

CHAPTER 61

ZOOLOGY

Doctoral Theses

01. ABRAHAM (Jeeva Susan)
Taxonomy, Phylogeny and Molecular Systematics of Ciliates from Delhi, India.
Supervisors : Dr. Seema Makhija and Dr. Renu Gupta
Th 25378

Abstract
(Verified)

Ciliates, single celled microorganisms are integral part of aquatic and terrestrial ecosystem. In the present study, ciliates diversity from three freshwater bodies from Delhi – Okhla Bird Sanctuary (OBS), Sanjay Lake (SL), and Raj Ghat Pond (RJ) were identified using microscopic and molecular methods. 48 ciliate species representing 8 classes, 16 orders, 28 families, and 38 genera of Phylum Ciliophora were identified. Maximum ciliate diversity was observed in the OBS and maximum species were reported from the class Spirotrichea. Sixteen ciliate species from the class Spirotrichea were characterized by morphological and molecular markers. Of these, 8 were identified as new species (*Aponotohymena isoaustralis* n. sp., *Gastrostyla indica* n. sp., *Tetmemena saprai* n. sp., *Anteholosticha foissneri* n. sp., *Uroleptus isogallina* n. sp., *Diaxonella multimarginata* n. sp., *Euplotes lynni* n. sp. and *Euplotes indica* n. sp). The remaining 8 were Indian populations of the known species (*Aponotohymena australis*, *Oxytricha granulifera*, *Paraurostyla coronata*, *Sterkiella multicirrata*, *Pseudokeronopsis erythrina*, *Pseudourostyla cristata*, *Euplotes aediculatus* and *Euplotes woodruffi*). Further, correlation among various physicochemical parameters and ciliate diversity of the three sites was carried out for different seasons. Ciliate diversity was positively correlated with temperature, phosphate, nitrite, nitrate and ammonia, whereas it was negatively correlated with pH, dissolved oxygen (DO), total dissolved solids (TDS), electrical conductivity (EC), water hardness (WH), chloride and sulphate. Desirable physicochemical parameters for ciliate diversity, richness and evenness were: temperature (22–29°C), neutral pH (7–7.5), DO levels (more than 2 mg/L), low level of TDS, EC, WH, chloride, sulphate and high levels of phosphate, nitrite, nitrate, and ammonia. Using metabarcoding approach eleven genera and one class was identified, however about 22 species revealed by classical methods were not revealed by this approach. This suggests that ciliate identification and status can be done by integrating morphology and molecular methods.

Contents

1. Introduction. 2. Review of literature 3. Materials and methods 4. Results and discussion 5. Outcomes. Bibliography.

02. BATRA (Twinkle)
Effects of Dim Light at Night on Sleep and Metabolism in Female Zebra Finch.
 Supervisor : Prof. Vinod Kumar
Th25378

Abstract
(Verified)

The earth's rotation on its own axis exposes organisms that inhabit the planet earth to daily cycles of the light-dark, and hence food availability. However, in about last 100 years, there has been a major alteration in the light-dark environment, particularly because of increasing usage of artificial lighting, which has vastly improved our living condition by adding efficacy and productivity in the work environment. The benefits of artificial light has also significantly added to the problems related to health and well being of humans and animals. One very visible consequence of illuminated nights is foraging; the availability of light at night can alter the feeding pattern. A diurnal species can spread its feeding activity at night, if it is illuminated enough to make the food resource visible and accessible. The light at night, now categorised as light pollution, is indeed one of the most pervasive forms of present-day alteration in our environment. It has blurred the temporal partitioning of the day and night by turning the night less dark. In this thesis, we have asked the question whether dim light at night disrupts circadian (daily) rhythms and associated biological functions, such as the activity-rest, sleep, feeding (eating), hormone secretions and metabolism by using Zebra finch (*Taeniopygia guttata*) as the experimental system. The results from present study provides evidence for disruptive effects of dim light at night, in particular, on the behaviour, physiology, hormones and gene expressions in a diurnal species. However, the negative effects of dLAN were ameliorated if food availability was restricted only during the day-time. The effects were also substantially reduced in birds exposed to red light at night; so, using a monochromatic long wavelength light could reduce the negative impact of light at night on the overall behaviour and physiology.

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1.General Introduction 2. Effects of dLAN-induced alteration in eating pattern on behaviour and physiology 3. dLAN-effects: role of light wavelength 4. Summary and Conclusions. References. Publications and Presentations.

03. BAKSHI (Amrita)
Studies on Leptin and Leptin Receptor in Spotted Snakehead Channa Punctata (Bloch,1793)
 Supervisor : Prof. Umesh Rai
Th 25379

Abstract
(Not Verified)

The structural, functional and regulatory aspects of leptin (Lep) and its receptor (Lepr) were investigated in spotted snakehead *Channa punctata* that significantly contributes to inland fisheries. The putative Lep and Lepr consisted of 159 and 1129 amino acids. Hydrophobic nature of Lep was predicted based on positive grand average of hydropathy score conjecturing existence of leptin binding proteins. Tertiary structure of Lep revealed four α -helices wherein conserved residues (Cys-108, Cys-159, Arg-42, Glu-88) were predicted crucial for providing structural

integrity to hormone. In *Lepr*, a pair of WSXWS motifs and three pairs of cysteine in extracellular domain and residues of homology box along with Tyr-969, Tyr-1063, Tyr-1128 required for downstream signalling were conserved. Evolutionary analyses revealed clustering of *Lep/Lepr* of *C. punctata* with respective homologs in *Channa striata*. Evolution of teleostean leptin genes was driven by positive and negative selection pressures. Ubiquitous expression of *lep/lepr* was found with maximal levels of *lep* in liver and *lepr* in middle brain, head kidney and gonads indicating pleiotropic roles of leptin in fishes. Expression of *lep/lepr* in lymphoid organs, brain, intestine, liver and gonads varied depending on reproductive state. Further, sex-related difference noticed in lymphoid organs, liver and gonads especially during reproductively active phase prompted to speculate the implication of sex steroids in transcriptional regulation of *lep/lepr*. Correlation analysis between *lep/lepr* and plasma sex steroids corroborated the assumption which was fortified by *in vivo* and *in vitro* experiments with dihydrotestosterone (DHT) and 17 β -estradiol (E2). A marked reduction in *lep/lepr* was observed in lymphoid organs and liver of both male and female *C. punctata*. In gonads, DHT and E2 had inhibitory effect on testis while stimulatory on ovary. These observations suggest tissue- and sex-specific involvement of sex steroids in transcriptional regulation of leptin and its receptor in *C. punctata*.

Contents

1. Introduction. 2. General Methodology 3. Molecular characterization of leptin and leptin receptor of spotted snakehead *channa punctata*: structural, functional and evolutionary analyses 4. Tissue distribution and differential expression of *lep* and *lepr* depending on sex and reproductive state of spotted snakehead 5. Transcriptional regulation of *lep* and *lepr* by sex steroids in male and female spotted snakehead. 6. Summary. References. List of Publications.

04. BHAT (Anjali)

Investigation of the Role of Exosomes in Cervical Cancer Angiogenesis and Endothelial Cell Conditioning.

Supervisor : Prof. Alok Chandra Bharti
Th25370

Abstract (Not Verified)

Cervical cancer, caused by persistent infection of high-risk human papillomavirus (HPV), poses a major reproductive health challenge for women. High risk HPV types, HPV16 and HPV18 collectively contribute to over 80% of invasive cervical cancers which develops over a long period of time via initiation of precursor metastatic lesions. Angiogenic switch is a hallmark feature of transition from low grade to high grade cervical intraepithelial neoplasia (CIN) lesions in cervical cancer progression. Recent leads indicate role of tumor-derived exosomes in altering the functions of endothelial cells, but their role in cervical cancer remains unexplored. Our data showed that cervical cancer cell exosomes are angiogenic in nature as seen via enhanced tube formation, increased migration rate and higher proportion of cells in S/G2/M phase in HUVEC. A high level of PTCH1 protein was detected in the exosome-treated endothelial cells. RT-PCR analysis showed increased transcripts of Hh-Gli downstream target genes like VEGF-A, VEGFR2, angiopoietin-2 and decreased expression of VEGF-B, and angiopoietin-1, suggestive of active Hh-Gli signalling in treated HUVEC. Our data showed enrichment of poly-A RNA transcripts in the exosomal cargo. The transcripts estimated using Illumina HiSeq X showed EVC2, LUZP1 and ANKS1B as the top 20 overexpressed transcripts, due to their involvement in Hh signaling, cellular migration and invasion, respectively. HPV

encoded viral oncoproteins E6 and E7 play a pivotal role in the tumorigenic transformation and our RT-PCR data revealed HPV18 E6*I splice variant in exosomal RNA of HeLa cells which were consistently retained even after 5-FU and cisplatin-induced oxidative stress. However, evaluation for HPV16 and18 E6 /E7 DNA, indicated towards the absence of HPV genomic fragments in these exosomes. The present investigation therefore, aims to create a holistic picture of cervical cancer-endothelial cell interaction, which could be, beneficial to design better therapeutic intervention strategies.

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1.Introduction 2.Review of Literature 3.Rationale and objectives 4.Materials and methods 5. Results 6. Discussion 7. Summary and conclusion. Bibliography.

05. BUNIYAADI (Amaan)

Study of Cognitive Performance in Indian House Crow: Impact of Light and Social Environment.

Supervisor : Prof. Vinod Kumar

Th25544

Abstract (Not Verified)

Avian cognition has been an element of fascination to humans since time immemorial. Cognition in birds encompasses the mental processing, transformation, storage, manipulation, and retrieval of information acquired through sensory modalities, experience, and thought. Among birds, corvids are considered 'feathered apes', as they possess cognitive feats that are otherwise not found outside primates, apes, and humans. To further maximize their fitness, birds possess endogenous clocks which interact with prevailing light, food, and social environment to generate temporal oscillations in crucial daily functions of birds, such as activity-rest, sleep-wake, and feeding patterns. An alteration in the physical environment, especially the temporal partitioning of the day and night, affects the endogenous circadian timekeeping and, in turn, daily periodic functions, and higher-order brain functions like cognitive performance. Since the last century, the increasing usage of artificial light at night (ALAN) has altered our nighttime environment and diminished the distinction between light and dark components of the day. In the present thesis, we first confirmed that crows possess the ability of self-recognition, which is an advanced cognitive trait. Then, we performed experiments to address the effects of dLAN (dim light at night) on daily activity and sleep patterns, physiology, and cognitive performance in Indian house crows. We observed that dLAN negatively impacted daily activity, sleep, and mood, and decreased cognitive performance as assessed by a motor-self regulation task, innovative problem-solving, and spatial and pattern learning memory retrieval (LMR) tasks. We also tested and confirmed the mitigating effects of a short dark period at night, exogenous melatonin, and social enrichment on the dLAN-induced negative alteration in behavior and cognition of the crows and their associated gene expression. These findings suggest like humans, crows possess remarkable cognitive feats and an alteration in the night environment can have detrimental effects on their overall health and brain functions.

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1.General Introduction 2. Role of exogenous melatonin 3. Role of social enrichment 4. Summary and conclusions. References. Publication and presentations.

06. CHATTERJEE (Megha)
Impact of Serine Mutations in Mutant Huntingtin on Huntington's Disease Pathogenesis.
 Supervisor : Prof. Namita Agrawal
Th25586

Abstract
 (Not Verified)

Poly-glutamine expansion near the N-terminus of the huntingtin protein (HTT) is the prime determinant of Huntington's disease (HD) pathology; however, post-translational modifications and protein context are also reported to influence poly-glutamine induced HD toxicity. The impact of phosphorylating serine 13/16 of mutant HTT (mHTT) on HD has been documented in cell culture and murine models. However, endogenous processing of the human protein in mammalian systems complicates the interpretations. Therefore, to study the impact of S13/16 phosphorylation on the subcellular behavior of HTT under a controlled genetic background with minimal proteolytic processing of the human protein, we employed *Drosophila* as the model system. We ectopically expressed full-length (FL) and exon1 fragment of human HTT with phosphomimetic and resistant mutations at serines 13 and 16 in different neuronal populations. Phosphomimetic mHTT aggravates and the phosphoresistant mutation ameliorates mHTT-induced neurotoxicity in the context of both FL- and exon1- mHTT in *Drosophila* although in all cases FL appears less toxic than exon1. Besides the neurological symptoms of HD, debilitating metabolic alterations including weight loss are also evident in pre-clinical and clinical HD studies. Moreover, metabolic changes associated with HD are reflected in the systemic levels of major metabolic markers like carbohydrates, lipids and proteins. The neuronal expression of exon1-mHTT induced a reduction in the body-weights as well as the carbohydrate levels of adult *Drosophila*. However, the phosphoresistant mutation increases the body weight and the levels of carbohydrate in exon1- mHTT flies. Carbohydrate levels were found to be significantly modulated on neuronal expression of exon1- mHTT in larval stages as well. Conclusively, serine 13 and 16 residues of mHTT might prove to be attractive therapeutic targets for effectual HD management and therefore, their role in HD toxicity needs to be rigorously investigated.

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1. Introduction 2. Material and methods 3. DNA sequence validation of huntingtin transgenes in transgenic *drosophila* and expression profile of gal4 drivers 4. Investigation of the impact of serine 13/16 mutations on huntington's disease neurotoxicity using transgenic *drosophila* 5. Effect of serine mutations on peripheral toxicity of huntington's disease using transgenic *drosophila* 6. Summary. References. List of publications.

07. CHAUHAN(Namita)
Unravelling the Role of Patterning Genes and Moulting Hormone in Maintaining Pattern Integrity and Development in Faster Developing *Drosophila Melanogaster*.
 Supervisor : Prof. Mallikarjun Shakarad
Th 25388

Abstract
(Not Verified)

The ability of biological systems to maintain a stable phenotype despite genetic, environmental or physiological perturbations is called as 'Developmental robustness'. The final phenotype is regulated by coordination between various developmental and molecular mechanisms. In holometabolous insects, accurate patterning and development is guaranteed by the alignment of final gene expression patterns in tissues at a specific developmental stage such as moulting and pupariation, irrespective of the individual rate of development. In the present study, I have used *Drosophila melanogaster* populations selected for faster pre-adult development and extended reproductive lifespan to understand the mechanisms regulating developmental robustness in insects. These populations show extremely rapid development compared to their ancestors with a ~22% reduction in the egg to adult development time. Despite a significant reduction in development duration, flies from the selected population exhibit stability of phenotype, albeit significantly small in size. My research shows that the flies from selected populations show significantly shorter larval phase and organ size compared to the controls. The reduced duration is a result of early as well as higher levels of moulting hormone ecdysone in the selected populations due to the relatively larger prothoracic gland and higher transcriptional activity of ecdysone biosynthetic genes. The selected populations also show higher expression of patterning genes such as wingless, achaete and cut in the wing imaginal disc. The phenotypic integrity even under reduced development time in these flies is ensured by coordination between higher ecdysteroid biosynthesis and higher expression of developmental genes that ensure appropriate pattern formation at the end of each development stage that is being attained early in these populations compared to their ancestral controls.

Contents

1. Introduction and Review of Literature 2. The experimental fly populations and their maintenance 3. The impact of selection pressure on development rate and organ size 4. Systemic regulation of faster development in the selected population 5. Evaluation of temporal and spatial expression patterns of key patterning genes in the imaginal disc tissues 6. Conclusion and future perspectives. References. List of publications.

08. DHINGRA(Neha)
Isolation and Characterization of Root Epiphytic Bacteria and their Protein Profiling under Heavy Metal Stress.
 Supervisors : Prof. Dileep Kumar Singh
Th 24793

Abstract
(Not Verified)

Bacterial isolates exhibited plant growth promoting characters that benefit plant directly, indirectly or synergistically. Both isolates displayed plant growth promoting properties. Heavy metal stress at higher concentrations, displayed varying extent of toxicity to these properties of the bacterial isolates. But the effect of heavy metal toxicity was less at lower concentrations as compared to higher concentrations of heavy metal. The bacterial isolates were subjected to immobilization using alginate, casein and gelatin beads. Their metal uptake capacity was studied. It was found that alginate beads showed higher heavy metal uptake as compare to casein and gelatin beads. Highest metal uptake by alginate beads was of Cadmium, Copper and the Chromium. This study helped us to understand that different plants harbour different heavy metal remediating bacteria. This is the first report to isolate and study heavy metal remediating bacteria from wetland plants *Acorus calamus*, *Typha latifolia* and *Phragmites karka*. This study can be very important in managing the environmental concerns. This study helped us to understand that different plants harbour different heavy metal remediating bacteria. This is the first report to isolate

and study heavy metal remediating bacteria from wetland plants *Acorus calamus*, *Typha latifolia* and *Phragmites karka*. This study can be very important in managing the environmental concerns.

Contents

1. Introduction 2. Review of Literature 3. Assessing the seasonal variation in bacterial community profiling from the rhizospheric zone of the wetland plants (*Acorus calamus*, *phragmites karka* and *typha iatifolia*) 4. Isolation, identification and characterization of heavy metal (Cadmium, copper and chromium) remediating root epiphytic bacteria 5. Characterization of PGPR properties and extracellular polymeric substance from *providencia rettgeri* strain KN1 and *serratia marcescens* strain KN2 under heavy metal stress. 6. Protein profiling of *providencia rettgeri* strain KN1 and *serratia marcescens* strain KN2 during heavy metal stress (Cadmium, copper and chromium) 7. Comparative study on metal adsorption properties of immobilized alginate, casein and gelatine beads of *providencia rettgeri* strain KN1 and *serratia marcescens* strain KN2. 8. Conclusion 9. Summary. References. List of Publications.

09. GOSWAMI (Ravi Kumar)

Evaluation of *Lemna Minor L.* As Fish Feed Ingredient, Its Mass Production and Estimation of Biochemical Composition.

Supervisors: Prof. Rina Chakrabarti

Th25375

Abstract (Not Verified)

Aquaculture is one of the fastest-growing food producing sectors in the world. It contributes immensely in food security, livelihood support and employment generation. The limited global production of fishmeal and its cost are major concerns in the present scenario to replace with non-conventional alternative feed ingredients. Freshwater duckweeds are a potential ingredient to replace the application of fishmeal in aquaculture. The present study aimed to standardize the culture technique of duckweed *Lemna minor* and evaluates the effect of plant-based diets on the performance of *Labeo rohita* (rohu), *Cyprinus carpio* (common carp) and *Oreochromis niloticus* (tilapia). Fish were fed with plant-based diets at different concentrations and control diet without supplementation of plant ingredients. The final average weight and specific growth rate were significantly ($P < 0.05$) higher in fish fed with duckweed-based diets compared to others. Duckweed-based diets influenced the amino acids and fatty acids compositions of fishes. All essential, non-essential and free amino acid levels were significantly ($P < 0.05$) higher in fish fed duckweed-based diets compared to the control group of fish. Amylase activity was significantly ($P < 0.05$) higher in fish fed duckweed-based diets compared to others, and lowest lipase activity was observed in fish fed control diet compared to other feeding regimes. The inclusion of duckweed in the diets of rohu, common carp and tilapia enhanced the levels of omega-3 fatty acids, eicosapentaenoic acid and docosahexaenoic acid of fishes. Expression levels of delta-6-desaturase (*fads2d6*), elongation of very long-chain fatty acids protein 2 (*elov2*), elongation of very long-chain fatty acids protein 5 (*elov15*) and fatty acid synthase (*fas*) were up-regulated in rohu and common carp fed duckweed-based diets compared to the others. The knowledge generated from the present study will help in the formulation of cost-effective diets and thereby, the production of nutrient rich fishes for consumers.

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1. Introduction 2. Review of literature 3. Materials and methods 4. Results 5. Discussion 6. Summary and conclusion, Reference, Publications.

10. JADLI (Mohit)
Role of NF- κ B and Interacting Cytokines During Prostate Cancer Induced Osteoclastogenesis.
 Supervisor : Prof. Alok Chandra Bharti
Th 25372

Abstract
(Not Verified)

Prostate cancer (PCa) frequently metastasizes to the bone leading to devastating complications such as severe pain and fracture. However, the mechanisms by which PCa cells cause bone loss remain less understood. We investigated the role and mechanisms by which PCa cells induce osteoclastogenesis using cultured monocytic osteoclast precursors. Treatment of RAW264.7 cells with PCa cell lines: DU-145, LNCaP, PC-3, or their conditioned media led to the formation of distinct multinucleated, TRAP+ osteoclasts. This phenomenon was associated with the increased activation of transcription factor NF- κ B. High transcript levels of RANKL, TNF- α , and IL-6 were detected in PCa cells. TNF- α and LT- α augmented, whereas IL-6 reduced the RANKL-induced osteoclast formation in RAW264.7 cultures. Our results also demonstrated that PCa cells-induced osteoclastogenesis involved the activation of the TRAF6-IKK-p65-NF- κ B signaling cascade. Together, our study demonstrates that PCa cells produce RANKL and several other proinflammatory cytokines, which collectively influence osteoclastogenesis by targeting NF- κ B signaling pathway.

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1.Introduction 2. Review of literature 3.Rationale and objectives 4. Materials and methods 5. Results 6. Discussion 7. Summary and conclusion. Bibliography. Annexures.

11. KHURANA (Himani)
Exploring the Gut Microbiome of Freshwater Fish from Gobindsagar Reservoir, Himachal Pradesh, India.
 Supervisor : Dr. Ram Krishan Negi and Prof. Rup Lal (Retd.)
Th 25377

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1. Introduction 2.Review of literature 3. Analysis of cultivable microbial diversity of tor putitora(Ham.) and hypophthalmichthys molitrix 4. Deciphering the gut microbiome of tor putitora (Ham.) using metagenome sequencing 5. Investigation of microbial diversity and their functional significance in different regions of the alimentary canal of hypophthalmichthys molitrix (Val.) using metagenome sequencing 6. In-silico identification of potential anti-microbial peptides (AMOs) from the fish gut microbiome 7.References. Appendices. List of Publications.

12. KHYATI
Circadian Rhythm and Associated Behaviour under Physical and Physiological Stress in Insects.
 Supervisor: Prof. Vinod Kumar
Th 25585

Abstract
(Verified)

Circadian rhythms are ubiquitous; they are exhibited in a myriad of functions, and at all the levels; i.e. molecular, physiological and behavioural levels. In fact, the

organisms use circadian rhythms to allow the anticipation of favourable times during the day by using one or more of the environmental zeitgebers (German word, zeit= time; geber = giver). Light-dark cycles act as a predominant zeitgeber for most circadian functions, since it is a stable environmentable variable and is also a predictor of the season because of consistent changes in the duration of light-dark component at places away from the equator. The circadian time is generated by the interaction of a host of genes in the interlocked auto regulatory transcription-translation feedback loops (TTFL). TTFL involves genetic transcription of “clock genes” and post-translational activities of the “clock proteins”, and is conserved through almost all the taxa. However, because of desynchronosis that can result from the asynchrony of endogenous circadian rhythms with endogenous and/ or exogenous factors, there can be the impairment of overall metabolism and the other functions. The present thesis addressed this question using insects whether physical and physiological stresses induce desynchronosis in circadian molecular clocks in the central and peripheral tissues. We mainly assessed changes in mRNA oscillations of genes that constitute core TTFL of the circadian clock in response to the unnatural all-light (constant light) or no-night (constant darkness) environment in an insect moth, and to the neurogenerative disorder (Huntington’s disease, HD) using transgenic HD flies.

Contents

1.General Introduction 2.Circadian clock gene expressions and reproductive performance under constant light and darkness in *spodoptera litura* 3. Trans-generational effects of gamma radiation on circadian clock gene expressions and reproductive performance in *spodoptera litura* 4. Restorative effect of curcumin and melatonin on clock gene expressions in transgenic HD flies 5. Summary and conclusions. References. Publications and presentations.

13. MALIK (Indu)

Effects of Photoperiod and Social Interaction on Behaviour, Physiology and Reproduction in Zebra Finch.

Supervisor : Dr. Vinod Kumar

Th 25389

Abstract (Verified)

Survival depends on how well an individual or a species adapts to its surrounding environment, particularly to the day-night cycle. Increased usage of the artificial light in about last 100 years has dramatically altered the daily light-dark environment to which animals and humans are getting exposed to. Recent studies have shown that illuminated night can adversely affect behaviour and physiology of various organisms. Besides, light-dark cycle, the interaction with conspecifics has been found to play a significant role in shaping daily activities; it is adaptive and plays a key role in both reproduction and survival. In fact, social grouping is ubiquitous in nature, and extends from foraging and defense to the courtship and mating. In present research, I focused on studying both short and long-term consequences of the exposure to constant light (no-night) and illuminated night (dim light at night), as well as of the social interaction on selected behaviors, physiology and reproduction, and associated gene expressions in a diurnal species. The present thesis has been a sincere research attempt to gain insights into the seemingly sophisticated light and social world by using an interesting experimental system of zebra finches (*Taeniopygia guttata*). Whereas the most part, the results provide insights into the effects of imposed abrupt light condition on the physiology and

reproduction, a section of thesis includes results, in particular, on the effects of social interactivity on the affiliation behaviour in zebra finches. My research generates some interesting and relevant questions in the area of vertebrate behavior, physiology and metabolism that will attract further research in future. Overall, the thesis findings seem to have broader implications for understanding the public health consequences at the present time when humans' lifestyle has become dependent on the excessive exposure to light at unnatural times (night) of the day.

Contents

1.General Introduction 2.Effects of no-night (LL) and dim light at night (dLAN) environment on gut microbial community and associated physiology 3. Impact of dim light at night (dLAN) on behaviour, physiology and reproduction 4. Effect of social interaction on affiliation behaviour and associated gene expressions. Summary and conclusions. References. Publications and presentations.

14. MOHIT KUMAR

Degradation of Penicillin G by Isolated *Serratia* sp.R1,its Impact on Protein Profile,and Synthesis of its Complex for the Enhanced Antibacterial Activity.

Supervisor : Prof. Dileep Kumar Singh

Th 25385

Abstract (Verified)

Serratia sp. R1 was isolated from the contaminated Yamuna river water, to check its potential for the bioremediation. Bacteria was purified, acclimatized, and identified through polymerase chain reaction, biochemical test, antibiotic resistant test, and scanning electron microscope. The isolated bacteria was found to have the potential of around 84% degradation of penicillin G in 14 days.

Contents

1. Introduction 2. Review of literature 3.Isolation and identification of potential, antibiotic resistant bacteria from the Yamuna River water 4. Study of the change in protein profile of *serratia* sp. R1 and identification of antibiotic resistant enzymes 5. Synthesis and characterization of antibiotic-metal complex [Penicillin G and iron] for the enhanced antibacterial activity 6. Summary. List of publications.

15. NAZ (Saba)

Investigating the Novel Mechanisms of Drug Resistance in *Mycobacterium Tuberculosis*.

Supervisor : Prof. Yogendra Singh

Th 25376

Abstract (Not Verified)

Drug resistance in *Mycobacterium tuberculosis* (Mtb) is a major public health concern, which is exacerbated by the emergence of multi and extremely drug-resistant tuberculosis. To identify novel mechanisms of drug resistance we investigated the role of two different cellular processes in either evolution or imparting drug resistance. We sought to decipher the biological role of a serine/threonine protein kinase PknL with the help of a gene replacement mutant RvΔpknL. Deletion of pknL results in the compromised growth under redox stress ,

ex vivo, establishing infection in vivo. The absence of *pknL* increases the survival ~1.5-2.5 log fold upon isoniazid or ethambutol treatment. Collectively, data suggests that *PknL* aids in combating stress conditions and reduces the efficacy of isoniazid and ethambutol. *Mtb* possesses a GC-rich genome, rendering it highly susceptible to cytosine deaminations, resulting in the occurrence of uracils in the DNA. UDGs encoded by *ung* and *udgB* initiate the repair; hence we investigated the biological impact of deleting UDGs in the adaptation of pathogen. We generated gene replacement mutants of uracil DNA glycosylases, individually (*RvΔung*, *RvΔudgB*) or together (*RvΔdKO*). *RvΔdKO* exhibited higher spontaneous mutation rate, higher survival rates in guinea pigs and accumulated large number of SNPs as revealed by whole-genome sequence analysis. Competition assays revealed the superior fitness of *RvΔdKO* over *Rv*, both ex vivo and in vivo. Importantly, this property allowed us to utilize *RvΔdKO* for the facile identification of drug targets. Next, we performed genome-wide association analysis (GWAS) using 2,773 clinical strains of *Mtb*. We identified a strong association between the mutations in the DNA repair genes and multidrug-resistant phenotype. We functionally validated the GWAS data by performing mutation rate analysis. Collectively, we propose that compromised DNA repair results in the accumulation of mutations and a subset of selected mutations drive adaptation and evolution of antibiotic resistance.

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1.Introduction. 2. Review of literature 3. Material and methods 4. A novel role of *PknL* in conferring drug resistance 5. Role of uracil DNA glycosylases in providing superior adaptability in the host 6. Role of DNA repair enzymes in drug resistance evolution. Bibliography. Appendix. List of Publications.

16. PRATEEK KUMAR

Structural Analyses of Bioactive Compounds from *Streptomyces* spp. and Identification of their Biosynthetic Gene Clusters.

Supervisor : Dr. Monisha Khanna Kapur

Th 25382

Abstract

(Verified)

Actinomycetes are considered as excellent reservoirs of natural bioactive compounds. Decreased efficacy of available medicines against drug-resistant pathogens and various diseases has resulted in dire need for the detection of compounds having unique modes of action. During our previous studies, actinomycetes were isolated from diverse habitats and screened for production of bioactive molecules. Studies of 16S rRNA gene homology revealed that isolated strains belong to genus *Streptomyces*. In current study, these compounds were characterized using GC-MS, LC-MS and NMR studies. MIC determination revealed that extracts from strains 196, 51, and RI.30 showed activity nearly in the range of commercial drugs. Strains were screened for the presence of PKS-I and NRPS gene-clusters. Strains 196, 51 and L3.41 were found to possess both PKS-I and NRPS, whereas RI.24 possess NRPS. Based on the results of structural analyses and screening of gene-clusters, strain 196 was identified as a potent strain and selected for further studies. Genome sequencing of strain 196 resulted in a draft genome of 7.4Mb. RAST results revealed the presence of 6,682 CDS, 64 tRNA genes and 7 rRNA genes. Comparative studies showed that strain 196 have 93.5% nucleotide and 96% protein similarities with *Streptomyces rhizosphaericola* 1AS2c. antiSMASH predicted the complete PKS-I and NRPS biosynthetic gene-clusters responsible for production of diverse compounds. During in-vitro studies, the extract from strain 196

demonstrated concentration and time-dependent cytotoxicity against lung cancer cells (A549) with IC50 at 0.5 mg/ml (6h) and 0.15 mg/ml (24h). Proliferation and metastatic potential of cancer cells decreased over-time in a concentration-dependent manner. Discrete changes in cellular morphology were noted as a result of the induced cytotoxicity. Apoptosis assay demonstrated 98.7% cell death at highest concentration of extract (1mg/ml). During in-silico studies, molecular docking revealed that compounds from strain 196 are effectively inhibiting the mutant EGFR (T790M/L858R).

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1. Introduction 2. Review of literature 3. Materials and methods 4. Results 5. Discussion. References. Annexure. Publications.

17.

PRIYA

Effects of Peripheral Expression of Huntingtin Protein on Metabolic Dysfunctions in Huntington's Disease.

Supervisor : Prof. Namita Agrawal

Th 25371

Abstract (Not Verified)

Metabolic disturbances including debilitating weight loss in Huntington's disease (HD) patients are complicated peripheral manifestations, and the cause remains poorly understood. In HD, besides the prominent corticostriatal atrophy, abnormalities are also noted in the peripheral tissues. Given the ubiquitous expression of mutant huntingtin (mHTT; the causative protein of HD) protein, these metabolic disturbances are speculated to occur as a result of direct effect engendered by mHTT expression in the peripheral tissues rather than being an indirect effect of hypothalamic neurodegeneration or general malaise. In my thesis, I investigated the effects of selective expression of human mHTT in the fat body (FB; functionally equivalent to human adipose tissue and liver) using transgenic Drosophila. I find that FB-autonomous expression of human mHTT exon1 is intrinsically toxic and causes chronic weight loss in the flies despite progressive hyperphagia, reminiscent of hyperphagic weight loss in patients with HD, and early adult death. Moreover, flies exhibit other metabolic defects that include a decline in the systemic levels of lipids and carbohydrates which worsen over time. Similarly, FB-autonomous expression of full-length mHTT causes weight loss, and a persistent decline in the systemic levels of a circulating carbohydrate, and reduced lifespan of flies. At the cellular level, cell death occurs along with the formation of exon1 mHTT aggregates in the FB. On the contrary, full-length mHTT accumulates in diffused forms in the FB tissue. Conclusively, my thesis work indicates that FB-autonomous expression of human mHTT alone is sufficient enough to cause metabolic abnormalities, and emaciation in vivo without any neurodegenerative cues. If this proves correct and mHTT has such profound effects on adipose tissue and the liver in HD patients, then inhibiting the pathological effects of mHTT in these peripheral tissues could be a valuable therapeutic intervention

Contents

1. Introduction 2. Materials and methods 4. Validation of the expression profile of a fat body specific driver, Cg-GAL4, throughout the developmental stages of drosophila 5. Evaluation of the impact of selective expression of exon 1 fragment of human mutant huntingtin in the peripheral tissue of transgenic drosophila 6. Elucidation of

the effect of selective expression of full-length human mutant huntingtin in the peripheral tissue of transgenic drosophila 6. Summary. References. List of Publications.

18. SAMAL (Roopa Rani)

Characterization of Mechanisms involved in the Development of Acetamiprid and Deltamethrin Resistance in an Indian Strain of Aedes Aegypti L.

Supervisor : Dr. Sarita Kumar

Th 25387

*Abstract
(Verified)*

Aedes aegypti is a vector of disease of supreme concern across the globe. Aedes-borne infections accounts for million deaths worldwide each year. Thus, current study was aimed to evaluate the efficacy of deltamethrin and acetamiprid against *Ae. aegypti* larvae; the possible development of resistance against them; and the mechanisms involved therein. The larvicidal efficacy of acetamiprid and deltamethrin against parent susceptible strain (PS) of *Ae. aegypti* revealed higher efficacy of deltamethrin than acetamiprid. Cross-susceptibility assays with different insecticides belonging to 4 chemical groups showed maximum efficacy of α -cypermethrin and fenitrothion. The larvae of PS strain subjected to the selection pressure of acetamiprid and deltamethrin, separately, for ten successive generations; to estimate the rate of development of resistance; registered a higher resistance to acetamiprid as compared to the deltamethrin. Both the selected strains of *Ae. aegypti* showed cross-susceptibility to the organophosphates and pyrethroids. The acetamiprid/deltamethrin selection also affected the growth and development parameters of *Ae. aegypti* larvae adversely inducing delayed toxic effects, growth inhibition, developmental abnormalities and reduced reproductive fitness. Investigations on the physiological, biochemical and molecular characterization of resistance development revealed involvement of multiple mechanisms. The cuticle of selected strains displayed higher thickness as compared to the PS strain causing decreased insecticide penetration. A significant rise in the activity of different metabolic detoxification enzymes; α -esterases, β -esterases, Glutathione S-transferase, Acetylcholinesterase and CYP450; was recorded. Both the selected strains of *Ae. aegypti* developed dominant mutations in the *vgsc* and *ace-1* gene and showed target-site insensitivity to these toxicants. Further selections of F10 strains with insecticides synergised with PBO reduced as well as reversed the resistance. Similar effects were recorded with the rotational selections. This study would help to devise a strategy for efficient mosquito management by combating the *problem of insecticide resistance in not only Ae. aegypti but also co-inhabiting mosquitoes.*

Contents

1. Introduction 2. Review of literature 3. Materials and methodology 4. To study the development of acetamiprid and deltamethrin resistance and cross resistance to different insecticide groups in *Aedes Aegypti* L.larva 5. Efficacy of acetamiprid and deltamethrin on the growth, development, reproductive fitness and cuticular thickness of parent and selected strains of *Aedes Aegypti* L. larva 6. Biochemical characterization of resistance in larvae of *Aedes Aegypti* L. selected with acetamiprid and deltamethrin, separately 7. Target site insensitivity of *ace* gene and *vgsc* gene in the larvae of *aedes aegypti* L. selected with acetamiprid and deltamethrin, separately 8. To study the resistance management strategy (Rotation of insecticides and synergistic use of PBO) in acetamiprid and deltamethrin-selected larvae of *aedes aegypti* L. 9. Discussion. Summary and conclusion. References. List of publications.

19. SIDHU (Harpreet Kaur)
Diversity and Taxonomic Characterization of Ciliated Protists from River Yamuna and Evolution of their Membrane Trafficking Proteins.
 Supervisor: Prof. Ram Krishan Negi
Th 25373

Abstract
(Not Verified)

Ciliated protists (Kingdom Protista, Phylum Ciliophora) are highly diverged single celled eukaryotes. The present study was focused on exploring the diversity of the ciliated protist community using classical and molecular approaches in the River Yamuna. Ciliate communities were correlated with environmental parameters to determine the potential of ciliates as bioindicators in the river. Ciliate communities at polluted sites in the Delhi NCR stretch of the river were compared with a less polluted site upstream in Uttarakhand. Ciliate diversity was maximum at the site where the river enters Delhi and reduces downstream. Significant correlations of ciliated protists with environmental parameters were found. There were 14 ciliate species found at all sites; 19 species were site-specific. One novel spirotrichean genus *Neogastrostyla aqua* nov. gen., nov. spec. was established. Another novel subspecies, *Oxytricha granulifera yamunii* nov. subspec., was proposed for the River Yamuna population of *Oxytricha granulifera granulifera*. A geographic isolate of *Aponotohymena australis* from the river was described. *Stylonychia notophora* sensu Sapra and Dass 1970 which was considered synonymous to *Tetmemena pustulata* Wirnsberger 1985 by several authors was redescribed to resolve its taxonomic status. Description of six populations of *T. pustulata* isolated from six selected sites in the river showed similar inter-population and intra-clonal variations and comparisons based on morphological, morphogenetic and molecular data confirmed that *S. notophora* sensu Sapra and Dass 1970 is a population of *T. pustulata* Wirnsberger 1985 and not *S. notophora* Stokes 1885. 18S rDNA molecular marker was used to study the systematic positions and evolutionary relationships of the ciliate protists isolated from the river. Survival of ciliates in extreme conditions such as pollution depends on the functioning of the membrane trafficking system. Lineage-specific modifications in the membrane trafficking proteins, SM proteins and their interactors Qa-SNAREs were found specifically in classes Oligohymenophorea and Heterotrichea in the present study.

Contents

1. Introduction 2. Review of literature 3. Spatial variation of ciliate communities in relation to abiotic factors along the river Yamuna 4. Classical and molecular characterization of ciliate species isolated from the river Yamuna 5. Evolutionary pattern of membrane trafficking proteins in ciliates 6. Summary. Bibliography. Publications and presentations.

20. SINGH (Tejveer)
Identification of the Herbal Homeopathic Formulations with Anti-Cervical Cancer and Anti-HPV Activity.
 Supervisor : Prof. Alok Chandra Bharti
Th 25381

Abstract
(Not Verified)

The present study carries out the comprehensive evaluation of anti-CaCx and anti-HPV activities of certain plant-derived Homeopathic preparations (HP) which supports their repurposing in management of CaCx as economical alternatives. HP mother tincture (MT) and 30C potencies of plants *Berberis aquifolium* (BA), *Berberis vulgaris* (BV), *Mentha piperita* (MP), *Curcuma longa* (CL), *Cinchona officinalis* (CO), *Thuja occidentalis* (TO) and *Hydrastis canadensis* (HC) were screened for their anti-proliferative activity on human papillomavirus (HPV)-negative (C33a) and HPV-positive CaCx cells (SiHa and HeLa) by MTT assay. Total phenolic content (TPC) and anti-oxidant ABTS and DPPH radical scavenging activity of each HP were also determined. In the next step, phytochemicals reportedly available in these HP were examined for their inhibitory action on HPV16 E6 by molecular docking. MT of all HP tested induced a differential dose-dependent cytotoxic response against CaCx that varied with cell lines. For HPV-negative C33a, HPV16-positive SiHa and HPV18-positive HeLa, the order of response was TO>CL>BA>BV>HC>MP>CO, HC>MP>TO>CO>BA>BV>CL and CL>BA>CO, respectively whereas, 30C potencies of HP showed inconsistent response. Further, anti-CaCx responses did not follow the order of HP's phenolic content (TO>CO>CL>HC>MP>BA>BV) or free radical-scavenging activity (ABTS: TO>CO>CL>HC>MP>BV>BA; or DPPH: CO>MP>CL>BV> TO>BA>HC). Analysis revealed anti-oxidant content of BA, BV and HC had lowest contribution to their anti-CaCx activity. Constituent lead phytochemicals berlambine, magnoflorine, berberrubine, palmatine and berberine, reported to be present in BV, BA and HC; and beta-sitosterol and campesterol in CL and TO strongly inhibited HPV16E6's carcinogenic interactions in molecular docking using E6's crystallographic structures (6SJA and 4XR8). A detailed study was carried out on *B. aquifolium* root for availability of similar anti-CaCx and anti-HPV activities and also the molecular cascade targeted by BAMT. On the molecular level revealed that BAMT-treatment resulted in reduced protein expression of key transcription factors, STAT3 with a decline of its active form pSTAT3 (Y705); and components of AP-1 complex, JunB and c-Jun. Immunocytochemistry experiment showed that BAMT did not prevent the entry of remnant active transcription factor to the nucleus, but loss of overall transcription factor activity resulted in reduced availability of transcription factors in the cancer cells. These changes were accompanied by gradual loss of HPV E6 and E7 protein in BAMT-treated HPV-positive cells. These plant derived HPs showed a multi-pronged therapeutic potential against HPV infection and cervical cancer, and described the underlying molecular mechanism of their action and the role of transcription factors like AP-1 and STAT-3 in the disease pathogenesis. Thus, these phytomedicines can potentially meet the clinical need in the form of first line or adjunct therapy of cervical cancer treatment.

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1. Introduction 2. Review of literature 3. Rationale and objective 4. Materials and methods 5. Results 6. Discussion 7. Summary and conclusion. Bibliography. Annexures.

21. SINGH (Amarjeet)
Evaluation of Immunostimulatory Properties of Seeds and Leaves of *Achyranthes Aspera* Linn (Amaranthaceae) in Rohu, Labeo Rohita and Magur, *Clarias Batrachus*.
 Supervisor : Prof. Rina Chakrabarti
Th 25384

Abstract
(Not Verified)

Aquaculture is the fastest growing food production sector. Fish and fishery products represent a very valuable source of protein and essential micronutrients for human beings. Various bacteria, fungi, viruses and parasites cause diseases to fish. Various antibiotics are used to prevent infections in fishes which may have negative impact on consumers. Immunostimulants are a group of natural and synthetic compounds that increase the non-specific cellular and humoral defense responses. Immunostimulation through medicinal plants is a natural, safe, sustainable and eco-friendly approach to enhance the fish immunity. The present investigation evaluates the immunostimulatory properties of *Achyranthes aspera* leaves and seeds incorporated diets on the performance of *Labeo rohita* and *Clarias batrachus*. The experiments were conducted in aquaria and hapas. Fish were fed with test diets containing leaves and seeds of *A. aspera* and control diet without supplementation. After feeding, fish were either challenged with virulent *Aeromonas hydrophila* or immunized with c-RBC. The survival, growth of fish, myeloperoxidase, nitric oxide synthase and lysozyme were significantly ($P < 0.05$) higher in 0.5% seeds supplemented diet fed rohu and magur compared to the other feeding regimes. The oxidative stress indicators TBARS, carbonyl protein were significantly ($P < 0.05$) lower and anti-oxidant enzymes such as SOD, GPx, GST, catalase and GSH were significantly ($P < 0.05$) higher in 0.5% seeds supplemented diet fed rohu and magur. The changes in innate immune system were also seen through up-regulation and down-regulation of immunological genes. The seeds contain fatty acids, ecdysterone, oleonic acids, saponins and amino acids which may be responsible for increased growth and improved physiological conditions of fishes. The plant is found throughout India as a weed so application of plant ingredients is commercially viable and easily acceptable to Indian Aquarists. The positive results of field study may be beneficial for Indian aqua farmers.

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1.Introduction 2. Review of literature 3.Materials and methods 4. Results 5. Discussion. 6. Summary and conclusion 7.References. 8. Publications.

22. SRIPOORNA (S.)

Ciliates as Cellular Tool to Assess Heavy Metal Toxicity.

Supervisor: Dr. Seema Makhija and Dr. Ravi Toteja

Th 25383

Abstract
(Verified)

Ciliates are unicellular eukaryotic micro-organisms. They play major role in designing the community structure of living organisms in the freshwater ecosystem. In the present study, freshwater ciliates, viz. *Tetmemena saprai* n. sp. and *Euplotes aediculatus* were selected to evaluate heavy metal toxicity. Globally, heavy metals are considered to be the major pollutants affecting terrestrial and aquatic ecosystems since their concentration is increasing in the environment due to various anthropogenic sources. In this study, effects of two important heavy metals, viz. cadmium (Cd) and copper (Cu) were observed in *T. saprai* n. sp. and *E. aediculatus* at cellular and molecular level. LC50 values were determined where Cu was found to be more toxic to both the ciliates than Cd. Also, growth rate of ciliates decreased with increase in metal concentration. Activities of antioxidant enzymes, namely superoxide dismutase, catalase and glutathione peroxidase, were determined. Significant increase in the enzyme activity was observed in the ciliates exposed to

metal stress. Quantitative real time PCR was employed to evaluate the metal effect on the expression of stress-responsive genes, viz., manganese superoxide dismutase (Mn-sod), catalase (cat) and cytosolic hsp70. Their expression increased significantly in metal exposed cells. These genes were further characterized to understand their structure and function. Finally, metalloproteins (Cd, Cu-binding and Cysteine-rich proteins) were identified from the first 2,378 contigs of the whole genome data of *Tetmemena* sp. SeJ-2015 using bioinformatic tools. Also, the active sites of metalloproteins involved in cell defense were identified to predict how heavy metals modulate the functioning of these metalloproteins. In future, metalloproteins will help to identify target proteins involved in metal detoxification. Therefore, present investigation affirms that Mn-sod, cat and cytosolic hsp70 genes act as suitable heavy metal biomarkers, making *T. saprai* n. sp. and *E. aediculatus* promising candidates for assessing heavy metal toxicity.

Contents

1. Introduction 2. Review of literature 3. Why ciliates? 4. Materials and methods
5. Results 6. Discussion 7. Conclusion. Bibliography. Publications.

23. SUR (Sayantan)
Molecular Correlates of Photoperiodic Vernal Phenotype in Palaearctic-Indian Migratory Buntings.
Supervisor : Dr. Vinod Kumar
Th 25054

Abstract (Verified)

Avian migration has fascinated humans since the ancient times. Each year, billions of Passeriformes birds (songbirds) undertake two highly energy consuming long-disatnce journeys along the latitudinal gradient. In order to time their seasonal journeys during the year, the birds depend upon various environmental cues, most importantly the photoperiod and ambient temperature. The roles of both photoperiod and temperature have been widely investigated in controlling the migratory and reproductive functions; yet, the molecular mechanisms involved are not well known. This thesis research centers on the molecular underpinnings of photoperiodic induction of the vernal migratory and reproductive (gonadal maturation) in Palaearctic-Indian migratory male redheaded buntings (*Emberiza bruniceps*). In the first study on the role of light wavelength, we found wavelength-dependent changes in the mRNA expression of genes involved in the photoperiod perception, transduction/induction, and neural responses, in parallel with photoperiod-induced migratory and reproductive phenotypes. The next study demonstrates the relationship of changes in the spleen-mediated innate immune responses in parallel with the photoinduction of the heightened energetic stress state of the migratory and reproductive functions. Further, we investigated in some details the role of temperature in photoperiodic induction of vernal migratory functions and gonadal maturation. There is indeed a significant role of the ambient temperature in the development of spring migration phenotype, with changes in expressions of genes with known functions in the hypothalamus, and peripheral tissues (skin, liver and muscle) of buntings. This demonstrates the mutiple molecular drivers of temperature effects, and suggests that the transcriptional responsiveness to temperature of is a significant component of the overall adaptive strategy for timely departure of latitudinal migrant songbirds from wintering areas in the spring.

Contents

1.General Introduction 2.Photoperiodic induction of the vernal response 3.Role of temperature in the photoperiodic vernal response 4. Summary and Conclusions. References. Publications and Presentations.

24. TALWAR (Chandni)

Exploring Fish Gut Microbiome: Characterization of the Microbial Diversity, predictive Functional Profiling and its Selective Manipulation to Mitigate Pathogen by using *Bdellovibrio* *Bacteriovorus*.

Supervisors : Dr. Ram Krishan Negi and Prof. Rup Lal (Retd.)

Th 25380

Abstract

(Verified)

Fish gut microbiome studies have paced up in the last decade from the use of culture-based methods to metagenomic analysis and have led to identification of several probiotic bacteria and suggest that gut microbiome is altered with respect to seasons, life cycle stages and surrounding environments. However, currently there are two major lacunae in this field. First, the differences in microbial community profiles in the anterior and distal gut regions are not fully understood. Second, studies concerning gut microbiome manipulation for host benefit in specific bacterial diseases which cause high fish mortality are limited. The present work was performed to addresses these lacunae and is described under three objectives. The first objective compares the structural and predictive functional profiles of foregut and hindgut microbiomes in *Cyprinus carpio* var. *specularis* using culture-dependent and metagenomics approaches. The study revealed that foregut microbiome was optimized for uptake of nutrients while a major role of hindgut microbiota was revealed to be in nitrogen assimilation as it remains one of the limiting nutrients within animal intestines. Further, abundance of ammonia oxidizing communities in hindgut were thought to oxidize it to molecular nitrogen which is further utilized by nitrogen-fixing commensals to generate nitrate and nitrite explaining the abundance of denitrifying bacteria as well. A bacterial strain belonging to the genus *Salinicoccus* was isolated from foregut contents was taxonomically characterized in the second objective as a novel species by integrating phenotypic, genomic, physiological and chemotaxonomic methods. The third objective tests the potential of predatory *Bdellovibrio* to control a key pathogen, *Aeromonas salmonicida* within the gut of *Labeo rohita*. *Bdellovibrio* administration successfully attenuated *Aeromonas* burden in-vivo and restored balance of Gram-staining-negative and -positive bacteria. This work provided support for the use of predatory bacteria as 'live antibiotic' in fish gut in the post-antibiotic era.

Contents

1. Introduction 2. Review of literature 3. To compare the foregut and hindgut microbiome of *cyprinus carpio* var. *Specularis* (Lacepede, 1803) by using culture-dependent and metagenomics approaches 4. To taxo- genomically characterize the novel bacterial species isolated from gastro-intestinal tract of *cyprinus carpio* var. *Specularis* (Lacepede, 1803) 5. To determine the potential of *bdellovibrio bacteriovorus* HD100 as a live antibiotic in the gut of *labeo rohita* (Hamilton, 1822) challenged with *aeromonas salmonicida* subsp. *Salmonicida* ATCC 33658 6. Summary of the thesis 7. References. Appendices. List of publications.