

List of Abstracts Published for National and International Conferences 2019-2020

Bioconversion of different agrowaste for the production and optimization of pectinase enzyme by native soil isolates – a study

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Abstract

Microorganisms and plants are the major sources of pectinase in which majority of the industrial enzymes are of microbial origin. The disposal of fruit peels becoming the threatening problem in the fruit industries. So, using the fruit peels will be used as a potential substrate for the production of pectinase. Pectinase enzymes which breaks pectin polysaccharides into simple molecules like sugars and other useful compounds. The present study aim for the isolation and screening of pectinase producing bacteria from different soil samples collected from dump yards of vegetable wastes. Isolation of bacteria was performed by serial dilution and plating method on pectin agar medium. The organisms were tested for various biochemical test which leads to their identification as *Bacillus sp* and *Pseudomonas sp*. Pectinolytic activity was analysed with different parameters such as pH, temperature and incubation time. The screened isolates were used as a source of pectinase production and acts on various substrates from orange peel extract, potato peel extract and banana peel extract. The pectinase enzyme was more active in the pectin extracted from the banana peel extract which was determined by titrimetric method. It has been identified that the pectinase shows its maximum activity at pH 5.5, temperature at 27 °C with an incubation period of 24 h. The efficient of de-esterases will have various applications including pre-treatment of plant biomass, food, beverages, pulp and paper pharmaceutical and biofuel industries. The optimized method from the present study helps in large production of pectinase enzyme with cost effective. Thus, the present study concludes that, the enzyme extracted from the bacteria was very useful in industrialization of food, textiles, animal feed and biochemical products.

Keywords: Pectinase, polysaccharides, *Bacillus sp*, *Pseudomonas*, Pectinolytic activity

Molecular cloning and Genomic Characterization of Pese Penaeidin from the haemocytes of Green Tiger Shrimp *Penaeus semisulcatus*

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Abstract: Aquaculture is a rapid and fast growing field in world due to their high protein source. Unfortunately, the aquaculture production rate was decreased due to the impact of diseases caused by a wide range of pathogens, which causes huge economic losses to the aqua farmers. Nowadays, the immune response of shrimp and their defence mechanisms have become a most important concern in shrimp culture for better production. In recent time, the culture of *Penaeus semisulcatus* has experienced serious problems associated to the outburst of microbial diseases caused by viruses and bacteria which affects all age of shrimps. To compensate this problem, many chemicals, antibiotics, immune stimulants and probiotics were applied in huge quantity but no proper recovery was reported. Penaeidins are commercially important species in aquaculture with unique family of antimicrobial peptide which take part in the immunological defense of shrimp. AMPs act as a first line of defense against pathogens so we are planned to isolate the gene responsible for generating AMPs. Amino acid sequences of Pese Penaeidin contain proline rich N-terminal domain and a carboxyl domain with six cysteine residues. Structural analysis of Pese Penaeidin shows alpha-helix in its secondary structure and the targeted 3D structure shows two-disulphide bridges in the alpha-helix. In this present paper, we mentioned about penaeidin sequence cloned from the green tiger shrimp *P. semisulcatus* (Pese Penaeidin) with an open reading frame of 77 amino acid peptide along with 19 amino acid signal peptides. In healthy and microbial challenged shrimp, Pese Penaeidin was tested which shows expression in heart, intestine, haemocytes, gills, muscles, hepatopancreas and eyestalk. As a result, microbial challenge determines mRNA up-regulation, with expression at 6 h post injection which indicates the role of penaeidin in innate immunity.

Insecticidal Pest Control for Coconut Palm Trees

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Abstract:

Rhynchophorus ferrugineus (Red Palm Weevil) is one of the most devastating pests of coconut crops throughout the world. The dangerous stage of the pest was its larvae which act a major role in destruction of the coconut palms. By tunneling the nutrient poor smooth surface of crown, trunk they destroy the vascular system and leads to the death of coconut palms which causes a tremendous loss to the Agrifarmers. Long back an Integrated Pest Management (IPM) program was inaugurated in 1990 to prevent and control the life threatening pest in Agriculture and Livestock. IPM programme, prevent spread of this pest through planting material and sustain control levels. Knowledge of the resistance status of pests is an important factor for researchers to guide the farming community in regarding pest problems. Presently many researchers are focusing to prevent the pest attack by using several pheromones mass trapping, biological control and bio insecticide spraying. Commonly used insecticides may include Carbosulfan, Pirimiphos, Ethyl Dimethoate, Phenthoate and Pyrethrum. Some synthetic insecticides have been also used as a foremost managing tactic of this pest. Currently we are planned to use the extract of *Calotropis gigantean* to control the pest *Rhynchophorus ferrugineus*. The main aim and objective of the study is to summarize the research works to reduce and manage the red weevil population by using bio insecticides produced from plant extract and to protect the coconut palm and improves the economic status of Agri farmers.

Structural Elucidation of α -Bungarotoxin and interaction with *Mycobacterium tuberculosis* and *Salmonella typhi*

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Abstract: In recent years the presence of biochemical, pharmacological and functionally important snake venoms classified as hemotoxins, neurotoxins, necrotoxins, cytotoxins, etc. A neurotoxin α -Bungarotoxin is isolated from the venom of the Bungarus snakes [*Bungarus multicinctus* and *B. caeruleus* (Indian krait)] which affects the nervous system by binding strongly with nicotinic acetylcholine receptors. Bungarotoxins are further categorized as alpha-bungarotoxin, beta-bungarotoxin, kappa-bungarotoxin and gamma bungarotoxin and among these α -bungarotoxin is more harmful. Many researches are focused on the pharmaceutical importance of α -bungarotoxin in therapeutic medicine. However, the clear evidence of interactions of membrane protein in *Mycobacterium tuberculosis* (OmpATb, a pore forming protein from *Mycobacterium tuberculosis*) and *Salmonella typhi* (antigenic outer membrane protein ST50) with α -bungarotoxin is still unclear (Figure). Hence, the present study

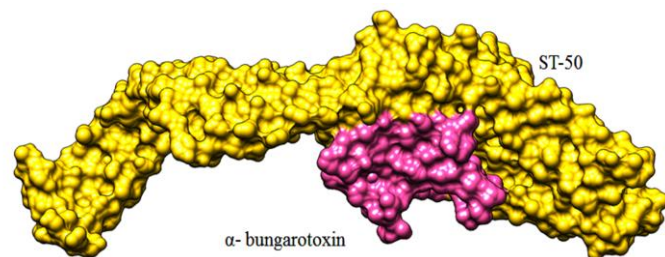


Figure: Molecular Interactions of snake α -bungarotoxin (Pink) with *Salmonella typhi* outer membrane protein ST-50 (Golden Yellow).

focused to evaluate the interactions of membrane protein in *Mycobacterium tuberculosis* and *Salmonella typhi* with

α -bungarotoxin through protein-protein interactions and Molecular Dynamics simulations, and in future

the results obtained from this study will be experimentally tested. The main aims and objective of our study is to determine the structural combination between α -bungarotoxin with *Mycobacterium tuberculosis* and *Salmonella typhi*. This study may also help to further investigate the possibility of using this α -bungarotoxin to avoid and reduce the adverse life-threatening diseases like *Mycobacterium tuberculosis* and *Salmonella typhi* in future generations.

**Cysteine Rich Antimicrobial Peptide Crustins Role in Biofilm inhibition of premoult field
crab *Paratelphusa hydrodromus***

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Crustins are antibacterial proteins 7-14kDa mol weight with a characteristic four-disulphide core-containing whey acidic protein (WAP) domain, expressed by the circulating haemocytes of crustaceans. Over 50 crustin sequences have been now reported from a variety of decapods, including crabs, lobsters, shrimp and crayfish. Three main types seem to occur but all possess a signal sequence at the amino terminus and a WAP domain at the carboxyl end. Differences between types lie in the structure of the central region. Those crustins purified as the native protein or expressed recombinantly all kill Gram-positive bacteria, and gene studies have shown that they are constitutively expressed, often at high levels, but show no consistent patterns of change in expression following injection of bacteria. This variable response to infection is enigmatic but indicates that these proteins could perform additional functions, perhaps as immune regulators in recovery from wounding, trauma or physiological stress. In situ visualization analysis of biofilm inhibition was observed through light and confocal laser scanning microscopy. Surface morphology and the bacterial biofilm inhibition were viewed by scanning electron and atomic force microscopy. This study emphasizes the potential activity of *Paratelphusa hydrodromus* crustin, an interesting candidate for the development of novel broad-spectrum antimicrobial agent against bacterial pathogens.