Abstract Book with Souvenir

International Colloquium
On
Regulatory Mechanisms underlying Behavior, Physiology and Development

Department of Zoology University of Delhi

24th-26th March, 2021

About the Colloquium

Development and differentiation, the hallmarks of living systems, lead organisms to adapt their behavior and physiology such that there is no mismatch between their internal environment and the external environment they inhabit.

This is, for example, seen in clear differences in the behavior and physiology between day and night. Diurnal species sleep at night and are active during the day; nocturnal are the reverse – they sleep during the day and are active at night. Various processes related to growth and repair are also linked to the day-night cycle. Hence, the regulation is important at two levels; one is the time-keeping of process, and the other is process itself. While biological clocks orchestrate the former, the latter involves an elaborate network of complex interacting neuroendocrine processes.

It is increasingly realized that all the regulatory processes are mutually inclusive, and involve close interaction within, and with the environment to maintain the homeostasis. In recent times, there has been an upsurge in scientific investigations in these areas. The Department of Zoology at University of Delhi has been engaged in research focusing on such regulatory mechanisms using diverse group of organisms from microbes to mammals including human.

The present International colloquium on **"Regulatory Mechanisms underlying Behaviour, Physiology and Development"** will enable us to discuss and exchange ideas to further the understanding of complex regulatory process, and to develop interdisciplinary research collaborations. The colloquium is being organized under the joint umbrella of Indian Society of Chronobiology and Indian Society of Comparative Endocrinology, and under the aegis of Centre of Advance Study in Zoology, University of Delhi. In this 3-day scientific meet, about 20 plenary speakers and hundreds of poster presenters will cover various aspects of the regulatory biology in different species, from insects to mammals including humans.

Web Link: www.rmbpd.zoology.du.ac.in

About the Department

The **Department of Zoology** is a constituent entity of the Faculty of Science, University of Delhi. Since its inception in 1947, it has been the foremost centre for learning in all aspects of Animal Sciences in India. Initial teaching efforts in the department was tailored to train students leading them to Bachelors degree and subsequently Masters and Ph.D. programme were rolled out in 1951. The present premise of the department was built in 1959 resulting in an expansion of research (representing a wide spectrum of disciplines in Animal Sciences) activities, coinciding with the attraction of eminent faculties to work in the Department.

Though being one of the youngest departments, it was selected as the maiden **Centre for Advanced Study in Zoology** by the UGC in recognition to its outstanding research profile in 1963 and it continues to hold this honour till date. Many extra mural funding grants was awarded to its faculties from different agencies like WHO, Ford Foundation, USDA, USAID, IAEC, DST-FIST, DST-PURSE, CSIR, ICAR, DBT, ICMR, AYUSH, etc, thus, enhancing the research infrastructure and help maintain its eminent position in the area of Animal Sciences. Being a part of this illustrious department, we are privileged to invite you to explore the website, wherein we have showcased the different facets of activities undertaken by our department. A glimpse of that journey in past decade in the form of souvenir is added at the end of this Abstract-cum-Souvenir book.

Website: www.zoology.du.ac.in

Memorial lectures

Professor M. L. Bhatia

(1896-1990)

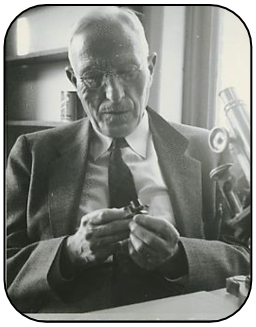
Professor M.L. Bhatia was born on December 30, 1896 in Sialkot. He studied in Punjab University and obtained his Ph.D. in 1937, and was awarded a D.Sc. degree in 1943. Dr. Bhatia was appointed a lecturer at Govt. College, Lahore in 1923. He shifted to Lucknow University in 1928, and in 1945 was appointed Reader in the Zoology Department of the same University. He joined the University of Delhi in 1948 and became the first Head of the newly established Department of Zoology. He served as Professor and Dean of Faculty of Science until 1960. During this period, he guided 32 students in their doctoral programme. He was Secretary of Garden Committee of Delhi University and started the University Flower Show. The present New Block of the Department was designed by him. He had conducted research on the morphology and physiology of Indian and foreign leeches and published many papers in reputed international journals. He worked with scientists in U.K., Switzerland, France and Italy in this branch of Zoology. Dr. Bhatia was President of the Zoology and Entomology Section of the Indian Science Congress in 1956. He was the Fellow of the 'Zoological Society of London' and 'Zoological Society of India'. The memorial lectures have been instituted by his illustrious son, Professor Balraj Bhatia in the memory of his eminent father.

Earlier Professor M.L. Bhatia Memorial Lectures

2015	Prof. Rajiv Raman	Sex determination in vertebrates: Diversity in the midst of unity
2013	Dr. Pradip Sinha	What is so exciting about biology in 21st Century
2011	Dr. Vidyanand Nanjundiah	Phenotypic Heterogeneity and Social Behaviour in the Cellular Slime Moulds
2009	Dr. Deepak Pental	Education - Research and Development Can they and should they be orchestrated?
2007	Dr. Girish Sahni	Tweaking Basic Research for 'Applied' Outputs: Old Challenges and Emerged Opportunities
2005	Dr. S. E. Hasnain	Mycobacterium tuberculosis: Geographic, Genomics, Functional, Promiscuity and Search for Novel Drug Targets.
2003	Dr. T. J. Pandian	Cloning for Conservation of Fishes.
2002	Dr. P. N. Tandon	Information Processing in the Human Brain
2000	Dr. S. M. Mohnot	Sociobiology & the Hanuman Langur.
1999	Dr. Ramesh Gulati	Eutrophication and Restoration of Temperate Lakes: Lake Biomanipulation and the Role of Zooplankton.
1998	Dr. Ishwar Prakash	Biodiversity-rich Spots in Rajasthan- Ecological Changes.
1997	Dr. P. V. Dehadrai	Status of Fisheries and Aquaculture in India.

Dr. Charles Paul Alexander

(1889-1981)



Entomology will never forget Charles Paul Alexander, "Doc Alex". The sheer numbers of his taxonomic accomplishments will not allow it: the description of some 11,000 species of flies in more than 1,000 publications. He dedicated his life to making better known a family of Diptera he found fascinating, the crane flies or Tipulidae. His prolific output of species descriptions, particularly the naming of more than 10,000 species in a single family (including more than 2000 species in India), most likely will never be surpassed. Professor Alexander was more than an outstanding taxonomist. He was a well-rounded student of natural history; an enthusiastic teacher who introduced the basics of entomology to an estimated 4,000 students at the University of Massachusetts, Amherst; an administrator, who at Amherst served as Chairman of the Department of Entomology and Zoology (1930-'59) and as Dean of the School of Science (1945-'52); and an active member of several scientific societies and as president of the Entomological Society of America, Royal Entomological Society (UK). He was decorated with the Commander Order All Merito Bernardo O'Higgins, Chile. To honor this illustrious scientist, the Department of Zoology, University of Delhi, organizes annually 'Dr. C. P. Alexander Memorial Lecture' through an endowment fund bequeathed by late Dr. Alexander to the University of Delhi.

Previous Dr. C.P. Alexander Memorial Lectures

2013	Dr. V.V. Ramamurthy	Reinventing Taxonomy-Traditional and Modern Methods
2011	Dr. T.M. Manjunath	Bt & Bt crops: Their Safety and Relevance in Insect Pest Management.
2009	Dr. M.B. Malipatil	The Critical Role of Taxonomy and Reference Collections in Bioprotection and Biodiversity
2007	Dr. Anantanarayanan Raman	The Gall problems and the Insect Factor
2005	Prof. A.P. Das	Malaria: Are we losing the battle?
2004	Prof. C.A. Viraktamath	Systematic and Biology of Leaf hoppers on the Indian Subcontinent
2003	Prof. A.F.G. Dixon	Ladybirds and the Biological control of Aphid population
2002	Prof. C.P.S. Yadav	Phytophagous Scarabs and their Management in India
2001	Dr. S.P. Singh	Progress and Potential of Biological Control in India
2000	Dr. J.R.B. Alfred	Getting the Measure of India's Insect Diversity
1999	Prof. R. Gadagkar	The Evolution of Sociality in Insects
1998	Prof. V.K. Sehgal	Insect Biosystematics and Sustainability in Agriculture
1997	Dr. A. K. Gosh	Biodiversity and Entomology
1996	Prof. K.S. Khushwaha	Diverse Behaviour of Insect-Pest Complex in Agro-ecosystem
1995	Prof. S. Jayaraj	Biological Control and Integrated Pest Management: Progress and Perspectives
1994	Prof. K.N. Mehrotra	Insecticide-resistant Pest Management
1993	Prof. Santokh Singh	Man-Machine Interference in Mountain Ecosystem and its Impact on Insect Life
1992	Prof. K.N. Saxena	Developing Biointensive Pest Management Strategies: An African Experience
1991	Prof. M. S. Mani	Insect Life in Himalaya: Ecology Origin and Evolution
1990	Prof. M.L. Roonwal	Biological and Ecological Importance of Wing Micro-sculpturing in Termites
1989	Prof. T.N. Ananthakrishnan	Perspectives in Insect Mycophagy

INDIAN SOCIETY FOR COMPARATIVE ENDOCRINOLOGY

Reg. No. S/47554

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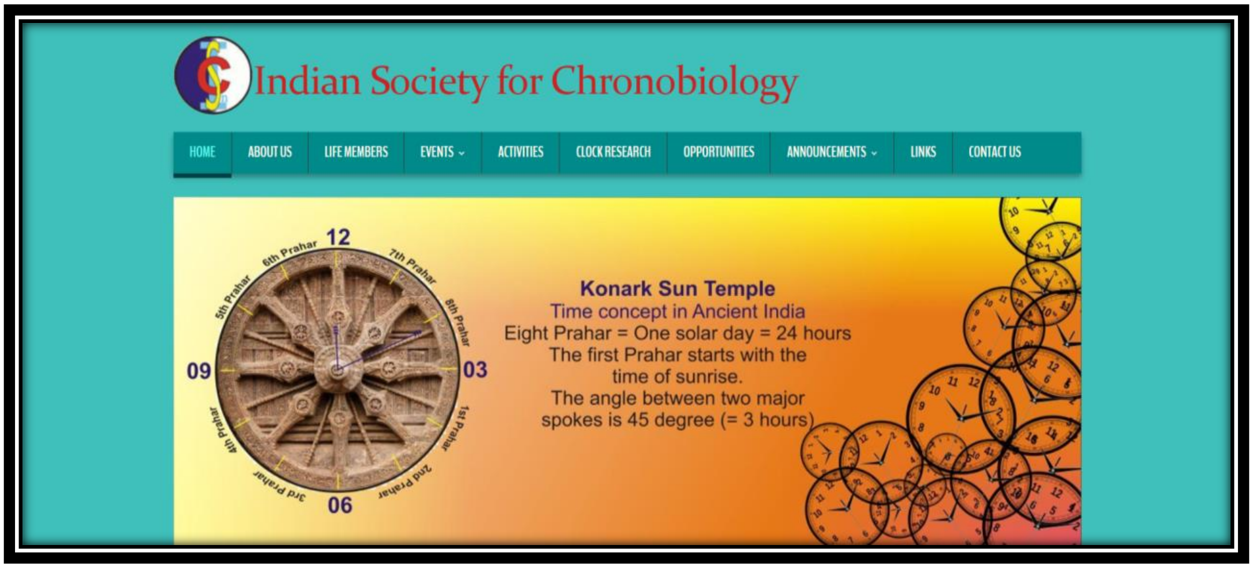
About Indian Society for Chronobiology (InSC)

The **Indian Society for Chronobiology (InSC)** was founded on the 12th of December 1977 in Mumbai (then Bombay). Today it has members ranging from active researchers to students from all over the country, and also a few members from abroad. The members share a common interest in understanding the biological rhythms ranging from ultradian, circadian (daily) to circannual (seasonal, annual) phenomena, and its application to human health.

The main aims of the society are: 1) To study the organisms in relation to the temporal order of the nature. 2) To study structure and mechanisms of temporal adaptation, both by empirical and theoretical approaches. 3) To promote the subject of Chronobiology both at the school and college level of education. 4) To promote the excellence in research in Chronobiology by organizing the workshops and schools. 5) To disseminate the importance and benefits of knowledge of Chronobiology to common man by carrying out frequent outreach activities. 6) To provide regular forum for discussion and exchange of ideas among the chronobiologists. 7) To interact with the other societies having similar areas of interest.

It has a dedicated website: https://chronobiologyindia.org

Currently, the XXVIII Biennial meeting of the Indian Society for Chronobiology is organized during March 24-26, 2021 together with Indian Society for Comparative Endocrinology in conjuction with International colloquim on "Regulatory Mechanisms underlying Behavior, Physiology and Development" under the joint umbrella of Indian Society of Chronobiology and Indian Society of Comparative Endocrinology.



Konark Sun Temple
Time concept in Ancient India
Eight Prahar = One solar day = 24 hours
The first Prahar starts with the time of sunrise.
The angle between two major spokes is 45 degree (= 3 hours)

Scientific Programme

International colloquium on "Regulatory Mechanisms underlying Behaviour, Physiology and Development"

March 24th - 26th, 2021

Day 1: Wednesday; March 24, 2021 (Session 1 to Session 4)

Session 1	**Chairpersons: Neeta Sehgal and Rina Chakrabarti**				
Lecture 1	9:15 to 10:00 AM	S. Unniappan	Professor, University of Saskatchewan, Saskatoon, Saskatchewan S7V 1H2, Canada	Online	Nucleobindin encoded peptides and the physiology of fish and mammals
Inaugural Function: 10:00 AM to 11:30 AM					
M L Bhatia Memorial Lecture	11:30 to 12:15 PM	Nishikant Subhedar	Professor, Indian Institute of Science Education and Research, Pune, India	Online	Reward circuits in the brain are modulated by CART neuropeptide
Session 2	**Chairpersons: Rita Singh and Sudipta Maitra**				
Lecture 1	12:30 to 1:00 PM	Rima Dada	Professor, Department of Anatomy, AIIMS, Delhi	Online	Your genes are not your destiny … Your choices are
Lecture 2	1: 00 to 1:30 PM	Bechan Lal	Vice Chancellor, Cluster University of Jammu, Jammu	**Offline**	A mini hypothalamo-hypophyseal axis in fish gonad
Lunch Time and Poster session: 1:30 PM to 3:30PM					
Poster Session1	**Chairpersons: Shaile Malik, Pankaj Kumar and Sunil Kumar**				
InSC and ISCE Executive Committee Meeting: 1:30 PM to 3:30 PM					
Session 3	**Chairpersons: Vinod Kumar and D. C. Bhatt**				
Lecture 1	3:30 to 4:15PM	Francis J. Ebling	Professor, School of Life Sciences, University of Nottingham, UK	Online	The role of tanycytes in seasonal cycles of reproduction and physiology

Tea Break: 4:15 PM to 4:30 PM					
Session 4	**Chairpersons: Anand Shankar Dixit and Sangeeta Rani**				
Lecture 1	4:30 to 5:15PM	Jacques Balthazart	Professor, University of Liège, GIGA Neurosciences, Belgium	Online	Endocrine and environmental controls of brain plasticity in songbirds
Lecture 2	5:30 to 6:15 PM	Erik Herzog	Professor, Washington University in St. Louis, USA	Online	"What wakes us? Networked circadian clocks in the brain and body"
7:00 PM to 9:30 PM Cultural Event and Dinner					
Day 2: Thursday; March 25, 2021 (Session 5 to Session 7)					
Session 5	**Chairpersons: Bechan Lal and Rakesh Kumar Seth**				
Lecture 1	9:30 to 10:15 AM	John F. Cockrem	Professor, Massey University, Palmerston North, New Zealand	Online	Glucocorticoid responses, personality and the ability of animals to cope with changes in their environment
C P Alexander Memorial Lecture	10:30 to 11:15 AM	Chandish Ballal	Director, ICAR-National Bureau of AICRP on Biological Control; Bangalore	Online	Biodiversity &biocontrol
Tea Break: 11:15 AM to 11:45 AM					
Session 6	**Chairperson: Madan Mohan Chaturvedi and Alok Chandra Bharti**				
Lecture 1	11:45 to 12:30PM	Mewa Singh	Distinguish Professor, University of Mysore, Mysore	Online	Behavioral research and its application for management of endangered species
Lecture 2	12:30 to 1:15PM	Rajagopal Raman	Professor, Department of Zoology, University of Delhi	**Offline**	Understanding the interactions between Bemisia tabaci, it's bacterial endosymbionts and geminiviruses

Lecture 3	1:15 to 2:00 PM	Arnab Mukhopadhyay	Scientist, National Institute of Immunology, Delhi	**Offline**	Regulatory mechanisms in longevity assurance
Lunch Time and Poster Session: 2:00PM to 4:00PM.					
Poster Session-2	**Chairpersons: Sanjay Kumar Bhardwaj, Brototi Roy, Amit Kumar Trivedi**				
Tea Break: 4:00PM to 4:15 PM					
Session 7	**Chairpersons: Sharmila Basu-Modak and Namita Agrawal**				
Lecture 1	4:15 to 5:00 PM	Christian Bartsch	Professor, Interfaculty Institute of Biochemistry, University of Tuebingen, Germany	Online	Modulation of longitudinal melatonin production in female rats during two 11-years solar cycles (1997-2020)
Lecture 2	5:15 to 5:45 PM	Yogendra Singh	Professor, Department of Zoology, University of Delhi	**Offline**	Chain length in *Bacillus anthracis* is regulated by protein kinase PrkC
InSC and ISCE General Body Meetings: 6:00 PM					
Day 3: Friday; March 26, 2021 (Session 9 to Session 10)					
Session 8	**Chairperson: D. K. Singh and Mallikarjun Shakarad**				
Lecture 1	9:30 to 10:15 AM	Shweta Saran	Professor, School of Life Sciences, JNU, Delhi	Online	A role played by AMPK in life of *Dictyostelium discoideum*
Lecture 2	10:15 to 11:00 AM	Udai Pratap Singh	Professor, Department of Pharmacy, University of Tennessee Health Science Center, Memphis, USA	Online	Obesity and inflammation: Cross-talk between adipocytes, macrophages and t cells
Lecture 3	11:00 to 11:30PM	Rakesh Kumar Seth	Professor, Department of Zoology, University of Delhi	**Offline**	Reconnaissance of nuclear energy in plant protection with special reference to insect pest management

Tea Break: 11:30AM to 12:00PM					
Session 9	**Chairperson: Yogendra Singh and R.K. Negi**				
Lecture 1	12:00 to 12:45 PM	Sheeba Vasu	Associate Professor, Jawaharlal Nehru Centre for Advanced Scientific Research, Bangalore.	Online	A role for electrical synapses in the circadian pacemaker neuronal circuit.
Lecture 2	12:45 to 1:15 PM	Savita Yadav	Professor, Department of Biophysics, All India Institute of Medical Sciences, New Delhi	Online	Exploring protein-protein interactions in seminal plasma and their clinical implications
Lecture 3	1:15 to 1:45 PM	Mallikarjun Shakarad	Professor, Department of Zoology, University of Delhi	**Offline**	Ecdysone and wingless- the Arundhati and Vashisht of phenotype constancy in faster developing *Drosophila melanogaster*
Lunch Time and Poster session: 1:45PM to 4:00PM					
Poster Session-3	**Chairpersons: Varsha Singh, Vinay Kumar Singh and Rajeev Singh**				
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Reward circuits in the brain are modulated by CART neuropeptide

ML-1

N K Subhedar

Indian Institute of Science Education and Research

Intracranial self-stimulation protocol (ICSS) is considered as gold-standard for the evaluation of brain reward system. Rats with electrode implanted in the lateral hypothalamus (LH)-medial forebrain bundle (MFB) area actively engage in lever press activity to self-stimulate. However, the neuronal substrate that translates the electrical pulses into activation of reward system has remained elusive. We test the hypothesis that the cocaine- and amphetamine-regulated transcript (CART) neurons in the LH-MFB area may support this function. The ICSS activity via an electrode in LH-MFB area was facilitated by CART (55-102) peptide injected in the posterior ventral tegmental area (pVTA), but attenuated by CART antibody. The LH of the animals conditioned to self-stimulate showed increase in the population of (a) CART cells, (b) CART + c-Fos colabeled cells, (c) CART + BDNF colabeled cells. Concomitantly 2 fold increase in CART mRNA expression was noted. The pVTA showed significant increment in the CART fiber terminals on the dopamine cells, increase in tyrosine hydroxylase (TH)-immunoreactivity, and CART and synaptophysin colabeled elements. Neuronal tracers revealed that CART cells of the LH-MFB project to the pVTA. The rats with stereotaxically implanted cannulae in pVTA avidly self-infused CART (55–102) suggesting a role for the peptide in motivation, however, CART (1–39) was ineffective. CART self-infusing activity was inhibited by dopamine D1 receptors antagonist, given directly in the nucleus accumbens shell (AcbSh). The rats trained to self-administer CART (55–102) showed enhanced TH immunoreactivity in the cells of pVTA and fibers in AcbSh. IntrapVTA administration of CART peptide promoted the release of dopamine, and its metabolite from the nucleus accumbens normal as well as ICSS animals. We suggest that CART neurons of the LH-MFB area may play a role in conveying reward information to the mesolimbic dopamine neurons, which in turn may arouse the goal directed behavior.

Biodiversity & Biocontrol

ML-2

Chandish R. Ballal

Director, ICAR-National Bureau of Agricultural Insect Resources & Project Coordinator, AICRP on Biological Control E-mail: ballalchandish@gmail.com

Biodiversity contributes to the maintenance of stability of ecosystems that provide essential life support and is the basis of adaptation and evolution. India has a rich biodiversity and sustainability of biodiversity is the need of the hour and a matter of concern to ecologists and biologists. Insects are one of the most crucial components of biodiversity, being the largest group of animals and closely associated with man's welfare in different forms not only as harmful pests, but also as natural enemies, producers of economic products and pollinators. There are millions of species of insects, mites and spiders still undescribed. Hence, systematics has a larger and prominent role to play in unearthing the species richness of various ecosystems. There is a need for a large number of trained taxonomists in the country to identify and document the Indian insect diversity.

Conservation of the beneficial insect diversity is extremely important considering the ecosystem services provided by them. Various in situ and ex situ strategies have to be taken up as a part of insect diversity conservation. At NBAIR, the ex situ conservation of biological control agents is taken up and live cultures of different bioagents are being maintained. The technologies developed for conservation and augmentation of biocontrol agents in the fields help the farmers to manage pests in a sustainable manner with minimal or nil chemical intervention. In India, innumerable attempts have also been made to augment populations of promising indigenous natural enemies including macrobials like trichogrammatids, braconids, bethylids, chrysopids, ladybird beetles and microbials such as nuclear polyhedrosis viruses, entomofungal pathogens, Bt, and entomopathogenic nematodes to control agricultural and horticultural pests. The biological control of rice pests in Kerala – the Adat Panchayat model - is one of the success stories, where Bio-intensive IPM was adopted in an area of 3000 ha in a year. Conservation biocontrol strategies have helped in tackling two invasive pests viz., the

Sugarcane Woolly Aphid and the Rugose Spiralling Whitefly. One of the notable successes in the field of classical biological control is that of the management of an invasive pest, papaya mealybug, Paracoccus marginatus in India, which was brought under control by introduction of an exotic parasitoid from Puerto Rico - Acerophagus papayae, which established well and brought about excellent control of the mealybug. The savings to our country through this intervention amounts to Rs. 1500 crores, besides the ecological benefits accrued through abstinence from usage of chemical insecticides.

In today's thrust for pesticide residue free produce and clean environment, it is imperative to focus on international bilateral exchange of biological control organisms leading to global biocontrol. India has definitely benefited through import of some of the effective exotic bioagents from other countries. Now, it is probably our turn to reciprocate and provide timely response to the needs of other countries and thus become active participants in global biocontrol initiatives. We have to ensure that all programmes on biodiversity conservation and utilization are implemented successfully, for which national and international networking and awareness creation amongst the farmers and other stakeholders are of prime importance.

Nucleobindin Encoded Peptides and the Physiology of Fish and Mammals

IL-1

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Nucleobindin 1 and 2 (NUCB1 and NUCB2) are DNA and calcium binding proteins. In 2006, nesfatin-1, a biologically active peptide encoded within NUCB2 was discovered. Nesfatin-1 was originally identified for its satiety and fat-influencing actions. The nesfatin-1 research from my lab and several other groups made several original contributions that helped expand our understanding of this peptide. More recently, we have identified a novel nesfatin-1-like peptide (NLP), which is encoded by NUCB1, a protein highly similar to the nesfatin-1 precursor, NUCB2. This talk will mainly focus on our discoveries on nesfatin-1 and NLP. For example, we first identified the insulinotropic and metabolic effects of nesfatin-1 and NLP in rodents. It was found that nesfatin-1 and NLP suppress feeding in fish. Further, a role for nesfatin-1 in regulating reproductive hormones from the hypothalamo-pituitary-gonadal axis of fish and mice, and oocyte maturation in fish was identified. More recently, we found evidence for direct actions of nesfatin-1 and NLP on pituitary somatotrophs to suppress growth hormone in rats and fish. Nesfatin-1 is present in the brain regions that regulate stress, and nesfatin-1 stimulates stress hormones in fish and mice. While both these peptides appear to have hormone-like actions, their receptors are currently unknown. However, new findings suggest that a G-protein coupled mechanism mediates the effects of nesfatin-1 and NLP. Together, our research has unravelled a number of biological functions for nesfatin-1 and NLP. This lecture will attempt to place nesfatin-1 and NLP within our existing knowledge on the endocrine physiology of metabolism, reproduction, growth and stress in vertebrates.

Your genes are not your destiny………….Your choices are….

IL-2

Rima Dada

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Family history is often one of the strongest risk factors for common diseases such as cardiovascular disease , diabetes, cancer, autoimmune disorders, and psychiatric illnesses. A person inherits a complete set of genes from each parent. Family history is thought to be a good predictor of an individual's disease risk and it is believed that our genes determine our destiny. Inherited genetic variation within families clearly contributes both directly and indirectly to the pathogenesis of disease. There is believed to be a direct link between gene mutation and disease. However the genome is highly stable and recent studies have shown that though genes play major role in determining our biology, but the they are just a small part of a much bigger picture. Our health and disease is determined by our choices; by our lifestyle, social interactions, what we eat , our thoughts as they modulate the epigenome. Epigenetics is the study of change in expression of genes which is independent of any change in the nucleotide sequence. This change is determined by the environment and our choices. As compared to the genome the epigenome is highly dynamic. Thus our epigenome influences our health, but we too can influence the epigenome by our choices. This talk would focus on how our unhealthy lifestyle choices, social habits, dysfunctional l eating habits and environmental pollutants have led to marked rise in complex diseases and how a simple lifestyle intervention (yoga) can impact our health.

A Mini Hypothalamo-Hypophyseal Axis in Fish Gonad

IL-3

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The physiological processes of reproduction in vertebrates primarily rely on complex signaling mechanism involving the secretions from the hypothalamo-hypophysial-gonadal axis. A variety of neuropeptides and neurotransmitters (GnRH, GHRH, PACAP, CRH, TRH, SRIH, Urotensins, Neuropeptide-Y, CCK, Tachykinins, serotonin, NOS/NO, dopamine, epinephrine, norepinephrine, etc.) from hypothalamus activate pituitary to secrete tropic hormones. Among them, gonadotropin-releasing hormone (GnRH), a principal neuropeptide, stimulates the anterior pituitary to release gonadotropins (follicle stimulating hormone - FSH and luteinizing hormone - LH), which in turn trigger gonad to undergo steroidogenesis and gametogenesis in sexually dimorphic manner to produce viable eggs and sperm. Nevertheless, some studies of the last three decades, report the paradoxical expression of these hypothalamic and hypophyseal factors in gonad at transcript level, largely in mammals, with very poor understanding of their role in gonadal activities. In last one decade, our studies have established the expression of some of the hypothalamic and hypophyseal factors such as GnRH, kisspeptin, NPY, NOS/ NO, BMP15, GH protein in fish gonad at cellular level. Their expressions varied temporally and spatially with changing reproductive status of the gonad suggesting their well controlled-secretion and physiological actions. Our *in vivo* and *in vitro* studies, using agonist and antagonist drugs, have further established their role in steroidogenesis employing well defined signally molecules, in paracrine /autocrine manner, independent of hypothalamic-hypophyseal factors and other regulators of steroid production in fishes. By modulating the steroid production, these intra-gonadally produced factors regulate production of viable eggs and sperms in fishes. It is postulated that the endocrine hypothalamo-hypophseal factors are relayed to the gonad primarily to synchronize the gonadal activities with environmental cues and time them to accomplish the successful reproduction.

The Role of Tanycytes in Seasonal Cycles of Reproduction and Physiology

IL-4

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Seasonal cycles in reproduction, appetite, fattening, hair growth and hibernation are widespread in mammals, and reflect an interaction of internal circannual rhythmicity and changes in the annual photoperiod, and modifying effects of local environmental cues. Our research focuses on how photoperiodic and circannual information reaches the neuroendocrine effector circuits in the hypothalamus. Hypothalamic glial cells known as tanycytes appear to be a crucial part of this circuitry. Tanycytes have cell soma embedded in the ependymal lining of the third ventricle, but send elaborate projections through the surrounding hypothalamus that appose neurons, capillaries in the median eminence, and cells in the surrounding *pars tuberalis* (pituitary stalk). Our studies in the Siberian hamster (*Phodopus sungorus*) maintained under changing photoperiods reveal profound seasonal changes in expression of many genes in tanycytes related to the transport and bioactivity of thyroid hormone (eg deiodinase II and III), retinoic acid signalling, and to metabolism. Manipulation of intrahypothalamic thyroid hormone concentrations in hamsters by surgical implantation of microimplants demonstrate a causal role for thyroid hormone in regulating seasonal changes in appetite and reproductive activity. However, although we have inferred that changes in thyroid hormone availability in the hypothalamus can regulate annual cycles in energy intake, storage and other physiological adaptations, analysis of tanycyte gene expression changes over the course of one year in natural photoperiod paint a more complex picture for thyroid hormone involvement. As tanycytes are also a stem cell niche and function as hormone, nutrient and metabolite sensors that impact upon neuronal function in the surrounding hypothalamus, we hypothesise that seasonal cycles in metabolism, reproduction and behaviour reflect long-term reversible plastic changes in the hypothalamus.

Endocrine and Environmental Controls of Brain Plasticity in Songbirds

IL-5

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The morphology of the oscine song control system is regulated by changes in the hormonal and social environment. This plasticity namely includes a modulation of neurogenesis in HVC and also changes in cell perineuronal nets (PNN) density. We review in this presentation recent studies from our laboratory devoted to these topics.

HVC neurogenesis was studied by quantifying cells expressing doublecortin (DCX), an endogenous marker of new neurons, in birds of both sexes in different photoperiodic conditions (sensitive, stimulated, refractory) or housed in variable social conditions: alone (M or F), male with a female (M-F) or male with another male (M-M) or in males castrated and treated or not with exogenous testosterone. Subjects in the social condition experiment additionally received injections of BrdU at the start of the experiment 21 days before brains were collected and of EdU 10 days before brain collection. All these experiments identified an active neurogenesis markedly modulated by all experimental factors tested. Together these data indicate that proliferation, recruitment and survival of new neurons can be independently affected by environmental conditions with DCX providing cumulative information not necessarily reflected in measures of single new populations (BrdU+ or EdU+).

PNN are aggregations of extracellular matrix components surrounding the soma of specific neurons that limit synaptogenesis and mark the end of sensitive periods. They were quantified in song control nuclei of canary brains collected in a variety of physiological conditions. During the first year of male canaries, brain PNN expression increased to reach its maximum in the fall in HVC and in early winter in the nucleus robustus arcopallialis (RA) when birds are crystalizing their song. Testosterone increased the number of PNN in castrated male and in female canaries, with the maximal density being reached after 21 days in females. PNN density also varied across seasons in the song control nuclei of adult males. Together these data suggest that changes in PNN densities in the song control nuclei might control changes in singing behavior plasticity during ontogeny and during the seasonal cycle. We started testing this conclusion by dissolving PNN in HVC via application of the enzyme chondroitinase ABC. To this date only marginal effects on song structure were observed and more work is needed to identify the potential role of PNN on singing plasticity.

We are currently investigating whether dissolution of PNN in HVC by application of chondroitinase sulfate affects song structure and song (re)learning in adult male canaries.

IL-6

"What Wakes Us? Networked Circadian Clocks in the Brain and Body"

E. Herzog

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We schedule our lives in anticipation of daily challenges. Daily rhythms in physiology and behavior arise from coordinated circadian clocks. This talk will review the molecules, cells and circuits that coordinate daily rhythms in the mammalian brain. I will focus on recent work connecting the central circadian pacemaker in the brain, the suprachiasmatic nucleus, to daily rhythms in glucocorticoids.

IL-7

Glucocorticoid Responses, Personality and the Ability of Animals to Cope With Changes in Their Environment

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When stimuli from the external environment are perceived by animals to be threatening or potentially harmful the hypothalamo-pituitary-adrenal (HPA) axis is activated and glucocorticoid hormones are secreted by the adrenal gland. The increased secretion of cortisol or corticosterone in response to a stimulus is commonly known as a stress response. However, stress is a term that has negative connotations whereas a glucocorticoid response is a natural response that helps an animal to adjust to a change in its immediate environment. There is considerable variation between animals in their glucocorticoid responses to the same stimulus, and some animals have little or no response to a stimulus that evokes a large response in other animals. These differences between animals in hormone responses reflect differences in the sensitivity of animals to changes in their environment. Individual animals also have characteristic patterns of behaviour, and the size of an animal's glucocorticoid response is linked with the type of behavioural response it has to environmental stimuli. Glucocorticoid responses and behavioural responses to environmental stimuli are together determined by individual characteristics called personality.

Animals with relatively low glucocorticoid responses and active behavioural responses are said to have proactive personalities, and animals with relatively high glucocorticoid responses and passive behavioural responses are said to have reactive personalities. Animals with low glucocorticoid responses and proactive personalities are likely to be more successful (have greater fitness) in constant or predictable conditions, whilst animals with reactive personalities and high glucocorticoid responses will be more successful in changing or unpredictable conditions. Studies of glucocorticoid responses and personality will be useful for understanding relationships between individual characteristics and success in animals, and for predicting how animals might cope with changing environmental conditions associated with climate change.

Behavioral Research and its Application for Management of Endangered Species

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Two branches of biology, Behavioral Biology dealing with functions, mechanisms, development and evolution of behavior studying individuals or social groups of animals, and Conservation Biology dealing with management of endangered species and ecosystems using landscape approaches, have traditionally been disassociated with each other. Research on animal behavior is generally seen to be an academic and theoretical pursuit aiming primarily at answering questions about ecology and evolution. I discuss how basic research on animal behavior can become a handy tool for conservation and management of species in their natural habitats as well as under altered environmental conditions such as zoological parks. I primarily discuss our long term data on two endangered species, the lion-tailed macaque and the elephant, in the Western Ghats. The study of behavior of these two species has helped us develop management strategies and ways to reduce human-animal conflict.

IL-9

Understanding the interactions between Bemisia tabaci, it's bacterial endosymbionts and geminiviruses

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Many of the viruses affecting animals and plants rely on arthropods as their vector. The whitefly Bemisia tabaci is a worldwide agricultural pest with wide range of host plant preferences and is capable of transmitting Geminiviruses in a circulative and persistent manner. This insect harbors two different types of bacterial endosymbionts the primary endosymbiont Portiera which alone is required for its survival since it provides essential non-dietary metabolites. The secondary endosymbionts are present in different combinations of Wolbachia, Rickettsia, Arsenophonus, Hamiltonella. Endosymbionts of B. tabaci as well as other insect vector hosts have been shown to play a major role in virus transmission. In both in-vitro and in-vivo studies, the GroEL protein of Arsenophonus was found to be interacting with the CLCuV coat protein. These results suggest the involvement of Arsenophonus in the transmission of geminiviruses by *B. tabaci*. We then attempted to eliminate Arsenophonus from B. tabaci to study its effects with regard to development and other fitness parameters. Our results revealed that Arsenophonus negative (A-) whiteflies had more fecundity, increased juvenile developmental time, increased nymphal survival and increased adult life span as compared to control (A+) whiteflies. Thus, our results demonstrate that A+ whiteflies have lesser fitness as compared to A- whiteflies. Experiments aimed at probing involvement of Arsenophonus in transmitting the ToLCNDV by B. tabaci revealed that A+ whiteflies transmit virus more efficiently as compared to A- whiteflies. These findings strongly implicated endosymbiont Arsenophonus for ToLCNDV transmission by this genetic group of B. tabaci. We performed a yeast two hybrid gut cDNA expression library screening against coat protein of ToLCNDV and CLCuV as bait. Midgut protein (MGP) was the common protein found interacting with both ToLCNDV and CLCuV. MGP was localized in whole mount B. tabaci as well as in dissected guts through confocal microscopy. Pull down and dot blot assays confirmed in vitro interaction between ToLCNDV and CLCuV coat protein and MGP. Immunolocalization analysis also showed colocalization of ToLCNDV and CLCuV particles and MGP within insect's gut. Finally, anti-MGP antibody fed B. tabaci, exhibited 70% reduction in ToLCNDV transmission, suggesting a supportive role for MGP in virus transmission.

IL-10

Regulatory mechanisms in longevity assurance

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The metabolic state of an organism instructs gene expression modalities, leading to changes in complex life history traits, such as longevity. How metabolic changes in one cellular organelle signals to the nucleus to affect gene expression is an interesting area of research. In my lab, we are using a simple genetic model, Caenorhabditis elegans, to tease out signalling cross-talks that regulate gene expression when metabolic state changes. As a paradigm, we modulate metabolism using Dietary Restriction, an intervention that increases life span and bestows health benefits across species. I will summarize our research findings of recent past and discuss ongoing studies where we are trying to understand how gut microbiota use micronutrients to regulate host gene expression and longevity.

IL-11

Modulation of Longitudinal Melatonin Production in Female Rats during Two 11-Years Solar Cycles (1997-2020)

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In 1994 we reported that the urinary excretion of 6-sulfatoxymelatonin (aMT6s) displays seasonal rhythms in laboratory rats under LD=12h:12h and hypothesized that the horizontal intensity H of the geomagnetic field acts as seasonal Zeitgeber. To test this hypothesis, a series of long-term experiments with female CD-rats was initiated in 1997 under highly controlled conditions which not only included constant photoperiods (LD=12h:12h) but also shielding from high-frequency electromagnetic fields (mobile phone signals).

The first part of these experiments was performed during 1997-2008 consisting of five sub-experiments in which 12-15 rats were observed over maximally two years collecting nocturnal urine in three intervals (19-23 h, 23-3 h, and 3-7 h) once a month to determine the excreted quantity of aMT6s. Here we focus on total overnight excretion (19-7h) as a measure for overall nocturnal melatonin production by the pineal gland. Winter-summer increments were detected in all five experiments, however with varying degrees. It was striking to see that longitudinal nocturnal aMT6s-excretion progressively increased during experiment II (1999-2000) and thereafter declined in experiments III-V (2003/4, 2005/6, 2007/8) to levels similar to experiment I (1997-9). As an extension of our initial hypothesis, we postulated an additional involvement of the 11-years sunspot cycle which is known to affect H depending on the degreee of solar activity. Incidentally, this first series of experiments was performed parallel to the 23rd sunspot cycle (1996-2008) thus indicating that increasing solar activity stimulates melatonin secretion by elevating the sympathetic tone which among others –controls pineal melatonin biosynthesis. To test the extension of our initial hypothesis regarding the mechanisms underlying seasonal melatonin changes under constant photoperiods, we performed a series of further five experiments throughout solar cycle 24 (2008-2019) which will be presented and discussed here.

Chain Length in *Bacillus Anthracis* is Regulated by Protein Kinase PrkC

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Anthrax is a bacterial disease caused by a gram positive bacterium known as *Bacillus anthracis*. This pathogen infects all animal species including human. The major virulence factors include a poly-D-glutamic acid capsule and anthrax toxin. In 2016, it was shown that longer chain of *Bacillus anthracis* blocks the lung capillaries causing hypoxia. However, how chain length is regulated is not well understood. While working with a ser/thr kinase, PrkC deleted strain of Bacillus anthracis, we noticed that the chain length were very small in comparison to wild type strain. Further examination revealed the reduced cell wall thickness and multi-septa phenotype in the mutant strain. We also found an upregulation in bacillus chain length determinant proteins - BslO, a septal murein hydrolase actively involved in the bacillus de-chaining process & Sap (surface layer protein), required for BslO localization. These results suggest that ser/thr kinase PrkC regulates chaining phenotype in *Bacillus anthracis*.

A Role Played by AMPK in Life of *Dictyostelium discoideum*

IL-13

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We focus on the protist, *Dictyostelium discoideum*, which has both uni- and multicellular stages incorporated in its life cycle. They remain as free living amoeba till sufficient amount of food is present but upon starvation, these free living amoebae come towards common collecting points in response to the chemoattactant cAMP to form multicellular structures that ultimately form a fruiting body comprising of two terminally differentiated cell types: the stalk (made up of dead vacuolated cells) and the spores (viable). *Dictyostelium* is a well-suited organism for studying autophagy, as it plays a key role in differentiation and development.

Autophagy is a degradation process, wherein long-lived proteins, damaged organelles and protein aggregates are degraded to maintain cellular homeostasis. AMPK is a highly conserved serine/threonine protein kinase consisting of a catalytic and two regulatory subunits and is conserved from yeast to humans. AMPK plays an important role in starvation responses and nutrient deprivation is necessary for the initiation of development in this organism. AMPK coordinates control of cell growth and autophagy, acting as a metabolic checkpoint and inhibits cellular growth via suppression of the mTORC1 (mammalian target of rapamycin complex 1) pathway This study was undertaken to explore the functions of AMPK during development of *D. discoideum*, which was found to be involved in regulating the aggregate size. We propose a key role of AMPK in pinocytosis and phagocytosis in *Dictyostelium*. In addition, AMPK play a role in basal autophagy induction through the AMPK–ATG1 axis.

Obesity and Inflammation: Cross-Talk between Adipocytes, Macrophages and T Cells

IL-14

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Obesity has become a global health problem affecting the life expectancy of people at epidemic proportions. Obesity is characterized as a state of low-grade chronic inflammation that influences the development and progression of many chronic and autoimmune diseases. A unique role of T cells in adipose tissue has been shown in the initiation and regulation of the inflammatory cascade. In this study, we investigated how a high-fat diet (HFD) influences the homeostatic expansion of T cells, macrophage phenotypes, and inflammation. HFD consumption alters the body weight, fat mass, and lean mass of mice when compared with those on a normal diet (ND). The HFD increased the frequency of $CD44^+$ and TCR $\alpha\beta^+$T cells in the epididymal adipose tissues as compared with ND. We also found a significant increase in the frequency of $CXCR3^+$ activated $CD8^+$ T cells and $CD8^+$ KLRG1 cells in mucosal and epididymal adipose tissues of mice that consume HFD. The systemic pro-inflammatory cytokines-chemokines and leptin concentration increased in the HFD group as compared to ND. Further, HFD consumption resulted in greater than 2-fold changes in 142 microRNAs (miRs) in epididymal adipose immune cells. Among these, ten inflammatory and obesity miRs were validated by RT-PCR analysis. Pathway analysis also validated that differentially regulated miRs target mRNAs are associated with T cell homeostatic expansion and macrophage function. Taken together, these results indicate that HFD modulates T cell homeostatic proliferation and expansion, CXCR3 expression, macrophage phenotype, and inflammatory miRs to sustain inflammation in adipose tissue. This study supports a key role of $CD8^+$ T cell homeostasis to maintain effector phenotypes by CXCR3 expression and macrophages function during HFD-induced obesity. Thus, this study augments our understanding of many pathophysiological consequences of obesity.

Reconnaissance of Nuclear Energy in Plant with Special Reference to Insect Pest Management

IL-15

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Nuclear energy has varied benefits due to its use in various disciplines of entomology ranging from basic to applied fields. Notwithstanding the non-interventionist use of broad-spectrum insecticides, especially in the tropical zones of the world, both pre- and post-harvest food losses due to these insect pests contribute significantly to the high prevalence of undernourishment in the tropical world. Current mercurial pest management methods have serious drawbacks such as the heavy reliance on chemicals, emerging genetic insecticide resistance in pests and high secondary exposure risks. Innovative, environment friendly and effective pest control tactics are therefore needed. Presently, various biological and para-biological control programmes are receiving major prominence. Nuclear technology is an innovative mode in plant protection, that relies on the use of isotopes and radiation techniques to combat pests and diseases, increase crop production, ensure food safety and increase livestock production. There are a number of applications of ionizing radiation in insect pest management, that includes disinfestation of commodities for quarantine and phytosanitary purposes, reproductive sterilization of insects for pest management programmes using the radio-genetic Sterile Insect Technique (SIT) and F_1 Sterility technique, etc. As part of the arsenal of environmentally-friendly control tactics, SIT has proven to be an effective tool against selected insect pests in an area-wide integrated pest management. SIT is an automatic birth control in which released sterile males induce sterility in field population through mating with wild females. Recently, more emphasis has been placed on the quality of the sterile insect that would be released in the field. Ionizing radiation can also be applied to greatly improve the efficiency of mass-rearing, handling and shipment of insect parasitoids and predators. Various perspectives of utilization of radiation as a tool in entomological research relevant to Indian climate need to be understood for pragmatic potential of nuclear technology

A Role for Electrical Synapses in the Circadian Pacemaker Neuronal Circuit

IL-16

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The fly *Drosophila melanogaster* has been a workhorse for the study of circadian biology, especially in the context of its cellular and genetic basis. The neuronal circuit that acts as the circadian pacemaker is composed of about 150 neurons in the fly brain. There have been many studies that examine this circuit and the interactions amongst its various nodes. Predominantly they have focussed on chemical neurotransmission. We find for the first time that proteins which form electrical synapses are critical for maintaining the speed of the circadian circuit - both at the level of the molecular clock oscillations as well as the behavioural rhythm. I will discuss these recent findings from our lab.

IL-17

Exploring Protein-Protein Interactions in Seminal Plasma and their Clinical Implications

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Infertility, one of the major health challenges, affects 15-20% of couples worldwide. Male associated factors contribute equally to the problem. Routine semen analysis, based on sperm factors such as concentration, motility, morphology, etc. is performed to screen fertility status; however, it fails in 30%-50% cases, highlighting high number of idiopathic cases. Advanced Research technologies like genomics, proteomics, transcriptomics, and metabolomics have allowed scientists to explore novel plausible biomarkers, together encompassing the "omics" era.

We are continuously engaged in this domain utilizing proteomics techniques and have identified several crucial proteins important for fertilization processes that can serve as markers of male fertility/infertility. Prolactin inducible protein (PIP) secreted from prostate gland, seminal vesicles or testis in seminal plasma is a ~17 kDa glycoprotein. It is known to play essential roles in various biological processes including male fertility/infertility; however precise physiological role remains unclear to date. Identification of protein–protein interactions is vital for complete understanding of a biological process and for functional characterization of a protein in related biochemical pathways. It has been found that PIP interacts with zinc-alpha-2 glycoprotein, human serum albumin and seminogelin I fragment in seminal plasma, during different studies conducted. These interactions highlight the role of PIP in male fertility related biological processes, specifically sperm functions and motility. We also found that PIP and seminogelin are up-regulated whereas PSA is down regulated in seminal plasma of Acute Lymphoblastic Leukemia survivors, though the survivors were found to have normal semen parameters in preliminary semen analysis. We believe that expression variations in seminal plasma proteins of cancer survivors may provide the information about the adverse effects of cancer treatment on male fertility.

Ecdysone and Wingless- The Arundhati and Vashisht of Phenotype Constancy in Faster Developing *Drosophila melanogaster*

N. Chauhan, N. K. Shrivastava, N. Agrawal and **M. N. Shakarad**

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Attaining species specific phenotype is prerequisite to attaining Darwinian fitness. The mapping of genetic information into a functional phenotype is a precise process rolled out in a specified time frame. The mapping can get perturbed under rapid development leading to phenotypically malformed individuals. We tested this hypothesis using *Drosophila melanogaster* populations simultaneously selected for faster pre-adult development and extended adult life span. Flies from selected populations showed phenotype integrity (although significantly small in size) despite significant reduction in development time. The reduction in development time is due to higher and earlier release of ecdysone leading to early exit from each developmental stage, while the phenotypic integrity is due to higher expression of wingless-one of the key patterning genes that might be ensuring appropriate pattern formation. The higher and early release of ecdysone was perhaps due to large prothoracic gland relative to the larval size and increased transcription of ecdysone biosynthetic and ecdysone responsive genes in the selected population. Our results clearly suggest that ecdysone and wingless maintain patterning pace in faster developing flies with significant reduction in development time thus ensuring Darwinian fitness.

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P-1

Role of Testes in Gene Expression in the Hypothalamus of a Migratory Songbird during Spring and Autumn Migratory States

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The biannual long-distance journeys are closely coupled to the reproductive cycle, but it is unclear whether seasonal gonadal state contributes to the spring and autumn migratory states. To investigate this, we examined gene expressions the hypothalamus, the key center regulating seasonal responses, in migratory male redheaded buntings that were reproductively inactive, as during early spring and autumn. Irrespective of season, both castrated and sham-operated birds showed photostimulated migratory phenotype under 12.5 h photoperiod, evidenced by nocturnal *Zugunruhe* and circulating thyroid hormone and testosterone levels. Using Kallisto, we pseudo-aligned RNA-Seq transcripts, and calculated the transcript abundance. Pairwise comparison suggested testis-dependent differentially expressed genes (DEGs) with seasonal differences. In particular, using collared flycatcher genome in DAVID, DEGs enriched G-protein coupled receptor and calcium ion signaling pathways in spring and autumn, respectively. qPCR validation of DEGs based on STRING analysis corroborated RNA-Seq results. Between seasons, *gabra5*, *ttr*, *thra* and *thrb* expressions were attenuated, suggesting reduced GABA and thyroid hormones effects on photo-sexual response during spring. Within season, castration-induced reduction in *npy*, *tac1* and *nrcam* and increase in *ank3* expression suggested testicular effects on appetite, prolactin release and neuronal functions during spring, whereas reduction in *rasgrp1*, *grm5* and *grin1* and increase in *mras* expression suggested testicular effects on Ras-mediated signaling regulating homeostasis during autumn. Similarly, castration-induced effects on *pomc* and *pdyn* genes suggested their reciprocal involvement in photoperiodic response in both seasons. These results demonstrate transcriptome-wide changes, and provide insights into season-dependent role of testes during spring and autumn migrations in latitudinal migratory songbirds.

P-2

Using Molecular Modeling Platform to Model Avian Chromatin Remodelling SWI/SNF-Like Complex

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Within the cell nucleus, the SWI/SNF complex family of chromatin remodelers form one of the most researched and well conserved groups of chromatin remodelers across the eukaryotes. Chromatin remodelling accomplished by these macromolecular multisubunit assemblies, expedites gene transcription through modulation of chromatin structure into its open and closed conformational states. Since an *in-silico* 3D model of chicken SWI/SNF-like complex (SLC) remains computationally uncharacterized hitherto, the recent reports of submission of high quality cryo-EM structures of human and yeast SWI/SNF complexes in RCSB PDB databank inspired us to forge ahead with *in-silico* modeling of the key subunits composing a canonical chicken SWI/SNF like complex. The PDB model of human SWI/SNF base module structure was decided to be used as a template. Thereafter, homology modelling based approach was undertaken to construct initial 3D models of chicken subunits BRG1, INI-1 and BAF170 through Swiss Model and visualized by Pymol visualizer software. The generated models depicted alpha-helices, beta-sheets and loops with several unstructured spans. These models were subsequently compared with respective human SWI/SNF subunits for evaluation of structural validity. Further, Ramachandran Plot analysis of the generated models revealed that the number of amino acid residues falling into allowed regions of the Ramachandran Plot were greater than that of outliers. Refinements with respect to re-structuring of the unstructured regions and of low identity regions of template-query alignments are currently underway, as is generating the models for rest of the chicken SWI/SNF like complex subunits. In near future, these will be docked together using protein-protein docking platforms to yield a 3D model of the *Gallus gallus* SLC; it will further be evaluated for appropriate RMSD values and energy minimizations using MD simulations.

P-3

Identification and Expression Analysis of Fgfs During Teleost Gonadal Development, Growth and Recrudescence

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Fibroblast Growth factors (FGFs) are polypeptide growth factors, well established for their role during embryogenesis. In higher vertebrates, significant role of FGFs have been reported during gonadal development, maturation and sex reversal. Among all FGFs, *FGF1*, *FGF2* and *Fgf9* are known for their role in testicular development in human and mice. However, regulatory influence of FGFs in gonadal development is still unclear. Till date most of the studies on FGFs were done in higher vertebrates with little or no information in lower animal models. Considering this, present work focused on elucidating the role of *fgfs* in the common carp, *Cyprinus carpio*. Nucleotide sequences were retrieved from NCBI database, one each from all the seven families of *fgfs* identified in common carp. Using this, primers were designed to amplify partial cDNA fragments using gonadal tissues of biannual breeder, common carp. Real time PCR was performed to envisage the expression pattern in some of the major tissues, different gonadal development and reproductive stages. The result of these studies indicated plausible roles of fgf families in gonadal growth and development. Gene silencing analysis is required to set more insights to the function of *fgfs* in teleostean reproduction.

A Study of Cellular and Molecular Mechanisms Underlying Aberrant Lipid Metabolism in Huntington's Disease (HD) Fly Model

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Huntington's disease (HD) is a dominantly inherited, progressively worsening disorder marked by prominent atrophy in striatal and cortical brain regions. HD is caused by $(CAG)_n$ repeat expansion in *huntingtin* (*HTT*) gene which translates into a mutant form of the ubiquitously expressed Huntingtin (HTT) protein. Disease phenotype sets in once the number of glutamines in the HTT protein crosses 35, wherein, extensive peripheral metabolic dysfunction coexists with overt neuropathy. Loss of body weight despite normal to high caloric intake remains a critical determinant of the disease progression and a challenge for therapeutic interventions. Earlier in HD fly model, we have reported amendment in level of major macromolecules with disease progression along with significantly dysregulated lipid levels. Furthermore, it was observed that the fatbody of diseased flies undergo immense structural and functional modification and therefore, we intended to monitor cellular and molecular perturbations, if any, contributing to metabolic changes caused by pan-neuronal expression of mHTT (mutant Huntingtin; 93 glutamine repeats) protein. Interestingly, in HD flies, we found aberrant transcription profile of the key lipolytic and lipogenic effector genes, *lipin* and *brummer* with disease progression. Moreover, we found that fat body undergoes extensive alteration in vital cellular processes and eventually surrenders to elevated apoptotic cell death at terminal stage of the disease. Extensive mitochondrial dysfunction at an early disease stage and calcium derangement at the terminal stage were observed in fat body which might be contributing to its increased apoptosis. Present study provides an insight into the mechanisms through which neuronal expression of mHTT might be inflicting profound systemic effects, specifically on lipid metabolism and may further open new therapeutic avenues for alleviation of this multidimensionally devastating disease.

P-5

Melatonin Rescues the Negative Effect of an Illuminated Night Environment on the Behaviour, Cognition and Associated Gene Expression in Diurnal Indian House Crows

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Previous studies from our laboratory have shown that ecologically relevant illumination (dim light at night, dLAN) affects the activity, sleep-wake pattern, mood states and reduced melatonin levels of diurnal birds. The “nocturnal” hormone, melatonin is a known regulator of circadian rhythms along with cognition, thus making it an important candidate molecule to play a role in dLAN-induced effects. Two groups of birds were exposed to dimly illuminated night (dLAN; 12L = 150 lux: 12D = 6 lux) and received intraperitoneal injections for 10 days, of either 50 µg melatonin per day (MT group) or vehicle (VH group) half-an-hour before the light off; another group exposed to complete dark night (LD group; 12L = 150 lux; 12D = 0 lux) was administered with vehicle at the same time, and served as control. Elevated melatonin levels at night and reduced night activity and enhanced sleep quality in MT group, but not in VH group, were similar to that of the LD group; this suggested physiological effect of the administered exogenous melatonin. We found no depressive like behaviour, as reflected by increased duration of feeding, preening and exploration of novelty, in the MT group, similar to that in the LD group. As compared to LD, hippocampal mRNA expression of genes associated with neurogenesis and synaptic plasticity (*bdnf*, *dcx*, *nr4a2*, *hat1*), and melatonin receptor (*mel1a*) was decreased and that of genes involved in depressive like behaviour (*tnfα, tnfr1, hdac2, hdac4)* was elevated in VH group; these were however unaltered in the MT group. In MT group, the cognitive performance, as assessed by motor self-regulation and innovative problem solving, was enhanced as compared to the compromised performance in the VH group. Further, MT treated birds had elevated mRNA levels of genes involved in the neurogenesis, synaptic plasticity (*bdnf, dcx, egr1, creb, hat1*) and dopamine synthesis and signaling pathway (*th*, *darpp32* and *taar1*) and decreased *hdac2* expression in the mid brain and nidopallium caudolaterale, as compared to the VH treated birds. These results demonstrate that disruption in daily pattern of melatonin secretion drastically affected both behaviour and mental health of a diurnal species.

P-6

Molecular Characterization of Leptin and Leptin Receptor of Spotted Snakehead *Channa punctata*: Structural, Functional and Evolutionary Analyses

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The present study, in addition to molecular characterization of leptin (*lep*) and its receptor (*lepr*) of spotted snakehead *Channa punctata*, is focussed on physicochemical, structural, evolutionary and selection pressure analyses which are poorly elucidated in teleosts. The putative full-length Lep and Lepr of *C. punctata* showed conserved structural and functional domains, especially the residues responsible for structural integrity and signal transduction. Conversely, residues predicted essential for Lep-Lepr interaction displayed divergence between teleosts and tetrapods. Impact of predicted substitutions/deletions highlighted species specificity in ligand-receptor interaction. Physicochemical properties of ligand and receptor predicted for the first time in vertebrates revealed high aliphatic and instability indices for both Lep and Lepr, indicating thermostability of proteins but their instability under ex vivo conditions. Positive grand average of hydropathy score of Lep suggests its hydrophobic nature conjecturing existence of leptin binding proteins in *C. punctata*. In addition to disulphide bonding, a novel posttranslational modification (S-126 phosphorylation) was predicted in Lep of *C. punctata*. In Lepr, disulphide bond formation and N-linked glycosylation near WSXWS motif in ECD, and phosphorylation at tyrosine residues in ICD were predicted. Leptin and its receptor sequence of *C. punctata* cladded with its homolog from *C. striata* of order Anabantiformes. Selection pressure analysis showed higher incidence of negative selection in teleostean leptin genes, though pervasive as well as episodic diversifying selection was also evidenced. Leptin system of Anabantiformes was phylogenetically closer to that of Pleuronectiformes, Scombriformes and Perciformes. Molecular evolution of teleostean leptin genes appeared to be driven by both negative and positive selection pressures. Higher incidences of negative selection pressure indicate limited adaptation in structure and function of these genes. However, evidence of pervasive and episodic diversifying selection laid a foundation of co-evolution of Lep and Lepr in teleosts.

P-7

Cardifoliside - A Novel Inhibitor of Crystathionine-ϒ-Lyase, an H_2S Synthesizing Enzyme: An In-Silico Study in Phytochemicals from *Tinospora cordifolia* for Exploring Anti-Tumor Mechanism

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Hydrogen sulfide (H_2S) is a gasotransmitter, synthesized endogenously in various tissues. Ample studies report its pro-tumorigenic role in the cancer microenvironment. Immune cells in tumor microenvironment show high expression of *Cystathionine-γ-lyase* (CSE), a key H2S synthesizing enzyme, and thereby contributes to the cancer growth. Nowadays, drug discovery using phytochemicals has become a thrust area in biomedical research. Recent reports and studies in our laboratory on *Tinospora cordifolia* (TC) against cancer gave us a lead to explore its bioactive compounds for the inhibitory potential against CSE.

In preliminary study, we assessed H_2S homeostasis in murine tumor model of Dalton's lymphoma (DL). We evaluated the H_2S-level in biological samples of DL using *in-vitro* and *in-vivo* studies. For *in-silico* studies, 3D-structure of CSE and bioactive compounds were retrieved from online databases. Various visualization, simulation software and online tools were used for energy minimization, ligand and protein preparation, binding-site prediction and docking analysis.

Wet-lab experiments showed increased levels of H_2S in serum and ascitic fluid in cancer bearing mice and tumor factor-induced macrophages. *In-silico* study revealed cordifoliside-A to be the most potent inhibitor of CSE among several bioactive compounds of TC, as its binding to CSE was found to be firm with lowest free energy. Its pharmacokinetic property was also found satisfactory. Finally, this study approves the Cordifoliside-A for further investigation, and possible therapeutic utilization against cancer.

Asprosin in Wall Lizard: A Preliminary Study

P-8

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Asprosin, a 140 amino acid long pleiotropic hormone derived from proteolytic cleavage of the precursor molecule profibrillin-1 at conserved RGRKRR/S furin cleavage site, regulates metabolic, immune and reproductive functions in mammals. Interestingly, this recently discovered peptide remains unexplored in non-mammalian vertebrates. Thereby, the current study is focused in a reptile, the group holding phylogenetic significance due to its taxonomic position. A partial profibrillin-1 transcript consisting of 4040 nucleotides encoding 909 amino acids long partial profibrillin-1 peptide lacking N-terminal region was identified from lizard ovarian transcriptome data (Bioproject Accession: PRJNA324371). Nonetheless, its C-terminal end encoded for a complete asprosin peptide. Multiple sequence alignment across vertebrates revealed that the furin cleavage site RGRKRR/S is conserved in lizard asprosin. The same was reaffirmed by ProP.1 software. In lieu of three glycosylation sites in mammals, analysis of post translational modifications showed the presence of two sites (NetNGlyc) in lizard asprosin. In addition, ten phosphorylation sites (NetPhos 3.1) and one acetylation site (NetAcet) were predicted. The three-dimensional structure prediction of wall lizard asprosin using Phyre2 showed the presence of 2 alpha helices and 10 beta sheets. This is in contrast to the 3D structure of mammalian asprosin which consists of 3 alpha helices and 11 beta sheets. In addition, mutational analysis of lizard asprosin in comparison to human employing the PROVEAN tool showed presence of four independent sites of deleterious mutations suggesting a probable change in functions or mode of action of the peptide. Phylogenetic analysis showed clading of reptilian asprosin with birds and mammals. Among reptiles squamates formed a separate clade while chelonia and crocodilia lie closer to mammalia and aves. The preliminary *in silico* analyses though suggest conservation of primary structure, deleterious substitutions and variation in 3-dimensional structure point towards possible deviation in mode of action and function.

P-9

Prevalence of Antibiotic Resistance and Associated Genes in *Escherichia coli* Isolated from Commercial Layer Chickens

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Antibiotic resistance has emerged as a major threat to public health sector which leads to 7 lakhs global deaths annually. Use of antibiotics in veterinary sector is twice as much as in humans which greatly contributes to the increase in the total resistome. Nevertheless, it still remains a poorly studied field in developing countries like India. As a pilot investigation, we assessed resistance in *Escherichia coli* isolated from layers being reared in three commercial poultry farms located in Sonipat, Haryana and Rampur, Uttar Pradesh. Twenty birds were sampled from each farm to finally assess 180 *E. coli* isolates for phenotypic susceptibility to 14 antibiotics encompassing all clinically important classes. Results showed high degree of resistance to Nalidixic acid (88.33%), Norfloxacin (74.44%), Tetracycline (68.33%), Ciprofloxacin (60%), Co-trimoxazole (43%), Ampicillin (41.66%), Amoxyclav (31%), and Streptomycin (27%). 58% of the isolates showed extreme resistance (>4 antibiotics), 36.7% showed moderate resistance (2-4 antibiotics) while only 2.25% of the isolates was susceptible to all drugs, indicating the heavy usage of antimicrobials in raising chickens. Sixty isolates were randomly selected for genotyping of antibiotic resistance targeting twenty-two different antibiotic resistance genes (ARGs). Selected isolates showed prevalence of *tetA* , *sul2, sul3, strA*, *aada1* and *qnrS* genes . Also, 17 of these isolates possessed more than three ARGs, 14 isolates possessed more than 4 ARGs which demonstrates widespread occurrence of multiple drug resistance in farm environment. Therefore, high usage of antibiotics in the poultry sector put the health of the consumers as well as farm workers at tremendous risk. Farm effluents can also contaminate the downstream environments with antibiotics and antibiotic resistance genes which can further gain entry into clinical environment. Personal hygiene, proper sanitation at the farms, and judicious use of antibiotics are the recommended measures for public health safety.

P-10

Lockdown as ‘clock disruptor’: Impact on daily behavior and mental health in Indian population

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The COVID-19 is a pandemic outbreak across the globe which has forced governments all over the world to impose the lockdown. It has restricted all the non-essential activities and essential services were permitted and people were forced to live in the condition of social isolation. In the present study, we hypothesized that (i) the lockdown would impact our daily behaviors (ii) prolonged exposure to this situation may lead to mental disorders like depression. We also studied the sensitivity of people towards the lockdown extension. The study was planned to be carried out after one month of the imposition of the lockdown between (April 26 – May 05, 2020) to observe the chronic effect of lockdown. A cross-sectional study was performed by an online questionnaire designed using google form. Our results showed a delay in daily rhythms such as sleep-wake cycle, sleep duration, eating time. The other routine activities were altered in their frequency. The further analysis shows that of the total volunteers 60% reported good sleep, 32% had increased daytime nap, the maximum time was spent in social media 29% and electronic gadgets usage 79%. The physical activity and work hours were reduced to 57% and 58% respectively. About 54% of the population were depressed. The impact of lockdown was in its favor as 97% and about 96% were mentally prepared for the extension of lockdown. Based on our results it can be speculated that the lockdown acted as a ‘clock disruptor’ and induced similar effects as that of weekends.

Food Choices Matter for Birds too, Insights from Behavioral and Physiological Responses

P-11

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Food is one of the key environmental factors affecting an organism's behavior and physiology on daily and seasonal basis. Over the years, studies' regarding human food choices and its subsequent impact on their behavior and physiology has been explored a lot but studies on same line are missing with reference to different animal taxa. Thus, in the present study, we investigated the impact of varied food availability on birds, and how it affects their behavior and physiology? The experiment was performed on migratory passerine finch (*Emberiza bruniceps*), where two groups of bird (N=10 each) were taken. Group I birds were fed only with seeds of *Setaria italica* (Kakuni) whereas group II was provided with seeds of kakuni along with sesame seeds (*Sesamum indicum*) and egg white, all three separately in different bowls. The results reveal the preference for seeds of *Setaria italica* over other food options. Behaviorally, group II birds were more active with higher gross food intake when compared with group I, along with increasing trend in average values of fat score, body mass and gonadal growth. Thus, the study clearly demonstrates the impact of food variety over a monotonous food schedule on the bird under study.

P-12

Bisphenol A (BPA) Modulation of Reproductive Parameters in Perch, *Anabas testudineus*

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BPA, a ubiquitous xenobiotics and a potent endocrine disrupting chemical, acts as a weak estrogen receptor agonists/antagonists and at higher concentration can compete with binding of endogenous estrogen to its cognate receptors. BPA alteration of early embryonic development, metabolic homeostasis, immune response, cell death, and reproductive parameters including gonadal growth, differentiation or even gametogenesis in teleosts has been documented earlier. Among others, reproduction is the unique physiological process through which an organism sustains its genetic trail. In the present study, adult perch (*Anabas testudineus),* both male and female, were exposed to environmentally relevant (sub-lethal) concentrations i.e., 1, 10, 100 µg/L of BPA for 15 days to observe influence of BPA exposure on reproductive health of this commercially important fish species. Significant attenuation in gonadosomatic index (GSI) in BPA exposed gonads corroborated well with heightened lipid peroxidation, nitric oxide (NO) synthesis, and differential regulation of anti-oxidant defence parameters (catalase, GPx, GSH, GST) indicating elevated oxidative and/or nitrosative stress in the gonads. Interestingly, major inflammatory markers, e.g. p-p65-NFκB, TNFα, IL-1β, and i-NOS at protein level underwent sharp change, albeit with differential sensitivity, in BPA-exposed testis and ovary. Moreover, DNA breakage, increase in BAX/Bcl2 ratio and activation of caspases in treated groups revealed good correlation with histopathological alteration like inhibited spermatogenesis, vacuolization within the lobule in testis and presence of atretic follicles in the ovary. Further, BPA exposure elicited significant alterations in transcript abundance of gonadotropin receptors (*lhcgr, fshr*) and major steroidogenic enzyme (*StAR, P450scc, 3β-hsd, aromatase*) genes in both sexes. Moreover, at protein level, dose dependent increase of ERα, ERβ, StAR and aromatase was observed in ovary while attenuated ERα, ERβ and increased aromatase were found in testis. Taken together, our findings demonstrate that BPA, a highly hazardous EDC, has widespread negative influence on reproductive parameters in *A. testudineus.*

P-13

Innovative Screening Tool for Progressive Cervical Cancer Lesions: Early Detection, Prevention and Elimination

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Cervical cancer is major threat to women's health globally and is caused by persistent infection of high risk Human Papillomaviruses (HR-HPVs). Over 90% of the pre-cervical lesions regress spontaneously whereas ~10% of these lesions progress to frank malignancy. There is a lack of clinically-available prognostic tool that could discriminate progressive vs. non-progressive cervical lesions with high sensitivity and specificity. Therefore, the efforts are required to explicitly address the identification of women with persistent HR-HPVs infection that have greater tendency of progression. This is essentially required to prevent overtreatment of patients, reduction of colposcopy referrals and better triaging of affected women. In the last decade, our laboratory has been actively engaged in identifying the role of a specific transcription factor signal transducer and activator of transcription 3 (STAT3), the expression and activity of which increases in cervical cancer with increasing disease severity. STAT3 plays an indispensable role in HPV replication, transcription, and expression of viral oncogenes E6/E7. These leads established a strong biomarker value of STAT3 in HPV oncogene expression and disease progression during cervical carcinogenesis. By combining STAT3 and HPV E6/E7 mRNA in the screening of cervical lesions, a 25% reduction in colposcopy referral rate have been reported by other investigators. Taken together, inclusion of STAT3 and HPVE6/E7 in a single diagnostic assay, we develop a cell based diagnostic assay that discriminate progressive cervical lesions with simultaneous quantitative measurement of active STAT3 and HPV E6/E7 using Flow-FISH.

P-14

Dim light at night negatively affects sleep and novel object exploration in diurnal male zebra finches

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Sleep plays an important role in almost all physiological processes. Illuminated night (light at night; LAN) disrupts sleep-wake rhythm and alters the daily behavioural processes. We exposed male zebra finches to a dim light at night (12L = 150 lux: 12 dLAN = 5 lux) with controls on complete darkness at night (12L = 150 lux: 12 d = 0 lux). Dim light at night altered the sleep-wake pattern in zebra finches. dLAN increased the sleep frequency and decreased sleep bout duration hence a reduced sleep duration. dLAN delayed the sleep onset and decreased the awakening latency with respect to lights on as compared to LD. We also tested effects of dLAN on the novel object exploratory behaviour in zebra finches since it is a measure of mood state and loss of interest in performing brain-dependent functions.In congruent with the reduced sleep, less number of birds approached novel object under dLAN. In dLAN birds, the total number of perch hops were reduced and birds spent lesser time on perch with novel object. None of the birds exposed to dim light directly associated (physical association) with the novel object. In general LD birds spent more time and also associated directly with the novel object, as expected. Overall, we found negative effect of dim light at night on sleep-wake cycle, total sleep and novel object exploration in diurnal male zebra finches.

P-15

Impact of *Spirodela polyrhiza* Containing Diets on Growth, Physiology and Nutritional Composition of Common Carp *Cyprinus carpio*

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Greater duckweed *Spirodela polyrhiza* is a good source of protein, amino acids and fatty acids and capable to replace very costly fish meal and soybean meal, the traditional protein sources in aquaculture feed industry. The present study aims to evaluate the effect of *S. polyrhiza* containing diet on common carp *Cyprinus carpio*. Five isoproteinous experimental feeds were prepared using soybean meal/ inclusion of *S. polyrhiza* powder with soybean meal as a protein source. The control feed (SP0) contained soybean meal as the only source of protein and in four experimental feeds SP5, SP10, SP15 and SP20, *S. polyrhiza* powder was incorporated at the rate of 5, 10, 15 and 20 g/100 g of feed. There was no significant difference in crude protein, lipids and ash contents among the feeds, but free amino acids and poly unsaturated fatty acids levels were lower in the control feed compared to other feeds. Common carp (0.475 ± 0.006 g) were fed *ad libitum* with prepared feeds for 60 days. The final average weight and specific growth rate were significantly ($P < 0.05$) higher in SP20 fed fish; this treatment was followed by SP15, SP10, SP5 and SP0. Significantly ($P < 0.05$) lower protein content was found in fish fed with control feed SP0. Essential and non- essential amino acids were significantly ($P < 0.05$) lower in fish fed SP15. Omega-3 and Omega-6 polyunsaturated fatty acids contents were significantly ($P < 0.05$) lower in control fish. Significantly ($P < 0.05$) higher activities of digestive enzymes, amylase, protease and trypsin were found in fish fed with feed SP20. The *delta-6-desaturase* (*fads2d6*), *fatty acid synthase* (*fas*) and *elongation of very long chain fatty acid 5* (*elovl5*) were up regulated in SP5 fed common carp.

P-16

In Silico Analysis of NOD1 and its Differential Expression during Bacterial Infection in Spotted Snakehead *Channa punctata*

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The nucleotide-binding oligomerization domain 1 (NOD1) receptor is a member of the cytosolic NOD-like receptor (NLR) family involved in innate immune responses. It recognizes pathogen-associated molecular patterns (PAMPs) and danger-associated molecular patterns (DAMPs) through its leucine-rich repeat (LRR) domain present at C-terminal. Binding of ligand results in activation of downstream signaling cascade leading to inflammation. In freshwater teleost *Channa punctata*, NOD1 consisting of 943 amino acids contains a caspase recruitment domain (CARD) at N-terminal, a central NACHT domain and 9 leucine rich repeat (LRR) regions towards the C-terminal. In the present study, we have focused on the interaction of NOD1-LRR domain with γ-D-Glu-m-DAP (iE-DAP), a cell wall component of Gram-negative bacteria. For this, a combinatorial approach involving 3D modeling, docking followed by molecular dynamics (MD) simulation and binding free energy calculation was employed. Structural dynamics study showed that C-terminal β-sheet LRR 4-7 region is implicated in binding to iE-DAP. The bacterial ligand formed hydrogen bonds with Lys109 (Lysine), Asp135 (Aspartate), Asn163 (Asparagine), Ser165 (Serine) and Arg190 (Arginine) residues of NOD1-LRR domain while it exhibited hydrophobic interaction with Val107 (Valine), Phe134 (Phenylalanine), Thr162 (Threonine), Ile191 (Isoleucine) and Trp193 (Tryptophan) residues. In addition, the differential expression of NOD1 induced by a Gram-negative bacterium, *Aeromonas hydrophila* was investigated. A significant ($p < 0.05$) downregulation of NOD1 expression was observed in primary as well as secondary lymphoid organs, and also splenic phagocytes from infected fish. The current study thus gives an insight into structural and functional dynamics of NOD1 which might have future prospects for structure-based drug designing in teleosts.

P-17

tsh-β, *dio2* and *dio3* mRNAs Expressions on the First Day of Photoperiodic Induction in Eurasian Tree Sparrow (*Passer montanus*)

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Photoperiodism is an adaptative mechanism that enables birds to predict seasonal changes in the environment. Increased thyroid-stimulating hormone β (*tsh-β*) expression in the pars tuberalis is supposed to be an early event in the molecular cascade involving neuroendocrine transmission of photoperiodic information in seasonal birds. Long-day (LD) photoperiod stimulates the synthesis of TSH from pars tuberalis, which acts on ependymal cells in the mediobasal hypothalamus (MBH) to induce expression of the iodothyronine deiodinases genes. We investigated the effects of single long day on the transcription of *tsh-β* and two iodothyronine deiodinases (type II iodothyronine deiodinase, *dio2* and type III iodothyronine deiodinase, *dio3*) in both sexes of Eurasian tree sparrow (*Passer montanus*). Two groups of photosensitive birds were exposed to short day length (SD: 9L/15D) for 4 days and on the 5th day one group was transferred to long day length (LD: 14L/10D) whereas other group was continued under SD for one day (control). We compared relative mRNA expressions of *tsh-β, dio2* and *dio3* using quantitative RT-PCR at different hours after dawn *i.e.*, ZT0, ZT11, ZT14, ZT16 and ZT18 and ZT20 (ZT0 = light on). The relative mRNA expression of *tsh-β* in pituitary showed an increase after 14 h of dawn (ZT14) followed by an increase in expression of *dio2* 2h later in the hypothalamus *i.e.*, at ZT16. Further, a significant increase in *dio3* expression was observed still later *i.e.*, at ZT18. No significant difference was detected in the expression of the above genes between sexes. The above observations clearly suggest that the photoinduction of *tsh-β* is critical for antiphasic switching of *dio2* and *dio3* mRNA expressions in the hypothalamus during photoinducible phase of circadian rhythm in the tree sparrow.

P-18

Effect of Irradiation on Gut Bacterial Microbiota in a Serious Noctuid Polyphagous Pest, *Spodoptera litura* (Fabricius)

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Gut microbiome constitutes the microorganism that colonize the insect gut and plays a crucial role in the physiology, nutrition, and behavior of the insects. Inherited sterility technique (IS) as a radio-genetic method has been proposed for the suppression of a serious tropical pest, *Spodoptera litura,* wherein the viability and reproductive competitiveness are vital for operating this nuclear technology. The objective of the present study is to (i) assess the gut bacterial diversity of the unirradiated insect, (ii) ascertain the impact of irradiation on gut bacterial diversity. This study might establish a correlation between gut microbiome and insect's viability, and degree of influence of irradiation might help us optimize this radio-genetic technique. In the present study, it is attempted to study the gut microbial diversity using Culture dependent and Culture independent techniques. The laboratory reared population of this pest were subjected to isolation of culturable microbes and 16S rDNA sequence-based identification using (8F/27F & 1492R). The gut microbiome of the control and irradiated larvae (130Gy) were studied using culture dependent method. Genus *Bacillus* and *Pseudomonas* were predominantly present in the control and irradiated larval gut. Culture independent method includes the Next Generation Sequencing analysis of 16S rRNA (a phylogenetic marker in metagenomics). The hypervariable V3 region of 16S rRNA can be amplified with specific primers (341F and 785R). Alpha diversity analysis showed that gut bacterial community was found to be diversified in all the examined regimens, viz., F_1 progeny L6 larvae of 0Gy, 100Gy and 130Gy treated male moths (x untreated female). Although, the principal component analysis plot showed a little similarity between 100Gy and Control (0Gy). Further, the rare fraction analysis showed the maximum gut bacterial diversity in F_1 progeny of 130Gy irradiated male parents. The gut bacterial diversity is being correlated with reproductive competence of irradiated male parent and their F_1 progeny.

P-19

Potential of Biosynthesized Gold Nano-Particles in Waste Water Management

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Rapid expansion in population, agricultural activities, industrialization and widespread disposal of various pollutants into water bodies have rendered freshwater into a cut-throat competitive resource in many parts of the world. Moreover, this stumbling block of water scarcity is also putting a damper on the economic development. So, in this present generation of inadequate fresh water resources, efficacious treatment of wastewater is an indispensable necessity for the expanding economy. It is, therefore, critical to develop competent and novel strategies to supplement existing approaches to manage water pollution with low capital requirement and among various outlooks, “Nanotechnology” came up as one of the most promising approach to combat this menace.

Nanotechnology exploits the unique size-dependent properties of nanoparticles to design a sensitive analytical approach for water remediation. However, the conventional methods of nanoparticle synthesis are being increasingly reported as toxic towards multiple aspects of human physiology, and the reaction by-products further loading the environment. To address these concerns, researchers working on the nanoscale therefore calls for green synthesis of nanoparticle as safer, inexpensive, and environment-friendly alternative.

In the present study, we used tyrosine mediated gold nanoparticles (AuNP^{tyr}) as sensitive colorimetric probes and explored their potential to formulate a cost-effective method to provide a sustainable and practical solution for water remediation. Results obtained from the study revealed that AuNP^{tyr} can be used for rapid tracking and quantitative estimation of heavy metals present in contaminated water.

P-20

Effects of Environmental Factors on Expressions of *GnRH-I* and *GnIH* mRNAs in Control of Reproductive Cycle in the Spotted Munia, *Lonchura punctulata*

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For successful survival in a seasonal environment, birds plan their life history stages such that they are best adapted to the changing environment by timing their reproduction to the time of the year which is best suited for survival of their offspring. Annual changes in environmental factors affect reproductive functions in many seasonally breeding avian species. In birds, changes in the hypothalamic gonadotropin-releasing hormone - I (GnRH-I) and gonadotropin inhibitory hormone (GnIH) content and release are correlated with reproductive stages which is critical for the regulation of reproduction. We investigated the effects of different environmental factors namely temperature, rainfall, relative humidity and photoperiod on the regulation of seasonal reproductive and related events in both the sexes of spotted munia (*Lonchura punctulata*) in their natural habitat from January, 2018 to December, 2018 for 12 months at Shillong. The mRNA expressions of *GnRH-I* and *GnIH* along with testicular volume, follicular diameter, bill colour, molt of body and primary feathers and body weight were observed at monthly intervals. Also, the annual changes in various environmental factors including temperature, rainfall and humidity were recorded. The above observations revealed that the annual changes in gonadal size, bill colour and feathers molt follow the annual variations in temperature, rainfall and humidity in natural conditions suggesting their roles in the control of reproductive and related cycles in the spotted munia. Further, although the relative mRNA expression levels of *GnRH-I* coincide with gonadal growth, *GnIH* levels decrease with an increase in gonadal growth. Thus *GnRH-I* and *GnIH* are expressed in an antiphasic manner. The changes in relative mRNA expressions of *GnRH-I* and *GnIH* show a significant correlation with temperature and humidity among different environmental factors. Our results thus suggest the role of temperature and humidity in regulation of reproductive cycle in spotted munia.

Sexual Dimorphism in Ultradian and 24h Rhythms in Plasma Levels of Growth Hormone in Indian Walking Catfish, *Clarias Batrachus*

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Growth hormone (GH), a key regulator of somatic and reproductive growth in vertebrates, has been extensively studied, although primarily in female fish. Despite numerous reports about sex- and species-specific growth patterns in fish, there is no report about the 24h rhythm of plasma GH in male fish. We aimed to investigate temporal variations in plasma GH levels and the existence of any rhythms therein during the reproductively active months in the male walking catfish, Clarias batrachus; and to compare the secretory temporal patterns of GH in male female specimens of C. batrachus to decipher sexual dimorphism in GH secretions in fish. After 14 days of acclimation to the natural environment, male catfish ($N = 240$) were sorted and randomly divided into eight groups for study at ZT0 (sunrise ~06:00h), 3, 6, 9, 12, 15, 18 and 21. Male catfish ($n = 40$/month) were sampled ($n = 5$/group) at each time point under the natural light-dark (LD) cycle. Catfish were anaesthetized and blood was collected through a caudal puncture, centrifuged, and plasma isolated. Plasma GH was measured using a competitive homologous enzyme-linked immunosorbent assay. A significant effect of time and season ($p < 0.05$) on plasma GH level was detected. Cosinor analyses verified existence of statistically significant ($p < 0.05$) ultradian (12h) and 24h rhythms of plasma GH in male C. batrachus. Acrophases (peak times) showed two ultradian and one 24h acrophase of GH during the early photophase and early scotophase from March to August. Distinct sexual-dimorphism in plasma GH was noticed between male and female catfish. Together, plasma GH show 24h and seasonal fluctuations in a sex-specific manner, suggest the importance of considering the effect of biological 24h and seasonal time and sex on the GH level in regulating the physiology of somatic growth and reproduction in catfish.

P-22

Role of Thyrotropin and Deiodinase Axis in the Regulation of Seasonal Reproduction in Indian Freshwater Catfish *Heteropneustes fossilis* (Bloch)

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Seasonal reproduction is an evolutionary adapted event regulated by the biological clock in an organism. Photoperiod, temperature and food availability are considered to be major environmental cues which guide the organism to speculate the optimum conditions for seasonality. Thyrotropin (TSH) from pars tuberalis has been identified as a regulator of seasonal reproduction in avian and mammalian system. It is known to regulate the basal metabolic rate of an organism via thyroid hormones T4 and T3. TSH from pars tuberalis induces the expression of deiodinase 2 enzyme in the ependymal lining of 3^{rd} ventricle, that leads to high T3 level which in turn releases the GnRH from the hypothalamus. In the absence of pars tuberalis thyrotropin is mainly synthesized in pars distalis under the influence of Thyrotropin stimulating hormone (TRH) from hypothalamus in fishes. Recently, in some teleosts, saccus vasculosus (SV) has been identified as a regulatory hub for photoperiodic information. In present study we have attempted to identify the key elements that link photoperiodic information with hypothalamo-pituitary-gonadal axis in the Indian freshwater catfish *Heteropneustes fossilis*. We have observed upregulation of *tsh-b*, *dio2* and *dio3* genes with increasing photoperiod and temperature, that enables the organism to reproduce in a particular season when the conditions such as sufficient water and food are available for the young ones to grow.

P-23

Aquatic Plants and Their Element and Fatty Acid Profiles

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The present study aims to evaluate the elements and fatty acids composition of twelve aquatic plants. Freshwater plants *Azolla microphylla*, *A. pinnata*, *Enhydra fluctuans*, *Hydrilla verticillata*, *Ipomoea aquatica*, *Lemna minor*, *Marsilea quadrifolia*, *Pistia stratiotes*, *Salvinia molesta*, *S. natans*, *Spirodela polyrhiza* and *Wolffia arrhiza* were cultured using organic manures, cattle manures, poultry wastes and mustard oil-cake (1:1:1). Among various aquatic plants significantly ($P<0.05$) higher crude protein and lipid were found in *L. minor* and *S. polyrhiza*. The ash content was significantly ($P<0.05$) higher in *H. verticillata*, *W. arrhiza* and *P. stratiotes* compared to others. Highest Na, Mg, Cr and Fe levels were recorded in *P. stratiotes*. *H. verticillata* was the rich source for Cu, Mn, Co and Zn; Ca, Mg, Sr and Ni contents were highest in *S. polyrhiza*; Se and K contents were higher in *S. natans* and *W. arrhiza*, respectively. The *n*-6 and *n*-3 polyunsaturated fatty acids (PUFA) levels were significantly ($P<0.05$) higher in *W. arrhiza* and *I. aquatica*, respectively compared to others. Linoleic acid (C18:2*n*-6) and alpha linolenic acid (C18:3*n*-3) were dominant *n*-6 and *n*-3 PUFA, respectively. Highest (4.04) *n*-3/*n*-6 was found in *I. aquatica*. The ratio ranged from 0.61-2.46 in other macrophytes.

P-24

Molecular Components of Ca^{++}- And Cyclic Nucleotides-Induced Signaling Pathways in Regulation of Arylalkylamine N-Acetyltransferase2 *(AANAT2)* Gene in Photosensory Pineal Organ of the Catfish, *Clarias gariepinus*

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In the fish, three *aanat* genes (*aanat1a, aanat1b* and *aanat2*) have been reported. However, photosensory fish pineal organ exclusively expresses *aanat2* gene, which regulates the rate of melatonin synthesis. Though there are reports on the presence of sympathetic nerve fibres, adrenergic receptors, cholinergic receptors, cAMP, cGMP and enzymes in the fish pineal organ, there is practically no information on the role of molecular components of Ca^{++}, cAMP and cGMP signaling pathway in regulation of *aanat2* gene. Therefore, we studied molecular components of Ca^{++}, cAMP and cGMP signaling pathway in regulation of *aanat2* gene in the fish pineal organ by investigating *in vitro* effects of db-cAMP (an analog of cAMP), db-cGMP (an analog of cGMP), Nitrendipine (specific blocker of L-type voltage-sensitive calcium ion channels), (±)- Bay K8644 (specific agonist of L-type voltage-sensitive calcium ion channels) IBMX (inhibitor of cyclic nucleotide-dependent phosphodiesterase) Chelerythrine chloride (specific inhibitor of PKC), H-89 dihydrochloride hydrate (selective inhibitor of PKA), KT5823 (specific inhibitor of PKG), Okadaic acid and Calyculin A (specific inhibitors of serine/threonine phosphatase types 1 and 2A), Cypermethrin (specific inhibitor of serine/threonine phosphatase 2B), CREB inhibitor (666-15-Calbiochem), CBP-CREB interaction inhibitor (CAS 92-78-4-Calbiochem), U0126 ethanolate (specific inhibitor of MeK), and SB 202190 monohydrochloride hydrate (selective inhibitor of p38 MAPK) on relative expression of *aanat2* gene by measuring *aanat2* mRNA using Real Time RT-PCR. Relative expressions of *aanat2* mRNA of all samples were calculated using the ΔΔCt (threshold cycle) method (Livak and Schmittgen, 2001). Based on our findings, we suggest for the first time that *aanat2* gene expression in the fish pineal organ is regulated by a complex intracellular signalling machinery involving both cAMP-PKA-CREB/CBP-CRE pathway and cGMP-PKG-serine/threonine phosphatases-MeK-MAPK pathway. Further, Ca^{++} seem to be a prerequisite for cAMP- and cGMP-induced transcription of *aanat2* in the fish pineal.

P-25

Constant Light Negatively Affects Activity Behaviour and Gene Expressions in Female Zebra Finches

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Exposure to light at night represents an undesirable consequence of technological progress and a modern lifestyle. A most crucial feature of biological adaptation is the maintenance of close temporal relationship of behaviour and physiology with periodic light-dark environment, which is rapidly changing with increasing night illumination. We continuously monitored activity behaviour and measured 24-h mRNA rhythm of clock genes (*Bmal1*, *Per2*, *Rev-erb β*) in the hypothalamus, liver and intestine of diurnal zebra finches that were born and raised under LL, with controls on 12L:12D. We also measured hypothalamic 24-h expression of *c-Fos* (a neuronal activity marker), *Rhodopsin* and *Mel1-a* (markers of photoperiod perception), hepatic expression of *Fasn* and *Cd36/Fat* (genes associated with fat biosynthesis and uptake) and gut expression of *Sglt1*, *Glut5*, *Cd36* and *Pept1* (genes associated with carbohydrate, fat and protein absorption). Under LD, all birds were entrained and showed a significant rhythm in activity behaviour and gene expressions. Under LL, the majority (4/5th) of birds tested showed circadian rhythm in activity behaviour, whereas hypothalamic expression of all genes was arrhythmic. However, there were variable responses in the liver and intestine. There was a significant 24-h mRNA rhythm of *Per2*, not *Bmal1*, in both tissues, and of *Rev-erb β* in the liver; similarly, *Fasn* and *Cd36* mRNA levels were attenuated under LL, compared to LD, as suggested by lower baseline mRNA expressions. Likewise, *Sglt1* and *Cd36* genes, acting as major transporter of glucose and lipids, respectively, showed loss of daily rhythms; however, *Glut5* and *Pept1* genes showed rhythms but with phase differences. These results demonstrate dissociation of circadian rhythms at different levels as the result of the loss of night, and provide insights into possible mechanism(s) that animals might employ to adapt to an emerging overly-lit urban environment.

P-26

Intercellular Communication through Exosomal Compartment in HNSCC: Transfer of Transcription Factor STAT3

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Background: Our prior reports have shown the elevated levels of STAT3 signaling in head and neck squamous cell carcinoma (HNSCC). STAT3 plays an important role in oncogenesis, however the carcinogenic role of STAT3 on tumor microenvironment (TME) of HNSCC is not known. Exosomes that can act as bridge between tumor cells and neighboring cells in the TME remains to be investigated.

Aim: The present study aims to investigate the physical transfer of STAT3 via exosomal compartments of HNSCC.

Material and Methods: We examined the exosomes and their biomolecular content in a panel of head and neck cancer cell lines, Oct-1, 93UV147T, and UDSCC 2. Exosomes were isolated using commercially available kits and their morphology, size and molecular profile were characterized using transmission electron microscopy, dynamic light scattering and western blotting (Tsg101, HSP70) respectively. Expression of STAT3 proteins in HNSCC cells and their respective exosomes were checked using immunblotting.

Results: Exosomes isolated showed cup-shaped morphology under transmission electron microscope and were homogenously distributed in the diameter size range of 30-150 nm. Our immunoblotting results showed that these exosomal preparations were enriched in exosomal marker proteins Tsg101, HSP70. We observed the overexpression of STAT3 in all HNSCC cell lines. However, the immunoreactive STAT3 protein was found truncated (approximate size 50kDa) in comparison to the full length STAT3 (91kDa) detected in corresponding cell lysates.

Conclusion: Overall, the preliminary findings support the transfer of STAT3 in HNSCC exosomes, however its biological significance in reconditioning of TME in HNSCC is yet to be established.

Keywords: Head and Neck squamous cell carcinoma (HNSCC), Extracellular vesicles (EVs), Exosomes, Human papillomavirus (HPV), Signal Transducer and Activator of Transcription factor 3 (STAT 3)

P-27

Non-Cell-Autonomous Effects of Mutant Huntingtin on Immune Cells in Transgenic *Drosophila* Model of Huntington's Disease

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Huntington's disease (HD) is dominantly inherited, progressive neurodegenerative disorder characterized by hallmark chorea, cognitive decline and psychological impairment. The causative factor behind HD is an unstable expansion of polymorphic trinucleotide (CAG) repeats beyond 35 in Interesting Transcript 15 (IT15) gene encoding ~348 kD Htt protein. Most prominent neuropathological feature in HD involves severe cell death of a specific set of neurons in the striatum and cortical regions of the brain. In addition to neurobiological anomalies, immune dysregulation is considered one of the clinical challenges and may critically contribute to the pathology of HD. *Drosophila* is widely used model to understand relationship between immunity and diseases. *Drosophila* cellular immunity comprises three distinct lineages of hemocytes. Plasmatocytes are the professional phagocytes most similar to vertebrate macrophages, crystal cells are responsible for melanisation during wound repair and lamellocyes involved in encapsulation of pathogen.

In present study, we used transgenic *Drosophila melanogaster* expressing human mHtt exon1 fragment with 93 glutamine repeats selectively in neuronal cells using pan-neuronal driver and evaluated its non-cell-autonomous effects on hemocyte population and their physiological functions. We found that non-cell-autonomous expression of mHtt has noxious effects on *Drosophila* hemocytes as evidenced by significant increase in crystal cell count in late 3rd instar larvae. Furthermore, phenoloxidase (PO) activity was significantly higher in diseased flies at different ages with disease progression as compared to age-match controls. We also found increased proliferation of circulating plasmatocytes in diseased 3rd instar larvae and an obstinate plasmatocyte count in hematopoietic pockets/hubs of diseased flies throughout disease progression whereas there was a gradual decline in plasmatocyte number of hematopoietic pockets of controls with aging. Consequently, we observed that plasmatocytes of diseased flies exhibit reduced phagocytic activity *ex vivo* despite an increase in their number. These findings indicate that neuronal expression of mHtt alone is sufficient to induce non-cell-autonomous immune dysregulation *in vivo*.

P-28

To identify and characterise the potential interacting protein partners of Dengue virus in the insect vector (*Aedes aegypti*)

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Dengue virus (DENV) is primarily transmitted by the insect vector *Aedes aegypti and Aedes albopictus*. DENV has four antigenically different serotypes (DENV1-4) which can cause range of disease in humans from mild fever to dengue hemorrhagic fever and lethal Dengue shock syndrome. The envelope protein(E) of DENV has major antigenic determinant property and domain-III(ED-III) is involved in receptor binding as well as endosomal fusion to the host cell. Despite of number of studies, very few interacting protein partners has been identified in the invertebrate host. To identify the potential interacting partner of DENV in the invertebrate host, we have performed phage display library screening against the envelope protein domain III(ED-III). The various interacting peptide partners was found. The various interacting peptide partners were identified, heterologously expressed, purified and used for in-vitro and in-vivo interaction.

P-29

Increase in Neutrophil Number and Function Contributes to Gradual Systemic Deterioration during Tumor Progression

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Chronic inflammation is known to be an important hallmark of cancer wherein inflammatory cells and their mediators play a crucial role. Among inflammatory cells, neutrophils recently became the subject of intense research with focus on the association between inflammation and cancer. The ratio of neutrophil to lymphocyte counts (NLR) in blood has been suggested as a simple measure of systemic inflammation in cancer patients. However, cancer progression has a systemic impact and affects multiple organs thus challenging the overall physiology of the host. Looking at the increased neutrophil count in circulation, it is worthwhile to explore whether and how neutrophils contribute to systemic deterioration with cancer progression. Therefore, we aimed to discern the systemic role of neutrophils via monitoring their number and function with tumor progression in the well accepted Dalton's lymphoma mice model.

We observed a gradual increase in neutrophil infiltration in blood as well as in the vital organs of tumor bearing mice. In parallel, we observed damaged histo-architecture of organs with significant alterations in serum biochemical parameters that aggravated with tumor progression. We next examined neutrophil function by assessing NE, MPO, and MMP-9 in liver, lungs, peritoneum and spleen. We found upregulation in their expression and activity in all the examined organs of tumor bearing mice. Taken together, our results demonstrate high infiltration and hyper-activation of neutrophils in peripheral blood and vital organs of tumor bearing host. We speculate that the systemic presence of hyper-active neutrophils may account for gradual systemic deterioration which is observed in the cancer patients. These findings also suggest neutrophils as therapeutic targets for immunomodulators that can reduce the systemic manifestations thus leading to improved survival of patients.

P-30

Ascorbic Acid Inhibits Tumor Growth in DL Mice via Regulation of HDAC 1, 2 & 6 Expression

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The purpose of the study was to evaluate the anti-tumor effects of ascorbic acid in DL mice, wherein it was directly infused in the tumor microenvironment. In addition, whether these effects manifest as a result of histone deacetylases (HDACs) regulation has also been investigated. Firstly, the effect of ascorbic acid therapy on tumor growth was determined by studying morphological, anatomical, hematological and histological parameters. This clearly demonstrated, dose-dependent effects of ascorbic acid on Dalton’s Lymphoma progression *in vivo*, wherein ascorbic acid therapy brought significant improvement in all the parameters studied. Therapy also prolonged survival time of DL mice significantly by impeding tumor growth. Further, for discovering underlying HDAC regulatory mechanisms, changes in mRNA expression of Class I and Class II HDACs in DL cells was also studied after ascorbic acid treatment. This showed that ascorbic acid modulates mRNA expression of HDAC 1,2 & 6 and may mediate its anti-tumor effects through this mechanism. For further elucidation, *in silico* analysis of the docking ability of ascorbic acid on HDACs was done in order to understand its interaction with these enzymes, thereby studying the possible change in their activities. However, *in silico* docking analysis showed no inhibitory effect of ascorbic acid on the activity of human HDAC 1, 2 & 6. Thus, suggesting that ascorbic acid affects acetylation status of cancer cells by regulating the expression of HDACs and probably not by inhibiting the activity. Taken together, this study provides a strong basis for advancing pharmacologic ascorbate in cancer treatment and also points towards the involvement of HDAC regulatory mechanisms for its anti- cancer potential, however further studies are required to work out the exact pathways and the genes involved.

Phylogenetic Analysis of Nesfatin-1, a Novel Peptide

P-31

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Nesfatin-1 is a pleiotropic hormone derived by proteolytic cleavage of the prepropeptide, nucleobindin 2 (NUCB2). Its recent discovery and involvement in several metabolic, reproductive and cardiovascular functions along with its implication in several diseased conditions in mammals prompted us to understand about this interesting molecule in other vertebrates. To generate putative protein sequence of nesfatin-1 from different vertebrates, their respective NUCB2 protein sequences were retrieved from NCBI and subjected to ProP 1.0 cleavage site prediction software. Multiple sequence alignment of the acquired nesfatin-1 protein sequences showed high conservation (>80%) between higher vertebrates, from reptiles to mammal. However, its homology with fishes and amphibians was quite low (55-70%). A maximum likelihood tree generated using MEGA 7 software showed a single clade comprising of reptiles, aves and mammals where chelonia, crocodilia, aves and mammals figured together while squamates formed a separate group. On the other hand, fishes and amphibians claded separately. Further, PROVEAN tool was employed to study the effect of substitution/deletion in nesfatin-1 of different vertebrates. Although majority of the substitutions were neutral across vertebrates, deleterious mutations concentrated towards N-terminal region of the peptide were observed. Interestingly, the highest number of deleterious mutations were seen in fishes. Selection pressure analysis using Datamonkey tool demonstrated episodic diversifying selection at the node constituted by fishes, reaffirming that high evolutionary pressure has acted on fish nesfatin-1. Nonetheless, midsegment of the peptide known as its bioactive core was seen to be under negative selection indicating its conservation across vertebrates. The current *in silico* analyses suggest that nesfatin-1 has evolved faster in fishes as compared to that of other vertebrates.

P-32

Deciphering STAT3 Regulatory Mechanism(s) in HPV Transcription in Cervical Carcinogenesis

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Background: Signal transducer and activator of transcription 3 (STAT3) plays an essential role in cellular proliferation, differentiation, and cell survival. In the last decade, our laboratory has been actively engaged in identifying the carcinogenic role of STAT3, the expression and activity of which increase in cervical cancer with disease severity. STAT3 plays an indispensable role in human papillomavirus (HPV) transcription and expression of viral oncogenes E6/E7. However, the underlying mechanisms are poorly defined.

Objective: To dissect the molecular events through STAT3 that influence HPV infection and subsequently the cervical carcinogenesis.

Materials and Methods: We examined HPV-positive (SiHa, HeLa) and HPV-negative (C33a) cervical cancer cell lines for the expression of viral oncoproteins (HPV16/18 E6 and E7) and host transcription factors STAT3, pSTAT3 (Y705 and S727) by immunoblotting and immunocytochemistry. The direct interaction of STAT3 with HPV LCR was determined using a bioinformatics tool FIMO (Find Individual Motif Occurrence; meme-suite.org) and using HPV18 ChIP-seq data. Experimental validation of the same is being carried out by ChIP-PCR. STAT3 reporter plasmids (pLucTKS3), internal control renilla luciferase (pRL) were expanded to measure endogenous STAT3 activity. HPV16 plasmid was cloned for its expression in HPV negative cells to examine the interaction of STAT3 with HPV LCR. Further, indirect functional interactions of STAT3 with other transcription factors having binding site on LCR like AP1 (JunB, JunD, c-fos) were examined by Co-IP and by supershift assay (Light Shift Chemiluminescent EMSA). Using the genome visualization tool, the co-expression and correlation studies of STAT3 and AP1 (JunB, c-Jun, JunD, c-Fos, FosB, FOSL1, FOSL2) genes were analyzed from TCGA data of cervical squamous cell carcinoma.

Results: Cytoplasmic expression of HPV16 E7, HPV18 E7 was noted in SiHa and HeLa cells respectively. Higher expression level of pSTAT3-S727 was detected in all the fractions (whole cell, cytoplasm and nucleus) of SiHa cells comparable to HeLa and C33a cells. Presence of STAT3 motif in HPV18 genome was mapped as 4bp spacer in LCR and near L1/LCR junction. Manual analysis of HPV16 genome revealed a series of atypical potential sites [TT(N4-6) AA] for STAT3. Transcription factor AP1 found predominantly localized in nuclei of cervical cancer cells with somewhat punctate signal in SiHa cell line whereas STAT3 expression was demonstrated in both the compartments (cytoplasm as well as nucleus). In silico results of cervical carcinoma revealed significant correlation between STAT3 and AP1 genes. NFkB probe demonstrated strong DNA-binding activity comparable to STAT3 and AP1 probes. The pLucTKS3, pRL and HPV16 construct will be used for expression analysis of HPV transcripts and reporter activity.

Conclusion: The study will provide the molecular insights into activated STAT3 signaling and its role in HPV integration in the host genome which could be utilized as a possible therapeutic, diagnostic and prognostic target for potentially-progressive cervical cancer and precancer lesions.

P-33

Annual profiling of multiple forms of vitellogenin (vg) and choriogenin (chg) genes in Indian fresh water murrel, *Channa punctatus*

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Endogenous rhythms, nutritional status and seasonal changes in day length and water temperature regulate the release of hormones from hypothalamo-hypophyseal gonadal axis. It is well established that estradiol-17β is released into the circulation that binds to specific estrogen receptors in liver to induce the synthesis of vitellogenin and choriogenin proteins. In the present study, hepatic expression of multiple forms of vitellogenin gene (*vga*, *vgb* and *vgc*) and choriogenin genes (*chgH*, *chgL*) has been correlated with seasonal changes in gonadosomatic index in the Indian fresh water murrel. To investigate temporal sequence of *vg* and *chg* genes expression, liver has been processed for RNA isolation followed by quantification of each gene using specific primers. Real Time PCR was performed. We have observed that lower dose of estradiol initiates choriogenesis preferentially over vitellogenesis. Expression of *chg* genes prior to *vg* genes suggests that choriogenin protein is synthesized early during oogenesis that helps in chorion formation around the egg. This process makes egg covering thicker so that oocytes can incorporate large amount of yolk into oocytes during exogenous vitellogenesis.

P-34

Isolation and identification of amoxicillin degrading bacteria from the Yamuna river water

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Antibiotic contamination in the environmental matrices is a serious global problem which leads to an increase in the proliferation of antibiotic resistance genes. Amoxicillin is ubiquitous in the environment, but there is hardly any information on the dissipation of amoxicillin by the microbial community. In the present study, amoxicillin-resistant bacteria were isolated using selective enrichment procedure. Many morphologically distinct colonies were obtained. The minimum inhibitory concentration was checked for all the isolates and only strain MMA, WA, and WA5 were able to grow at increasing concentration of the amoxicillin. The isolates were subjected to 16S rRNA gene sequencing and phylogenetic analysis, and were identified as *Alcaligenes* sp. MMA, *Burkholderia* sp. WA, and *Stenotrophomonas* sp. WA5. The amoxicillin removal of the strains was carried out in M9 minimal media and the removal was checked by Ultra Power Liquid Chromatography (UPLC). The UPLC results showed that the bacterial strains were able to remove amoxicillin in 14 days. *Alcaligenes* sp. MMA could remove 84% of the amoxicillin whereas *Burkholderia* sp. WA removed 69 % of amoxicillin, and *Stenotrophomonas* sp.WA5 removed 97% of amoxicillin in 14 days. Further, the metabolites were identified for *Alcaligenes* sp. MMA and *Stenotrophomonas* sp. WA5 using mass spectrometry (LC–MS/MS) analysis. Various metabolites including the degradation products of amoxicillin ex: penicillic acid, benzoic acid, benzothiazole, 2-Amino-3-methoxyl benzoic acid, 4-Hydroxy-2-methyl benzoic acid, 5-Amino-2-methylphenol and 3,5-Bis(tert-butyl)-2-hydroxybenzaldehyde were identified at the end of 14 days which further confirms the degradation of the amoxicillin by the bacteria.

P-35

Irradiation impact on sexual behaviour of female moth, *Spodoptera litura* (Fabricius) and its potential role in operating 'Inherited sterility technique' for pest suppression

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Inherited Sterility technique (IS) as a modified Sterile Insect Technique (SIT) is a radio-genetic and eco-friendly method, that has a noteworthy potential towards management of a serious noctuid pest, *Spodoptera litura* (Fabr.). The traditional approach of the IS technique involves male-only field release and the methodology includes sex based segregation before the mass release.

The objective of this research study involves the inclusion of irradiated female moths along with the irradiated male moths for IS technique so as to avoid the tedious sex segregation of moths and to ensure the substantial inherited sterility in F1 generation. This would warrant the determination of a suitable single gamma dose that could fully sterilize females and partially sterilize males in view of differential sexual radio-sensitivity (females being more radio-sensitive than males).

The radio-biological investigations on the females, irradiated with 100 -250 Gy, showed a protracted calling and mating behaviour and exhibited a decrease in oviposition, fertility and longevity with increase in radiation dosage. The sterilizing dose without compromising the mating competence significantly, was identified as 130 Gy for females. The same dose (130Gy) could induce partial sterility (ca. 56%) in males, followed by 74-87% sterility in F1 generation. A marked impact of irradiation was noticed in pheromone titres and their composition in the irradiated females. GC MS analysis of pheromonal glands of irradiated females, indicated a distinctive change in the titres of sex attractants (Eicosyl acetate, 9-Octadecenoic acid (Z)-methyl ester), copulation releasing pheromone (Deoxy-nonacosane, Heneicosane) and ovipositor releasing pheromone (2,6,10,15-Tetramethyl heptadecane) at 200 Gy but the effect was not significant at 130 Gy irradiated female moths which supports the suitability of 130Gy to be used in operating IS technique. Further, the studies on using 130Gy to both sexes is underway to assess the quantum of sterility induction in F1 progeny towards pest suppression.

P-36

Applications of L-Tyrosine Mediated Gold Nanoparticles in Remediation of Contaminated Water

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Rapid expansion in population, agricultural activities, industrialization and widespread disposal of various pollutants into water bodies have rendered freshwater into a cut-throat competitive resource in many parts of the world. Moreover, this stumbling block of water scarcity is also putting a damper on the economic development. So, in this present generation of inadequate fresh water resources, efficacious treatment of wastewater is an indispensable necessity for the expanding economy. It is, therefore, critical to develop competent and novel strategies to supplement existing approaches to manage water pollution with low capital requirement and among various outlooks, “Nanotechnology” came up as one of the most promising approach to combat this menace.

Nanotechnology exploits the unique size-dependent properties of nanoparticles to design a sensitive analytical approach for water remediation. However, the conventional methods of nanoparticle synthesis are being increasingly reported as toxic towards multiple aspects of human physiology, and the reaction by-products further loading the environment. To address these concerns, researchers working on the nanoscale therefore calls for green synthesis of nanoparticle as safer, inexpensive, and environment-friendly alternative.

In the present study, we used tyrosine mediated gold nanoparticles (AuNPtyr) as sensitive colorimetric probes and explored their potential to formulate a cost-effective method to provide a sustainable and practical solution for water remediation. Results obtained from the study revealed that AuNPtyr can be used for rapid tracking and quantitative estimation of heavy metals present in contaminated water.

P-37

Molecular Mechanism and Transient Silencing of GDNF/Gfrα-1: Possible Implication on DA-Ergic System

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Potent signalling molecule glial cell line-derived neurotropic factor (GDNF) which preferentially binds to GDNF family receptor α-1 (GFRα-1) to signal the GDNF-GFRα-1/–RET complex which promotes differentiation of dopaminergic (DA-ergic) neurons. The recent study aimed to evaluate the significance of GDNF/GFRα-1 in the functions of DA-ergic system during early brain and gonadal development in catfish. Tissue distribution analysis revealed ubiquitous expression with high levels in female brain and ovary. Differential expression analysis showed high expression was evident in 75 and 100 days post hatch females than the respective age-match males during brain development. Further, transient silencing of GFRα-1 through siRNA significantly lowered the GFRα-1 mRNA levels and certain in brain specific genes, *in vivo* and *in vitro.* Similarly, flow cytometry analysis and cytoxicity has been done after the exposure of neurotoxin MPTP to check damaged DA apoptotic cells using primary brain cell line and C6 glial cell *in vitro* and the changes in the levels of biogenic amines measured. GFRα-1 has been localized in preoptic area and hypothalamus which correlated well with the expression analysis in different regions of brain. Hence, the involvement of GDNF/GFRα-1 might be critical for brain to regulate gonadal function as well as considered as an excellent candidate molecule to protect and /or regenerate the DA-ergic system.

Key words: GDNF/GFRα-1, Dopamine neurotoxin, Transient Silencing

P-38

Ovarian Progesterone Receptor in *Hemidactylus flaviviridis*: Reproductive Phase-Dependent Expression Pattern, Gonadotropic Regulation and Correlation with Plasma Progesterone Level

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Sequence characterization of progesterone receptor (PR), its temporal expression pattern along with plasma profile of progesterone during different reproductive phases of the wall lizard, *Hemidactylus flaviviridis* enrich our comprehensive understanding of intraovarian functions of progesterone receptor in reptiles. A 1688 bp long *pr* transcript was obtained from ovarian transcriptome data (Bioproject I.D PRJNA32437) of the wall lizard. The 384 amino acid long putative partial peptide encoded by the transcript showed high homology with mammalian PR and consisted of a DNA binding domain, a hinge region and a ligand binding domain. Further, ovarian *pr* expression estimated during different reproductive states showed a marked increase in ovaries with early/late vitellogenic follicles implicating *pr* in final follicular development and ovulation in wall lizards. The role of *pr* in wall lizards may be extended to maintenance of corpus luteum and consequently retention of egg in the oviduct during early gestation. This is proposed based on high expression of *pr* even in postovulatory ovary and the single peak of plasma progesterone during early gestation period. The current study also examined the gonadotropic regulation of progesterone production and ovarian *pr* expression. Administration of follicle stimulating hormone (FSH) induced follicular growth, development and vitellogenesis. Rise in plasma progesterone and ovarian *pr* paralleled each other in lizards receiving 7/11 injections of FSH. Our *in vivo* observations were corroborated by *in vitro* study wherein FSH directly upregulated *pr* expression in early vitellogenic follicles while it had no effect on gene expression in early growing and previtellogenic follicles.

P-39

Triazophos Suppresses the Leucocyte Immune Responses in Freshwater Teleost, *Channna punctatus*

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Triazophos is a commonly used organophosphate insecticide, which suppresses the acetylcholinesterase enzyme and causes paralysis and ultimately death of insects. Effects of the organophosphate pesticides on fish immunity have rarely been investigated. The present study was planned to evaluate the immunotoxic role of in vitro triazophos exposure to the leucocytes in a freshwater teleost fish, *Channa punctatus*. Different concentrations of in vitro triazophos (0.1, 0.5, and 1 µg ml^{-1}) were used to study lymphocyte proliferation, superoxide production, leucocyte phagocytosis and nitrite release. Dose-dependent reduction in various immune responses was observed. Mitogen induced blood lymphocyte proliferation was significantly reduced at 0.5 and 1 µg ml^{-1} but not at 0.1 µg ml^{-1} in vitro concentration of pesticide. Superoxide production and nitrite release by blood leucocytes were reduced in cultures having triazophos. The suppressive effect was also found while analyzing phagocytic response. These investigations describe the effects of pesticides on immune responses in *C. punctatus* and are helpful in giving an insight about immunotoxicity in fish. However, more researches are essential to help design the strategies to combat ecotoxicity in aquatic bodies.

P-40

Expression of Bacteriophage Endolysins for Mitigation of Methicillin Resistant *Staphylococcus aureus* Infection

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MRSA (Methicillin-resistant *Staphylococcus aureus*) one of the major pathogens in hospital, community-associated infections causing blood stream infections, endocarditis, skin and soft tissue infections. This pathogen is also associated with live-stock known as LA-MRSA (live-stock associated MRSA). The development of resistance against antibiotics in *Staphylococcus aureus* is increasing gradually, elevating the risk of infection. As an alternative to antibiotics, bacteriophage derived proteins known as Endolysins with lytic property against peptidoglycan layer of bacterial cell wall act as a promising antimicrobial agent when externally applied against Gram positive bacteria. Bacteriophage endolysins are lytic enzymes secreted by phage at the end of lytic life cycle to release phage progenies. Endolysin LysK derived from bacteriophage K (*Staphylococcal* phage) and its different domains including catalytic domain CHAP have shown effective lytic activity against *Staphylococcus aureus*. Present study is focused on expression of different domains of bacteriophage endolysin LysK in bacterial system and to observe their lytic activity on MRSA bacteria. pET22b plasmid with T7 promoter, pelB leader sequence for subcellular targeting and C- terminal His-Tag was used as expression vector. LysK-CHAP and LysK-SH3b domain constructs cloned in pUC57 vector was prepared. Using double digestion of gene of interest and pET22b, CHAP and SH3b were cloned into expression vector. Both the domains of LysK CHAP and SH3b have been successfully cloned in pET22b expression vector, in future we wish to express these proteins in *E. coli* BL21(DE3) and isolate it to check its lytic activity.

P-41

Divergence Pattern of Teleost TLRs With Emphasis on their Repertoire in the Walking Catfish, *Clarias batrachus*

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The significance of toll-like receptors (TLRs) as critical molecular tools for understanding the evolution of vertebrate immunity has been validated by multiple studies across vertebrate and invertebrate classes. However, in fish, their status remained scarcely investigated till date with only few reports available, based on intra-species assessment. The present study was undertaken to evaluate the nature of selection constraints active on the teleost TLRs with a special emphasis on the TLR repertoire in the Walking catfish, *Clarias batrachus*. A total of 228 teleost TLRs were analyzed in this study including the eleven newly identified *C. batrachus* TLRs (TLR1, 2, 3, 5, 7, 8, 9, 13, 22, 25, 26) on the basis of phylogenetic proximity to its *Siluriformes* orthologues. The analyses showed a relaxation in the selection constraints for TLR1, 7, 8 and 9 wherein our species of interest, *C. batrachu,s* was found to be under significant episodic selection for TLR1 and 7 alignments. Based on our results, we hypothesized a trend of diversification in the teleost TLR repertoire which may account for species-specific ligand recognition in the vertebrate group. Apart from enhancing our insight on molecular evolution of TLRs, this study would also guide the functional experiments for ligand promiscuity of teleost TLRs. The findings pave way for exploring disease resisting mechanisms and consequent design of ligand-based vaccines in aquaculture candidates like *C. batrachus*.

Effect of Bedtime on Salivary Melatonin Rhythm and Chronotype in Young Human Female Volunteers

P-42

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An understanding of the relationship between the sleep-wake cycle and endogenous circadian system is important to promote good health in a society. Therefore, the present study was aimed to study the effect of bedtime on salivary melatonin rhythm in young female volunteers in Raipur, India. Twenty three female volunteers aged 25.30±0.72 (mean±SE) years were selected for the study. Necessary ethical permission from the Institutional Ethical Committee and written consent from the participants were obtained prior to start the study. Diurnal preference was measured using the Morningness-Eveningness Questionnaire (MEQ) (Horne and Östberg, 1976) and sleep quality was measured by using Pittsburgh Sleep Quality Index (PSQI) (Buysse et al., 1989). Salivary melatonin was measured by using commercially available ELISA kits from IBL International Hamburg, Germany (www.IBL-international.com.). Saliva sample were collected at four time points on daily time scale i.e. at 18:00-19:00 hrs (evening time), 22:30-01:30 hrs (bed time), 06:04-09:25 hrs (morning time) and 12:00-14:00hrs (noon time) for three consecutive days during the course of a year i.e. summer, winter, spring and autumn. Results exhibit a significant effect of bed time on mid sleep only. Higher percentage of morning chronotype in early sleepers was observed as compared to late sleepers. Whereas, evening chronotype was higher in late sleepers as compared to early sleepers. Results of two factor ANOVA revealed a statistically significant effect of daily time and season on the level of salivary melatonin in both early and late sleepers. Results of cosinor rhythmometry revealed a statistically significant 24-h rhythm in the level of salivary melatonin in early sleepers during the summer and winter seasons. It can be concluded that late bed and wake-up time of sleep may delay the circadian pattern of melatonin rhythm and may be associated with evening chorotypes.

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Light at Night Alters Daily Behavioural Pattern and Physiology in Male Zebra Finches

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We investigated the effects of dim light at night (dLAN) on behaviour and physiology in male zebra finches. Light at night disturbs the light:dark cycle and in turn can disrupt the 24-h daily behaviours. Birds were exposed to dLAN of 5 lux with controls on dark night (LD; 0 lux) for 6 weeks. We measured different daily behaviours (feeding, drinking, perch hopping and preening) to assess the effects of dLAN. We also monitored changes in body mass, fat score, food intake, crop content and blood glucose level to examine the effects on physiology. dLAN negatively affects the daily behaviours. In particular, due to presence of light at the nighttime birds extended their feeding hours in the night also, which disrupted the daily feeding pattern. However, the overall daily food intake remain unchanged as compared to LD. dLAN induced perch hopping, preening and drinking at nighttime which also suggest alterations in the activity-rest rhythm as compared to the controls under dark nights. Interestingly, birds under dLAN increased their body fat score and hence, gained body mass which remained unchanged in LD. We also observed that, birds under dLAN have more crop seed content than in LD at the time of lights on. Our results suggest that feeding at the wrong time due to dLAN induced the changes in body mass, fat content and daily behaviours in male zebra finches which are diurnal, akin to human.

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Characterization of A Novel Histone H2A Specific Protease from Chicken Liver Nuclear Extract

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The histones are subjected to diverse arrays of posttranslational modifications such as methylation, acetylation, phosphorylation, sumoylation, ubiquitylation and citrullination etc. Histones are also subjected to irreversible posttranslational modification such as histone tail proteolysis. The N-terminal cleavage is reported in histone H3, whereas, C-terminal cleavage has been observed in histone H2A. We have reported a novel aspartic acid protease specific to H2A from chicken liver nuclear extract that cleaved the C-termini of histone H2A at the site between 90th and 91st amino acids. However, the protease is yet to be identified. In the present study, efforts were taken to purify the H2A specific protease from chicken liver nuclear extract to homogeneity by an empirically designed purification strategy. The protease activity was enriched by a series of column chromatography and the major bands were sequenced using MALDI based sequencing. However, the major protein band was identified as vinculin. Further, vinculin could immunoprecipitate (ip) actin from the chicken liver nuclear extract. Furthermore, the ip demonstrated H2A specific protease activity. It strongly suggested that probably the H2A specific protease was a part of a larger protein complex, which had at least the actin and vinculin. Efforts are being taken to purify the H2A specific protease to homogeneity and investigate its physiological relevance in terms of regulation of gene expression by modulating the chromatin structure and function.

P-45

Impact of Neuro-Immune mediated regulatory mechanisms during pathogenesis in the Model Host, *Caenorhabditis elegans*

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The interplay between neuron and immune system had been known in many conditions of a cell, but only few studies described the inter-players involved in their communication. This study tried to understand the consequence of neurotransmitters for the cross talk between Neuro and immune system during Host-Pathogen Interaction using *Caenorhabditis elegans* as a model host. *Cronobacter sakazakii,* Gram negative bacterium is seriously implicated in cases of neonatal septicemia, necrotizing enterocolitis, and meningitis in neonates and infants globally. It is one among the bacteria which can cross Blood-Brain Barrier. *C. elegans*, a well known nematode model organism already been explored for studying the immune regulatory mechanism and neuronal connections. It is built-up with 306 individual neurons and has its own innate immune response against the invading pathogenic microbes. In case of *C. sakazakii* and *C. elegans* interaction, it appeared that it was attracted towards the pathogen. In addition, survival of the host was drastically reduced, pharyngeal pumping rate was very low and ROS level was higher during their interaction. Further, we attempted to monitor the impact of sensory neurons, influence of neurotransmitters and the sequel for the immune regulations in the host during *C. sakazakii* infection. The metabolic footprinting obtained from LC-MS/MS of *C. sakazakii* infected *C. elegans* was analyzed for the derivatives or interacting metabolites of neurotransmitters, excitatory amino acids and biogenic amines. It was observed that the small molecules involved in cholinesterase activity, anticholinergic and serotonin inhibition were upregulated during *C. sakazakii* infection. The study is expected to pave a way for understanding the importance of neurotransmitters and the neuronal receptors activity during immune regulatory response pathway/players during *C. sakazakii* infection in the model host *C. elegans*.

P-46

Assessment of Immunostimulatory Properties of Achyranthes Aspera Seeds and Leaves Supplemented Diets in *Clarias batrachus* Fry

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The effect of Immunostimulatory properties and their remedial measures have been studied in catfish *Clarias batrachus* (magur) fry (352.4 ± 7.91 mg). Fish fry were acclimatized for 10 days and then fed with four different diets: 0.5% seeds (D1), 0.5% leaves (D2), 0.25% leaves (D3) of *Achyranthes aspera* and control (D4). After 60 days, all groups were immunized with c-RBC @ 50 µl/fish. Various tissues samples were collected on 7th, 14th and 21st days after immunization. The average weight, feed conversion ratio (FCR) and specific growth rate (SGR) were significantly higher in D1 diet fed magur compared to other feeding regimes. Serum lysozyme, myeloperoxidase, nitric oxide synthase and superoxide dismutase levels were significantly higher in D1 diet fed magur compared to rest experimental groups. Thiobarbituric acid reactive substances and carbonyl protein level were significantly lower in D1 fed magur compared to rest experimental groups. Tumour necrosis factor alpha (*TNF-α*), B-cell lymphoma 2 (*Bcl-2*), nuclear factor kappa B (*NF-kB*), *caspase-3*, *caspase-9*, Bcl-2-associated X (*BAX*), cytochrome complex, superoxide dismutase C (*SOD-C*) and inducible nitric oxide synthase (*iNOS*) were significantly up-regulated in D1 diet fed fish compared to other feeding regimes. Seeds and leaves supplemented diets showed immunomodulatory properties in and seeds were more effective than leaves.

P-47

Long Term Consequences of Constant Bright Light Environment on Reproduction and Associated Behaviours in Zebra Finches

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Aperiodicity in the light environment can induce widespread negative effects on circadian clock-controlled behaviour and physiology, since periodic day-night environment is critical for temporal organization in animals. Here, we hypothesized that a constant light environment would disrupt circadian rhythms and consequently affect singing behaviour and reproductive physiology in parents (P), F1 and F2 generation of zebra finches (*Taeniopygia guttata*). In total, sixteen zebra finch pairs were kept constant bright light (LL) environment, with controls under 12 h light: 12 h darkness (12L:12D). Over several weeks, we raised two generation of birds and recorded their 24 activity rest, singing and reproductive parameters, and measured hormone profiles of parents and offspring when adult. Exposure to LL decayed rhythmicity in activity and singing pattern in P but not in F1 and F2 birds. However, LL induced negative effects on song with reduced daily song bouts, unique syllables and song syntax. Circulating corticosterone (in males), testosterone and estradiol levels were significantly lower under LL than under 12L:12D. Furthermore, long term effect of LL in P birds reflected in reduced number of fledgling and viable offspring, reduced reproductive success and increased fledging duration and offspring mortality in C3 as compared to C1 and C2. The effects of LL on reproductive performance of F1 was more pronounced with longer initiation to breed, more attempts to nest and breed but failing significantly to do so, lesser eggs incubated to producing less number of viable offsprings, increased fledging duration and offspring mortality and decreased reproductive success. Both sexes differed in morphometric and phenotypic measurements. Overall, our results give insights into the possible impact of changing light environment in urban landscape on behaviour and physiology of animals.

P-48

Radiation Hormesis as an Augmentative Approach to Improve Radio-Genetic F1 Sterility Technique towards Suppression of a Polyphagous Pest, *Spodoptera litura* (Fabr.) [Lepidoptera: Noctuidae]

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Radiation hormesis is a biphasic phenomenon which gives positive response when biological agents are exposed to low dose and increase in dose decreases the benevolent effects. It stimulates the various behavioural and physiological activities of organisms. This property of radiation hormesis can be exploited in various biorational approaches for insect pest control. Although, much work has been done on high dose of gamma radiation, the effect of low dose of this stressor is not known in the insects. Thus, the objective this work was to investigate the effect of low range gamma radiation on the behaviour and viability of *Spodoptera litura* that would be reflected in life span and other physiological parameters. In this study, the hormetic dose range of radiation from 0.25 to 1.25 Gy was examined on various ontogenic stages (egg, larva and pupa) with an aim to rearing quality moths that would exhibit better viability and also retain better competitiveness (in terms of longevity, oviposition, fertility, mating success) when subjected to the proposed substerilizing doses (100-130 Gy), after hormetic irradiation, to be utilized in radio-genetic F_1 Sterility technique. The present results indicated the potential hormetic gamma doses as 0.75 Gy and 1.0 Gy in the case of egg, 1.0 Gy for larva and 1.0 Gy for pupal stage. These hormetic doses showed enhanced longevity and showed better mating performance as compared to control. Further, the study on the viability and competitiveness of substerilized (130 Gy irradiated) adults, preceded by hormetic irradiation in their ontogeny, is under progress to assess their reproductive fitness and the expression of certain physiologically vital genes (related to survival, antioxidant defence and reproductive performance) in correlation with F1 sterility induction. This study might further support this phenomenon of radiation hormesis and optimization of radio-genetic technique for Lepidopteran pest suppression.

Gonadotropin Imbalance and Progression of PCOS

P-49

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Background: Polycystic ovary syndrome (PCOS) is associated with higher levels of LH, and arrested ovarian follicular growth. High LH in PCOS patients may have deleterious impact on the FSH-stimulated metabolism in granulosa cells (GCs) leading to subfertility. However, the direct role of high LH on FSH mediated metabolic responses in PCOS patients is not clear.

Objective: To understand the potential role of high LH on FSH-stimulated metabolism in preovulatory GCs.

Methodology: In order to explore the role of gonadotropins in glucose metabolism in preovulatory granulosa cells (GCs), we examine the glucose uptake and its storage as glycogen through [U-^{14}C]-2 DG, and 2-NBDG. The role of IRS-2/PI3K/Akt2 pathway was studied through siRNA knockdown technique. To evaluate the specific role of IRS2, GS and PP1 in metabolism immunoprecipitation and specific assays were performed. Also, effect of hCG on FSH mediated glucose uptake and glycogen storage in control and PCOS patients were studied. The HEK293 cells co-expressing FSHR and LHR were used to demonstrate glucose uptake and BRET change by FSH and hCG.

Results: FSH found to be more potent than hCG in stimulating glucose uptake in control human and rat granulosa cells, where FSH stimulates the activity of glycogen synthase via IRS-2/PI3K/Akt2 pathway leading to increased glycogen synthesis. The FSH-stimulated glucose metabolism is found to be defective in GCs of PCOS-patients indicating defective FSHR activity. Administration of high concentration of hCG in HEK293 cells overexpressing Flag-LHR and HA-FSHR inhibited FSH-stimulated glucose uptake. Also, the increased BRET change was observed in HEK293 cells expressing FSHR-Rluc8 and LHR-Venus signifying increased heteromerization of LHR and FSHR in the presence of both hCG and FSH as compared to FSH-hCG alone.

Conclusion: The high level activation of LHR in GCs of PCOS patients instigates the attenuation of FSH mediated metabolic responses through inhibition of IRS-2 pathway, causing depleted energy stores and leading to follicular growth arrest.

Deciphering immune system in faster developing *Drosophila melanogaster*

P-50

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Every living organism attempts to maximize its Darwinian fitness by optimal allocation of energy reserves in somatic maintenance and reproductive effort. The somatic maintenance involves resistance/tolerance to various biotic and abiotic stresses, efficient scavenging of reactive oxygen species (ROS), repair of damage in body and countering infections through immune responses. However, organisms with rapid growth and short life spans are reported to invest relatively less resource in defence in favour of growth and early reproduction, as against those with slower growth and longer life spans due to increased exposure to pathogen.

Therefore, we tested the veracity of these claims using six *Drosophila melanogaster* populations; three of which are simultaneously selected for rapid development and extended adult lifespan while the other three are the ancestral controls. To evaluate if immune system is able to keep pace with faster developing flies, we monitored major lineages of hemocytes like plasmatocyes and crystal cells. Interestingly, faster developing populations had significantly higher number of circulating plasmatocytes alongwith the upregulation of two of the anti-microbial peptides, namely, Diptericin and Drosomycin under non-challenged condition; suggesting that the selected populations were investing more in defence mechanism despite having lower energy reserves as indicated by significantly lower levels of lipid reserves. However, when the flies were challenged with *Drosophila* pathogen *Pseudomonas entomophila* and *Bacillus thurengiensis* during larval stage; the selected populations were able to survive as well as the control populations.

Study of Sleep Pattern during Lockdown

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Global pandemic has caused sudden change in the daily routine. Along with all the zeitgebers of the body's clock, social zeitegeber is also tightly linked with regulation of sleep cycle. Since COVID-19 restrictions compelled people to waive the social obligations, which were linked to various events like school, offices, and meals. It provided us with an opportunity to compare the social pressure on the daily schedule and its impact on sleep regulation. The comparison in the sleep times before and after the imposed restrictions was calculated by measuring Social Jet Lag (SJL). SJL is the difference between the sleep duration in work day and free days. The data was collected from the residents of Pune city of Maharashtra, using an online Google form. The questionnaire was based on the Global Chrono Corono Survey (GCCS) by T. Roenneberg et al. It consisted of 47 questions related to sleep, meal, activity, and sunlight exposure time. A total of 151 participants participated in the survey during the period of May and June 2020. The data was grouped into three categories: students, employed, and unemployed /homemaker. Sleep debt analysis showed statistically significant change in all the three groups. The two groups, 'students' and 'employed' showed 2 fold decrease, while the group 'unemployed /homemaker' showed approx. 7 fold decrease in the sleep debt during lockdown. Analysis of social jet lag showed statistically significant reduction in the groups 'student' and 'unemployed', while does not show significant social jet lag in the group 'employed'. It was observed that there was approx. 7 fold and 10 fold increase in social jet lag before lock down in homemakers/unemployed, and students respectively, indicating the need for awareness about the importance of lifestyle preferences.

P-52

Transcriptional Regulation of Human Papillomavirus in Head and Neck Squamous Cell Carcinoma Cells

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Background: Human Papillomavirus (HPV)-positive head and neck squamous cell carcinomas (HNSCC) represent a distinct group of diseases that differ in their clinical presentation, disease progression and therapeutic response. However, oncogenic role of HPV in HNSCC is not established. For tumorigenic-transformation, HPV essentially requires a permissive cellular environment and host cell factors for induction of viral transcription, which remains to be investigated.

Aim: In the present study, we aimed to decipher the spectrum of host transcription factors in HPV-positive and HPV-negative HNSCC and their impact on HPV transcription using ectopically-expressing viral genome in experimental systemm.

Material and Methods: We examined HPV-negative HNSCC (Oct-1, SCC131, SCC84) and HPV-positive HNSCC (93VU147T, UDSCC2) cell lines for expression/activity of HPV LCR-related transcription factors namely AP1, NFkB and STAT3 by ICC. HPV16 whole genome present in pBR322 was transferred to eukaryotic expression vector pCDNA3.1(-) for stable propagation and expression of HPV16 full length construct.

Results: All the three transcription factors i.e. AP1 (c-fos), NF-KB-p65, NF-KB-p50, showed a prominent nuclear localization in UDSCC-2 cell line. In OCT-1, the localization of STAT3 was seen in the extranuclear space, whereas for the AP1 (c-Jun), the localization signal was seen in the nuclear space. HPV16 full-length construct was cloned in pCDNA3.1 and verified with PCR. Both pBR322_HPV16 and pCDNA3.1_HPV16 were characterized with HPV specific PCR. pCDNA3.1_HPV16 construct will be used for expression analysis of HPV transcripts in HPV-negative HNSCC cells.

Conclusion and Future prospects: HNSCC cells show expression of HPV-related transcription factors. Transfection of HPV-negative HNSCC (Oct-1, SCC131, SCC84) with pCDNA3.1_HPV16 and comparison with HPV-positive HNSCC (VU147t, UDSCC2) cell lines will provide necessary insights of HPV-permissive transcriptional milieu of HNSCC.

Keywords: Head and Neck squamous cell carcinoma (HNSCC), Human papillomavirus (HPV), pCDNA3.1_HPV16, Transfection

P-53

Influence of Radiation on Female Sex Peptide Receptor (Spr) to Assess the Frequency and Quality of Insemination in a Tropical Pest, *Spodoptera litura* (Fabr.) [Lepidoptera: Noctuidae]

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Spodoptera litura (Lepidoptera: Noctuidae) is a serious polyphagous tropical pest of several cultivated crops and has attained a global importance. Radio-genetic method- Inherited sterility technique (IS) has been proposed as an integral component of pest management strategy for this moth pest. IS involves inundative release of irradiated (sterile / partially sterile) insects to decrease the target pest population in the field. The effectiveness of sterile insect programs depends on successful mating of sterile males with the wild females. The sterile males need to copulate and effectively inseminate; cause infertility after amphimixis and induce reproductive refractoriness in female to check its remating propensity.

The secretions from male accessory gland (MAG) play a key role in the mated female behavior like calling, oviposition, remating, etc. It is reported that in *Drosophila* female, sex peptide receptor (SPR) detects male sex peptide (SP) and triggers post-mating changes in female. SPR expression (assessed by Real-time PCR analysis) was correlated with satisfactory mating and quality insemination. The females mated to radio-sterilized males (250Gy) showed significant decrease in SPR expression unlike the female mated with substerile males (130Gy) with respect to control (0Gy, non-irradiated). Further, the effect of male irradiation on female receptivity was studied which indicated a decrease in refractory period when female was mated with irradiated (sterile) male. Hence, the female after mating with sterile male (250Gy) was ready to remate more frequently with less refractoriness as compared to the remating propensity of female mated to substerile male (130Gy) or control. These results suggested that the male subjected to sterilizing gamma dose could influence the quality of insemination. Further, the degree of irradiation impact on insemination response is being correlated with sterility induced and mating competitiveness of the irradiated moths in order to optimize the F_1 sterility technique.

P-54

Urban and Rural Differences in Sleep Behaviour and Fatigue: The Consequence of Mobile Involvement and Internet usage among School going Female Adolescents

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Urban and rural habitats offer different and often contrasting lifestyle in terms of the light exposure due to difference in the electrification and technology reach. The continuous electric supply and advanced technologies like mobile and internet in urban areas are found to be associated with health hazards, such as the obesity, cardiovascular diseases, poor sleep quality, insomnia, and many other sleep related disorders. This study assessed the impact of urban and rural settlement on sleep related parameters and fatigue as a results mobile and internet addiction among school going female adolescents in the age group 14-18 years.

We surveyed randomly chosen students from both urban and rural settlement, and asked to respond to validated questionnaires formulated to assess the chronotype and sleep related parameters. We used Munich chronotype questionnaire for chronotype, the Epworth sleepiness scale for daytime sleepiness, Pittsburgh sleep quality index for sleep quality, fatigue severity scale for fatigue level, Young's internet addiction scale for technology addiction (mobile phone involvement scale and internet addiction). The results show that a larger proportion of rural population consisted of morning chronotype (50 %), as compared to the urban population (21%). Female students in rural settlements showed an early sleep onset and offset, a longer sleep duration, lesser total time in bed, lesser social jet lag and weekly sleep loss, lower daytime sleepiness and fatigue, and a higher percentage of good sleepers than the urban counterparts. The higher usage of mobile and internet was also observed among urban female adolescents. The study overall suggests that urban environment has negative effects on sleep-wake patterns and associated effects among young school going female adolescents.

P-55

Understanding the Genetic Basis of the High Degree of Quinolone Resistance Detected in Escherichia coli Isolated from Commercial Chickens from North India

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Antibiotic resistance has become a global healthcare challenge that leads to 750,000 annual deaths worldwide. Overwhelming use of antibiotics in farm animals for growth promotion is responsible for the occurrence and dissemination of antibiotic resistance from farms to various environments, including human. Chicken and eggs are the most favoured source of animal proteins in India. Quinolones, a class of clinically indispensable antibiotics, are one of the most abused growth enhancing drugs in poultry industry, which has resulted in a high prevalence of resistance concerning these antibiotics. Our study was an effort to understand the extent and genetic basis of quinolone resistance in microbes associated with commercial chickens. We collected cloacal swabs from 120 chickens from six geographically separated farms located in Sonepat, Haryana and Rampur, Uttar Pradesh to isolate *Escherichia coli* for the assessment of phenotypic resistance to three different fluoroquinolones (viz., nalidixic acid, norfloxacin, and ciprofloxacin). Isolates were subjected to PCR screening for plasmid-mediated quinolone resistance (PMQR) determinants (*qnrA, qnrB, qnrS, qepA and aac(6)-Ib-cr*). Eighteen nalidixic acid-resistant isolates were selected to identify quinolone resistance determining region (QRDR) mutations within *gyrA* and *parC* genes which encode gyrase A and topoisomerase IV, respectively. Isolates showed unprecedented levels of resistance against all three quinolones (nalidixic acid-91%, norfloxacin- 73%, ciprofloxacin- 66%). Among screened PMQR determinants, *qnrS* showed the highest prevalence (38%), followed by *aac(6)-Ib-cr* (16%) and *qnrB* (6%). QRDR mutations within *gyrA* and *parC* genes were found to be the major determiners of quinolone resistance. Commonest QRDR mutation, which also showed correlation with phenotypic quinolone resistance reported in our study was gyrase A-associated leu83 (replacing serine). The occurrence of both plasmid-borne and chromosome-borne resistance towards quinolones can have serious ecological implications. Therefore, our findings must encourage the authorities to impose strict restrictions on the use of quinolones in poultry sector.

P-56

Characterization of the Methanolic Seed Extract of Two Medicinal Plants, *Putranjiva roxburghii* and *Bryonia laciniosa* and its Effects on Gonads of Albino Mice

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The changing lifestyle in recent years has dramatically influenced the reproductive health of humans leading to infertility issues globally. One of the prominent approaches to address infertility issue has been the use of plant-based safe and affordable drugs with no or minimal side effects. The seed of two such plants, *Putranjiva roxburghii* and *Bryonia laciniosa* when co-administered is believed to help couples conceive and are used for gynaecological disorders and fertility. *Putranjiva roxburghii* (commonly known as putranjiva) belongs to the family Euphorbiaceae; while *Bryonia laciniosa* (commonly called shivlingi) belongs to the family Cucurbitaceae. Hence, methanolic extracts were prepared and characterized by thin-layer chromatography (TLC) and high-performance liquid chromatography (HPLC). Further, two experiments were out with the methanolic extract of the seeds of these two medicinal plants at a dose of 100mg per kg body weight to observe its effect on the reproductive physiology of albino mice. Experimental mice (Male and female) of two age groups - 3-week old (Experiment-I) and 8-week-old (Experiment-II) were administered with methanolic extract (ME) in normal saline, while the controls for the respective male and female mice for the two experiments received normal saline for continuous 42 days. Male and female mice were sacrificed at the interval of 14, 28 and 42 days of treatment. The TLC analysis of the methanolic extract (ME) showed five fractions which were named as Spot1, 2, 3, 4 and 5. These are being further analysed and characterized. HPLC analysis showed the presence of three phytocompounds, i.e. flavonoids - Quercetin (peak 4.867), Tannic acid (peak 2.497) and Rutin (peak 3.440) in the methanolic extract of the seeds of the two medicinal plants. Further, in both the experiments, no significant change in the body weight was observed in both male and female mice, irrespective of the treatment group. Histology of liver showed no toxicity at the

administered dose in either of the male and female mice groups in both the experiments. Histology of testis showed an increased number of Sertoli cells, interstitial cells, spermatozoa and Leydig cells with more vascularization and sperm count highly significant ($p<0.05$) in ME than NS treated mice in both the experiments. Ovarian histology in ME showed a more substantial number of follicles in the stage of secondary antral follicle maturing towards the Graafian follicle with increased vascularization in both the experiments. This result is in consensus with the estrous cycle of the females where ME-treated mice prolonged their cycle at the estrous phase (heat phase). The uterus histology also showed increased proliferation of uterine lumen with numerous epithelial glands in both the experiments. These changes observed may be due to the presence of the phytochemicals/flavonoids present in the plant extract, which may enhance reproductive efficiency of mice. Further extensive research along with proper screening of phytosteroids of the methanolic extract of the seeds of these two medicinal plants is under process.

P-57

Immunohistochemical Analysis of Heme Metabolizing Enzymes in Late Gestation Heme oxygenase 1 Knockout Mouse Embryos.

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Heme is an essential cofactor in several biological processes, but in its free state it is highly toxic. Therefore its metabolism is finely regulated within cells. Heme oxygenase (Hmox) is the first and rate limiting enzyme of heme degradation pathway. The inducible isoform Hmox1 is involved in mammalian development as partial to complete pre-natal lethality has been reported in the gene-targeted Hmox1 knockout (KO) mouse model. The role of Hmox1 in heme metabolism during embryogenesis has not been deciphered. This study addresses the consequences of Hmox1 deficiency on the expression of genes involved in heme degradation (BVRA and BVRB) and the rate limiting enzyme in heme synthesis (ALAS1) in late-gestation KO mouse embryos. The iron transporter FPN1 was also included in the analysis as Hmox1 has been reported to play important role in exporting iron from the cell via this iron transporter. Protein localization in intact tissue sections was detected by IHC and staining was compared between wildtype (wWT) and KO mouse embryos in five organs namely brain, heart, lung, liver and kidney. At 8X magnification low staining intensity was found for ALAS1, BVRA and BVRB in all the organs analysed in KOs. Such a comparison for FPN1 showed that the staining intensity was higher in brain, heart and liver of KOs in comparison to wWTs. Analysis of immunoreactive protein signal intensities at higher magnification (400X) showed statistically significant differences between wWT and KOs in all organs for ALAS1, BVRA, and BVRB whereas FPN1 was found to be higher in KOs and the difference was statistically significant in all organs except lungs. These results taken together indicate that there is some compromise in heme metabolism in KO embryos suggesting the role of Hmox1 in heme degradation during embryogenesis. The significance of higher protein signal for FPN1 in the absence of Hmox1 needs further investigation.

P-58

Understanding Transcriptional Regulation of Gonadotropin-Releasing Hormone in the Asian Stinging Catfish, *Heteropneustes fossilis*

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Onset of puberty and reproduction are controlled by coordinated regulators in brain-pituitary-gonadal axis wherein gonadotropin-releasing hormone (*gnrh*) plays a crucial role. It stimulates pituitary gonadotropin secretion and regulates the tertiary regulators such as steroids, peptides and growth factors in gonads. In addition to this, kisspeptin, encoded by kiss gene, binds to G protein-coupled receptor to stimulate hypothalamic *gnrh* and its isoforms thereby regulating the central reproductive axis in vertebrates including teleost. Fish have been an ideal model of study for *gnrh* multiple forms due to structural diversity and distribution. Furthermore, *gnrh* forms can be broadly classified into three types, wherein type I and type III may be the same variant in teleost whereas type II is common to all vertebrates. However, studies on transcriptional regulation of these correlates are meagre in fishes. Hence, to investigate these, *gnrh1* and *gnrh*2 promoter analysis was performed using *Heteropneustes fossilis* as a model organism by cloning of 5' upstream fragments of *gnrh1* and *gnrh*2. *In silico* promoter motif analysis revealed putative transcription factor binding motifs such as sox/SRY, oct, pax family of transcription factors and TATA/GATA/cAMP-responsive element binding proteins. The present study highlights novel genes/factors that may regulate *gnrh* action on fish reproduction that may provide new insights to understand the regulation of gametogenesis.

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Comparative account of sleep in Adolescents and Young Adults

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Sleep is important for maintaining overall physical and mental health. Adolescents and young adults (AYAs) at growing age need more sleep because it acts as the fuel for rapidly growing brain and bodies. Many physicians encounter young people having health issue developed due to improper sleep. Understanding the connection between sleep and health in AYAs is important as the sleep problem is coming up as a global pandemic that can seriously harm the health, safety, productivity of our nation's young generation, thus, is a major public health concern. The current study investigates the sleep behaviours of adolescents in comparison to young adults. Present study is based on self-reported sleep-log entries made by subjects. The collection of data is done on a random basis from school and university set up. Sleep log sheets is an instrument that elicits sleep-related data (sleep onset/offset, latency/inertia, etc.) on a day-to-day basis. Statistical analysis was done using the Mann-Whitney U test at a significance level of $p < 0.005$. To conduct this study, individuals of two different age groups were selected; adolescent group (age = 14±01 year; n = 45) and young adult (age = 23±01 year; n = 43). The study shows a significant difference between adolescents and young adult's timings for various sleep variables such as time to bed ($p<0.0001$), sleep onset ($p<0.0001$), sleep offset ($p<0.0001$), sleep inertia ($p= 0.0156$). Although, no significant difference was reported in actual sleep duration and sleep latency between the groups. Outcomes of the study are indicative of sleep deprivation in adolescent students. This information can help us to further understand the sleep-related differences in the behaviour of adolescent and young adults. This can aid in device a better work schedule to optimize their performance.

P-60

Behavioural and Metabolic Perturbations in PTSD

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Objectives

To identify and co-relate the behavioural and metabolic perturbations in Post Traumatic Stress Disorder (PTSD) rats using Open Field Test and NMR urinary metabolomics.

Background and Aims

Post-Traumatic Stress Disorder (PTSD) animal model reveals its metabolic and behavioural aspects, which can be translated to humans. NMR based metabolomics, have proved to be an efficient in identification of the metabolites in biofluids. Aim of the study was to develop clinical understanding of the metabolites and their pathways as well as the behavioural changes brought about by PTSD to aid in development of medical procedures and treatment.

Materials and Methods

Underwater trauma (UT), rat model of PTSD model was developed in male Sprague Dawley rats (n=10) (Richter-Levin, G. 1998). Validation and documentation of the pre and post trauma behaviour in rats was conducted using the open field test. Urine samples were collected before and after exposure. NMR spectroscopy was performed in samples prepared as reported earlier (Lindon, J. C. et al, 1999). The behavioural and metabolic data was compared and evaluated for the changes before and after the trauma.

Results

The behavioural as well as the metabolic profiles showed substantial changes pre and post trauma. Behavioural discrepancy pre and post trauma included changes in central square crossing, peripheral square crossing, first-minute activity, climbing, rearing, and grooming. In metabolic pool analysis the statistical technique Partial Least Square Discriminant Analysis (PLS-DA) showed a good separation between the two groups pre PTSD and post PTSD. Results depicted alterations in major metabolic pathways.

Conclusions

The pattern in weight gain and the behavioural study shows a close correlation to that of the metabolic data acquired through NMR metabolomics. Grooming and rearing, both the activities had been linked to recreational activities shown by the rats. Drastic reduction in both these activities post trauma clearly indicates, the inculcation of trauma and exhibition of the depressed symptoms in the rats. Irregular feeding and sleeping patterns were exhibited by rats, after they were exposed to trauma. This behavioral discrepancy arises from the various hormonal changes occurring in the body ensuing the traumatic experience. The metabolites α-ketoglutarate, succinate and citrate were lowered in PTSD animals indicates, decreased central energy production, citric acid cycle and electron transport chain. The increased n-methyl nicotineamide and nicotinate shows up-regulation of Tryptophan-Nicotinate pathway. Changes in Hippurate and β-hydroxybutyrate signify altered renal clearance, intestinal microbiota, and anxiety levels respectively. These findings may lay the groundwork for the future development of a urine-based diagnostic test and behavioural analysis.

P-61

Targeting Sperm Activating Proteins to Devise Biorational Modalities to Couple with Inherited Sterility (Is) Technique for Controlling a Serious Polyphagous Pest *Spodoptera Litura* (Fabr.) [Lepidoptera: Noctuidae]

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Spodoptera litura (Fabr.) is a nocturnal tropical pest damaging a wide range of important agricultural crops. Ecologically sound strategies are required to control this pest due to its immense resistance against all conventional pesticides. In this paper a novel strategy is discoursed for the development of bio-rational inhibitor molecules to target sperm activity in males and females (after copulation). In vitro-sperm activation assays using secretions of different parts of the male reproductive tract as activators confirmed the presence and its higher concentration in the lower prostatic part of the reproductive tract. The apyrene sperm activity was further pronounced by accessory glands secretion. Sperm activation bioassay using synthetic trypsin indicated sperm activation within optimum concentration range (0.0039mg/ml-0.5mg/ml). As per LC-MS investigation, the proteome-profiling of prostatic part further confirmed the presence of trypsin like serine protease of molecular weight 27kDa with 254 amino acids as an activator molecule. PAGE results showed the transfer of 27kDa protein from male to female reproductive tract within spermatophore during copulation. Gene for trypsin like serine protease was amplified using specific primers and was sequenced, that indicated 100% homology with trypsin like serine protease gene in *Spodoptera litura.* dsRNA (pertaining to trypsin like serine protease) is being designed to check the sperm activity. The role of sperm activation inhibitors (through protein inhibitors and RNAi technology) are discussed to act as potent bio-rational pest control molecules to be integrated with Inherited Sterility(IS) technique for an effective suppression of this serious polyphagous pest.

P-62

Exploring Fibrillin 1 Gene and its Product Asprosin in Spotted Snakehead *Channa punctata*

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Asprosin, a recently discovered fasting-induced gluconeogenic protein hormone, is involved in various metabolic functions such as glucose homeostasis, appetite regulation, reproduction, inflammation and apoptosis in mammals. It is the cleavage product of C-terminal region of preprofibrillin protein, encoded by fibrillin 1 gene (*FBN1*) and majorly produced by white adipose tissue. In humans, *FBN1* encodes 2871 amino acids long preprofibrillin protein which is cleaved by furin enzyme resulting in fibrillin 1 and asprosin proteins. However, no report is available on *Fbn1*, or asprosin in non-mammalian vertebrates. In view of this, the current study in *Channa punctata* was undertaken in which *in silico* analysis of fibrillin 1 was performed. The longest transcript of *fbn1* obtained from testicular transcriptome data of *C. punctata* (Bioproject accession PRJNA304088) subjected to nucleotide BLAST suggests the existence of this gene in teleosts. Using Gene Runner software, 8454 base pair long coding sequence of the *fbn1* was deduced. To validate the transcript sequence, primers were designed and reverse transcriptase polymerase chain reaction was performed. The transcript encoded 2817 amino acid long putative protein. Domain analysis predicted the presence of epidermal growth factor-like (EGF) domain, numerous EGF-like domains for calcium binding (EGF-CA) and transforming growth factor (TGF)-β binding (TB) protein domain as in humans. Phylogenetic tree for fibrillin 1 protein showed a separate cluster for fishes wherein the fibrillin 1 of *C. punctata* was placed along with *Anabas testudineus* belonging to the same order. *In silico* analysis also revealed the presence of conserved furin enzyme cleaving site in the putative profibrillin protein suggesting that there is a possibility of cleavage of profibrillin into fibrillin 1 and asprosin as seen in mammals. Hence, using the C-terminal region of fibrillin 1 implicated in coding for asprosin, 3D model of snakehead asprosin protein was constructed and compared with 3D models of representative members across the vertebrates. Post-translational modifications such as phosphorylation and glycosylation sites which are essential for signaling, intermolecular interactions and protein secretion were predicted in asprosin.

P-63

Effect of *Groundnut bud necrosis virus* on the Developmental Period on its Vector (*Thrips palmi*) and Non-Vector Species (*Thrips tabaci)*

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Thrips are minute insects with fringed wings belonging order Thysanoptera. They cause direct damage to the plant by feeding on its sap. They also transmit a virus called *Tospovirus* that belongs to the genus *Orthotospovirus*, family *Tospoviridae*, and the order *Bunyavirales*. Tospoviruses cause various diseases in plants that create huge economic loss worldwide. During course of virus transmission, thrips are also infected by tospoviruses. Many studies have been done to check the effects of tospoviruses on vector thrips species but very few studies are conducted on non-vector thrips species. In this study, we focused on the effects of *Groundnut bud necrosis virus* (GBNV) on the developmental period of *Thrips palmi* (a vector species) and *Thrips tabaci* (a non-vector species). The first instar larvae of *T. tabaci* and *T. palmi* were allowed to feed on GBNV infected cowpea leaves for 24 h and then transfer to the healthy leaves and analyzed the development period till they emerged into adults. Our study shows that the developmental period of GBNV exposed larval *T. tabaci* do not differ significantly as compared to the non-exposed *T. tabaci* larvae. However, in case of *T. palmi* we observed that the development period of GBNV infected thrips was decreased as compared to the healthy thrips. The result of our study will be useful for improving our knowledge regarding the early events of virus–vector interaction leading to successful virus transmission.

P-64

Effect of Light at Night (LAN) on Blood Biochemistry of Indian Baya Weaver

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The animal life, having endogenous biological rhythms, evolved closely coupled with natural light and dark cycle which at present, with the introduction of light at night (LAN), has interrupted the close coupling between the aforementioned rhythms. The find the role of artificial light at night (LAN) on some physiological parameters of baya weaver (Baya weaver; *Ploceus philippinus*), we have exposed the birds ($n=8$) under 12L:12D photoperiodic conditions with 5 lux constant night light intensity for five weeks. We found that the body mass, post-prandial blood glucose, haemoglobin significantly decreased while that of triglycerides, creatinine and AST showed a significant increase in its levels after LAN exposure. Pre-prandial blood glucose and bilirubin direct did not showed any significant change. A negative correlation in post prandial blood glucose and haemoglobin after the exposure of LAN indicates the negative effects of the LAN exposure to avian physiology (reported in literature). Thus the study reveals the deteriorating effect of night light on the physiology of birds.

P-65

Gut Microbiome of Freshwater Fish

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The gastrointestinal tract of vertebrates is a complex environment which harbours pathogenic bacteria in addition to symbiotic bacteria. These symbiotic bacteria suppress the growth of opportunistic pathogens by competing for nutrients available in the host and by production of various antimicrobial peptides, helping in host nutrition and digestion, development of effective immune system. Dysbiosis leads to diseased condition. Although fish represents the greatest diversity among all vertebrates yet there are important gaps in our present understanding of their resident microbiota and its functional significance. Thus, knowledge of gut microbiota will help enumerate the intricate mechanisms of host-microbe relationships. An increased demand on aquaculture industry has led to the surge of antimicrobial resistance. Therefore, insights into such genes will help design antimicrobial peptides as a substitute over conventional antibiotics.

P-66

Therapeutic Potential of Tinospora cordifolia: Multiple Effects on Lymphoma-Induced Neovascularization

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Neovascularization is an important hallmark of cancer wherein endothelial cell (EC) proliferation and matrix degradation plays a crucial role. This activated angiogenic switch is a consequence of the imbalance in expression of pro-and anti-angiogenic genes which are known to be immensely impacted by ROS and epigenetic regulation. Many complementary therapeutics, particularly, herbal formulations have been reported to have beneficial effects in cancer management. One such nature's elixir, *Tinospora cordifolia*, is also known to have multiple properties and is being used for curing many diseases with least side effect in traditional Ayurvedic practices. However, their impact in cancer is not extensively studied. Therefore, in the present study we investigated potential of *Tinospora cordifolia* extract (TCE), majorly its impact on angiogenesis.

For the present study, we used a well-established murine model of Dalton's lymphoma (DL) and studied the effect of TCE treatment on neovascularization by evaluating blood vessel sprouting, matrix degradation and expression of angiogenic genes. For evaluating direct effect of TCE on EC proliferation and ROS production, we utilized an *in vitro* EC model developed from thoracic aorta. MMP9 level and activity were assayed using ELISA and gelatin zymography, respectively. Expression of angiogenesis-related genes and their promoter hypermethylation status were studied using qRT-PCR and MSP-PCR, respectively. We observed that TCE treatment showed significant reduction in tumor load with concomitant inhibition of neovascularization in DL mice. This effect was corroborated in *in vitro* study wherein TCE inhibited DLA-induced EC proliferation in a dose-dependent manner. Further, TCE reduced the DLA-induced ROS level in ECs. Reduction in MMP9 level and activity further supported the anti-angiogenic potential of TCE treatment. TCE modulated the expression of pro- and anti-angiogenic genes via impacting their promoter hypermethylation status. Our data strongly suggest that *Tinospora cordifolia* exerts anti-tumor activity by acting upon multiple targets involved in neovascularization. Thus, it may serve as an effective complementary therapeutic agent in cancer management via its impact on angiogenesis.

P-67

Testis-specific Estrogen Receptor Subtypes in Spotted Snakehead *Channa punctata*: Reproductive Phase-dependent Expression and Gonadotropic Regulation

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The present study identified transcripts for three subtypes of estrogen receptor (*er*), *eralpha* (*cperα*), *erbeta1* (*cperβ1*) and *erbeta2* (*cperβ2*), from testicular transcriptome data of spotted snakehead *Channa punctata*. The characteristic domains of nuclear receptors were delineated by *in silico* analysis of their protein sequences. Phylogenetic analysis and multiple sequence alignment indicated closeness of these receptor subtypes with their homologues from other teleosts and conservation of various receptor properties. Interestingly, subtype-specific properties such as ligand binding, phosphorylation and ligand-dependent transcriptional activity were observed. Reproductive phase-dependent expression analysis of *cper* subtypes showed low level of their expression in testis during preparatory and spawning phases while high level in postspawning and resting phases. In addition, treatment of *C. punctata* with human chorionic gonadotropin during resting phase induced spermatogenesis and spawning but decreased the expression of *cperα*, *cperβ1* and *cperβ2*. Taken together, it appears that the female sex steroid estrogen is involved in regulating the testicular events of the inactive reproductive phases in *C. punctata*, *i.e.*, maintaining testicular regression and repopulating testis with spermatogonia.

P-68

Tumor-Derived Exosomes as a Salient Protagonist in Mediating Pro-Tumoral Activation of Macrophages

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Exosomes are nano-vesicles that form intercellular communication networks to mediate normal physiological functions in the host. However, in cancer conditions, their dysregulated release, principally by tumor cells, governs aggressive tumor behavior. Tumor-derived exosomes (TEXs) support tumor growth and metastasis by promoting its various hallmarks, including immune evasion. Recent reports suggest that macrophages, the key immune cells, are the major target of TEXs. Macrophages, depending upon the stimuli, can be either classically activated or alternatively activated to form M1, anti-tumoral or M2, pro-tumoral type, respectively. The TEXs mediate pro-tumoral M2 activation, a known prognostic marker in many cancer types. Therefore, the pro-tumoral macrophages could be a potential target in cancer therapeutics, wherein exploration of mechanism behind TEXs-mediated M2 activation is a pre-requisite. To investigate this, we used the murine model of Dalton's lymphoma (DL) and isolated exosomes from its fully-grown ascites. These lymphoma-derived exosomes were characterized and then used for *in vitro* studies by incubating macrophages with them. In the *in vitro* system, we assessed macrophage morphology and level of reactive oxygen and nitrogen species (ROS/RNS). Also, the M1/M2-specific markers together with TLR2 expression were investigated. We observed vesicle-like structures in electron microscopy which was further confirmed by immunoblotting using exosome-specific markers. The macrophages incubated with exosomes showed spindle-shaped morphology and produced high ROS, characteristic of M2 type. Nitrite release is an important characteristic of M1 macrophages and we observed significant reduction in nitrite release in LPS-stimulated macrophages by exosomes. We also observed upregulation of arginase1, an M2-specific marker, and TLR2 expression in macrophages incubated with lymphoma-derived exosomes. Our results suggested that lymphoma-derived exosomes polarize macrophages towards pro-tumoral M2 type by upregulating TLR2 expression. But there is still a need to explore the involvement of other TLRs that could be playing a role in TEX-mediated activation of macrophages. If unravelled, TLR signalling would offer a strong prospect to activate anti-tumor immune response using a potent immunomodulator in cancer therapeutics.

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Prenatal exposure to Endocrine disrupting chemicals induces anxiety-like behaviour?

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Bisphenol-A (BPA) is one of the extensively studied estrogenic endocrine disrupting chemicals (EDC) with ubiquitous exposure among humans and wildlife. While there are literature reporting the association of dysregulated Brain-derived neurotrophic factor (BDNF) expression levels with altered cognitive and emotional behaviour such as anxiety-like and stress behaviour in animal models, there are no studies in BPA that investigate these altered neurobehavioural outcomes in parallel with the expression of intracellular proteins involved in BDNF signaling pathway.In this study, pregnant Wistar rats were exposed to BPA through water (25 µg/L, 250 µg/L, and 2.5 mg/L) during gestation day (GD) 9-21. Prenatal BPA exposure, increased anxiety-like behaviour in males and decreased exploratory behaviour in both male and female offspring. Downregulation of both BDNF and CYP19A1 genes were observed in male BPA-exposed offspring, whereas in females, the expression was upregulated. The expression of p-AKT, p-MEK and p-ERK proteins were increased in males, while in females, it decreased. Both the male and the female BPA-exposed offspring exhibited elevated levels of DNMT1 protein. The sex-specific alteration in the expression of CYP19A1 and DNA methyltransferase 1 (DNMT1) suggests that both hormonal and epigenetic dysregulation could underlie the long-term BPA-induced effect on anxiety-like behaviour in the offspring.

Role of Wnt/β-catenin Signalling in *M. fortuitum*-Induced CNS Tuberculosis

P-70

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CNS tuberculosis accounts for the most rare and severe implications of mycobacterial infections. As of now, there is no universal animal model for studying the pathogenesis underlying CNS tuberculosis. In this study, adult zebrafish (*Danio rerio*) were injected intraperitoneally (i.p.) with *Mycobacterium fortuitum* and the prognosis of CNS tuberculosis studied. *M. fortuitum* is a non-tuberculous mycobacterium residing in aquatic and soil habitats. The spectrum of disease caused by this pathogen ranges from pulmonary to systemic infections. Results suggested *M. fortuitum* invades zebrafish brain, triggering extensive pathology such as neuropil vacuolation and lymphocytic infiltration as evident by CFU and histopathological studies. *M. fortuitum* affects blood brain barrier (BBB) integrity as evident by decreased expression of tight junction and adherens junction complex molecules (claudin5a, occludin and α-catenin) and Evans blue dye extravasation assay. RT-qPCR studies suggested upregulated expression of *wnt2*, *wnt3a*, *fzd5*, *lrp5/6* and *ctnnb1*, along with concordant downregulation in *axin* and *gsk3ba* (components of β-catenin degradation complex) and *capn2a* (β-catenin regulator) in the infected brain. *M. fortuitum* infection upregulated expression of pro-inflammatory cytokines (*ifng1* and *tnfa*) at early stages of infection and anti-inflammatory cytokines (*il4* and *il10*) at later stages of infection. We conclude that *M. fortuitum* represses tight junction and adherens junction complex proteins affecting BBB permeability and invades into zebrafish brain. Our results suggest the involvement of Wnt/β-catenin pathway in *M. fortuitum*-induced CNS tuberculosis. We propose the surge in pro-inflammatory cytokine aid in bacterial clearance and the anti-inflammatory cytokines assist in averting the sequel of CNS tuberculosis, suggesting that the interplay of cytokines is critical in *M. fortuitum*-induced CNS tuberculosis.

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Annual variations in Expression of kiss1, kiss2, gnrh1, gnrh2 in the Hypothalamus and lbβ and fshβ genes in the Pituitary of an Air-breathing Catfish, *Clarias magur* under Natural Climatic Conditions

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We studied monthly variations in expression of *kiss1*, *kiss2*, *gnrh1*, *gnrh2* in the hypothalamus and of *lhβ* and *fshβ* genes in the pituitary gland of both male and female catfish, *Clarias magur* maintained under natural climatic conditions. After acclimatization under natural conditions for 15 days, the fish was decapitated at 12:00 (Mid-day) and 24:00 (Mid-night) under MS-222 anesthesia, hypothalamus and pituitary dissected out rapidly, and processed for quantification of transcripts of *kiss1*, *kiss2*, *gnrh1*, *gnrh2* genes in the hypothalamus, and of *lhβ* and *fshβ* genes in the pituitary using qPCR. Expression patterns of *kiss1*, *kiss2*, *gnrh1*and *gnrh2* genes in the hypothalamus and of *lhβ and fshβ* genes in the pituitary exhibited prominent monthly and diurnal variations in both the sexes. Transcript levels of all the studied genes were comparatively higher during the mid-day as compared to that in mid-night. Expression of *kiss1* and *kiss2* genes in the hypothalamus of both the sexes exhibited two peaks, first during February-March and then in October-November in females, while in the male fish the two peaks were recorded in April and October during both mid-day and mid-night. In the hypothalamus of the female fish, transcript levels of only *gnrh2* gene exhibited monthly pulsatile expression during both mid-day and mid-night, while *gnrh1* gene expression remained basal during different months. In the hypothalamus of the male fish, the transcript levels of both *gnrh1* and *gnrh2* genes exhibited pulsatile expression during different months with a peak in April. In the pituitary of both the sexes, transcript levels of *lhβ* and *fshβ* genes during mid-day and mid-night started increasing in April and reached maximum levels in May-July, and declined gradually thereafter. Based on these findings, we suggest for the first time that there are prominent monthly/seasonal and diurnal variations in expression of all the studied genes in the fish. Early increase in expression of *kiss1* and *kiss2* genes is followed by increased expression of *gnrh2* gene in the hypothalamus, while increased expression of *lhβ* and *fshβ* genes in the pituitary was recorded during the breeding phase (May-July) of the fish, and both the genes seem to be controlled by *gnrh2* gene only.

P-72

Melatonin ameliorates diabetes-induced oxidative stress in spleen of laboratory mice in dose dependent manner

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Hyperglycaemic condition induced oxidative stress in diabetic individuals caused oxidative damages of internal organs including immune organ spleen. The effect of low doses of melatonin (25, 50 and 100µg/100g. B.wt./day) was studied on histoarchitecture and oxidative stress in streptozotocin-induced diabetic mice. Melatonin significantly resisted the increase in blood glucose levels and showed dose-dependent effect on body weight and relative spleen weight in diabetic mice. Melatonin suppressed diabetes-induced lipid peroxidation and increased the antioxidant enzymes (SOD and catalase) activity and also increased the GSH level in spleen tissue of diabetic mice in dose dependent manner. Melatonin treatment improved the reactivity of Nrf-2 and HO-1 in the spleen of diabetic mice. Present study may suggest the dose-dependent effect of melatonin in attenuation of oxidative stress in spleen of diabetic mice.

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Role of host irradiation on the viability of entomopathogenic nematode, Steinernema thermophilum and their potential as an adjuvant to F1 sterility technique against a polyphagous pest, *Spodoptera litura* (Fabr.)

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Entomopathogenic nematodes (EPNs) are multi-cellular metazoans occupying a bio control niche between microbial pathogens and parasitoids, and are habitually grouped with pathogens, due to their symbiotic relationship with bacteria. EPNs have been utilized in classical, conservation, and augmentative biological control programs. The vast majority of applied research has focused on their potential as inundatively applied augmentative biological control agents. In this paper, the bio-efficacy of an EPN, *Steinernema thermophilum* as a potential biocontrol agent was studied against a noctuid pest, *Spodoptera litura* (Fabr.) in India. The main purpose is to establish a safe mode of transport and dispersal of EPNs without concern that uninfected, reproductively competent hosts would be inadvertently released. The parasitization capability of EPNs *Steinernema thermophilum* was assessed against normal and irradiated host (70 Gy). There was no significant difference in the parasitization capacity of EPNs on the normal and irradiated host however, the mortality time of the irradiated host was significantly reduced by 17 hours. The efficacy of EPNs cultured in radio sterilized host, was studied vis-à-vis radiation mediated F1 sterility technique (radio-genetic tactic) on *Spodoptera litura*. *S. thermophilum* harvested from irradiated host (70 Gy) were almost equally effective (>90% parasitization efficacy) on normal and F1 sterile *S. litura* larvae (derived from cross of substerilized male and normal female) acting as hosts. The total harvesting of EPNs (IJs/host) was reduced by > 30% in case of F1 sterile host as compared to normal host. The overall findings indicated the suitability of treated insects (produced during operation of F1 sterility technique) as viable host for EPNs and feasibility of integrating EPNs with F1 sterility technique in efficacious management of this lepidopteran pest.

Correlation between plasma GtH (LH), E2 and Vg (Vg1 and Vg2) levels in Catfish

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Vitellogenin (Vg), the egg yolk precursor glycolipophosphoprotein is the prerequisite for the oocyte growth during oogenesis in fish (see Wallace and Selman 1981). Environmental changes provide cues to the central nervous system activating hypothalamus to secrete gonadotropin releasing hormone (GnRH). GnRH acts on hypophysis to secrete Gonadotropic Hormones (GtHs), which regulates the ovarian activities. However, the action of gonadotropin is not direct but mediated via the ovarian production E_2. So involvement of GtH and E_2 is essential in the process of Vitellogenin synthesis (Vitellogenesis).

In our present study annual profile of plasma GtH(LH), E_2, Vg1 and Vg2 levels in relation to ovarian growth of the female catfish, *C. batrachus* has been evaluated during one complete breeding cycle to observe the correlation between the expression levels of plasma GtH (LH), E_2 and Vg (Vg1 and Vg2). The primary change was an increase in plasma levels of GtH (LH) during the mid preparatory period (March) when ovarian growth was not significant. Similar changes in GtH (GtH II) have been demonstrated in brown trout (Billiard et al., 1978), rainbow trout (Bromage et al., 1982), and mrigal (Maitra et al., 2007). The increase in LH levels may be responsible for the stimulation of E_2 production as revealed from the present study that just after the small LH peak E_2 levels increased in plasma. GtH administration into female fish induces E_2 production has been demonstrated in many fish species (Sundararaj et al., 1982; Billiard et al., 1978; see Swanson et al., 2003 for review). A second major peak of LH had occurred in August during which this fish spawns and thus, indicates that a high concentration of LH requires for maturation, ovulation and spawning. A surge of LH (GtH II) has been demonstrated for maturation, ovulation and spawning in many teleosts (see Sundararaj, 1981; Swanson et al., 2003; Nagahama, 2000 for review). Throughout the annual ovarian cycle of the catfish, which includes vitellogenesis and maturation ovulation and spawning there was a significant negative correlation between LH and E_2 levels, which indicates the negative feedback of E_2 on LH during vitellogenesis. The increase in E_2 levels resulted in vitellogenin synthesis and secretion from the liver as evidenced by parallel increase in both E_2 and Vg (Vg1 and Vg2) levels. The increased plasma E_2 with simultaneous increase in Vg levels indicates the onset of vitellogenesis so as to form yolky oocytes, thereby increasing the ovarian weight. The highly significant correlation between E_2 and Vg (Vg1 and Vg2) levels seen in May-June was not observed later in the cycle suggesting that once Vg synthesis stimulated by E_2 it continues despite the E_2 returns to basal level. Similar findings have been reported in different fish species by others (Elliot et al., 1979; koya et al., 2003; Lee et al., 2000). Such findings thus, suggest that the accumulation of Vg in plasma may act as negative feedback to ovarian E_2 production.

Promoter Regulation and Expression Analysis of *11β-Hydroxylase* and its Associated Factors during Spermatogenesis and After HCG Induction in Catfish

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Regulation of steroidogenesis and gonadal development is controlled by the expression of steroidogenic enzyme genes and their associated transcription factors in teleosts. Interestingly, previous study using the walking catfish, *Clarias batrachus* reported the existence of four forms of *11β-hydroxylase* (*11β-h)* in contrast to a single form in the African catfish, *C. gariepinus*. Hence, the current study aims to compare *11β-h* of both the species at promoter level to unravel the key factors that entrain the regulation of *11β-h* which has not been analyzed in any lower vertebrates till date. To investigate the transcriptional regulation of *11β-h*, 5' upstream regions of *11β-h* were cloned in both the animal models followed by *in silico* promoter analysis wherein *foxp1*, *sox9/10* and *sf1* were found to be crucial and were selected for further characterization and luciferase reporter assay using TM3 cells indicated the promoter motifs were active. Expression of *11β-h and* its sensitivity to gonadotropin was analyzed by qPCR in *C. gariepinus*. Tissue and phase-dependent expression analysis of *11β-h* indicated its role in testicular cycle in *C. gariepinus*. Transcriptome analysis data from *C. gariepinus* gonads (naturally spawning vs hCG induced) were used to retrieve the cDNA fragments for the factors of interest for further analysis. The present study warrants for molecular characterization and functional validation of the identified transcription factors (*foxp1*, *sox9/10* and *sf1*) to indicate their role in 11β-*h* regulation, vis-a-vis, androgen production in catfish.

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Bisphenol A (BPA) Exposure Modulates Ovarian Nos/NO/sGC and Nppc/Npr2 Signaling Cascades in Zebrafish (*Danio rerio*)

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In recent years, nitric oxide (NO), one of the most significant free radicals synthesized in biological systems, has become a popular theme of research for its versatile regulatory actions in vertebrates. These short-lived molecules are synthesized via three types of tissue specific nitric oxide synthase (NOS) isoforms, neuronal NOS or NOS1 in neurons, inducible NOS or NOS2 in macrophage or inflammatory responsive tissues and endothelial NOS or NOS3 in vascular endothelial tissues. NO binding to soluble guanylate cyclase (sGC) catalyses the formation of second messenger cyclic GMP (cGMP) from guanosine tri-phosphate (GTP). The high load of cGMP maintains meiotic arrest in oocytes to prevent precocious oocyte maturation. Moreover, peptide hormone ligands (natriuretic peptide type C, NPPC) interact with membrane-bound or particulate guanylate cyclase (natriuretic peptide receptor 2, NPR2) to elevate cGMP accumulation in ovarian follicles. High load of cGMP may interfere with functioning of intra-oocyte phosphodiesterase (PDE3) and increase cAMP pool, which in turn activates protein kinases (PKA) to restrain the oocyte maturation.

At present, indiscriminate release of estrogenic endocrine disruptors (such as BPA, 4-nonylphenol, octyl phenol) in aquatic environment poses serious threat to fish reproduction. Present data demonstrate that congruent with a sharp increase in NO level, BPA exposure *in vivo* at three different sublethal concentrations, promote significant increase in the expression of ovarian inducible *nos2a*, at both mRNA and protein levels, in zebrafish (*Danio rerio*) ovary. Further, elevated expression of *sGC* mRNA in BPA-exposed ovary, indicating altered cGMP level, corroborates well with the expression of *nppc*/*npr2* suggesting EDC modulation of ovarian Nos/NO/sGC and Nppc/Npr2 cascades may perturb with reproductive fitness in this species.

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Potential Influence of Estrogen on Oxidative and Nitrosative Outburst in Macrophages

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Production of reactive oxygen and nitrogen species including free radicals is an integral part of metabolic activities and can damage vital biological processes. Inflammation is the body's attempt of self-protection to remove pathogens and begin the healing process. When inflammation threatens to damage critical body organs, steroids can be organ-saving and in many instances, life-saving. Estrogens have been proposed to exert antioxidant effects in *in vitro* models as well as in many biological systems. In the present study, thioglycollate elicited peritoneal macrophages from male swiss albino mice were exposed to graded levels of endotoxin (LPS) for three different time points (6h, 12h, 24h). Upregulation of nitric oxide (NO) level in LPS-treated groups corroborated well with heightened ROS generation. Conversely, priming with estradiol-17 β (E2) could abrogate ROS generation in LPS-treated cells. Interestingly, recombinant human insulin, in association with E2 could further attenuate LPS action on inflammatory response in peritoneal macrophages cultured in high glucose medium *in vitro*. These results prompted us to examine the profile of inflammatory cytokines (*tnfα, il-1β, inos, il-10, arginase-2*) at transcript level. While expression pro-inflammatory cytokines was elevated in LPS treated group, E2 pre-incubation significantly alleviated transcriptional activation. Interestingly, we observed significant downregulation of pro-inflammatory cytokines when co-treated with insulin and estrogen in combination indicating potential synergism. Taken together, impact of estrogen priming on oxidative and nitrosative outburst in macrophages, maintained either in normo-or hyper-glycemic condition, may provide important insights on macrophage polarization and disease outcome or sets the stage for further in-depth investigation in future.

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Protective Effects of Gonadotropin-Induced Steroid Biosynthesis on Follicular Redox Homeostasis and Igf Axis in Zebrafish Ovary

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Background: The prevalence of infertility among women is approximately 13% and poses a global concern in spite of current treatment strategies. An oocyte being the functional unit of the ovary and the most common candidate involved in implantation failure, the molecular and cellular processes regulating its quality and competence is of particular significance. Ovarian steroids and local growth factors, specifically insulin-like growth factors (IGFs), are indispensable for growth, differentiation and folliculogenesis in vertebrate ovary. The intrafollicular redox balance is also of immense importance wherein low levels of ROS are being utilized for regulation of gene expression, its excess interferes with normal physiological processes. However, possible association between steroid biosynthesis and redox homeostasis in ovarian physiology is less investigated. Accordingly, the present study sought to examine the effect of pharmacological inhibition of steroidogenesis on follicular redox homeostasis vis-à-vis its Igf network and meiosis resumption *in vitro*.

Results: Using zebrafish full-grown (FG) ovarian follicles, our study showed that blocking steroid biosynthesis with anti-steroidal drugs, DL-aminoglutethimide (AG) or Trilostane (Trilo), prevented hCG (LH analogue)-induced *StAR* expression concomitant with a robust increase in intrafollicular ROS levels. Congruent with heightened positive staining in NBT assay as well as NOX4 expression, priming with AG or Trilo down-regulated the transcript abundance of major antioxidant enzyme genes (SOD1, SOD2, and CAT) and eminent heat-shock protein (HSP70) in hCG-stimulated follicles. Disrupted oxidant/antioxidant balance in steroid-depleted follicles negatively impacted hCG-mediated transcriptional activation of *igf* ligands by targeting the activation of PKA/CREB protein. Resultant elevated ROS, attenuated antioxidant defense system and altered endocrine or autocrine/paracrine homeostasis culminated into dysregulated oocyte maturational competence and reduced p34cdc2 (Thr-161) phosphorylation, a reliable marker for MPF activation and meiotic resumption. Collectively, present study demonstrated the relative importance of follicular steroidogenesis on regulation of redox homeostasis, Igf synthesis and meiosis resumption in FG follicles *in vitro*.

Identification of Some Important Freshwater Zooplankton

P-79

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Zooplanktons are free swimming minute organisms, found in marine as well as freshwater bodies. They vary in size from microscopic to larger such as jelly fish. They are heterotrophic in nature and feeds on phytoplankton. Zooplankton are considered as important natural basic diet for many fish and shrimps as they are serving as an intermediary species in food chain that transfers energy from small planktonic algae to larger fish who in turn feed on them. Identification of the planktonic organisms is a very important first step. The organisms are classified either on the basis of morphological features or molecular markers. DNA barcoding is the most widely used molecular technique for plankton identification. This technique used short sequences of one or a few genes in order to classify known organisms and use this information to detect new ones. The morphological approach is simple and less expensive than molecular approach. In this study some important freshwater zooplankton are characterized on the basis of their morphological features and some identification keys are also specified to identify them.

P-80

Comparative Genomics Approach for Identification of Drug Resistance Markers in *Leishmania*

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Leishmaniasis is a vector-borne disease caused by a digenetic protozoan parasite of the genus *Leishmania*. Currently, VL therapy is trailing behind because of drug resistance, toxicity due to off-target effect, high cost, declining efficacy, and bioavailability. Hence, there is an urgent therapeutic demand for the identification of target-specific anti-leishmanial drug. We have analysed genomic and transcriptomic alterations associated with *in vitro* paromomycin and artemisinin tolerant *Leishmania* field isolates. Genomic data analysis of drug sensitive wild type (K133WT) vs. artemisinin resistant (K133AS-R) parasites revealed substantial genomic variation, including 240 single nucleotide polymorphisms (SNPs), 237 insertion deletions (InDels), 616 copy number variations (CNVs) and trisomy of chromosome 12 in AS-R parasites, while whole-genome sequence analysis of K133WT vs. K133PMM parasites showed 259 SNPs, 187 InDels and 546 CNVs. Chromosome 9 and 12 were found in trisomy condition while chromosome 5 is in tetrasomy condition, a unique observation in K133PMM. Comparative transcriptome profiling showed modulated expression of 500 genes in PMM-R parasites whereas 208 genes (fold change ≥ 2) in K133AS-R parasites compared to sensitive isolate. Functional classification and pathway analysis of modulated genes indicated probable adaptations in drug resistant lines by alternate metabolic adaptation, decreased protein synthesis, increased DNA damage repair and active drug efflux. The up-regulated expression of cathepsin-L like protease, amastin-like surface protein, amino acid transporter and down-regulated expression of ABCG2, pteridine, adenylate cyclase-type receptor and certain hypothetical proteins were found to be in concordance with genomic alterations suggesting their potential role in drug resistance. Overall, our study provides an understanding of the molecular basis linked to drug resistance in *Leishmania* parasites, which may help identify drug resistance mechanisms further and safeguard the few novel drugs for future use.

P-81

Experience Window Influences Development and Retention of Memory to Recognise Predators in *Euphlyctis cyanophlyctis* Tadpoles

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Learning and memory are the critical components of predator recognition as they allow prey to develop an adaptive response to a novel situation that increases its survival. In prey animals that lack innate predator recognition, associative learning plays a crucial role in the recognition of novel predatory cues by associating them with familiar conspecific alarm cues. On perceiving novel predator odours along with alarm cues, prey animals learn to recognise predatory odours alone in their future encounters. Studies on different model systems have shown that a single event of exposure (conditioning) is sufficient for prey to associate novel predatory cues with alarm cues. However, the minimum period required for learning and memorizing information about predator identity is not known. Hence, we used *Euphlyctis cyanophlyctis* tadpoles to determine the association between experience window and development of memory and its retention. We conditioned tadpoles with a mixture of dragonfly nymphs' odours and conspecific alarm cues for 1, 3, 6, 12, and 24 h and subsequently recorded their antipredator behaviour at 1, 5, 10, 15, 20 days post-conditioning. The results show that the minimum duration required to learn about predatory cues is ~6 h. Interestingly, the intensity of antipredator response was proportional to the duration of conditioning. Moreover, retention of memory increased with an increase in the duration of conditioning. Therefore, our study for the first time shows the importance of experience window in the development of learning. We also show an association between duration of conditioning and retention of memory i.e. more the conditioning, the stronger is the memory retention. In aquatic ecosystems, where prey animals are exposed to a wide array of chemical cues from diverse predators at different stages of their ontogeny, our findings open a new avenue in understanding complex aspects of prey-predator interaction.

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Expression Profiling of AP-1 Family Genes, *C-Jun*, *C-Fos* and *Junb* in Common Carp Testis Shows Seasonal and Testosterone Dependence

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Transcriptome analysis using immature gonads of the common carp, *Cyprinus carpio* revealed the presence of transcription factor genes such as *activator protein-1*(*AP-1*) family namely, *jun proto-oncogene* (*c-jun*), *fos proto-oncogene* (*c-fos*) and *junB proto-oncogene* (*junB*). AP-1 family is known to be involved in a wide variety of signaling pathways, one of which being the protein kinase C pathway which is influential to regulate the expression of steroidogenic acute regulatory protein thereby steroidogenesis. In view of this, present study attempted to unravel the role of AP-1 family in steroidogenesis vis-à-vis spermatogenesis. Transcripts of *c-jun, c-fos* and *junB* were retrieved from transcriptome and sub-cloned to confirm the sequence data. Partial cDNA fragments of *c-jun*, *c-fos* and *junB* were obtained from common carp testis authenticating the transcriptome data on these correlates. Quantitative PCR of *c-jun*, *c-fos* and *junB* and was done in tissues, phase-wise and after testosterone treatment, *in vitro* in carp testis. Significant expression of *c-jun*, *c-fos* and *junB* was observed during spawning phase. Testosterone treatment of testicular slices, *in vitro* elevated the expression of *c-jun*, *c-fos* and *junB*. Over expression of *c-jun*, *c-fos* and *junB* during spermiating phase and testosterone dependency implicate their significance in carp spermatogenesis. It seems activation of AP-1 family might be essential to induce steroidogenesis to stimulate testicular function. Gene silencing of crucial factor belonging to *AP-1* family is required to elucidate their role in testicular recrudescence and maturation.

Development of Plant Derived Anti-Cervical Cancer and Anti-HPV Therapeutics

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Cervical cancer is caused by high-risk HPV (Human Papillomavirus). Among 14 high-risk HPV types HPV16 and HPV18 are the most prevalent, constituting 50-70% of all HPV induced cancers. Cervical cancer which has an infectious etiology can be prevented by prophylactic vaccines targeted to HPV coat proteins. However, there is no plant derived pharmacological therapeutics that can cure women already infected with HPV.

Oncogenic potential of HPV is manifested by its key oncoproteins E6 and E7 that are exclusively coded by viral genome. It has been shown in classical experiments that E6 plays a cell-cycle and apoptosis destabilizing role by interacting with p53 leading to ubiquitin mediated degradation of p53. Later researches have reported several other cellular targets of E6. This might aid E6 in causing carcinogenesis. Therefore, E6 plays a central role in carcinogenic progression of cervical cancer and has become a molecular and therapeutic target.

Even though the molecular mechanism of HPV-mediated cervical carcinogenesis is fairly known, there is a lack of pharmacological inhibitors that could be used as therapeutic drugs against HPV and associated carcinogenic events. Therefore, in present investigation we have attempted to screen selected plant-derived active principles that are chemically characterized and have shown anti-cancer activity for their capability to interact with HPV16 E6 by *in silico* and *in vitro* methods.

Present study demonstrates a multifactorial action of BAMT on CaCx cells. BAMT induced cell death and G1 growth arrest in CaCx cells irrespective of their HPV status. Molecularly, this HP targeted oncogenically-relevant transcription factors of STAT3 and AP-1 family that result in loss of oncoprotein expression. Among various constituents, berberine, magnoflorine and palmatine were found capable of targeting E6 functions by strong cooperative binding. Collectively, these leads show that commercially available BAMT can be an effective and economic broad-spectrum therapeutic option against cervical cancer.

P-84

Illuminated Night Negatively Affects Sleep and Associated Hypothalamic Gene Expressions in Diurnal Zebra Finches

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Exposure to light at night can disturb the cyclic feature of the day-night environment resulting in several deleterious effects, including disruption in the sleep-wake cycle. Here, we report the results of a study that investigated the effects of ecologically relevant levels of dim light during the night on sleep and hypothalamic expression of genes constituting the circadian clock circuitry (*per2*, *bmal1*) and sleep regulatory pathways (cytokines: *tlr4*, *tnf-α*, *il-1β*, *nos*; Ca^{2+}-dependent pathway: *camk2*, *sik3*, *nr3a*; cholinergic receptor, *achm3*) in female zebra finches (*Taeniopygia guttata*). Birds were exposed daily to 12 h light (150 lux) coupled with 12 h darkness without or with 5-lux dim light at night (dLAN). dLAN fragmented the nocturnal sleep with decreased frequency and length of sleep bouts, and caused sleep debt as confirmed by reduced plasma oxalate levels. Hypothalamic mRNA expression patterns further evidenced dLAN-induced negative genetic effects. Reduced daily peak level (amplitude) and altered expression time (acrophase) of *per2*, not *bmal1*, mRNA expression indicated differential involvement of clock genes in dLAN-induced nocturnal sleep disruption. Concomitantly, decreased *tlr4*, *il-1β* and *nos* mRNA levels suggested attenuated inhibition of the arousal system; in turn, the wake state promotion in dLAN birds. The parallel changes in *tlr4*, *il-1β*, and *nos* gene expressions suggested their close linkage with dLAN-induced sleep fragmentation. Furthermore, whereas changes in *camk2* and *sik3* expressions suggested dLAN-induced effects on Ca^{2+}-influx pathway, the lack of diurnal difference in *achm3* mRNA levels could account for sleep loss under dLAN. These results demonstrate dLAN-induced negative effects on sleep and associated hypothalamic genetic pathways in diurnal zebra finch, and provide insights into health risks of an illuminated night exposures to animals including humans in an urban setting.

Gut Metabolites Dysbiosis in Tuberculosis Patients

P-85

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Tuberculosis (TB) is an ancient disease that killed millions of people worldwide and has claimed 1.41 million deaths in 2019 alone. It is caused by *Mycobacterium tuberculosis* (Mtb), which tends to infect mainly lungs causing pulmonary disease but can also infect any organ of the body as extrapulmonary manifestation. The disease usually presents as a latent infection with no clinical symptoms but may develop into an active disease in the future. This progression from latent to active disease is influenced by many factors such as host immunity, genetic background of the *bacilli, age, gender,* co-infection and recently gut microbiota has been shown to be associated with the pathogenesis of TB. However, despite the advent of next-generation sequencing platforms that allow profiling these complex microbial communities through 16S rRNA sequencing, the knowledge regarding the gene functional annotation is still sparse. In the present study, we examine the functional readout of the gut community in the host milieu through fecal metabolomics. In particular, ^{1}H-NMR metabolomics was performed for the comprehensive analysis of metabolite composition in the stool samples from the TB infected cases (n=20) and unrelated healthy subjects (n=20). The metabolome analyses showed that few branched-chain amino acids were significantly higher in TB infected group. The difference in the abundance of different metabolites in TB patients and healthy individuals in our data indicated the role of complex metabolic pathways in the etiology of TB infection. Examination of fecal metabolites provides a non-invasive way to analyse the host-gut microbiome interactions. The findings can potentially go a long way in the development of nutritional and personalized therapies for the restoration of alteration and subsequent relief.

Hypothalamic Neuropeptide Y in Wall Lizard

P-86

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Neuropeptide Y (NPY), an orexigenic peptide, is widely distributed throughout the central nervous system and peripheral tissues of mammals. An emerging body of evidence implicates NPY in the regulation of feeding behaviour, energy homeostasis and reproductive functions, though studies are largely restricted to mammals and fishes. The current study was thereby planned in a reptilian model as this group phylogenetically connects the lower and higher vertebrates. Histological images of wall lizard brain were compared with MRI brain atlas of tawny dragon to demarcate the hypothalamic region in our animal model. For computational analysis of NPY, a 1815 bp long NPY transcript encoding 97 amino acid long complete NPY protein was selected from splenic transcriptome data of wall lizard (Bioproject id: PRJNA313009). Multiple sequence alignment demonstrated a high conservation of the protein across vertebrates. Phylogenetic tree showed a separate clade for reptiles and birds. Among reptiles, chelonia and crocodilia were closer to birds while squamates formed a separate group. In order to study the temporal variation in hypothalamic NPY expression, brain of female wall lizards were dissected during different reproductive phases and its hypothalamic region was used for gene expression analysis using densitometry. The lowest expression of NPY was observed during regressed phase while early and late recrudescence as well as breeding phase had higher expression. The association of differential hypothalamic NPY expression with feeding behaviour/energy homeostasis or reproductive activities or both needs to be explored.

P-87

Cloning and Expression of the Chicken Liver Glutamate Dehydrogenase (GDH) in Bacteria

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Glutamate dehydrogenase is an NAD(P)$^+$ dependent homo-hexameric enzyme, majorly found in the matrix of mitochondria that catalyses the reversible conversion of glutamate to α-ketoglutarate and ammonia. It is conserved in all living organisms with differences in the coenzyme specificity. In case of mammals, the GDH is primarily encoded by *GLUD1* gene; however, human and apes in addition have acquired a second gene *GLUD2*. The GLUD2 encoded GDH is refractory to allosteric regulation by GTP and ADP. On the contrary, GTP and ADP act as allosteric inhibitor and activator, respectively, for the GLUD1 encoded GDH. Preliminary investigation revealed that the chicken liver GDH is encoded by a single GLUD1 gene.

A histone H3 specific protease activity (named as H3ase) from chicken liver nuclear extract has been established in our laboratory and subsequently, the H3ase was identified as GDH. Hence, in the present study, full length GDH (GLUD1 gene) from chicken liver was cloned without its N-terminal signal pre-sequence and expressed in a heterologous system of bacteria and its H3ase activity was investigated in the bacterially expressed GDH. Analysis of the cloned nucleotide sequence of the GDH revealed various gaps in the N-terminal region. Comparative analysis of the nucleotide sequence in the unique N-terminal region of the cloned chicken GDH revealed repetitive nucleotide sequences and high G and C's. Repetitive nucleotide sequences with higher GC content suggested heterogeneity in cDNA population of chicken GDH; also it increased the chances of formation of higher order secondary structure like hair pin loops, assembly of G-quadraplex in the transcripts. Subsequently, the protein encoding GDH gene minus the N-terminal sequence was further sub cloned and expressed in *E. coli* as a His-Tagged protein. Efforts are being taken to purify the bacterially expressed GDH and explore the H3ase activity in it.

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Determination of the Optimum Concentration of Various Anaesthetics for two Channid Species

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Fish anaesthetics are very useful in aquaculture practices for reducing stress during different processes such as transportation, sorting, tagging, vaccine administration and surgical procedures. However, information related to optimum dose of an anaesthetic for various fish species is essential because improper dosages may lead to stressful condition. The present work was designed to investigate stress induced alterations caused by improper concentrations of anaesthetizing agents viz. Clove oil, Paraldehyde and MS-222 (Tricane methane sulphonate) in *Channa punctatus* and *Channa gachua* on various target organs. Well acclimatized fishes were exposed to three different concentrations (Clove oil= 50, 100, 200 µl/l; Paraldehyde=3, 6, 9 ml/l; MS-222= 75, 100, 200 mg/l) of each anaesthetic. To determine the optimum concentrations, induction-recovery times were recorded and histological preparations of gills and buccal tissues were examined to monitor the architectural anomalies viz. epithelial uplifting, lamellar fusion, mucus exudation, dermal lifting and distorted epidermis. The stress effects of clove oil and paraldehyde were comparatively higher than MS-222 in both channid species. The degrees of alteration were much higher in 75 mg/l and 100 mg/l than 200 mg/l concentration of MS-222 in both channid species. Interestingly, 50 and 200 µl/l and 50 and 100 µl/l concentrations of clove oil as anaesthetic were found to be stressful in *C. punctatus* and *C. gachua* respectively which is evident from discernible histological disruptions in the gills and buccal tissues. Similarly, in both channid species, paraldehyde at 3 ml/l and 6 ml/l presented high stress associated variations than 9 ml/l in selected tissues. The level of damage may be due to defensive reaction against improper concentrations of anaesthetic agents. Therefore, from the above study it can be stated that 200mg/l of MS-222 and 6 ml/l of paraldehyde are considered to be optimum concentrations to induce total loss of equilibrium for both channid species whereas clove oil at 100 µl/l and 200 µl/l seem optimum for *C. punctatus* and *C. gachua*, respectively.

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In vivo and *in vitro* study of Organophosphorous Pesticide Triazophos on Super Oxide anion Production and Nitrite Release by Spleen and Head kidney the cells of Teleost fish, *Channa punctatus*

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Fishes are the first group of organisms that have adaptive and cell mediated immune responses. Immune system is first line defence against pathogenic organisms, however it is very sensitive to the factors present in the environment. Triazophos is an organo-phosphorous pesticide used to protect the crops from a wide range of pests. The aim of the present study was to analyse the effect of triazophos on various innate and cell mediated immune functions in *Channa punctatus*. Triazophos toxicity was determined by calculating LC_{50} in 96 hrs of exposure. Fishes were invivo exposed to 1/10 and 1/20 th of LC_{50} for 10 and 20 days and in invitro study three different concentration (0.01, 0.5 and 1.0 µg/ml) of TZ was used . After expiry of experiment, animals were cold anaesthetized, spleen and head kidney were isolated aseptically and single cell suspension was prepared from each tissue. Super oxide production by cells from both the tissues were analysed by nitro-blue tetrazolium assay. Nitrite assay was performed to evaluate the production of nitric oxide. Lymphocytes were isolated through density gradient centrifugation and were subjected to proliferation assay. Mitogen induced proliferation was also assessed using concanavalin A and Lipopolysaccharide. Results of the present study showed that oxidative stress was decreased when the fishes were invivo and invitro treated with triazophos. Lymphocyte proliferation also decreased significantly in treated animals. It was concluded the pesticide adversely affected the immune system of the fishes and the effect was more pronounced when exposure time was increased. Pesticides pose threat to non-target animals specially fishes and the later suffer mortality loss may be due to weakened immunity.

Role of Serotonin and Dopamine in Regulation of Reproductive Cycle in the Freshwater Murrel, *Channa punctatus* (Bloch)

P-90

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The neuroendocrine mechanism regulates reproduction through a complex interaction via the Hypothalamus-Pituitary-Gonadal (HPG) axis. The main hormone regulating HPG axis is gonadotropin releasing hormone (GnRH) which is produced in the hypothalamus. In addition, various neurotransmitter of central nervous system (CNS) regulates the synthesis of GnRH such as serotonin and dopamine. Serotonin (5-hydroxytryptamine, 5-HT), a monoamine is involved in wide range of functions including reproduction. In mammals, sexual behavior, gonadotropin release and GnRH secretion are regulated by serotonin. Accordingly, serotoninergic system may play a unique role in control of reproduction in fishes. Expression of 5-HT, tryptophan hydroxylase (Tph) and 5-HT receptor (HTr) can be used to identify and localize serotonergic neurons mainly in diencephalon, hind brain and spinal cord. In addition, Dopamine (DA) acts as functional antagonist of GnRH and inhibits the secretion of adenohypophyseal hormones thereby blocking the reproductive process. Inhibition of LH release is mediated by dopamine D2 like receptor (D2). In this study, we have characterized and localized the putative serotonergic and dopaminergic neurons in the brain of freshwater murrel, *Channa punctatus*.

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Internal & External Factors Affect Reproduction in Different Ways in Japanese quail, *Coturnix coturnix japonica*

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It is well known fact any factor whether external (such as photoperiod, temperature, rainfall, food availability) or internal (hormonal neurotransmitter etc), influences gonadal activity via hypothalamo-hypophyseal-gonadal axis. In our study, we have focused neurotransmitters as internal factors and photoperiod or light durations as external factors. We used precursors (5-HTP and L-DOPA) of neurotransmitters (serotonin and dopamine respectively) in firsts experiment. In the first experiment/case, the effect varies with the interval between the two injections (5-HTP and L-DOPA) and the trend of the effect although linear, was in two opposite direction in the quail of two subsets of the groups. On the other hand, all the day length ranging from 6-12 hrs of light in the L:D cycle, did not induce initiation of gonadal development in these quail until the age of 13 weeks. However, after a period of such a long sexual quiescence (scotosensitivity) gonad develop spontaneously and were moderately developed by 15 week of age (scotorefractory). But, in case of 16L and 24L quail, immediate development leading to full breeding condition was evident These two analogous conditions induced gonadal responses but the degree and the trend of effect was different. Thus, bird's gonadal system can recognize even one hour change in the phase relation of circadian neural oscillations and responds accordingly. In addition to the regulation of seasonal gonadal cycle, the relative position of the two circadian oscillations also appears to determine the rate and the trend (suppression or stimulation) of gonadal development in Japanese quail. This indicates that linear relation observed between photoperiod and gonadal response is not applicable to another mechanism which is specific to the phase angle of the neural oscillations and is a non-linear effect.

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Cocaine and amphetamine regulated transcript peptide (CART) in the tadpole brain: response to different energy states

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Cocaine- and amphetamine-regulated transcript peptide (CART) is an anorexigenic neuropeptide known to play a key role in energy homeostasis across the vertebrate phyla. In the current study, we have investigated the response of the CART immunoreactive system to varying energy states in the brain of a tadpole model. The pro-metamorphic tadpoles of *Euphlyctis cyanophlyctis* were fasted, or intracranially injected with glucose or 2-deoxy-D-glucose (2DG; an antagonist to glucose inducing glucoprivation) and the response of the CART containing system in various neuroanatomical areas was studied using immunohistochemistry. Glucose administration increased the CART immunoreactivity in the entopeduncular neurons (EN), preoptic area (POA), ventral hypothalamus (vHy) and the Edinger Westphal nucleus (EW) while CART positive cells decrease in response to fasting and glucoprivation. A substantial decrease in CART was noted in the EW nucleus of tadpoles injected with 2DG. These regions might contain the glucose-sensing neurons and regulate food intake in anurans. Therefore, we speculate that the function of central CART and its antagonistic action with NPY in food and feeding circuitry of anurans is evolutionary conserved and might be responsible for glucose homeostasis.

Sleep Behavior in Shift-Working Paramilitary Personnel

P-93

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A questionnaire based study was carried out on 508 shift personnel of paramilitary forces to reveal the association between sleep behavior and other parameters, such as general health, fatigue, job satisfaction, etc. They worked in counterclockwise fast rotating shift system, which has several drawbacks. Various parameters, like chronotype, excessive day time sleepiness, general health, and fatigue level and job satisfaction were considered to exhibit their relationship with sleep disturbances. 90.2% subjects complained about moderate sleep disturbances. Sleep disturbances were more pronounced in evening type individuals. A negative relationship between sleep disturbances and chronotype was reported. A significant positive relationship between age and chronotype noticed in the present study, and we documented that about 71.1% shift personnel reported moderate level of fatigue. We also demonstrated that fatigue has strong relationship with daytime sleepiness and sleep disruption. In the present study fatigue showed negative association with chronotype. With reference to psychological problems, we noticed that regardless of shift work 99% of shift personnel did not report any kind of psychological poor health. Factors such as change of shifts, disciplined life, emergency duties, maintaining performance, job stress etc. in combination may lead to sleep disruptions, fatigue, and daytime sleepiness. Among 508 subjects 11% were discontented with their job. Also evening type individuals found to be more satisfied with their job. Despite, sleep disturbances and fatigue, most of the shift personnel are adapting to shift work and found to be psychologically normal and satisfied with their job. Similar studies on abnormal patterns in sleep-wake behavior and depressive moods of farmers and daily wage workers have been performed and research is going on.

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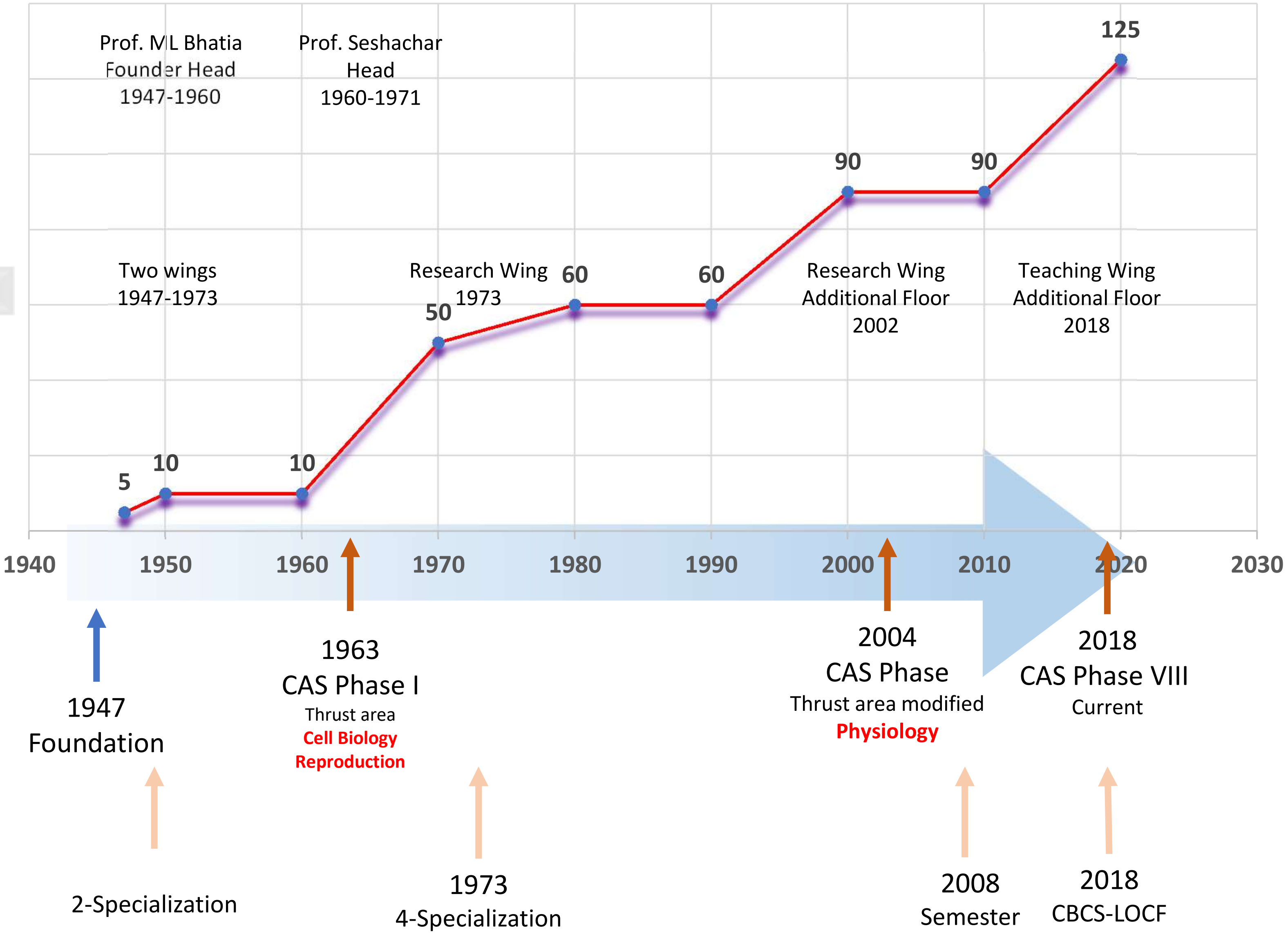
microbes to human

THRUST AREA(S)

- Regulatory mechanisms associated with Physiology and development
- Mechanisms to understand how genes and/ or gene networks regulate physiology and development in organisms

DEPARTMENTS GROWTH PROFILE



Department Head

Prof. ML Bhatia
Founder Head
1947-1960

Prof. Seshachar
Head
1960-1971

Infrastructure

Two wings
1947-1973

Research Wing
1973

Research Wing
Additional Floor
2002

Teaching Wing
Additional Floor
2018

Students Intake

CAS-SAP Program

1947
Foundation

1963
CAS Phase I
Thrust area
Cell Biology
Reproduction

2004
CAS Phase
Thrust area modified
Physiology

2018
CAS Phase VIII
Current

Teaching Program

2-Specialization

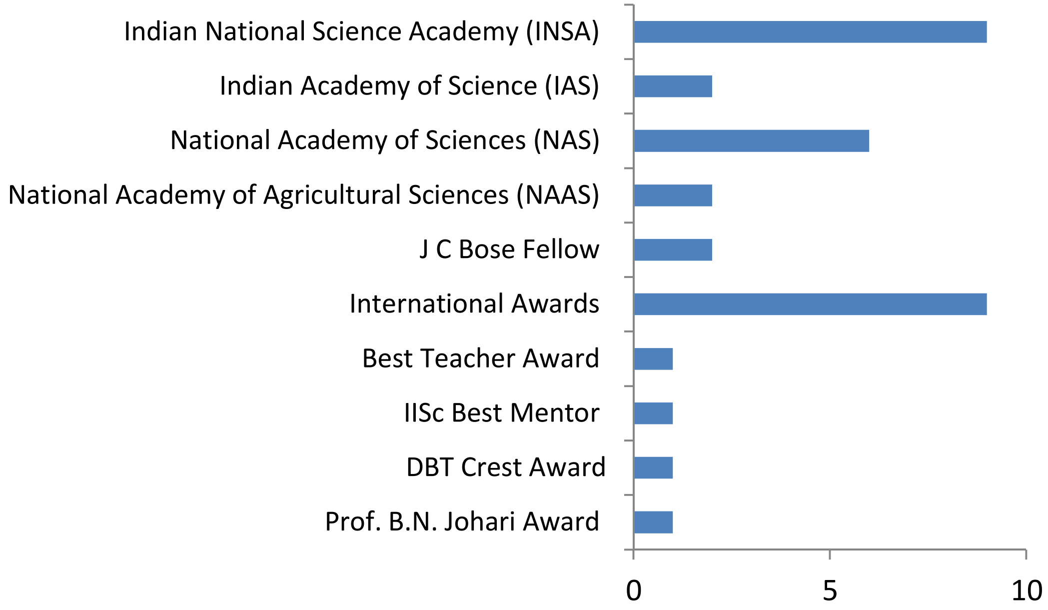
1973
4-Specialization

2008
Semester

2018
CBCS-LOCF

AWARDS AND RECOGNITION

(Faculty)



- Elected Fellows of number of Scientific Academies and Scientific Bodies: **13**
- Members of editorial boards of Scientific Journals: **9**
- Committee members Academy Boards/Committees of several Institutions: **All**
- Individual extramural grants: **Fairly good**
- Collaborative research: **National and International**
- Good publications: **>400**

FACULTY MEMBERS: AREA OF SPECIALIZATION

Prof. M.M. Chaturvedi	Biochemistry & Molecular Biology
Prof. Umesh Rai	Comparative Immuno-endocrinology & Reproductive Physiology
Prof. Rina Chakrabarti	Fish Nutrition and Aquaculture
Prof. Neeta Sehgal	Molecular Endocrinology and Reproductive Biology of Fish
Prof. Vinod Kumar	Chronobiology, Physiology of seasonal reproduction & migration
Prof. R. K. Seth	Applied Entomology & Radiation Biology
Prof. Dileep K. Singh	Insect and Environmental Pesticide Toxicology and Bioremediation
Prof. Rita Singh	Molecular Reproduction, infertility and Cancer
Prof. S. Mazumder	Immunobiology of host pathogen interactions & Immunotoxicology
Prof. Anju Shrivastava	Cell Signaling, Molecular Immunology and Tumor Biology
Prof. S. Basu-Modak	Molecular Cell Biology
Prof. Rajagopal Raman	Gut Microbiology, Vector Biology, Xenobiotic degradation
Prof. M. Shakarad	Evolutionary, Population and Behavioral Genetics
Prof. Namita Agarwal	Developmental Biology
Prof. Yogendra Singh	Bacterial Pathogenesis
Prof. Alok C. Bharti	Molecular Oncology
Prof. R.K. Negi	Biodiversity

M.SC. ZOOLOGY SYLLABUS REVISION

Syllabus-M.Sc Zoology Under CBCS Scheme 2018.pdf

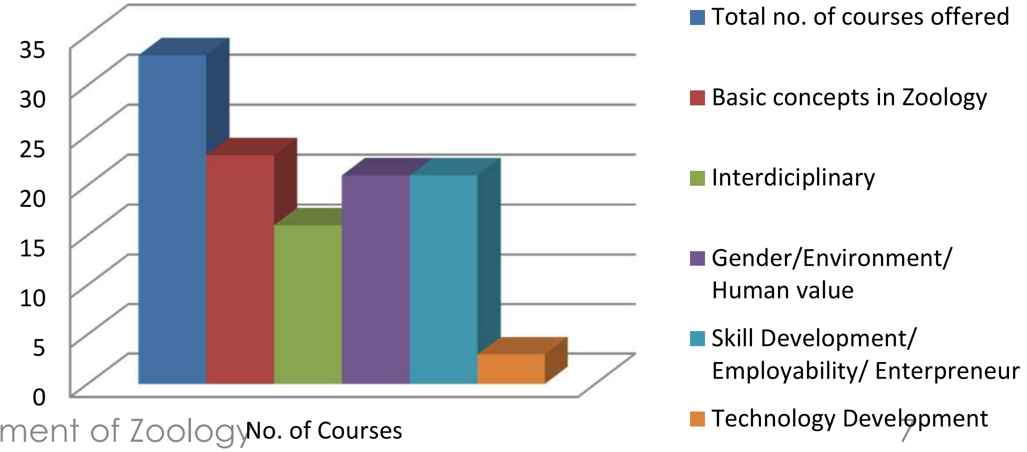
Type	Number	Semester	To be selected
Core	10	I,II,III	ALL
Electives/Open E	6/1	III	2/1
Electives (in stream)	16 (4 in each stream)	IV	4 (1 stream)
Dissertation	Optional, student depending on their interest can opt for it.		

Recent advances in Zoology from organismic to reductionist biology

Understanding the **challenges of society and the country** that falls into the realms of Zoology

- ***Physiology,***
- ***Neurobiology,***
- ***Behavior and Biological time keeping,***
- ***Reproductive health,***
- ***Cancer Biology,***
- ***Microbiome and their roles in health and diseases,***
- ***Aquaculture,***
- ***Bioremediation of pollutants and pesticides,***
- ***Environment and animal interaction, etc.***

Program Objective



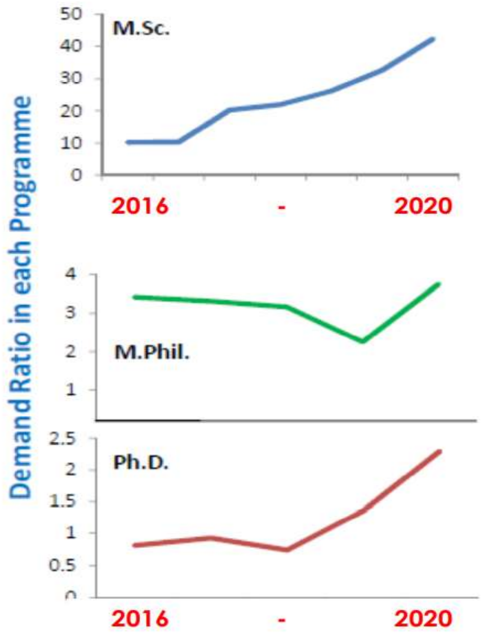
TEACHING PROGRAM

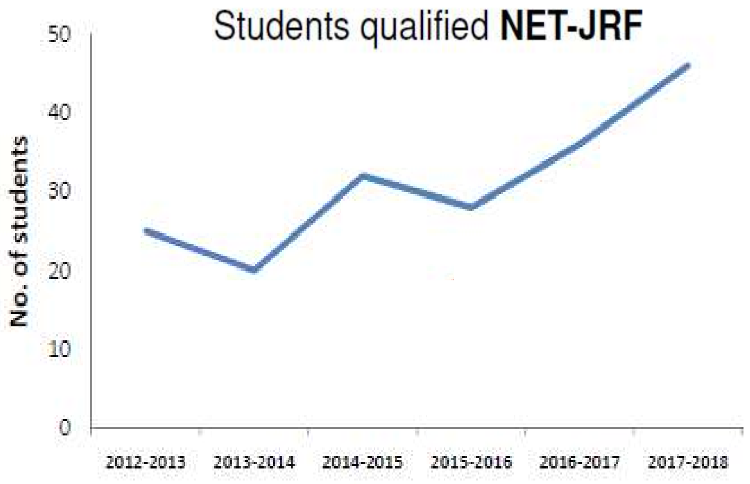
PROGRAMMES OFFERED

I. M.Sc. in Zoology

II. M.Phil. in Zoology

III. Ph.D. in Zoology





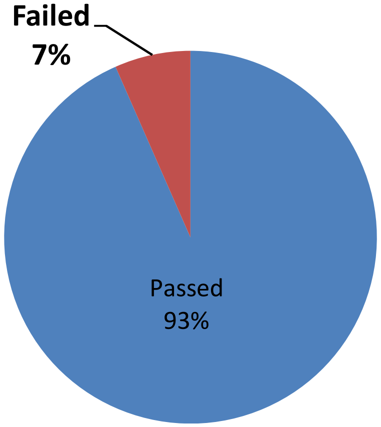
Students are well placed: **85%** (during 2012-2018)

- In teaching both at school and
- At college/university level- **60%**
- Research institutions- **21%**
- In R&D of drug companies -**2%**
- GOI-**2%**

STUDENT SUPPORT & PROGRESSION

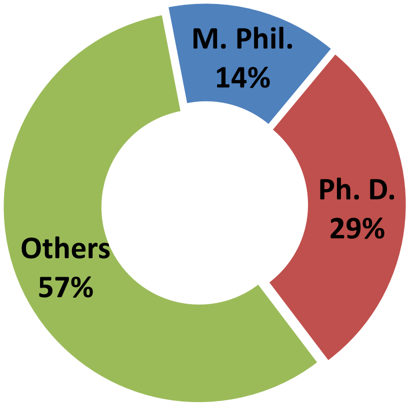
M. Sc. awarded during 2012-2018

M.Sc. Pass percentage

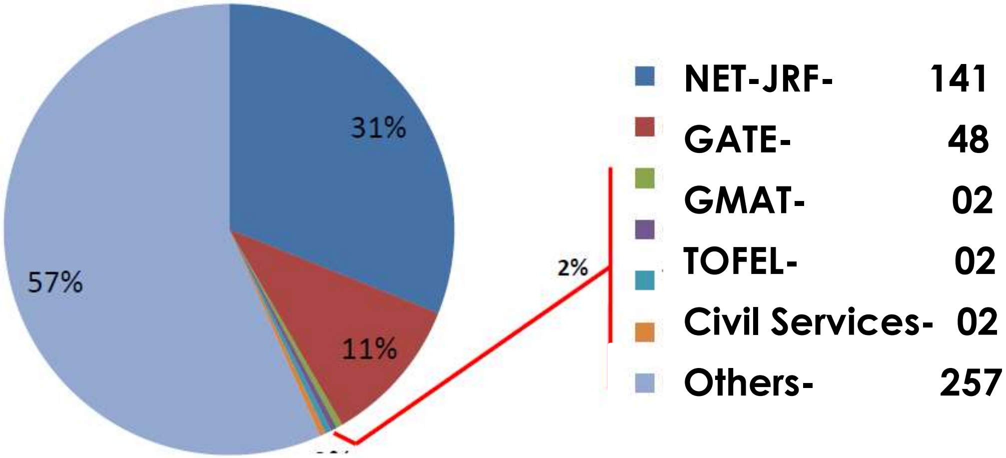


Appeared - 486
Passed M.Sc.- 454

After M.Sc.



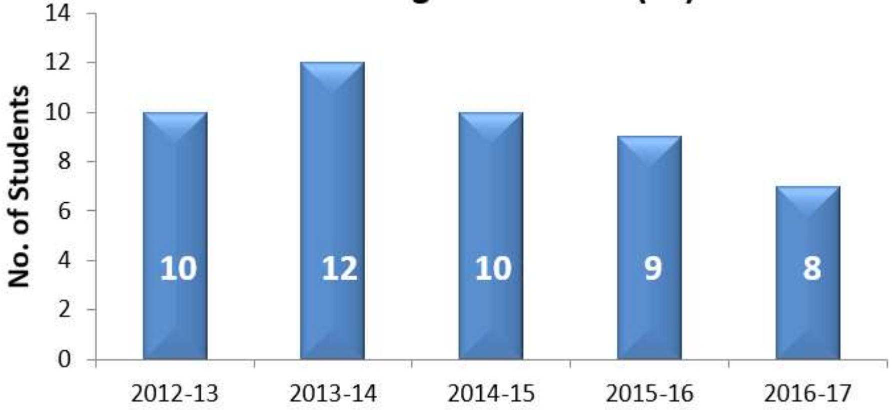
Competitive Exams qualified by M.Sc. Students



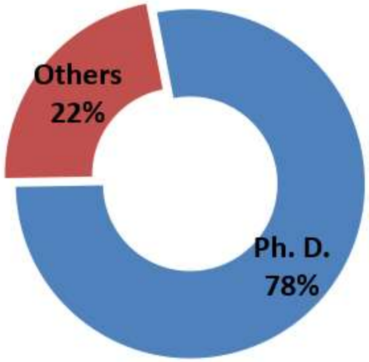
STUDENT SUPPORT & PROGRESSION

M.Phil. and Ph.D. awarded during 2012-2018

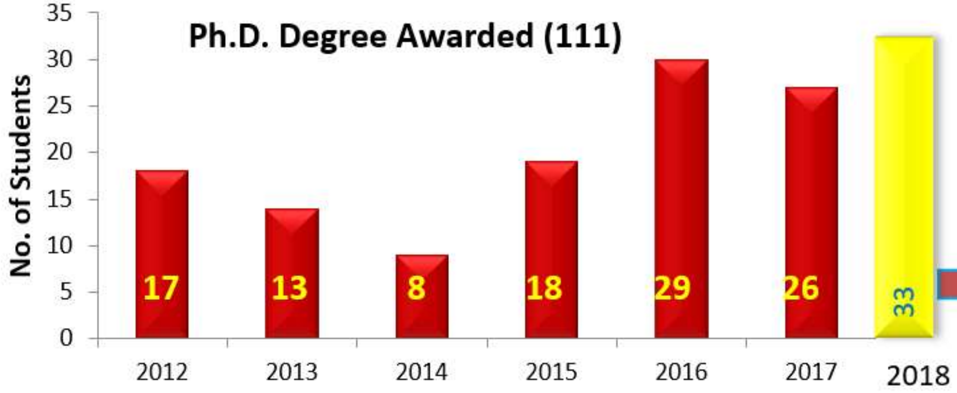
M.Phil. Degree Awarded (49)



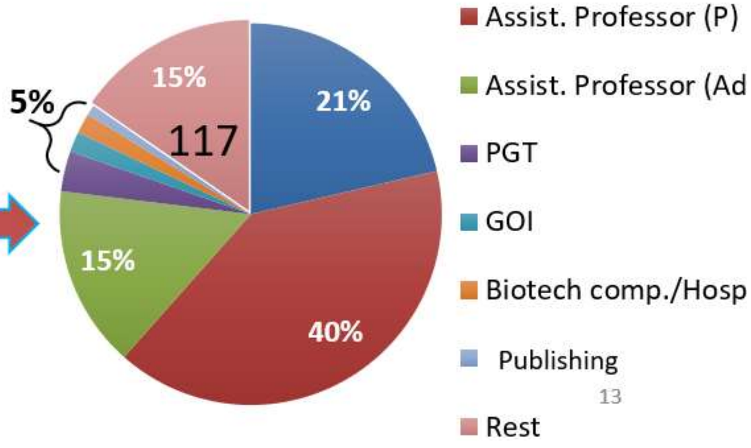
After M.Phil.



Ph.D. Degree Awarded (111)



After Ph.D.



UNDERGRADUATE TEACHING

- Serve as the Nodal point, and responsible for revision of curriculum
- Administrative support for examination
- Conduct regular workshops and training courses for college teachers for course updates
- Hand-holding with college teachers in supervising doctoral research
- Mentoring of undergraduate research
- Faculty mentors college teachers awarded with innovation Projects
- Facility open to college teachers for their own research and for the doctoral students enrolled in colleges

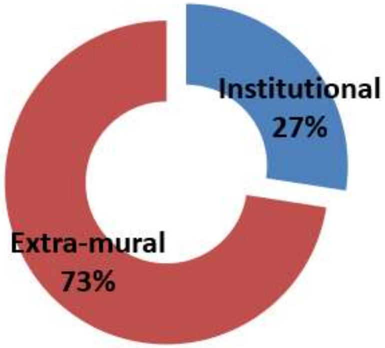
Revised the undergraduate B.Sc. Zoology (Honors) Syllabus under CBCS Scheme in 2019

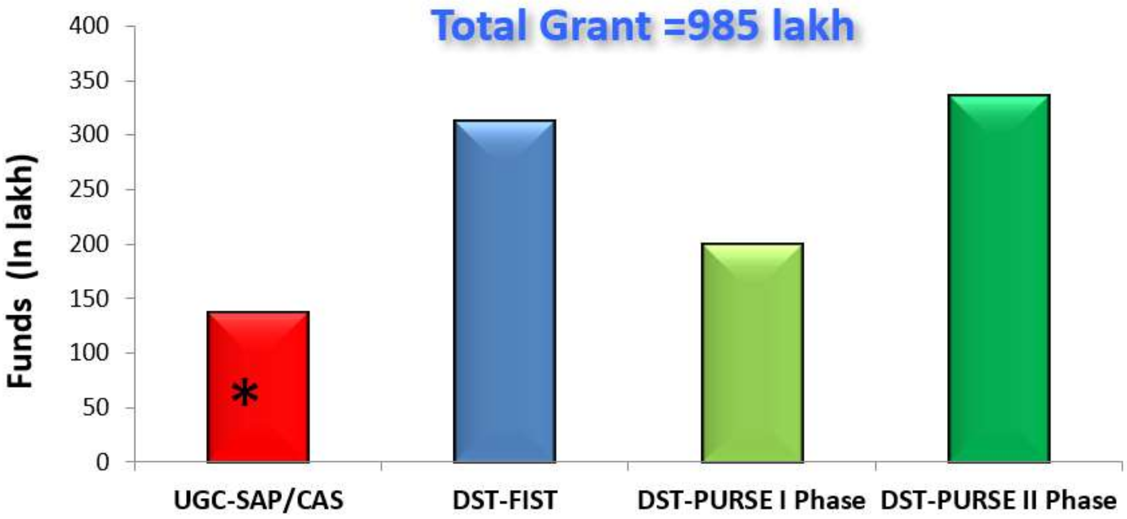
Research Profile

PROJECTS FUNDED BY DST-FIST, UGC-SAP/CAS, DST-PURSE ETC. -TOTAL GRANTS

(DURING 2012-2017)

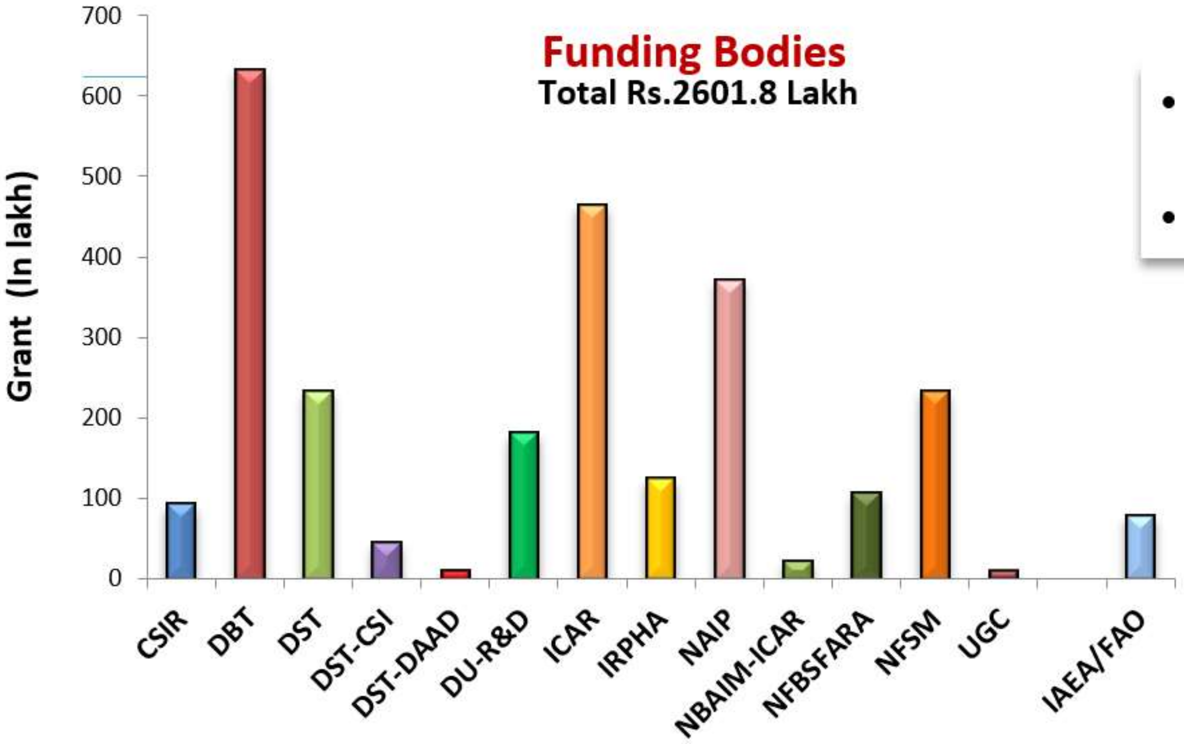
Total funding during 2012-2017
(Total 3586.8 lakh)





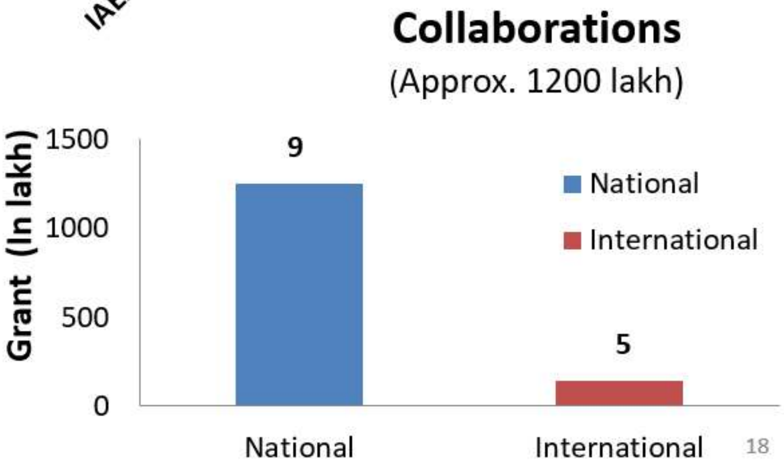
EXTRA-MURAL FUNDING

DURING 2012-2017



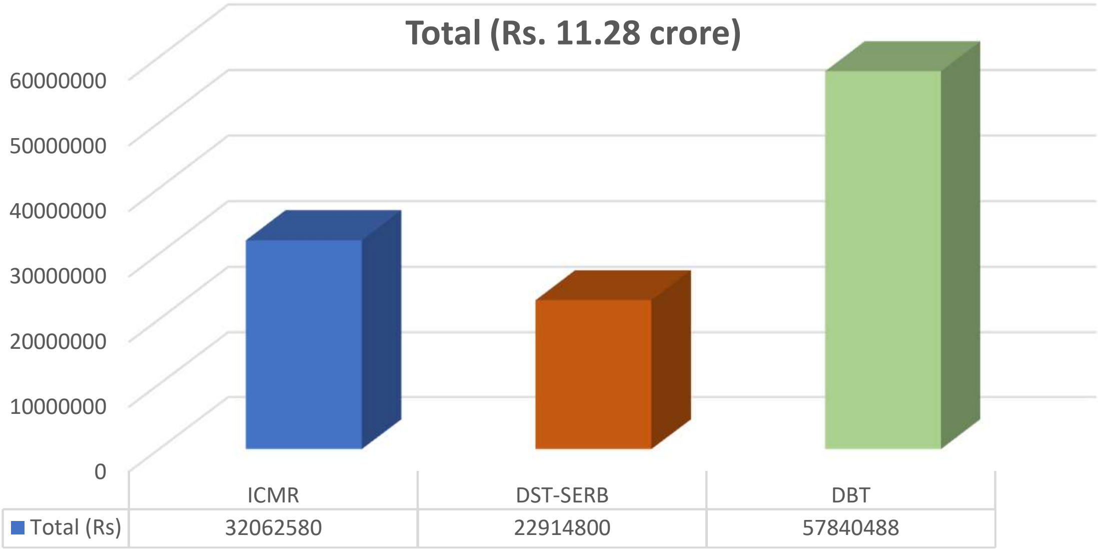
- Fairly good extra-mural funding
- Good collaboration

National & International Collaborative Research

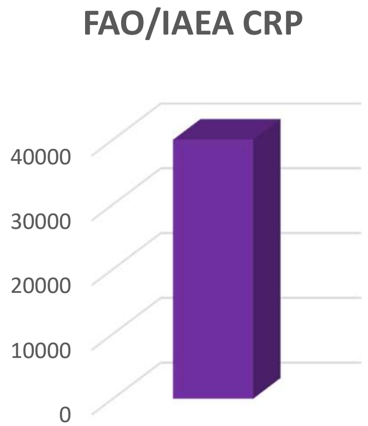


Recent (2018-2020)

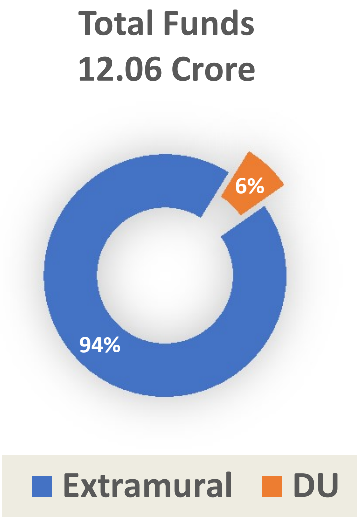
Extramural Grants to Faculty



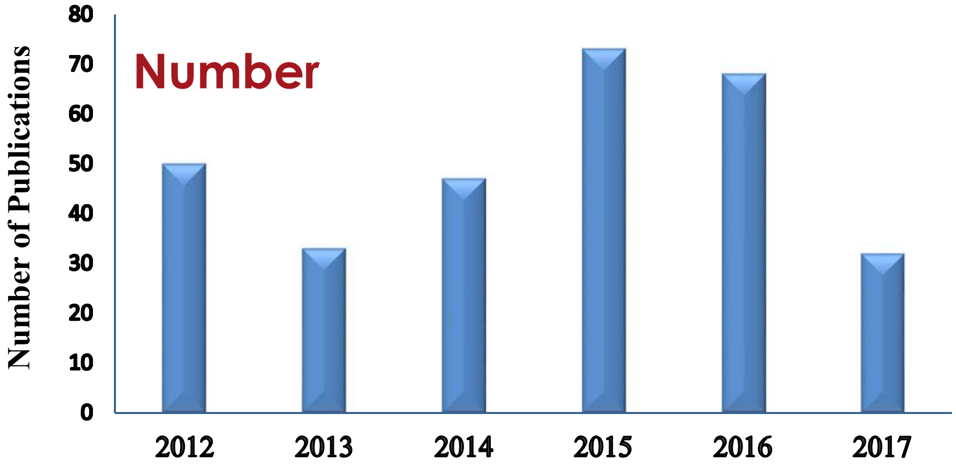
	ICMR	DST-SERB	DBT
🟦 Total (Rs)	32062580	22914800	57840488

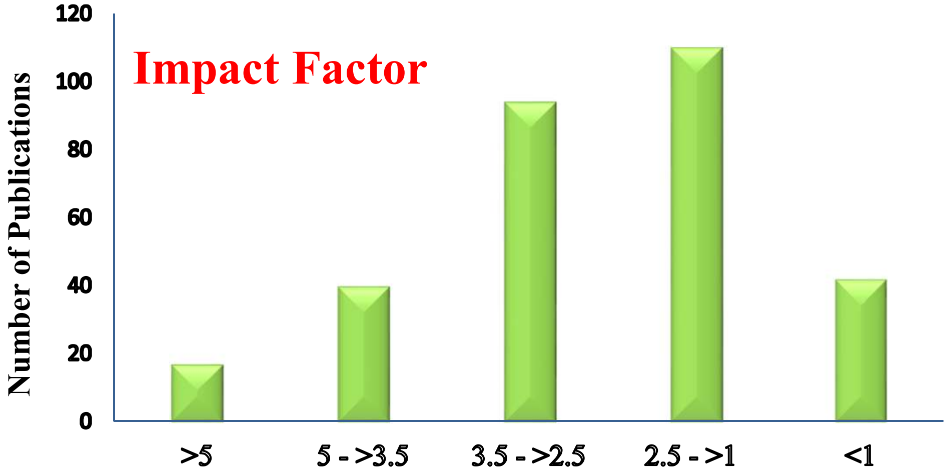


Euro 40000



PUBLICATION PROFILE





Total number 322

h-index of Faculty ranges from 10-44

Overall Citation- 16500
Citation index- 2306

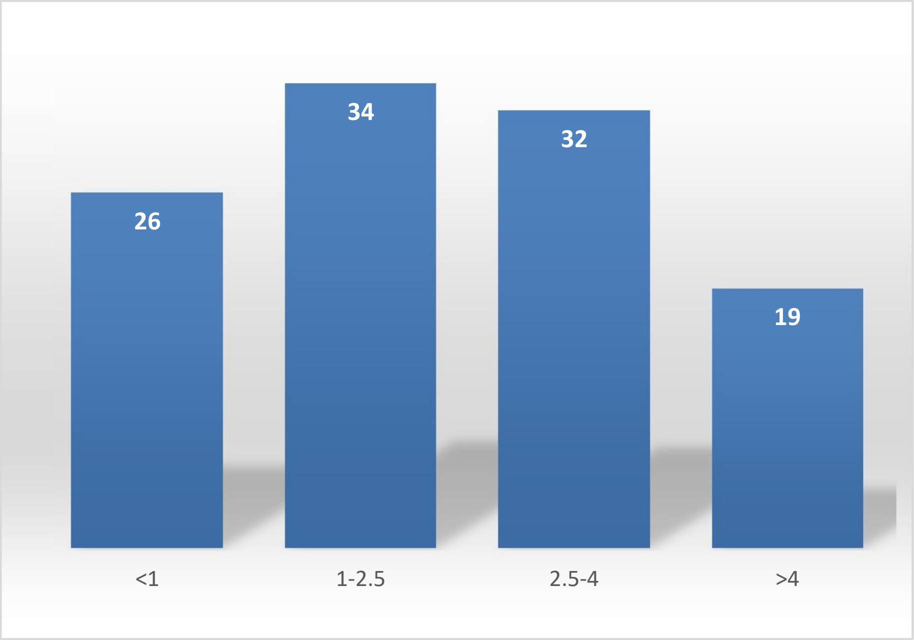
Impact factor 0.6-16.77

Books edited- 4
Chapters in books- 16

Recent Publication (2018-2020)

Publications in Peer Reviewed Journals (as per www.scopus.com)

Number of Publications	**:**	**111**
Impact factor of Journals	**:**	**0.2 to 8.0**
Citations till 2020	**:**	**16,500** (*overall from 2012*)
Chapters in Books/Edited Books/Books	:	**09**



PUBLICATIONS: REPRESENTATIVE JOURNALS

Microbiology/ Molecular Biology	IF
Microbiology & Mole. Biology Review	16.77
ISME J	9.2
PloS Pathogens	8.0
Age	4.0
BMC Genomics	3.9

General	IF
Scientific Reports	5.5
Proc. Royal Soc. Biological Science	5.2
The FSAEB Journal	5.1
Cell and Tissue Research	3.6
PLoS One	3.5
Journal of Experimental Biology	3.0
International Journal of Radiation Biology	2.3
Journal of Bioscience	2.1

Physiology/ Biochemistry	IF
Journal of Biological Chemistry	4.5
Physiology and Behavior	3.0
Photochemistry & Photobiology	2.9
Comparative Biochemistry & Physiology	2.8
Journal of Comparative Physiology	2.6

Environment/ Pesticides	IF
Journal of Hazardous Materials	4.3
Chemosphere	3.5
Food Chemistry	3.3

Neuroscience/ Chronobiology	IF
European J. Neuroscience	3.5
Journal of Chemical Neuroanatomy	3.6
Journal of Biological Rhythms	3.3
Chronobiology International	3.3
Neuropeptides	2.6

Endocrinology/ Reproduction	IF
J. Clinical & Endocrine Metabolism	6.21
Fertility and Sterility	4.6
Molecular and Cellular Endocrinology	4.5
Hormones & Behavior	4.6
Journal of Neuroendocrinology	3.5
General and Comparative Endocrinology	2.8

Fish Biology	IF
Fish and Shellfish Immunology	3.0
Journal of Fish Diseases	2.0
Fish Physiology and Biochemistry	1.6

Entomology	IF
Advances in Insect Physiology	7.3
Journal of Insect Physiology Fish	2.0
Bullentin of Entomological Research	2.0

Research Profile (2018-2020) contd….

Collaborating Partner Institutions

National:

- TERI, NBRI, IITR, IMTECH, IARI,, IIT, NEERI, IGIB, ICGEB, CDFD, NII, ICPO, NIHFW, JNU, NEHU, NISER, CCSU, Other Universities

International:

- DBT, India – BBSRC, UK: University of Stirling, Scottish Association for Marine Science
- Africa: Sokoine University of Agriculture, Aqua cultural Association of Kenya, State Department of Fisheries
- Austria: International Atomic Energy Agency (IAEA) Vienna
- Norway: Norwegian University of Science
- Australia: IACB CSIRO

INFRASTRUCTURE & LEARNING RESOURCES

Department of Zoology
University of Delhi

S.No.	Infrastructure Head	Department of Zoology
1	Library	**10293 Books (Recent, Archives, Rare books)**
2	Internet facilities for staff and students	**100 computers, Wi-Fi enabled**
3	Total number of class rooms	**3, all ICT equipped, Smart boards**
4	Class rooms with Computers and ICT facility	**Yes**
5	Teaching Laboratories	**7, all ICT equipped, Smart boards**
6	Research Laboratories	**18, Well equipped**
7	Museum	**Specimens, Skeletons, Stuffed animals**
8	Animal House	**Mice, Birds, Lizards, Fishes, Insects, Microbes**

LIBRARY

Rich library - **> 10,000 Books**

Multiple copies of **reference books** (Recent editions)

Books on **Advance Research Topics**, **Methodologies /protocols**, etc.

- **Enough seating arrangement**
- **Equipped with computers/ laptops**
- **Wi-Fi facility**

INTERNET FACILITIES FOR STAFF AND STUDENTS

- **> 100 Computers** all connected to internet
- Used by students, faculty and staff.
- ‘Bioinformatics & Computational Biology’ class in M.Sc.
- Department is Wi-Fi enabled

CLASS ROOMS

- 3 Class rooms
- Smart Boards &
- ICT facilities
- Wi-Fi enabled

TEACHING LABORATORY


Genetics lab

- **Laboratories** as per GLP standard
- **Equipment** used for teaching
  - Spectrophotometer
  - Refrigerated incubator shaker
  - Data Acquisition system
  - Centrifuges
  - Electrophoresis units
  - Thermocycler
  - Laminar Flow
  - Microscopes , etc.

TEACHING LABORATORY(CONTD.)


Physiology lab


Fish biology lab


Entomology lab


New lab

CENTRAL INSTRUMENTATION FACILITY

- Flourescence Microscopes
- HPLC, FPLC, GLC, GC, 2D PAGE,
- Lyophilizers,
- Nanodrop, Spectrophotometers,
- ELISA Reader
- Ultracentrifuges & High Speed Centrifuges
- Gradient PCR & Real Time PCR
- Gel-documentation system,
- FACS

First 'Natural History Museum' in the country which is still functional

ANIMAL HOUSE

ANIMAL MODELS


Drosophila Facility


Aquaculture Facility


Avian Facility

Insects
Reptiles
Murine Model

ANIMAL HOUSE (CONT...)

- Registered with CPCSEA
- The department has CPCSEA approved IAEC
- All protocols of experiments on animals are approved by IAEC
- The biological waste are disposed through the waste disposal service provider

Evolvera-Zoological Society

Department of Zoology, University of Delhi

OUR MOTO : "An innovation for today, an invention for tomorrow"

"आज की नवीनता, कल का आविष्कार"

Team Evolvera

Chief Patron:	Prof. Umesh Rai Head
Patrons:	Prof. Namita Agrawal, Prof. Neeta Sehgal & Prof. R.K. Seth
President:	Mr. Chetkar C. Keshavam
Vice President:	Ms. Nidhi K. Shrivastava
Treasurer:	Ms. Priya
General Secretary:	Mr. Chandrakant Singh
Joint Secretary:	Ms. Neha Vimal

Activities

- Invited lectures
- Journal Club
- Annual Festival
- Conference & Celebrations
- Fun for togetherness
- NGO donation drive

Founded in: March 2015

RECENT EVENTS

Workshops organized in departments/ colleges/other universities

We have been instrumental in organising workshops in colleges, departments and universities

Workshops

- Physiology
- Drosophila Stock Centre
- Animal Behaviour
- Animal Handling

Topics covered:

- Art of Science Communication
- Scientific Writing and Communication
- Culture of Responsibility

Workshops were organised at:

- Ramjas College
- Maitreyi College
- Sri Venkateswara College
- Department of Chemistry, DU
- MDU, Rohtak
- Panjab University, Chandigarh
- IMTECH, Chandigarh
- Jawaharlal Nehru University
- Amity University
- Goa University
- NIIT, Neemrana
- Department of Zoology, DU
- Institute of Home Economics, DU
- University of Guwahati
- Tamil Nadu Agricultural University
- KIIT, Bhubaneshwar

Collaborators from United Kingdom, Kenya, Tanzania and India attended the Third Annual Meeting of the DBT (India)-BBSRC (UK) sponsored Project during February 1-3, 2019.

Honourable Pro Vice-Chancellor, Prof. J. P. Khurana, University of Delhi released the Training Manual “Recent Advances in Fish Nutrition” on March 15, 2019.

Honourable Pro Vice-Chancellor, Prof. J. P. Khurana, University of Delhi visited out door the Macrophytes culture facility of Department on March 15, 2019.

AMI Conference 3rd to 5th February, 2021
(Hybrid mode)

61st Annual International Conference of

The Association of Microbiologists of India (AMI) &

Indian Network for Soil Contamination Research (INSCR)

in association with

The Energy and Resources Institute (TERI),
University of Delhi (DU),
Indian Agricultural Research Institute (IARI) &
Indian National Science Academy (INSA)

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UNIVERSITY OF DELHI


Gunjan Shukla


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By Gunjan

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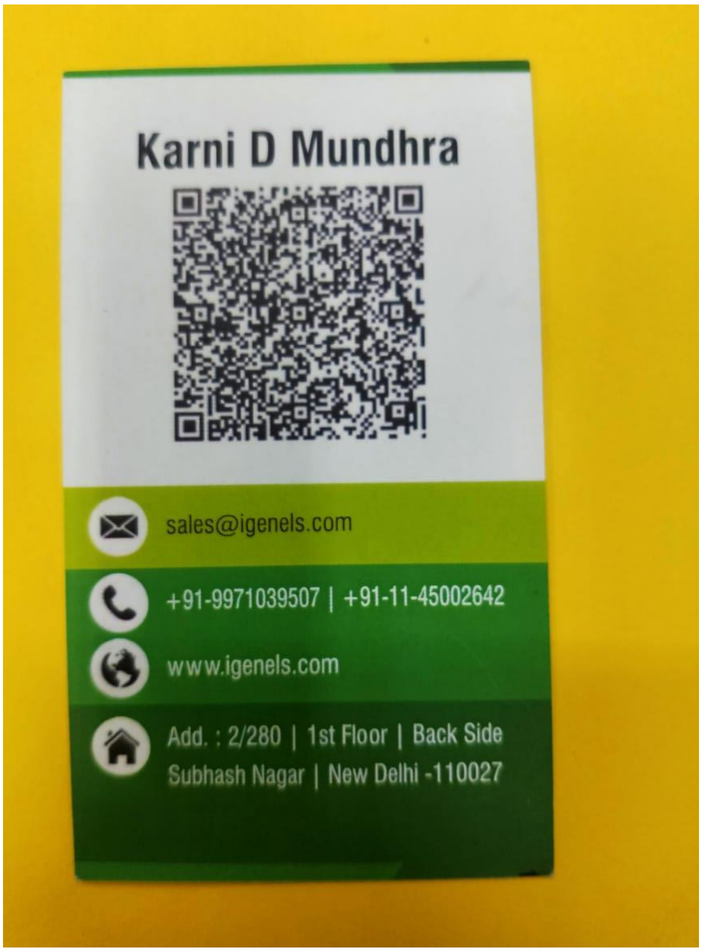

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