

6th World Congress on **Biotechnology**

October 05-07, 2015 New Delhi, India

Extraction and characterization of chitosan nanoparticles from fish waste and its applications on waste water treatment of fish food processing industry

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Fish waste is considered to be one of the major bio-pollutants which are generally discarded in coastal regions through local markets and fish processing industries. Nowadays, it is being eyed as a newer Bio-resource and few of the bio-products commercially marketed are oil, bioactive peptides, collagen, chitosan and gelatin. In the present study we have used fish scales waste generated through local market to synthesize chitosan nanoparticles. Antimicrobial activity for different pathogens like *staphylococcus aureus*, *Salmonella*, *Vibrio cholera*, *V. parahaemolyticus*, *E. coli*, was performed out of these *V. cholera*, *E. coli* showed a zone formation of 30 mm. Antioxidant assay various concentration of 20-100 was performed and the scavenging activity of the sample is calculated as 11%. Haemolytic activity using goat's blood is done in various concentration 10^1 - 10^8 activity showed is the haemolysis or the RBC break down is noted only from the 10^6 where as each cell carries the 2^n amount of haemolysis thus the factor is $2^6=64$ Hu (haemolytic units). Further characterization of chitosan nanoparticles was performed using SEM and FT-IR. Treating the obtained bio-products with effluent obtained from the fish processing industries is studied. The pH and turbidity of the effluent was measured by checking the BOD and COD after treating the effluent with the immobilized chitosan nanoparticles. The highest flocculation efficiency of chitosan observed under these conditions was 80% COD removal and 90% of turbidity removal.

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Phylogeny of the freshwater crab, *Parasesarma* sp: An assessment using molecular taxonomy and sperm ultra structure

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This is a first time report on the molecular taxonomy and spermatozoal ultra structure to elucidate the phylogeny of the freshwater crab, *Parasesarma* sp. The genomic DNA of the candidate specimen was isolated and purified and the gene for ITS (Internal transcribed spacer) was amplified using the ITS1 (TCCGTAGGTGAACCTGCGG) and ITS2 (GCTGCGTTCTTCATCGATGC) primers. Sequence comparisons of the amplicons were performed by in silico methods. BLAST and CLUSTAL W alignments have shown 93% identity with the Chinese mitten crab, *Eriocheir sinensis* with *E. rectus*, the alignment has shown 96% identity. Ultra structural investigations revealed that the spermatophores of *Parasesarma* are coenospermic and the spermatozoa displayed typical grapsid (family) features: Presence of a centrally placed operculum filled by an apical button, the loss of acrosome ray zone and the concentric acrosomal zonation, periopercular rim, lateral arms and a long cylindrical capsule have been the signifying features. The distinguishable variations (from other grapsid family members) have been the absence of concentric onion-ring lamellations of the outer acrosome and the tongue and groove connection between the operculum and the acrosomal zonation. Interestingly, the spermatozoa of *Parasesarma* sp. are encircled individually by an electron-dense protective sheath, which has hardly been reported in any other decapod spermatozoa. The results of the present study not only depict the presence of several grapsid characters in terms of the spermatozoal ultra structure, but it as well reports the occurrence of features unique to the candidate specimen (*Parasesarma* sp.), the species level identification of which is yet to be accomplished.

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