
8. Others (Specify)		-		-
TOTAL		-		-
Note: Amount due within one year				

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MAR 2017

(Amount - Rs.)

Particulars	Current Year		Previous Year	
SCHEDULE 6 - DEFERRED CREDIT LIABILITIES :				
a) Acceptances secured by hypothecation of capital equipment and other assets		-		-
b) Others		-		-
TOTAL		**-**		**-**
Note: Amount due within one year				

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MAR 2017

(Amount - Rs.)

Particulars	Current Year		Previous Year	
SCHEDULE 7 - CURRENT LIABILITIES AND PROVISIONS				
A. CURRENT LIABILITIES				
1. Acceptances	-		-	
2. Sundry Creditors	-		-	
3. Advances Received	22,086.00		-	
4. Interest accrued but not due on:	-		-	
5. Statutory Liabilities:	-	22,086.00	-	-
6. Other current Liabilities				
NIAB.CP Fund A/C	-		-	
EMD	-		-	
Security Deposit	33,000.00	33,000.00	80,102.00	80,102.00
TOTAL (A)		**55,086.00**		**80,102.00**
B. PROVISIONS				
1. For Taxation	-		-	
2. Gratuity	-		-	
3. Superannuation/Pension	-		-	
4. Accumulated Leave Encashment	-		-	
5. Trade Warranties/Claims	-		-	
6. Others (Specify) (Annexure-G)	2,589,987.00	2,589,987.00	2,325,189.00	2,325,189.00
TOTAL (B)		**2,589,987.00**		**2,325,189.00**
TOTAL (A+B)		**2,645,073.00**		**2,405,291.00**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MAR 2017

(Amount - Rs.)

SCHEDULE 8 - FIXED ASSTES :	GROSS BLOCK				DEPRECIATION				NET BLOCK	
Particulars	Cost/valuation As at beginning of the year	Addition during the year	Deductions during the year	Cost/Valuation at the year end	As at the beginning of the year	On additions during the year	On Deductions during the year	Total up to the year end	As at the Current year end	As at the Previous year end
A. FIXED ASSETS:										
1. LAND:										
a) Freehold ***	1.00	-	-	1.00	-	-	-	-	1.00	1.00
b) Leasehold	-	-	-	-	-	-	-	-	-	-
2. BUILDINGS										
a) On Freehold Land	-	-	-	-	-	-	-	-	-	-
b) On Leasehold Land	-	-	-	-	-	-	-	-	-	-
c) Ownership Flats/Premises	-	-	-	-	-	-	-	-	-	-
d) Superstructures on Land not belongs to the entity	-	-	-	-	-	-	-	-	-	-
3. PLANT MACHINERY&EQUIPMENT	156,048,213.00	1,145,994.00	-	157,194,207.00	49,241,622.00	16,173,907.00	-	65,415,529.00	91,778,678.00	106,806,591.00
4. VEHICLES	2,240,610.00	-	-	2,240,610.00	1,080,935.00	173,951.00	-	1,254,886.00	985,724.00	1,159,675.00
5. FURNITURE, FIXTURES	300,379.00	95,998.00	-	396,377.00	92,602.00	30,378.00	-	122,980.00	273,397.00	207,777.00
6. OFFICE EQUIPMENT	3,325,715.00	98,000.00	-	3,423,715.00	1,148,581.00	341,270.00	-	1,489,851.00	1,933,864.00	2,177,134.00
7. COMPUTER/PERIPHERALS	2,203,905.00	-	-	2,203,905.00	1,577,072.00	376,100.00	-	1,953,172.00	250,733.00	626,833.00
8. ELECTRIC INSTALLATIONS	-	-	-	-	-	-	-	-	-	-
9. LIBRARY BOOKS	599,985.00	10,618.00	-	610,603.00	594,912.00	15,691.00	-	610,603.00	-	5,073.00
10. TUBEWELLS & WATER SUPPLY	-	-	-	-	-	-	-	-	-	-
11. OTHER FIXED ASSETS	730,573.00	6,800.00	-	737,373.00	324,104.00	103,317.00	-	427,421.00	309,952.00	406,469.00
TOTAL	**165,449,381.00**	**1,357,410.00**	**-**	**166,806,791.00**	**54,059,828.00**	**17,214,614.00**	**-**	**71,274,442.00**	**95,532,349.00**	**111,389,553.00**
B. CAPITAL WORK-IN-PROGRESS	**452,829,056.00**	**269,022,720.00**	**-**	**721,851,776.00**	**-**	**-**	**-**	**-**	**721,851,776.00**	**452,829,056.00**
TOTAL	**618,278,437.00**	**270,380,130.00**	**-**	**888,658,567.00**	**54,059,828.00**	**17,214,614.00**	**-**	**71,274,442.00**	**817,384,125.00**	**564,218,609.00**
***** LAND OF 100 ACRES ALLOTTED BY GOVT. OF AP. WORTH OF RS. 306.822 CRORES TO NIAB AT FREE OF COST VIDE G.O.MS.NO. 566, DT. 13/09/2012 AT SY NO. 37, GOPANAPALLY VILLAGE, SERILINGAMPALLY VILLAGE, R R DIST. *****										
Assets bifurcation by funding :										
Core grant	617,326,506.00	270,070,089.00	-	887,396,595.00	53,991,982.00	17,120,000.00	-	71,111,982.00	816,284,613.00	563,334,524.00
Extra mural projects	951,931.00	310,041.00	-	1,261,972.00	67,846.00	94,614.00	-	162,460.00	1,099,512.00	884,085.00
TOTAL	**618,278,437.00**	**270,380,130.00**	**-**	**888,658,567.00**	**54,059,828.00**	**17,214,614.00**	**-**	**71,274,442.00**	**817,384,125.00**	**564,218,609.00**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MAR 2017

(Amount - Rs.)

Particulars	Current Year	Previous Year
SCHEDULE 9 - INVESTMENTS FROM EARMARKED/ENDOWMENT FUNDS :		
1. In Government Securities	-	-
2. Other approved securities	-	-
3. Shares	-	-
4. Debentures and Bonds	-	-
5. Subsidiaries and Joint Ventures	-	-
6. Others (to be specified) - STDRs	-	-
TOTAL	**-**	**-**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MAR 2017

(Amount - Rs.)

Particulars	Current Year	Previous Year
SCHEDULE 10 - INVESTMENTS - OTHERS :		
1. In Government Securities	-	-
2. Other approved securities	-	-
3. Shares	-	-
4. Debentures and Bonds : UTI Bonds	-	-
5. Subsidiaries and Joint Ventures	-	-
6. Others (to be specified) - STDRs,(CPF), NIAB CP FUND A/C	-	-
TOTAL	**-**	**-**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
SCHEDULES FORMING PART OF BALANCE SHEET AS AT 31st MAR 2017

(Amount - Rs.)

Particulars	Current Year		Previous Year	
SCHEDULE 11 - CURRENT ASSETS, LOANS, ADVANCES ETC.:				
A. CURRENT ASSETS				
1. Inventors				
a) Stores and Spares	-		-	
b) Loose Tools	-		-	
c) Stock-in-trade				
Finished Goods	-		-	
Work-in-progress	-		-	
Raw Materials	-	-	-	-
2. Sundry Debtors:		-		
a) Debts Outstanding for a period exceeding six months			-	
b) Others-Life Membership Fees	-	-		
3. Cash balances in hand (including cheques/drafts and imprest)				
4. Bank Balances:				
a) With Scheduled Banks:				
-On Current Accounts	-		-	
-On Deposit Accounts (includes margin money)	-		-	
-On Savings Accounts	17,566,320.40	17,566,320.40	16,858,926.21	16,858,926.21
b) With non-Schedules Banks:				
-On Current Accounts	-		-	
-On Deposit Accounts	-		-	
-On Savings Accounts	-	-	-	-
5. Post Office-Savings Accounts				
TOTAL (A)		**17,566,320.40**		**16,858,926.21**
B. LOANS, ADVANCES AND OTHER ASSETS				
1. Loans:				
a) Staff	-		-	
b) Other Entities engaged in activities/objectives similar to that of the Entity	-	-	-	-
2. Advances and other amounts recoverable in cash or in kind or for value to be received				
a) On Capital Account (Annexure-H)	718,034.11		794,653.00	
b) Prepayments - Deposits (Annexure-I)	22,078,843.00		12,352,599.00	
c) Others	-	22,796,877.11	-	13,147,252.00
3. Income Accrued:				
a) On Investments from Earmarked/Endowments Funds	-		-	
b) On Investments - Others	-		-	
c) On Loans and Advances	-		-	
d) Others	-	-	-	-
4. Claims Receivable	-			-
TOTAL (B)		**22,796,877.11**		**13,147,252.00**
TOTAL (A+B)		**40,363,197.51**		**30,006,178.21**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MAR 2017

(Amount - Rs.)

Particulars	Current Year	Previous Year
SCHEDULE 12 - INCOME FROM SALES/SERVICES		
1) Income from sales		
a) Sale of Finished Goods	-	-
b) Sale of Raw Material	-	-
c) Sale of Scraps	-	-
2) Income from Services		
a) Labour and Processing Charges	-	-
b) Professional/Consultancy Services (Analysis Charges)	-	-
c) Agency Commission and Brokerage	-	-
d) Maintenance Services (Equpiment/Property)	-	-
e) Others (Specify)	-	-
TOTAL	**-**	**-**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MAR 2017

(Amount - Rs.)

Particulars	Current Year	Previous Year
SCHEDULE 13 - GRANTS/SUBSIDES :		
(Irrevocable Grants & Subsides Received)		
1) Central Government (DBT Plan Grant-in-Aid)	82,800,000.00	89,187,800.00
2) State Government(s)	-	-
3) Government Agencies	-	-
4) Institutions/Welfare Bodies	-	-
5) International Organisations	-	-
6) Others (Specify)	-	-
TOTAL	**82,800,000.00**	**89,187,800.00**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MAR 2017

(Amount - Rs.)

Particulars	Current Year	Previous Year
SCHEDULE 14 - FEES/SUBSCRIPTIONS		
1) Entrance Fees	-	-
2) Annual Fees/Subscriptions	-	-
3) Seminar/Program Fees	-	-
4) Consultancy Fees	-	-
5) Others (Specify)	-	-
TOTAL	**-**	**-**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MAR 2017

(Amount - Rs.)

Particulars	Investments From Earmarked Fund		Investments - Others	
SCHEDULE 15 - INCOME FROM INVESTMENTS:	Current Year	Previous Year	Current Year	Previous Year
(Income on Invest from Earmarked/Endowment Funds transferred to Funds)				
1) Interest:				
a) On Govt. Securities	-	-	-	-
b) Other Bonds/Debentures	-	-	-	-
2) Dividends:				
a) On Shares	-	-	-	-
b) On Mutual Fund Securities	-	-	-	-
3) Rents	-	-	-	-
4) Others (Specify) STDRs	-	-	-	-
TOTAL	**-**	**-**	**-**	**-**
TRANSFERRED TO EARMARKED/ENDOWMENT FUNDS	-	-	-	-

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MAR 2017

(Amount - Rs.)

Particulars	Current Year	Previous Year
SCHEDULE 16 - INCOME FROM ROYALITY, PUBLICATION ETC.:		
1) Income from Royalty	-	-
2) Income from Publications	-	-
3) Others (Specify)	-	-
TOTAL	**-**	**-**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MAR 2017

(Amount - Rs.)

Particulars	Current Year	Previous Year
SCHEDULE 17 - INTEREST EARNED :		
1) On Term Deposits		
a) With Schedule Banks	1,201,024.62	1,042,271.00
b) With Non-Scheduled Banks	-	-
c) With Institutions	-	-
d) Others	-	-
2) On Saving Accounts		
a) With Schedule Banks	409,578.00	493,205.00
b) With Non-Scheduled Banks	-	-
c) Post Office Savings Accounts	-	-
d) Others	-	-
3) On Loans		
a) Employees/Staff	-	-
b) Others	-	-
4) Interest on Debtors and Other Receivables	-	-
TOTAL	**1,610,602.62**	**1,535,476.00**
Note :- Tax deducted at source to be indicated		

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MAR 2017

(Amount - Rs.)

Particulars	Current Year	Previous Year
SCHEDULE 18 - OTHER INCOME :		
1) Profit on Sale/disposal of Assets:	-	-
a) Owned assets	-	-
b) Assets acquired out of grants, or received free of cost	-	-
2) Export Incentives realized	-	-
3) Fees for Miscellaneous Services	-	-
4) Miscellaneous Receipts	526,500.00	220,000.00
5) Other Receipts		
Sundry Receipts	5,230.00	17,250.82
Application Fee	121,500.00	-
Sales Of Tender Forms	46,000.00	268,000.00
Licence Fee	-	-
Interest On Computer Advance, Conveyance Advance And HBA	-	-
Leave Salary-Pension Contribution	-	-
Provident Fund Salvage	-	-
Free Gifts-Donations	-	-
TOTAL	**699,230.00**	**505,250.82**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MAR 2017

(Amount - Rs.)

Particulars	Current Year	Previous Year
SCHEDULE 19 - INCREASE/(DECREASE) IN STOCK OF FINISHED GOODS & WORK IN PROGRESS :		
a) Closing stock		
-Finished goods	-	-
-Work-in-progress	-	-
TOTAL (a)	**-**	**-**
b) Less: Opening stock		
-Finished goods	-	-
-Work-in-progress	-	-
TOTAL (b)	**-**	**-**
NET INCREASE/(DECREASE) [a-b]	**-**	**-**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MAR 2017

(Amount - Rs.)

Particulars	Current Year	Previous Year
SCHEDULE 20 - ESTABLISHMENT EXPENSES :		
a) Salaries and Wages	9,043,554.00	9,032,230.00
b) Allowances and Bonus	10,114,536.00	8,054,354.00
c) Contribution to Provident Fund	58,646.00	-
d) Contribution to Other Fund (NPS)	1,084,878.00	851,858.00
e) Staff Welfare Expenses - Medical charges	475,789.00	539,700.00
f) Expenses on Employees Retirement and Terminal Benefits	-	-
g) Others (specify) - Staff leased House	-	-
TOTAL	**20,777,403.00**	**18,478,142.00**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MAR 2017

(Amount - Rs.)

Particulars	Current Year	Previous Year
SCHEDULE 21 - OTHER ADMINISTRATIVE EXPENSES :		
a) Purchases	14,420,904.00	31,155,049.00
b) Electricity and power	6,792,922.00	6,306,793.00
c) Water charges	128,028.00	173,364.00
d) Insurance	34,453.00	41,181.00
e) Repairs and maintenance	414,001.00	324,806.00
f) Rent, Rates and Taxes	24,974,160.00	23,324,144.00
g) Vehicles Running and Maintenance	236,116.00	158,433.00
h) Postage, Telephone and Communication Charges	233,210.00	280,365.00
i) Printing and Stationary	463,365.00	525,708.00
j) Travelling and Conveyance Expenses	1,386,189.00	1,410,072.00
k) Expenses on Seminar/Workshops	47,932.00	88,783.00
l) Subscription Expenses	28,229.00	169,866.00
m) Expenses on Fees	-	-
n) Auditors Remuneration	34,500.00	28,090.00
o) Hospitality Expenses	172,046.00	105,619.00
p) Professional Charges	-	-
q) Advertisement and Publicity	188,071.00	795,681.00
r) Bank Charges	356.32	2,464.13
s) Security & Cleaning Contract Charges	6,159,776.00	4,802,396.00
t) Training Course /Symposia	7,500.00	-
u) Other Contingencies	247,867.00	254,474.00
v) Liveries & Blankets	-	-
w) Other Research Expenses	2,200,871.00	1,396,803.00
x) Office Books	3,660.00	-
TOTAL	**58,174,156.32**	**71,344,091.13**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MAR 2017

(Amount - Rs.)

Particulars	Current Year	Previous Year
SCHEDULE 22 - EXPENDITURE ON GRANTS, SUBSIDES ETC. :		
a) Grants given to Institutions/Organisations	-	-
b) Subsidies given to Institutions/Organisations	-	-
TOTAL	**-**	**-**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
SCHEDULES FORMING PART OF INCOME & EXPENDITURE AS AT 31st MAR 2017

(Amount - Rs.)

Particulars	Current Year	Previous Year
SCHEDULE 23 - INTEREST :		
a) On Fixed Loans	-	-
b) On Other Loans (including Bank Charges)	-	-
c) Others	-	-
TOTAL	**-**	**-**

Schedule 24: Significant Accounting Policies &
Schedule 25: Contingent Liabilities & Notes on Account for the period ended 31/03/2017

1. Method of Accounting:

a.The accounting system adopted by the organization is on "Accrual basis".

b.The organization has been allocating plan grant-in-aid under the "Non-recurring" & "Recurring" heads.

2. Revenue recognition:

Income comprises of Grant-in-Aid, Internal Resources through services and interest from short term deposits.

Income accounted on the basis of the Cash/DD/Cheques/Cr notes received.

3. Fixed Assets:

a. Fixed assets are stated at cost. Cost includes freight, duties, and taxes etc.,

b. Depreciation: Based on the recommendation of the Finance Committee and approval of the Governing Body of the institute, Depreciation Account on Fixed Assets has been prepared at the rate prevailing to the concerned Fixed Assets as specified in the Income Tax Act, 1961 on Written Down Value Method of Depreciation. This has been set off against the Grant in Aid (Non Recurring) in the concerned account.

c. Capital work in progress has been entered to the extent of the last running account bills paid.

d. Realization on sale of obsolete/surplus fixed assets which is not required for the purpose of research activities are adjusted against capital cost.

4. Inventories:

All purchases of chemicals, glassware and other consumables have been charged to consumption at the time of purchase.

5. Foreign Currency transactions:

Foreign Currency transactions are recognized in the books at the exchange rates prevailing on the date of transaction.

6. Investments:

Investments in STDR's are stated at book values.

7. Interest earned on STDRs made out of own funds earlier has been shown against Schedule-15 Since the STDRs are not under the preview of Schedule-15 the same has been shown against Schedule-17 under Interest on Term Deposits. Further pervious year figures are regrouped/ rearranged accordingly.

8. The previous year balances have been regrouped/rearranged, wherever necessary.

for B Purushottam& Co
Chartered Accountants,
Reg.No. 002808S

Director	Finance Officer	Manager Office	[CH SATYANARAYANA]
NIAB	NIAB	(Accounts), NIAB	Partner M. No. 019092

Place: Hyderabad
Date: 11/05/2017

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
HYDERABAD

CLARIFICATION ON NOTES ON ACCOUNTS: 2016-17

- **Notes on Accounts 1 to 2 & 4 to 6 & 8:** Method of Accounting / Revenue recognition / Fixed Asset/ Inventories / Foreign Currency transactions / Investments:
  These are all only informatory items.

- **Notes on Accounts 3:** Fixed Assets:
  Depreciation has been calculated on Written Down Value method and at the rates prevailing to the concerned Fixed Asset as specified on the Income Tax Act, 1961 and set off against the Grant-in-aid (non-recurring). The details of the Depreciation on Fixed Assets are at Schedule – 8 is an integral part of the financial statements.

- **Notes on Accounts 7:** Interest earned on own funds has been reclassified from Schedule -15 to Schedule -17 to reflect the factual position.

Finance Officer,NIAB **Manager Office (Accounts)**

Place: Hyderabad
Date: 11/05/2017

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
Details of Closing balances of various Earmarked / Endowment Funds (Refer Sch-3)
For the Year Ended 31 MAR 2017

Annexure-I (Amount in Rs.)

Previous year	Proj No	Particulars	Current Year
243,043.00	FS002	DBT - Research Associate	-
206,613.00	FS003(PJ)	DST-INSPIRE Fellowship	169,120.00
32,554.00	FS004	DBT-JRF Programme	101,205.00
-	FS005(NAT)	DBT JRF	33,583.00
-	FS006(PN)	CSIR JRF	-240,080.00
-	FS-009(NN)	CSIR-UGC Fellowship	-242,177.00
-	FS-011(SR)	DBT-JRF Fellowship	32,500.00
-444,030.00	SP001	NMMP - Model Nursery - to meet the requirement of quality plating material for cultivation, and to maintain clonal / seed orchids	-444,030.00
1,193,107.00	SP002	Characterization of Cell Cycle regulators associated with DNA replication machinery in Toxoplasma Gondii - DST INSPIRE Faculty	1,373,983.00
66,258.00	SP003	Understanding the host response and molecular pathogenesis of Leptospira interrogans infection - Ramalingaswamy Fellowship	82,847.00
-468,409.00	SP004	Evaluation of Anti-inflammatory Natural Compounds for Therapeutic use in Mastitis of Dairy Animals - NMPB	-250,783.00
-485,532.00	SP005	Role of gamma delta T cells in inflammation - DST Women Scientist Scheme	413,448.00
100,566.00	SP006 (VB)	Characterization of vancomycin resistant Staphylococcus aureus strains - SERB Young Scientist Scheme	-
339,666.00	SP007(PS)	Identification of disease related markers for the diagnosis of Subclinical Mastitis	327,174.00
456,253.00	SP008(GKR)	Understanding the immune mechanism of host disease and development of marker vaccines and DIVA test for Peste des Petits ruminants	1,007,270.00
360,450.00	SP009(SV)	Effect of Kisspeptin on endocrine profile and follicular dynamics in buffaloes	-378,229.00
213,390.00	SP010(MS)	Collaborative work for genotyping of Newcastle Disease Virus Strains - Biological and Molecular Characterization	81,671.00
1,386,800.00	SP011(PS)	Genome-wide association study for identification of novel loci associated with resistance to Theileriosis in India	126,475.00

Previous year	Proj No	Particulars	Current Year
1,146,705.00	SP012(MS)	Elucidation of the role of nonstructural (W) protein of Avian Paramyxoviruses	138,756.00
1,586,800.00	SP013(GKR)	To develop novel therapeutics for brucellosis: Identification and characterization of host factors supporting Brucella replication	118,958.00
-	SP014(PS)	Identification of Virulence factors associated with Theileria annulata infection in Indian Cattle	388,107.00
-	SP015(MS)	A study to understand the genetic variations among the filed isolates of porcine circo viruses from piggery farms in Mizoram, with ultimate aim to engineer an effective recombinant chimeric DIVA Vaccine	1,208,148.00
-	SP016 (VB)	DST INSPIRE FACULTY-Charterization of transglycosylases associated with cell wall biogenesis in Vancomycin resistant Staphylococcus aureus	196,064.00
-	SP017 (AS)	Elucidation of mechanism(s) of transformation of host cells by Theileria annulata	697,000.00
-	SP018 (SM)	Towards establishing an efficient animal-based production of thrapeutic Protein in Milk of farmed animals using various modes of gene delivery	2,109,075.00
-	SP019	Development of peptide based anti-inflammatory drug for septicemia	3,178,000.00
5,934,234.00		**TOTAL**	**10,228,085.00**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
Details of Fixed Assets Fund (Capitalised Portion of Project Grants)
For the Year Ended 31 MAR 2017

Annexure-II

(Amount - Rs.)

Previous year	Proj No	Particulars	Current Year
270,063.00	SP002	Characterization of Cell Cycle regulators associated with DNA replication machinery in Toxoplasma Gondii - DST INSPIRE Faculty	219,815.00
71,883.00	SP003	Understanding the host response and molecular pathogenesis of Leptospira interrogans infection - Ramalingaswamy Fellowship	47,226.00
96,700.00	SP007(PS)	Identification of disease related markers for the diagnosis of Subclinical Mastitis	-
-	SP016 (VB)	DST INSPIRE FACULTY-Charterization of transglycosylases associated with cell wall biogenesis in Vancomycin resistant Staphylococcus aureus	43,000.00
438,646.00		**TOTAL**	**310,041.00**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
For the Year Ended 31st MAR 2017

Annexure: A Forming part of Receipts and Payments a/c

(Amount - Rs.)

Previous Year	Particulars	Current Year
	I-Remittances	
-	GSLI	2,800.00
755,135.00	Income Tax	1,492,747.00
-	Others (I-Remittances)	4,025.00
45,350.00	Professional Tax	57,000.00
585,035.00	Service Tax	745,100.00
2,026,132.00	TDS	2,355,522.00
3,411,652.00	**TOTAL**	**4,657,194.00**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
For the Year Ended 31st MAR 2017

Annexure: B Forming part of Receipts and Payments a/c

(Amount - Rs.)

Previous year	Particulars	Current Year
	Advance refunds/recovery/Adjustments.	
330,007.00	LTC [Advance]	210,959.00
2,000.00	Medical [Advance]	-
54,106.00	TA India & Abroad [Advance]	47,395.00
30,000.00	Transport maintenance [Advance]	98,000.00
17,625.00	Advertisement & Publications [Advance]	-
14,894.00	Printing & Stationery [Advance]	50,000.00
41,181.00	Insurance [Advance]	34,453.00
63,000.00	Others [Contingencies Advance]	27,000.00
51,600.00	Others [Maintenance Advance]	-
7,298,317.00	Chemicals [Advance]	2,783,975.00
4,875,549.00	Consumables, glassware and Spares [Advance]	2,678,524.00
15,000.00	Computer maintenance [Advance]	-
10,000.00	Others [Including Animal House Advance]	277,814.00
32,000.00	Scientific Workshops Symposiums Seminars [Advance]	-
12,500.00	Other Research Expenses [Advance]	-
6,296,379.00	Equipment [Advance]	794,653.00
762,958.00	Major Software [Advance]	-
10,147.00	Library Books [Advance]	-
1,657,624.00	General Deposits And Advances	9,405,679.00
10,000.00	EMD	-
9,000.00	Security Deposit	30,000.00
-	Revolving Advance	85,635.00
1,675,354.00	Prepaid Expenses	273,600.00
23,269,241.00	**TOTAL**	**16,797,687.00**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
For the Year Ended 31st MAR 2017

Annexure: C Forming part of Receipts and Payments a/c

(Amount - Rs.)

Previous year	Particulars	Current Year
	Projects-Receipts	
806,600.00	FS002	-
410,000.00	FS003(PJ)	385,887.00
280,000.00	FS004	420,000.00
-	FS005(NAT)	420,000.00
-	FS-011(SR)	285,645.00
-	FS-012(MPSM)	250,914.00
2,944,868.00	SP002	1,757,623.00
1,860,000.00	SP003	1,528,000.00
-	SP004	1,013,000.00
-	SP005	1,800,000.00
1,280,000.00	SP007(PS)	1,023,539.00
1,055,000.00	SP008(GKR)	1,410,505.00
1,461,800.00	SP009(SV)	-
300,000.00	SP010(MS)	900,000.00
1,386,800.00	SP011(PS)	-
1,470,000.00	SP012(MS)	-
1,586,800.00	SP013(GKR)	-
-	SP014(PS)	1,230,000.00
-	SP015(MS)	1,400,000.00
-	SP016 (VB)	1,107,320.00
-	SP017 (AS)	847,000.00
-	SP018 (SM)	2,109,075.00
-	SP019	3,281,000.00
14,841,868.00	**TOTAL**	**21,169,508.00**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
For the Year Ended 31st MAR 2017

Annexure: D Forming part of Receipts and Payments a/c

(Amount - Rs.)

Previous year	Particulars	Current Year
	Advances	
217,901.00	LTC [Advance]	279,494.00
2,000.00	Medical [Advance]	-
51,406.00	TA India & Abroad [Advance]	47,395.00
-	Rent [Advance]	36,000.00
75,000.00	Transport maintenance [Advance]	53,000.00
17,625.00	Advertisement & Publications [Advance]	-
-	Printing & Stationery [Advance]	318,037.00
41,181.00	Insurance [Advance]	34,453.00
63,000.00	Others [Contingencies Advance]	126,850.00
51,600.00	Others [Maintenance Advance]	-
3,199,461.00	Chemicals [Advance]	5,058,769.00
2,570,837.00	Consumables, glassware and Spares [Advance]	5,211,542.00
287,814.00	Others [Including Animal House Advance]	94,062.00
32,000.00	Scientific Workshops Symposiums Seminars [Advance]	-
7,500.00	Other Research Expenses [Advance]	-
1,060,534.00	Equipment [Advance]	12,600.00
10,147.00	Library Books [Advance]	-
-	Vehicles [Advance]	705,434.11
1,164,127.00	General Deposits And Advances	8,618,164.00
10,000.00	EMD	-
19,706.00	Security Deposit	77,102.00
-	Revolving Advance	85,635.00
-	GDA [Others]	4,927,191.00
11,400.00	Prepaid Expenses	786,600.00
8,893,239.00	**TOTAL**	**26,472,328.11**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
For the Year Ended 31st MAR 2017

Annexure: E Forming part of Receipts and Payments a/c

(Amount - Rs.)

Previous year	Particulars	Current Year
	I-Remittances	
-	GSLI	2,800.00
755,135.00	Income Tax	1,492,747.00
-	Others (I-Remittances)	4,025.00
45,350.00	Professional Tax	57,000.00
585,035.00	Service Tax	745,100.00
2,026,132.00	TDS	2,355,522.00
3,411,652.00	**TOTAL**	**4,657,194.00**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
For the Year Ended 31st MAR 2017

Annexure: F Forming part of Receipts and Payments a/c

(Amount - Rs.)

Previous year	Particulars	Current Year
	Projects - Expenditure	
155,390.00	FS001	-
720,276.00	FS002	243,043.00
203,387.00	FS003(PJ)	423,380.00
247,446.00	FS004	351,349.00
-	FS005(NAT)	386,417.00
-	FS006(PN)	240,080.00
-	FS-009(NN)	242,177.00
-	FS-011(SR)	253,145.00
-	FS-012(MPSM)	250,914.00
1,776,355.00	SP002	1,576,747.00
1,877,713.00	SP003	1,511,411.00
1,311,124.00	SP004	795,374.00
795,028.00	SP005	901,020.00
899,434.00	SP006 (VB)	100,566.00
940,334.00	SP007(PS)	1,036,031.00
598,747.00	SP008(GKR)	859,488.00
1,101,350.00	SP009(SV)	738,679.00
86,610.00	SP010(MS)	1,031,719.00
-	SP011(PS)	1,260,325.00
323,295.00	SP012(MS)	1,007,949.00
-	SP013(GKR)	1,467,842.00
-	SP014(PS)	841,893.00
-	SP015(MS)	191,852.00
-	SP016 (VB)	911,256.00
-	SP017 (AS)	150,000.00
-	SP019	103,000.00
11,036,489.00	**TOTAL**	**16,875,657.00**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
For the Year Ended 31st MAR 2017

Annexure: G Forming part of Balance sheet

(Amount - Rs.)

Previous year	Particulars	Current Year
1,331,525.00	March Salaries	1,899,964.00
34,350.00	Audit Fee	34,500.00
461,165.00	Electricity Charges	537,132.00
10,289.00	Water Charges	14,279.00
12,159.00	Telephone Charges	12,519.00
386,056.00	Security Contract Bill	-
9,503.00	Website maintenance Charges	9,545.00
5,000.00	Bio Waste maintenance Charges	-
1,032.00	Photo Copier maintenance Charges	1,236.00
74,110.00	NPS Employer Contribution	80,812.00
2,325,189.00	**TOTAL**	**2,589,987.00**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
For the Year Ended 31st MAR 2017

Annexure: H Forming part of Balance sheet

(Amount - Rs.)

Previous year	Particulars	Current Year
	LOANS AND ADVANCES	
794,653.00	Equipment [Advance]	12,600.00
-	Vehicles [Advance]	705,434.11
794,653.00	**TOTAL**	**718,034.11**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
For the Year Ended 31st MAR 2017

Annexure: I Forming part of Balance sheet

(Amount - Rs.)

Previous year	Particulars	Current Year
	PREPAYMENTS / DEPOSITS	
2,783,975.00	Chemicals [Advance]	5,058,769.00
2,502,559.00	Consumables, glassware and Spares [Advance]	5,035,577.00
5,957,169.00	GDA [Others]	10,884,360.00
765,429.00	General Deposits And Advances	-
9,253.00	LTC [Advance]	77,788.00
-	Others [Contingencies Advance]	99,850.00
277,814.00	Others [Including Animal House Advance]	94,062.00
11,400.00	Prepaid Expenses	524,400.00
-	Printing & Stationery [Advance]	268,037.00
-	Rent [Advance]	36,000.00
45,000.00	Transport maintenance [Advance]	-
12,352,599.00	**TOTAL**	**22,078,843.00**

NATIONAL INSTITUTE OF ANIMAL BIOTECHNOLOGY
For the Year Ended 31st MAR 2017

Annexure: J Forming part of Income and Expenditure statement

(Amount - Rs.)

Previous year	Particulars	Current Year
	Provision For Salaries and other Expenses	
	Addition during the year :	
1,331,525.00	Salaries for March	1,899,964.00
74,110.00	NPS (Employer contribution)	80,812.00
34,350.00	Audit Fee	34,500.00
461,165.00	Electricity	537,132.00
10,289.00	Water charges	14,279.00
12,159.00	Telephone Charges	12,519.00
386,056.00	Security contract Bill	-
9,503.00	Website maintenance charges	9,545.00
5,000.00	Bio Waste management contract bill	-
1,032.00	Photo copier maintenance charges	1,236.00
2,325,189.00	**Sub total**	**2,589,987.00**
1,577,548.00	Less : Adjustments during the year (Refer Annexure-G)	2,325,189.00
747,641.00	**TOTAL**	**264,798.00**

NIAB
Hyderabad
FS002: DBT - Research Associate
P.I: Dr. Dileep Kumar
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
156719.00	Opening Balance	243043.00			
806600.00	Grant In Aid	0.00	673400.00	Salaries - Manpower	197600.00
0.00		0.00	42281.00	Consumables	39255.00
0.00		0.00	0.00	Contingencies	6188.00
0.00		0.00	4595.00	Travel	0.00
0.00		0.00	0.00	Overheads	0.00
0.00		0.00	0.00	Equipment	0.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
963319.00		**243043.00**	**720276.00**		**243043.00**
0.00	Excess of Expenditure over Income	0.00	243043.00	Closing Balance	0.00
963319.00		**243043.00**	**963319.00**		**243043.00**

NIAB
Hyderabad
FS003(PJ): DST - INSPIRE Fellowship
P.I: Dr. Padmaja Jakka, DST JRF
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
0.00	Opening Balance	206613.00			
410000.00	Grant In Aid	385887.00	203387.00	Salaries - Manpower	390000.00
0.00		0.00	0.00	Consumables	21800.00
0.00		0.00	0.00	Contingencies	7981.00
0.00		0.00	0.00	Travel	3599.00
0.00		0.00	0.00	Overheads	0.00
0.00		0.00	0.00	Equipment	0.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
410000.00		**592500.00**	**203387.00**		**423380.00**
0.00	Excess of Expenditure over Income	0.00	206613.00	Closing Balance	169120.00
410000.00		**592500.00**	**410000.00**		**592500.00**

NIAB
Hyderabad
FS004: DBT-JRF Programme
P.I: Dr. Hiral Mistry, DBT JRF
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
0.00	Opening Balance	32554.00			
280000.00	Grant In Aid	420000.00	227500.00	Salaries - Manpower	347750.00
0.00		0.00	19946.00	Consumables	0.00
0.00		0.00	0.00	Contingencies	0.00
0.00		0.00	0.00	Travel	3599.00
0.00		0.00	0.00	Overheads	0.00
0.00		0.00	0.00	Equipment	0.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
280000.00		**452554.00**	**247446.00**		**351349.00**
0.00	Excess of Expenditure over Income	0.00	32554.00	Closing Balance	101205.00
280000.00		**452554.00**	**280000.00**		**452554.00**

NIAB
Hyderabad
FS005(NAT): DBT JRF
P.I: Neelam A Topno
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
0.00	Opening Balance	0.00			
0.00	Grant In Aid	420000.00	0.00	Salaries - Manpower	356417.00
0.00		0.00	0.00	Consumables	0.00
0.00		0.00	0.00	Contingencies	30000.00
0.00		0.00	0.00	Travel	0.00
0.00		0.00	0.00	Overheads	0.00
0.00		0.00	0.00	Equipment	0.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
0.00		**420000.00**	**0.00**		**386417.00**
0.00	Excess of Expenditure over Income	0.00	0.00	Closing Balance	33583.00
0.00		**420000.00**	**0.00**		**420000.00**

NIAB
Hyderabad
FS006(PN): CSIR JRF
P.I: PRACHITA NANDINI
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
0.00	Opening Balance	0.00			
0.00	Grant In Aid	0.00	0.00	Salaries - Manpower	240080.00
0.00		0.00	0.00	Consumables	0.00
0.00		0.00	0.00	Contingencies	0.00
0.00		0.00	0.00	Travel	0.00
0.00		0.00	0.00	Overheads	0.00
0.00		0.00	0.00	Equipment	0.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
0.00		**0.00**	**0.00**		**240080.00**
0.00	Excess of Expenditure over Income	240080.00	0.00	Closing Balance	0.00
0.00		**240080.00**	**0.00**		**240080.00**

NIAB
Hyderabad
FS-009(NN): CSIR-UGC Fellowship
P.I: Mr. B. Nagaraj Nayak
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
0.00	Opening Balance	0.00			
0.00	Grant In Aid	0.00	0.00	Salaries - Manpower	242177.00
0.00		0.00	0.00	Consumables	0.00
0.00		0.00	0.00	Contingencies	0.00
0.00		0.00	0.00	Travel	0.00
0.00		0.00	0.00	Overheads	0.00
0.00		0.00	0.00	Equipment	0.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
0.00		**0.00**	**0.00**		**242177.00**
0.00	Excess of Expenditure over Income	242177.00	0.00	Closing Balance	0.00
0.00		**242177.00**	**0.00**		**242177.00**

NIAB
Hyderabad
FS-011(SR): DBT-JRF Fellowship
P.I: Mr. Sonti Roy
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
0.00	Opening Balance	0.00			
0.00	Grant In Aid	285645.00	0.00	Salaries - Manpower	232742.00
0.00		0.00	0.00	Consumables	0.00
0.00		0.00	0.00	Contingencies	20403.00
0.00		0.00	0.00	Travel	0.00
0.00		0.00	0.00	Overheads	0.00
0.00		0.00	0.00	Equipment	0.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
0.00		**285645.00**	**0.00**		**253145.00**
0.00	Excess of Expenditure over Income	0.00	0.00	Closing Balance	32500.00
0.00		**285645.00**	**0.00**		**285645.00**

NIAB
Hyderabad
FS-012(MPSM): DST-ISRF Research Trainee
P.I: Dr. Manjula P.S. Magamage
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
0.00	Opening Balance	0.00			
0.00	Grant In Aid	250914.00	0.00	Salaries - Manpower	220914.00
0.00		0.00	0.00	Consumables	22201.00
0.00		0.00	0.00	Contingencies	7799.00
0.00		0.00	0.00	Travel	0.00
0.00		0.00	0.00	Overheads	0.00
0.00		0.00	0.00	Equipment	0.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
0.00		**250914.00**	**0.00**		**250914.00**
0.00	Excess of Expenditure over Income	0.00	0.00	Closing Balance	0.00
0.00		**250914.00**	**0.00**		**250914.00**

NIAB
Hyderabad
SP001: NMMP - Model Nursery - to meet the requirement of quality plating material for cultivation, and to maintain clonal / seed orchids
P.I: Prof. P Reddanna
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
0.00	Opening Balance	0.00	444030.00	Opening Balance	444030.00
0.00	Grant In Aid	0.00	0.00	Salaries - Manpower	0.00
0.00		0.00	0.00	Consumables	0.00
0.00		0.00	0.00	Contingencies	0.00
0.00		0.00	0.00	Travel	0.00
0.00		0.00	0.00	Overheads	0.00
0.00		0.00	0.00	Equipment	0.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
0.00		**0.00**	**444030.00**		**444030.00**
444030.00	Excess of Expenditure over Income	444030.00	0.00	Closing Balance	0.00
444030.00		**444030.00**	**444030.00**		**444030.00**

NIAB
Hyderabad
SP002: Characterization of Cell Cycle regulators associated with DNA replication machinery in Toxoplasma Gondii - DST INSPIRE Faculty
P.I: Dr. Abhijit S Deshmukh
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
24594.00	Opening Balance	1193107.00			
2944868.00	Grant In Aid	1757623.00	1004802.00	Salaries - Manpower	943925.00
0.00		0.00	414371.00	Consumables	337980.00
0.00		0.00	52119.00	Contingencies	376.00
0.00		0.00	0.00	Travel	4651.00
0.00		0.00	35000.00	Overheads	70000.00
0.00		0.00	270063.00	Equipment	219815.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
2969462.00		**2950730.00**	**1776355.00**		**1576747.00**
0.00	Excess of Expenditure over Income	0.00	1193107.00	Closing Balance	1373983.00
2969462.00		**2950730.00**	**2969462.00**		**2950730.00**

NIAB
Hyderabad
SP003: Understanding the host response and molecular pathogenesis of Leptospira interrogans infection - Ramalingaswamy Fellowship
P.I: Dr. Syed Faisal
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
83971.00	Opening Balance	66258.00			
1860000.00	Grant In Aid	1528000.00	1386807.00	Salaries - Manpower	1196112.00
0.00		0.00	349456.00	Consumables	242051.00
0.00		0.00	14559.00	Contingencies	13516.00
0.00		0.00	55008.00	Travel	12506.00
0.00		0.00	0.00	Overheads	0.00
0.00		0.00	71883.00	Equipment	47226.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
1943971.00		**1594258.00**	**1877713.00**		**1511411.00**
0.00	Excess of Expenditure over Income	0.00	66258.00	Closing Balance	82847.00
1943971.00		**1594258.00**	**1943971.00**		**1594258.00**

NIAB
Hyderabad
SP004: Evaluation of Anti-inflammatory Natural Compounds for Therapeutic use in Mastitis of Dairy Animals - NMPB
P.I: Prof P Reddanna & Dr. Paresh Sharma
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
842715.00	Opening Balance	0.00		Opening Balance	468409.00
0.00	Grant In Aid	1013000.00	467800.00	Salaries - Manpower	438830.00
0.00		0.00	694279.00	Consumables	283044.00
0.00		0.00	69600.00	Contingencies	5000.00
0.00		0.00	19445.00	Travel	0.00
0.00		0.00	60000.00	Overheads	68500.00
0.00		0.00	0.00	Equipment	0.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
842715.00		**1013000.00**	**1311124.00**		**1263783.00**
468409.00	Excess of Expenditure over Income	250783.00	0.00	Closing Balance	0.00
1311124.00		**1263783.00**	**1311124.00**		**1263783.00**

NIAB
Hyderabad
SP005: Role of gamma delta T cells in inflammation - DST Women Scientist Scheme
P.I: Dr. Aparna Rachamallu
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
309496.00	Opening Balance	0.00		Opening Balance	485532.00
0.00	Grant In Aid	1800000.00	700000.00	Salaries - Manpower	660000.00
0.00		0.00	70028.00	Consumables	136020.00
0.00		0.00	0.00	Contingencies	5000.00
0.00		0.00	0.00	Travel	0.00
0.00		0.00	25000.00	Overheads	100000.00
0.00		0.00	0.00	Equipment	0.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
309496.00		**1800000.00**	**795028.00**		**1386552.00**
485532.00	Excess of Expenditure over Income	0.00	0.00	Closing Balance	413448.00
795028.00		**1800000.00**	**795028.00**		**1800000.00**

NIAB
Hyderabad
SP006 (VB): Characterization of vancomycin resistant Staphylococcus aureus strains - SERB Young Scientist Scheme
P.I: Dr. Vasundhra Bhandari
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
1000000.00	Opening Balance	100566.00			
0.00	Grant In Aid	0.00	565172.00	Salaries - Manpower	0.00
0.00		0.00	171000.00	Consumables	0.00
0.00		0.00	52655.00	Contingencies	0.00
0.00		0.00	10607.00	Travel	0.00
0.00		0.00	100000.00	Overheads	0.00
0.00		0.00	0.00	Equipment	0.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	100566.00
1000000.00		**100566.00**	**899434.00**		**100566.00**
0.00	Excess of Expenditure over Income	0.00	100566.00	Closing Balance	0.00
1000000.00		**100566.00**	**1000000.00**		**100566.00**

NIAB
Hyderabad
SP007(PS): Identification of disease related markers for the diagnosis of Subclinical Mastitis
P.I: Dr. Paresh Sharma
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
0.00	Opening Balance	339666.00			
1280000.00	Grant In Aid	1023539.00	100296.00	Salaries - Manpower	187893.00
0.00		0.00	727024.00	Consumables	804696.00
0.00		0.00	2191.00	Contingencies	34642.00
0.00		0.00	14123.00	Travel	8800.00
0.00		0.00	0.00	Overheads	0.00
0.00		0.00	96700.00	Equipment	0.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
1280000.00		**1363205.00**	**940334.00**		**1036031.00**
0.00	Excess of Expenditure over Income	0.00	339666.00	Closing Balance	327174.00
1280000.00		**1363205.00**	**1280000.00**		**1363205.00**

NIAB
Hyderabad
SP008(GKR): Understanding the immune mechanism of host disease and development of marker vaccines and DIVA test for Peste des Petits ruminants
P.I: Dr.Girish K Radhakrishnan
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
0.00	Opening Balance	456253.00			
1055000.00	Grant In Aid	1410505.00	106080.00	Salaries - Manpower	353717.00
0.00		0.00	479829.00	Consumables	377675.00
0.00		0.00	1764.00	Contingencies	8341.00
0.00		0.00	11074.00	Travel	119755.00
0.00		0.00	0.00	Overheads	0.00
0.00		0.00	0.00	Equipment	0.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
1055000.00		**1866758.00**	**598747.00**		**859488.00**
0.00	Excess of Expenditure over Income	0.00	456253.00	Closing Balance	1007270.00
1055000.00		**1866758.00**	**1055000.00**		**1866758.00**

NIAB
Hyderabad
SP009(SV): Effect of Kisspeptin on endocrine profile and follicular dynamics in buffaloes
P.I: Dr. Satya Velmurugan
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
0.00	Opening Balance	360450.00			
1461800.00	Grant In Aid	0.00	67947.00	Salaries - Manpower	396500.00
0.00		0.00	1023327.00	Consumables	283854.00
0.00		0.00	10076.00	Contingencies	34048.00
0.00		0.00	0.00	Travel	24277.00
0.00		0.00	0.00	Overheads	0.00
0.00		0.00	0.00	Equipment	0.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
1461800.00		**360450.00**	**1101350.00**		**738679.00**
0.00	Excess of Expenditure over Income	378229.00	360450.00	Closing Balance	0.00
1461800.00		**738679.00**	**1461800.00**		**738679.00**

NIAB
Hyderabad
SP010(MS): Collaborative work for genotyping of Newcastle Disease Virus Strains - Biological and Molecular Characterization
P.I: Dr. Madhuri Subbiah
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
0.00	Opening Balance	213390.00			
300000.00	Grant In Aid	900000.00	53040.00	Salaries - Manpower	145718.00
0.00		0.00	33570.00	Consumables	836962.00
0.00		0.00	0.00	Contingencies	36690.00
0.00		0.00	0.00	Travel	12349.00
0.00		0.00	0.00	Overheads	0.00
0.00		0.00	0.00	Equipment	0.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
300000.00		**1113390.00**	**86610.00**		**1031719.00**
0.00	Excess of Expenditure over Income	0.00	213390.00	Closing Balance	81671.00
300000.00		**1113390.00**	**300000.00**		**1113390.00**

NIAB
Hyderabad
SP011(PS): Genome-wide association study for identification of novel loci associated with resistance to Theileriosis in India
P.I: Dr. Paresh Sharma
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
0.00	Opening Balance	1386800.00			
1386800.00	Grant In Aid	0.00	0.00	Salaries - Manpower	327683.00
0.00		0.00	0.00	Consumables	898616.00
0.00		0.00	0.00	Contingencies	0.00
0.00		0.00	0.00	Travel	34026.00
0.00		0.00	0.00	Overheads	0.00
0.00		0.00	0.00	Equipment	0.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
1386800.00		**1386800.00**	**0.00**		**1260325.00**
0.00	Excess of Expenditure over Income	0.00	1386800.00	Closing Balance	126475.00
1386800.00		**1386800.00**	**1386800.00**		**1386800.00**

NIAB
Hyderabad
SP012(MS): Elucidation of the role of nonstructural (W) protein of Avian Paramyxoviruses
P.I: Dr.Madhuri Subbiah
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
0.00	Opening Balance	1146705.00			
1470000.00	Grant In Aid	0.00	0.00	Salaries - Manpower	192920.00
0.00		0.00	320987.00	Consumables	778491.00
0.00		0.00	2308.00	Contingencies	21152.00
0.00		0.00	0.00	Travel	15386.00
0.00		0.00	0.00	Overheads	0.00
0.00		0.00	0.00	Equipment	0.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
1470000.00		**1146705.00**	**323295.00**		**1007949.00**
0.00	Excess of Expenditure over Income	0.00	1146705.00	Closing Balance	138756.00
1470000.00		**1146705.00**	**1470000.00**		**1146705.00**

NIAB
Hyderabad
SP013(GKR): To develop novel therapeutics for brucellosis: Identification and characterization of host factors supporting Brucella replication
P.I: Dr. Girish K Radhakrishnan
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
0.00	Opening Balance	1586800.00			
1586800.00	Grant In Aid	0.00	0.00	Salaries - Manpower	299419.00
0.00		0.00	0.00	Consumables	1124267.00
0.00		0.00	0.00	Contingencies	0.00
0.00		0.00	0.00	Travel	44156.00
0.00		0.00	0.00	Overheads	0.00
0.00		0.00	0.00	Equipment	0.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
1586800.00		**1586800.00**	**0.00**		**1467842.00**
0.00	Excess of Expenditure over Income	0.00	1586800.00	Closing Balance	118958.00
1586800.00		**1586800.00**	**1586800.00**		**1586800.00**

NIAB
Hyderabad
SP014(PS): Identification of Virulence factors associated with Theileria annulata infection in Indian Cattle
P.I: Dr. Paresh Sharma
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
0.00	Opening Balance	0.00			
0.00	Grant In Aid	1230000.00	0.00	Salaries - Manpower	183083.00
0.00		0.00	0.00	Consumables	648710.00
0.00		0.00	0.00	Contingencies	10100.00
0.00		0.00	0.00	Travel	0.00
0.00		0.00	0.00	Overheads	0.00
0.00		0.00	0.00	Equipment	0.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
0.00		**1230000.00**	**0.00**		**841893.00**
0.00	Excess of Expenditure over Income	0.00	0.00	Closing Balance	388107.00
0.00		**1230000.00**	**0.00**		**1230000.00**

NIAB

Hyderabad

SP015(MS): A study to understand the genetic variations among the filed isolates of porcine circo viruses from piggery farms in Mizoram, with ultimate aim to engineer an effective recombinant chimeric DIVA Vaccine

P.I: Dr. Madhuri Subbiah

Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
0.00	Opening Balance	0.00			
0.00	Grant In Aid	1400000.00	0.00	Salaries - Manpower	31619.00
0.00		0.00	0.00	Consumables	77438.00
0.00		0.00	0.00	Contingencies	12795.00
0.00		0.00	0.00	Travel	0.00
0.00		0.00	0.00	Overheads	0.00
0.00		0.00	0.00	Equipment	70000.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
0.00		**1400000.00**	**0.00**		**191852.00**
0.00	Excess of Expenditure over Income	0.00	0.00	Closing Balance	1208148.00
0.00		**1400000.00**	**0.00**		**1400000.00**

NIAB
Hyderabad
SP016 (VB): DST INSPIRE FACULTY-Charterization of transglycosylases associated with cell wall biogenesis in Vancomycin resistant Staphylococcus aureus
P.I: DR VASUNDHRA BHANDARI
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
0.00	Opening Balance	0.00			
0.00	Grant In Aid	1107320.00	0.00	Salaries - Manpower	240000.00
0.00		0.00	0.00	Consumables	488666.00
0.00		0.00	0.00	Contingencies	0.00
0.00		0.00	0.00	Travel	0.00
0.00		0.00	0.00	Overheads	35000.00
0.00		0.00	0.00	Equipment	147590.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
0.00		**1107320.00**	**0.00**		**911256.00**
0.00	Excess of Expenditure over Income	0.00	0.00	Closing Balance	196064.00
0.00		**1107320.00**	**0.00**		**1107320.00**

NIAB
Hyderabad
SP017 (AS): Elucidation of mechanism(s) of transformation of host cells by Theileria annulata
P.I: Dr. Anand Srivastava
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
0.00	Opening Balance	0.00			
0.00	Grant In Aid	847000.00	0.00	Salaries - Manpower	0.00
0.00		0.00	0.00	Consumables	0.00
0.00		0.00	0.00	Contingencies	0.00
0.00		0.00	0.00	Travel	0.00
0.00		0.00	0.00	Overheads	150000.00
0.00		0.00	0.00	Equipment	0.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
0.00		**847000.00**	**0.00**		**150000.00**
0.00	Excess of Expenditure over Income	0.00	0.00	Closing Balance	697000.00
0.00		**847000.00**	**0.00**		**847000.00**

NIAB
Hyderabad
SP018 (SM): Towards establishing an efficient animal-based production of thrapeutic Protein in Milk of farmed animals using various modes of gene delivery
P.I: Dr. Subeer S Majumdar
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
0.00	Opening Balance	0.00			
0.00	Grant In Aid	2109075.00	0.00	Salaries - Manpower	0.00
0.00		0.00	0.00	Consumables	0.00
0.00		0.00	0.00	Contingencies	0.00
0.00		0.00	0.00	Travel	0.00
0.00		0.00	0.00	Overheads	0.00
0.00		0.00	0.00	Equipment	0.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
0.00		**2109075.00**	**0.00**		**0.00**
0.00	Excess of Expenditure over Income	0.00	0.00	Closing Balance	**2109075.00**
0.00		**2109075.00**	**0.00**		**2109075.00**

NIAB
Hyderabad
SP019: Development of peptide based anti-inflammatory drug for septicemia
P.I: Dr. Girish K Radhakrishnan
Receipts and Payments Account from 01/04/2016 to 31/03/2017

Previous Year Amount Rs.	Receipts	Current Year Amount Rs.	Previous Year Amount Rs.	Payments	Current Year Amount Rs.
0.00	Opening Balance	0.00			
0.00	Grant In Aid	3281000.00	0.00	Salaries - Manpower	0.00
0.00		0.00	0.00	Consumables	0.00
0.00		0.00	0.00	Contingencies	0.00
0.00		0.00	0.00	Travel	0.00
0.00		0.00	0.00	Overheads	103000.00
0.00		0.00	0.00	Equipment	0.00
0.00		0.00	0.00	Books	0.00
0.00		0.00	0.00	AMC	0.00
0.00		0.00	0.00	Others	0.00
0.00		0.00	0.00	Transfer of Funds	0.00
0.00		**3281000.00**	**0.00**		**103000.00**
0.00	Excess of Expenditure over Income	0.00	0.00	Closing Balance	3178000.00
0.00		**3281000.00**	**0.00**		**3281000.00**