CHAPTER 64

ZOOLOGY

Doctoral Theses

01. AKANKSHA RAJ
Evaluation of Dose-Dependent Impact of Nanoparticles (NPs) in Drosophila Melanogaster.
Supervisor: Prof. Namita Agrawal
Th 23688

Abstract
(Not Verified)

The enormous implications of silver nanoparticles (AgNPs) and gold nanoparticles (AuNPs) in wide array consumer goods and biomedical applications are raising concerns about their potential effect on human health. Therefore, to assess their safety issues, dose-dependent impact of AgNPs and AuNPs on different aspects like fertility, survival, behavior and metabolism was investigated by rearing *Drosophila* on food without and with NPs-supplemented food. *Drosophila* with distinct developmental stages, short life cycle and significant homology with human serves as an ideal organism to study nanomaterial-mediated toxicity. Our studies suggest that ingestion of higher doses of AgNPs compromises fertility by impairing egg laying capability and ovary development in adults. Additionally, dietary intake of AgNPs from larval stage has more deleterious effects that result in reduced survival, ovary size and egg laying capability at a further lower dosage. Interestingly, the trans-generational effect of AgNPs was also observed without feeding progeny with AgNPs, thereby suggesting its impact from previous generation. Moreover, AgNPs ingestion causes behavioral abnormalities such as poor crawling in larvae and climbing and flying ability in adults. Interestingly, intake of higher dose of AgNPs at larval stage causes reduction body size and weight and significantly alters metabolic activity that includes lipid, carbohydrate and protein levels in adult flies. We also evidenced increased ROS production in AgNPs fed larval tissues. These results strongly imply that higher dose of AgNPs ingestion has systemic impact on fertility, survival, behavior and energetics which could be due to increased level of ROS production. Further, dosage study using AuNPs showed that at its administration at larval stage had have moderate effect on survival, body weight and carbohydrate levels. These observations indicate that evaluation of safe dose of NPs is a necessary prerequisite before incorporating these in various consumable products.

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02. ANUPMA KUMARI
Immunotherapeutic Function of Melatonin: Modulation of L-Arginine Metabolism in Tumor-Associated Macrophage
Supervisor: Prof. Anju Srivastava
Th 23684

Abstract
(Verified)

Looking at macrophage number and important role in tumor progression, tumor associated macrophages (TAMs) have been targeted for tumor therapy majorly by re-polarization of tumor associated M2 macrophage into M1-phenotype by the use of effective biological response modifiers (BRMs) such as melatonin. Melatonin has immunomodulatory and antitumor activity. Arginine metabolism plays central role in immune system. Tumors negatively regulate macrophage response by switching arginine metabolism from NO to arginase so as to support tumor growth and proliferation. Increasing TAMs population in T cell lymphoma has been correlated with poor prognosis of the disease We were interested to know the fate of L-arginine metabolism in TAMs in T cell lymphoma and can it be reinstated by melatonin? We established an *in vitro* model of TAMs, evaluated the effect of melatonin on arginine metabolism. Macrophages grown in presence of Dalton's lymphoma milieu factors change to TAMs representing M2 phenotype and can serve as an effective model to study TAMs function. DL-induced TAMs (DL-TAMs) showed many tumor promoting activities such as increased arginase expression and activity, enhanced production of cytokines like TGF-β, IL-10, IL-6 known to be involved in suppression of immune surveillance, promoting tumor cell migration, compromised anti-tumor activity such as reduced release of cytolytic molecules like NO, pro-inflammatory cytokines like IFN-γ, IL-12, TNF-α upon activation. DL-TAMs also showed high arginase expression and activity which was suppressed upon Melatonin treatment. In *in vivo* study we observed significant increase in survival of DL-bearing mice with melatonin treatment. Modulation of arginase expression and activity was conclusively reflected by increase in NO level and suppression in urea level in ascetic fluid obtained from melatonin-treated DL mice. Thus from present study we conclude that melatonin can effectively repolarise TAMs towards beneficial phenotype thereby controlling tumor growth and progression by multiple ways including immunomodulation and anti-tumor activity.

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1. Introduction. 2. Establishment of in vitro model of tumor-associated macrophages 3. Evaluation of L-arginine metabolism in tumor-associated macrophages 4. To study the effect of melatonin on L-arginine metabolism in tumor-associated macrophages 5. To monitor in vivo anti-tumor and immunomodulatory activity of melatonin in mice bearing dalton's lymphoma. Summary and publications

03. CHOUDHARY (Shreya)
Effect of Nutrition on the Ontogeny of Fertility in Insect Systems.
Supervisor: Prof. Mallikarjun N. Shakarad
Th 23690

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1. Introduction. 2. Basic biology of primitively eusocial and solitary wasps 3. Role of diet in evolution of sociality 4. Validation of role of diet in laboratory sytem under controlled conditions 5. Effect of altered conditions, on the changes produced n the physiology of lab system. References and list of publications

04. Das (Payal)
Microbial Extracellular Enzymes: Purification, Molecular Characterization and Applications.
Supervisor: Dr. Monisha Khanna Kapur
Th 23681

Abstract
(Not Verified)

Due to their vast availability, low cost, high stability and productivity, microbial enzymes are extensively used in industries. Actinomycetes are widely tapped group for production of extracellular enzymes. In the present study, approximately 646 actinomycetes were isolated from various ecological habitats and were screened for production of cellulase, xylanase, chitinase, phosphatase by plate assay method. Based on the results, isolates along with their positive control were selected for secondary screening and purification. Enzyme activity was estimated in crude cell free extract, partially purified and purified samples. In case of highest enzyme producers, isolates 194, 169, 130 and 165, effect of various fermentation conditions (pH, temperature and substrate concentration) was studied in crude extract. The Km and Vmax values of the purified fractions for isolates 169 and 130 was found to be 56.03mg/ml and 2.04µg/ml/min and 53.11mg/ml and 2.11µg/ml respectively. This shows that the enzyme has high affinity for the substrate. SDS gel electrophoresis of the purified fraction of isolate 169 showed presence of a dimer of approximately 50-55KDa and 60-65KDa and in case of isolate 130, a monomer of approximately 65-70KDa was observed. Analyses of purified xylanase and chitinase were done using MS/MS technique. N-terminal sequence corresponded to endoxylanase in case of isolate 169 and chitinase in case of isolate 130, the gene encodes a protein of 495 and 453 amino acid residues respectively. Comparison of deduced amino acid sequence to other xylanases and chitinases in the database indicated that in case of isolate 169, enzyme showed 65% similarity with *Streptomyces lividans,* family 10 endoxylanase and isolate 130 showed 70% similarity with chitinase from *Streptomyces plicatus,* family 18. Homology modeling and activity site analysis was also done in each case. Identification of secondary structure was done by CD spectroscopy. Isolates were also find efficient in degrading biodegradable wastes.

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05. DEEPIKA RASHMI

Estimating the Role of Isotopic, Analytical and Molecular Methods in Traceability of Indian Wheat and Determining its Pesticide Residues

Supervisor: Prof. D.K. Singh
Th 23683

Abstract
(Not Verified)

Present study was undertaken to develop a method for tracing wheat by identifying isotopic, elemental and genetic markers along with development and identification of an efficient method for determination of commonly used pesticides on wheat. In the first objective, study was done to evaluate effectivity and applicability of stable isotope ratios in tracing the geographic origin of wheat. Authentic wheat samples (n=20) were obtained from six adjoining states in India and their stable isotope ratios (δ C, δ N) were estimated utilizing isotope ratio mass spectrometry (IRMS) technique. Based on the δ C values unique fingerprint for wheat of some geographical origin was observed. The second objective was undertaken to study the distribution and accumulation of different elements in wheat grains obtained from different states. In total 14 elements were selected for this study based on the physiology of wheat. The discrimination of geographical origins of wheat samples based on multi-element data was substantially helpful in delivering some distinct identifications of wheat from different states. Identification and application of biochemical and molecular methods to distinguish the durum wheat and bread wheat was studied in the third objective. Assessment of genetic diversity was done and a primer SCAR 3 specific to durum wheat was developed which can be used as a reliable molecular marker for rapid detection and identification of durum wheat from the bread wheat. In the fourth objective, development of an effective method for detection of pesticide residues in wheat samples was carried out. Method C showed the highest recovery 93% and 99% for Chlorpyrifos and Malathion respectively. Overall it can be thus concluded that by combining Isotopic, Elemental and Molecular markers along with methods for Pesticide Residue determination we can achieve the objectives of food security, safety and authenticity and contribute to successful traceability of wheat in India.

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1. Introduction. 2. Stable isotope ratio analysis of carbon and nitrogen in determining the traceability of geographical origin of Indian wheat 3. To study the distribution and accumulation of different elements in wheat grains obtained from different states 4. Identification and application of molecular and biochemical methods to distinguish different wheat varieties 5. Development of an effective method for detection of pesticide residues in wheat samples 6. Summary and references

06. DWIVEDI (Satyam Ravi)

Physiological Stress Response in the Murrel, Channa Punctatus in Relation to Seasonal Variations in Water Quality of Yamuna River Catchment from Delhi.

Supervisor: Prof. Neeta Sehgal

Th 23750

Abstract
(Not Verified)

River Yamuna plays a key role in development and sustenance of socio-economic region of Delhi- NCR. However, increased human population involving agriculture, industries, and settlement has caused deterioration in water quality of river hence posed a serious threat to aquatic life inhabiting the river. In present study, physicochemical properties of Yamuna water were analysed at ten stations and parameters were compared for three seasons (early summer, early monsoon and winter). Water quality of river Yamuna at entry station (Alipur) met prescribed criteria (CPCB), and worsened as river reached exit stations near Okhla. Dissolved Oxygen levels were poor and Biological Oxygen Demand was higher than recommended limits set by CPCB. Regular influx of organic waste, from various sources combined with lack of flow in river during nonmonsoon seasons causes severe deterioration of water quality at aforementioned stations. Channa punctatus were maintained under laboratory in water collected from selected stations and under riverine conditions in hapa at Kalindi Kunj. Ratio between, change in weight and length of fish was calculated. Lipid peroxidation and Superoxide dismutase activity in gills, liver, gonads were estimated which are indicators of oxidative stress. These parameters were correlated with the water quality of river Yamuna. Fish exposed to water from exit stations showed increased levels of oxidative stress indicating that riverine water was contaminated as it passed through Delhi. High frequency of micronuclei in RBCs of fish exposed to water collected from exit stations, suggests presence of genotoxic contaminants in water Structural integrity of scale of the fish under the stress of heavy metals and pollutants was heavily compromised. Fish scales showed uprooted lepidonts and accumulation of heavy metals. Fish inhabiting contaminated water of river Yamuna in Delhi are under stress and unable to grow optimally

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1. Introduction. 2. Materials and methods 3. Results 4. Discussion 5. Summary 6. References

07. DUBEY (Neha)

Role of Peptidy1 Proly1 Isomerases in the Pathogenesis of Mycobacterium Tuberculosis.

Supervisor: Prof. Yogendra Singh

Th 23689

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1. Introduction 2. Review of literature 3. Materials and methods 4. Role of Mtb PPiA in bacterial survival and pathogenicity 5.Role of Mtb PPiB in bacterial survival and pathogenicity 6. Discussion. Bibliography, appendices and buffers and reactions

08. GUNJAN KUMAR SAURAV

Studies on Molecular Interaction and Diversity of Begomoviruses in the Insect Vector Bemisia Tabaci.

Supervisor: Prof. Rajagopal Raman

Th 23691

Abstract
(Not Verified)

Begomovirus, with more than 320 species recognized by the International Committee on Taxonomy of Viruses (ICTV), is the largest of all genera of viruses having either monopartite (DNA-A) or bipartite (DNA-A and DNA-B) genomes. Monopartite begomoviruses are associated with alphasatellites and/or betasatellites. Begomovirus-satellite DNA complexes cause devastating diseases in dicotyledonous plants resulting in huge economic loss. Begomoviruses are exclusively transmitted by *Bemisia tabaci* in persistent and circulative manner. The information on interaction of begomoviruses with *B. tabaci* at molecular and cellular level is scarce. This study was focused on understanding interactions of begomoviruses with *B. tabaci* with two objectives. In first objective, thioredoxin like protein (TLP) of *B. tabaci* was identified as potential candidate receptor since it interacted with coat protein (CP) of both *Cotton leaf curl Rajasthan virus* (CLCuV) and *Tomato leaf curl New Delhi virus* (ToLCNDV) in yeast two hybrid assays. *In-vitro* pull down assays suggested that TLP interacts with CP of both CLCuV and ToLCNDV showing 18.5% more binding for CLCuV CP than ToLCNDV CP. TLP also interacted with ToLCNDV particles isolated from tomato leaves. The expression of *tlp* gene was localized in abdominal part of insect where TLP was colocalized with ToLCNDV. *B. tabaci* with *tlp* gene knocked down showed 26.7% less transmission efficiency for ToLCNDV. The second objective was to study diversity of begomoviruses and their associated satellite DNAs in *B. tabaci* collected from 5 different locations in India by using Illumina sequencing for vector-enabled metagenomics (VEM). We found that a population of *B. tabaci* from a single field was able to harbor different begomovirus-satellite DNA complexes which vary based on locations and host plants. It suggests the possibility for presence of other new begomovirus-satellite DNA complexes. The entire genome needs to be cloned and sequenced before these could be classified as a strain/species.

Contents

09. MISHRA (Neha)

Biodegradation of DDT by Pseudomonas sp. Strain Y8B and its Protein Analysis.

Supervisor: Prof. Dileep K. Singh

Th 23687

Abstract

(Not Verified)

Ubiquitous presence of DDT owing to its excessive use and recalcitrance has been a matter of concern worldwide. The present study is an attempt to solve that problem by observing the spatial and temporal variations in physico-chemical properties (Temperature, pH, DO, EC and TDS), distribution of DDT residues in Yamuna river water and soil and isolating DDT degrading bacteria from river water. To achieve this, sampling of Yamuna river water and soil was done from 2012-2014. TDS and EC values were absorbed to be above permissible limits. DDT, DDE and DDD residues were found in water and soil samples. Bacterium capable of degrading DDT was isolated from river water using selective enrichment technique. The strain was identified on the basis of 16S rRNA gene similarity as belonging to *Pseudomonas* sp. degrading 40.06% DDD, 67.86% DDE and 81.25% DDT, in MSM during 15 days of incubation period. Under optimum environmental conditions (pH 7.0, 30 C temperature and 10ppm DDT concentration), degradation of DDT by the isolated strain was escalated to 91.18±2.86 %. Four unique polypeptide bands from the bacterial cell cultures in MSM with DDT, DDE and DDD as a sole carbon source were identified using SDS-PAGE and MALDI-TOF MS/MS technique to be significantly similar with peroxidases, ABC sulphate ABC transporter periplasmic sulphate binding protein, outer membrane porin, catalase/peroxidase. These proteins have already been reported for their role in the active transport of toxins inside the bacterial cell and thereby making them bioavailable for degradation. These enzymes provide protection against oxidative stress which occurs due to entrance of toxic substances inside the cell. Hence, it can be concluded that *Pseudomonas* sp. strain Y8B can be used as biodegrading agent in the bioremediation of DDT contaminated sites as well as a source of enzymes for the more advance enzymatic bioremediation process.

Contents

10. SHREE (Pallee)

Isotopic, Analytical, Molecular and Physicochemcial Methods for Traceability of Indian Rice and Detection of Pesticides as Food Adulterant.

Supervisor: Prof. D.K. Singh

Th 23677

Abstract
(Not Verified)

Traceability system which is having prime focus on safety, quality and security of food, is fundamental prerequisite. δ C and δ N of rice analyzed to distinguish geographical origin and variation ranged from -27.14 % to −28.97% and 7.58 ‰- 2.48 ‰ respectively. W.B. Assam and basmati δ C value do not differ significantly. PCA was performed using elemental content and different geographical location samples clustered together. On basis of dominated elements in different Principal components, radar plot drawn, it gives more visual distinction of rice origin. For molecular analysis important characters of Basmati rice that is grain length, aroma and cooked kernel elongation were considered. For differentiating aromatic rice primers were designed for *Badh2* gene result revealed 8bps deletion in aromatic rice. Grain elongation ratio evaluated and in basmati ratio was double. Pentagonal Radar plot was drawn with important physical parameters; there was a difference in basmati and non-basmati rice plotting. RAPD performed using 9 primers, 2 primers OPB-01 & OPA-13 showed clustering of all basmati cultivar. Phenolic content of rice determined result obtained in order of Unpolished grain of Black>Red>White>Basmati White. Basmati rice phenolic content does not differ significantly in some white rice. In microbial content determination, open rice has higher microbial load when compared with packed rice. Moisture content in open unpacked samples was high and is directly proportional to the growth of microbes. Microbial flora study of rice in the Indian market was done to draw attention and awareness for good quality branded rice. Method to determine incidental adulterant pesticides developed and tested and it was observed method2A had high efficiency for detecting residues of Dicofol, Aldrin, Chlorpyrifos, Malathion and Atrazine and therefore it will ensure safe and healthy rice products. Using this method, 12 samples tested of which 7 showed the presence of pesticides residue.

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1. Introduction

11. POOJA RANI
Characterization and Genome Diversity of Luteimonas Tolerans and Pedobacter Sordidisoli, and Pseudomonas Fluorescens Isolated from Hexachlorocyclothexane Contaminated Soil and Acidic Respectively.
Supervisors: Dr. Komal Kamra and Prof. Rup Lal
Th 23680

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1.Introduction. 2. Taxonomical characterization of Luteimonas sp. Nov., isolated from hexacholrocyclohexane (HCH) contaminated soil 3. Taxonomical characterization of pedobacter sordidisoli sp. Nov., isolated from hexachlorocyclohexane (HCH) contaminated soil 4. Genome analysis of luteimonas tolerans UMI^{T} and comparative genome study of luteimonas spp. 5. Genome analysis of pseudomonas fluorescens Pt 14 isloated from acidic soil (P^{H} 4.65) and comparative genomic account of pseudomonas fluorescens subspp. Appendices and list of publications

12. S K TAHAJJUL TAUFIQUE
Effects of Light at Night on Cognitive Performance and Associated Neural Changes in Indian House Crow, Corvus Splendens (Vieillot, 1817).
Supervisor: Prof. Vinod Kumar
Th 23675

Abstract
(Verified)

Organisms show adaptations to the day-night cycle, and exhibit distinct daily rhythms in physiology and behaviour, including the cognitive performance. However, the prevailing night illumination (light at night; LAN) has been found to have negative effects on the circadian rhythms and cognition. Therefore, the aim of the present thesis was to investigate the effects of LAN and dim LAN (dLAN) on circadian rhythms and its linkage with cognitive performance and associated brain functions in a diurnal species, Indian house crow (*Corvus splendens*). Particularly, we have tested the effects of LAN on learning using spatial and pattern associated learning paradigms, and the object exploration, and motor and mood performance. At the brain level, we have examined the neuronal plasticity by changes in the neuronal activity, neuron morphology and neurogenesis. We found LAN-induced disruption in the circadian rhythm in the activity behaviour. dLAN also disrupted the sleep-wake pattern and decreased the night melatonin levels. LL-induced negative effects were also found on both, the spatial and pattern associated learning and memory in crows. Also, dLAN affected the object exploration and motor learning. Furthermore, there was a significant reduction in grooming and feeding behaviours, along with an increased self-mutilation of feathers under dLAN, suggesting the development of depressive-like disorders. Interestingly, LL caused decline in the neuronal activity u in the hippocampus (HP) and caudal nidopallium (NC). LL also negatively affected the neurogenesis and dendritic maturation of newborn neurons in HP and NC. Effects of dLAN on mood and learning appear to involve changes in the expression of BDNF both at the mRNA and protein levels via epigenetic modifications. Overall, these results on a diurnal corvid species give insights into possible impact of emerging ecosystem with light environment having increased night illumination on brain health and functions in vertebrates, including humans.

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1. General introduction. 2. Circadian rhythms is activity, feeding and grooming behaviours 3. Effect of no-night light environment on activity behaviour, and learning performance and associated neural changes 4. Effect of 'dim light at night' environment on activity and sleep behaviour, mood and motor performance, and associated neural changes. Summary, references and publications.

13. SINGH (Tanvi)
Rhizoplane Bacteria for Phytoremediation of Lindane and their Interaction with Host Weedy Plants.
Supervisor: Prof. D. K. Singh
Th 23686

Abstract
(Not Verified)

Lindane is notorious organochlorine groups of pesticides. It is highly toxic and has been banned for manufacture and use, however owing to its chemical properties, it persists in environment. Therefore development of technologies aiming to decontaminate Lindane polluted environment is of utmost concern. Phytoremediation is a promising technology, utilizing plants and associated microorganisms to clean up organic contaminants in water, soils or sediments. Little work has been done on bioremediation of Lindane by rhizoplane bacteria of wetland plants. So, current study attempts to assess capability of root epiphytic bacteria of plants *Acorus calamus*, *Typha latifolia* and *Phragmites karka* in Lindane degradation and to study plant bacterial interaction during contaminant removal. Isolation of Lindane degrading root epiphytic bacteria of wetland plants was done by enrichment culture method. *Achromobacter* sp. strain A3 and *Ochrobactrum* sp. strain A15, belonging to phylum Proteobacteria, *Arthrobacter* sp. strain T16 belonging to phylum Actinobacteria, *Sphingobacterium* sp. Strain P18 and *Microbacterium* sp. strain P27 belonging to phylum Bacteroidetes and Actinobacteria respectively, were the potential Lindane degraders, residing on the root surface of *A.calamus*, *T. latifolia* and *P. karka*, Assessment of bacterial communities associated with the roots of focal plants using T-RFLP showed the presence of these phyla in dominance. Study of protein profiling of potential Lindane degrading bacteria showed that exposure of bacterial cells to Lindane resulted in regulative expression of certain proteins. Further, supplementing bacterial strains with root exudates resulted in increased Lindane degradation efficiency. All Lindane degrading bacterial isolates exhibited some plant growth promoting characters that might benefit plant directly, indirectly or synergistically. Lindane at all tested concentration, displayed varying extent of toxicity to plant growth promoting traits of all bacterial strains. The bacterial strains with intrinsic capability to promote plant growth even in the presence of Lindane can be exploited for the bioremediation of Lindane.

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14. SHARMA (Anukriti)

Microbial and Viral (META) Genomic Profiling of Stressed Niches: Hexachlorocyclohexane Contaminated Site and Manikaran Hot Springs.

Supervisor: Prof. Rup Lal

Th 23682

Abstract

(Verified)

This study has employed recent advances in the field of (meta)genomics to elucidate gene-level modulations driven by the environmental factors at both HCH contaminated soil and Manikaran hot springs. The genomic analyses of *Pseudomonas* sp. strain RL-a HCH dumpsite (450 mg/g) isolate and a HCH non-degrader revealed different strategies to counter the HCH stress; to name few, metabolic enrichment of TCS, flagellar biosynthesis, Type II secretion system and increased abundance of integron associated TnpA*6100*across the increasing gradient of HCH contamination. At Manikaran hot springs, *Cellulosimicrobium* sp. strain MM (microbial mat isolate) along with its two reference genomes i.e. *C. cellulans* J36 and *C. cellulans* LMG16121 were compared in order to delineate the pathogenome since *C. cellulans* has been already established as opportunistic pathogenic species. The pathogenicity markers behind pathogenesis of this species however remain unexplored with no genome-wide study as of yet. This report documents 49 virulence markers associated with human infections, thus delineating cause of potential pathogenesis across *C. cellulans.* Subsequently, the prokaryotic virosphere was also explored at Manikaran hot springs that led to recovery of 65 bacteriophage genomes from the shotgun metagenome data from microbial mats and sediment samples. This was followed by the genetic characterization of these phages and reconstruction of potential bacterial phage-hosts to reveal gene-level interactions between phages and their hosts. Further electron and helium ion microscopy was also performed across the hot spring samples in order to supplement the sequence based analyses which is makes characterization of novelgenotypes beyond the bounds of possibility. Viral enrichments followed by microscopy revealed enrichment of archaeal viruses belonging to *Fuselloviridae* family across the sediments and all the three major morphotypes of bacteriophages i.e. *Myoviridae, Siphoviridae,* and *Podoviridae* across microbial mat samples. This study used advanced (meta)genomic approaches investigating two extreme environments with respect to prokaryotic community.

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1. Introduction 2. Pangenome structure of pseudomonas inhabiting hexachlorocyclohexane (HCH) contaminated soils 3. Community wide insights into the pathogenome of cellulosimicrobium cellulans isolated from microbial mat at manikaran hot springs 4. Characterization of prokaryotic virome across manikaran hot springs using sequence –based and scanning electron & helium ion microscopy 5. Reconstruction of potential phage hosts and CRISPR mediated phage-host interactions across manikaran hot springs. Appendix and list of publications

15. SHELLY (Asha)
Delineating the Role of Ca^{2+} Signaling in Aeromonas Hydrophila-induced Headkidney Macrophage Apoptosis of Clarias Gariepinus.
Supervisor: Prof. Shibnath Mazumder
Th 23678

Abstract
(Not Verified)

Aeromonas hydrophila-induced pathological alterations are reported in fish as well as in mammals. Several previous reports have extensively implicated “macrophages” as an important cellular model to study the signaling mechanism underlying *A. hydrophila* pathogenesis. The major outcome of this host pathogen interaction is the apoptosis of the host cells however our understanding regarding the molecular signaling machinery responsible for the process still lags in fish, the natural host of the pathogen. In the present study, headkidney macrophages (HKM) isolated from *Clarias gariepinus* has been used in order to contribute towards better understanding of *A. hydrophila* pathogenesis at the cellular level. *A. hydrophila*-induced intracellular Ca (Ca) alterations are reported in HKM. An early activation of PI3K/PLC axis appeared to be indispensable for inducing Ca alterations from the intracellular stores *i.e.* ER. Altered Ca homeostasis led to the activation of conventional isoforms of PKC referred to as cPKC which was also found to be pro-apoptotic. Activated cPKC resulted in the phosphorylation of MEK1/2-ERK1/2 in *A. hydrophila*-infected HKM. Significant TNFα levels were recorded in the infected HKM which was detected downstream to PI3K/Ca /ERK1/2 axis. The activated PI3K/PLC axis also affected the CHOP expression, an ER stress marker which is reported to be involved during *A. hydrophila*-induced HKM apoptosis. During *A. hydrophila* infection, Ca is released from the ER and is eventually taken up by mitochondria leading to mitochondrial Ca overload. These events resulted in enhanced production of mitochondrial ROS (mtROS). Heightened caspase-1 activity and IL1β production was detected which was dependent on ER stress and mtROS. IL1β finally affected iNOS expression and NO production. Finally, TNFα and NO both converged at activating caspase-8 contributing in caspase-3 mediated apoptosis of *A. hydrophila*-infected HKM.

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1. Introduction 2. Review of Literature 3. Materials and methods 4. Results 5. Discussion. Conclusion and references

16. SINGH (Ambika)
Studies on Midgut Remodeling in Thrips tabaci and Drosophila Melanogaster.
Supervisor: Prof. Rajgopal Raman
Th 23692

Abstract
(Not Verified)

First, we detailed the structural organization of gut in different developmental stages in *Plicothrips apicalis* and *Thrips tabaci*. Next, we studied the process of midgut reorganization through different stages in *Thrips tabaci*. Finally, we dealt with the process of gut remodeling with respect to growth and tissue homeostasis in larval instars in *Drosophila melanogaster*. The digestive tract of *P. apicalis* was observed to be a linear structure in both the larval and the adult stages. Examining the gut structure in all the developmental stages of *T. tabaci* we noted that the midgut of the larval stages was looped in such a manner that it appeared circularized. In the pre-pupal and pupal stage the gut opens as a linear tube and in adult stages the midgut remains looped inside the abdomen but attains the state of undulating linear tube after dissection. In the second aspect, that is, post-embryonic midgut reorganization in *Thrips tabaci*, both morphological and cellular changes were evident during larval-pupal-adult transition. The structural difference of the gut between different stages along with degeneration of larval gut tissue was observable. Thrips one of the few hemimetabolous insect to bear a pupal stage (observed in holometabolous insects) display changes during metamorphosis (degeneration and regeneration of gut cells) which confirms the occurrence of midgut reorganization. In the third aspect, we took up the remodeling process in the larval stages of *Drosophila*. Very little is known about the midgut growth and process of tissue turnover in the larval stages of *Drosophila.* Midgut cell population, once laid down during embryonic development, persists throughout the larval period. Investigating the larval gut development under normal as well as in stressed conditions, we noted cellular damage and death. In response, the gut undergoes cell multiplication that was evident by apparent increase in the cell numbers.

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17. TRIPATHI (Charu)
Geonomics and Functional Diversity of Thermus Paravatiensis and Lampropedia Cohaerens Isolated from Manikaran Hot Springs Located Atop the Himalayan Ranges in Himachal Pradesh, India.
Supervisors: Dr. Komal karma and Prof. Rup Lal
Th 23679

Abstract
(Verified)

Thermophiles are essentially heat loving organisms and present intriguing questions related to survival adaptations at high temperatures. This work describes the genomics and functional analysis of two microorganisms isolated from the hottest water spring of India, situated at Manikaran, Himachal Pradesh with water temperature reaching ~96°C. The first part of the thesis describes the complete genome sequencing of *Thermus parvatiensis*, leading to the assembly of two replicons: a chromosome and a plasmid, with total genome size of 2.01 Mb. Further, a comparative genome analysis was performed with 17 *Thermus* genomes. The core (1177 genes) and pan (5188) genomes were identified for the genus *Thermus.* Metagenomic islands were delineated and annotated on the replicons of *T. parvatiensis*. The frequency and diversity of phage infections were analyzed by the analysis of CRISPR elements. The abundance of phage invasions was attributed to the natural competence *PilA* locus widespread among the genus members. *T.parvatiensis*, being a thermophile can be a potential candidate for obtaining novel thermophilic enzymes. With

this purpose, a novel gene for DNA polymerase was synthesized and expressed in heterologous host system. The thermostable enzyme was purified. The unit activity and optimum parameters for the activity of the enzyme *Tpa* polymerase were accessed. The second part of the thesis describes the characterization and genomic analysis of a novel species of *Lampropedia*isolated from the microbial mats of the hot spring. Taxonomic characterization of the novel strain CT6 was performed in comparison to *L. hyalina*, after which strain CT6 was designated as *Lampropedia cohaerens* on the basis of genotypic, phenotypic and chemotaxonomic properties. The genome of this biofilm forming and arsenic tolerating bacterium was sequenced. *L.cohaerens* had a total genome size of 3.15 Mb. Annotations revealed heavy metal resistance genes, biofilm forming genes and potential for mineral phosphate solubilization.

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1. Introduction. 2. Whole genome sequence and analysis of thermus parvatiensis, and comparative genomic analysis of thermus species 3. Characterization of thermostable DNA polymerase (Tpa) from thermas parvatiensis 4. Characterization of lampropedia cohaerens isolated from the microbial mats of hot water spring at manikaran, India 5. Genome sequencing and analysis of lampropedia cohaerens, a biofilm forming, arsenic tolerant bacterium. Appendices and list of publications.

18. VIJAY KUMAR
Design and Development of pH Responsive Chitosan and Glycol Chitosan Nanoparticles to Ameliorate Experimental Inflammatory Arthritis in Rat Model.
Supervisor: Dr. Anita Kamra Verma
Th 23676

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1. Introduction of rheumatoid arthritis 2. Review of literature 3. Material and methods 4. Preparation of nanoparticles 5. Characterization of prepared nanoparticles 6. In vitro release kinetics studies 7. In vitro cell culture studies 8. Biocompatibility, pharmacokinetics & bio-distribution of nanoparticles 9. In vivo anti-arthritic and antioxidant activity of MTXCHNP and DEXCHNP 10. In vivo anti-arthritic, antioxidant and anti-inflammatory activity of MFGCN. Discussion and summary and references.

19. VENKATESWARAN (Kavya)
Mitigation of Radiation Injury in Total Body-Irradiated Mice and Radio-Sensitization in Human Tumor Cells by Polyphenolic acetates.
Supervisors: Prof. Anju Shrivastava and Dr. B.S. Dwarakanath
Th 23685

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1. Introduction 2. Scientific background 3. Methods 4. Results 5. Discussion 6. Summary and conclusions. Publications