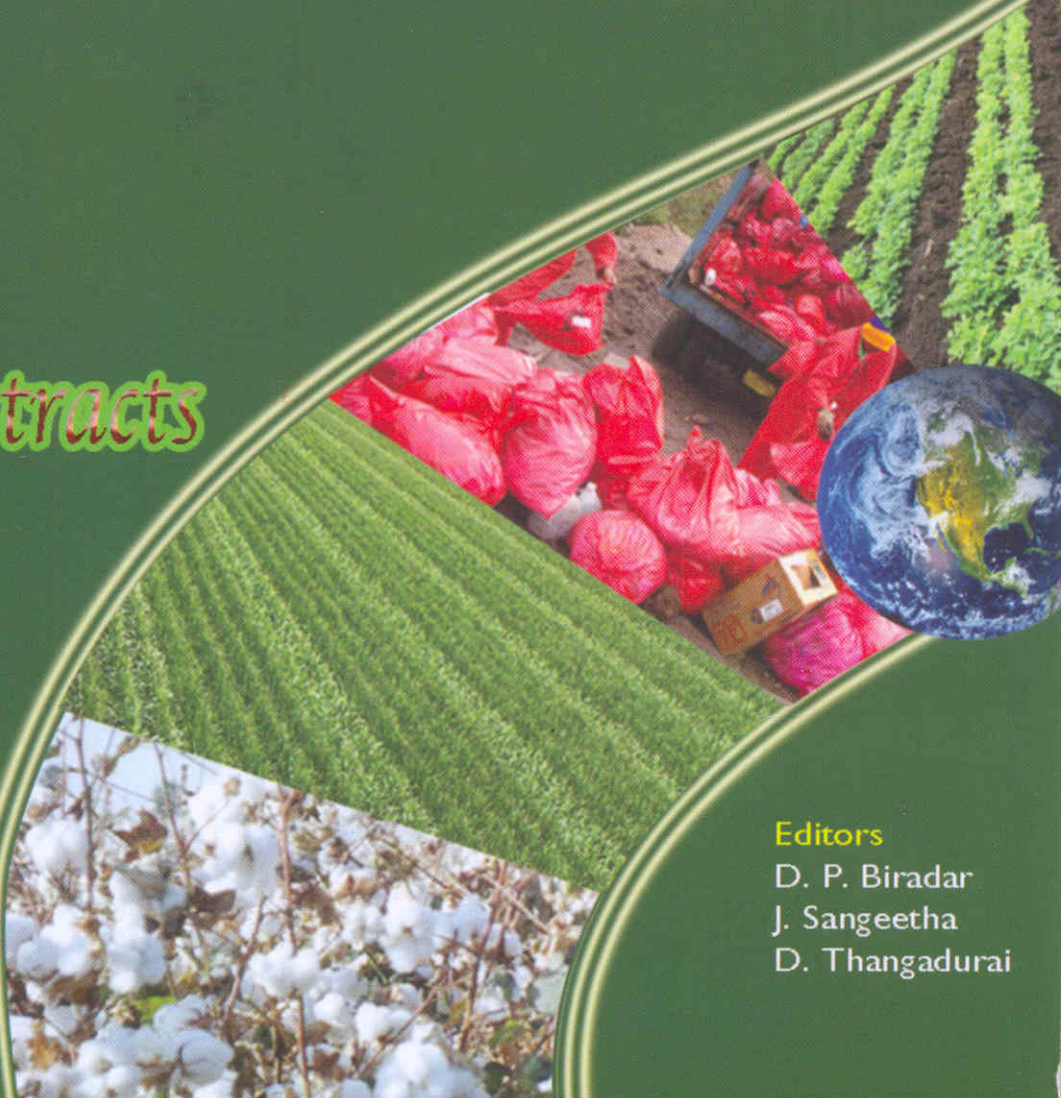


NATIONAL SYMPOSIUM

Innovative and Modern Technologies for Agricultural Productivity, Food Security and Environmental Management

Abstracts



Editors

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For every pollutant there is a microbe or a group of microbes that can transform it into harmless or less toxic forms. The biotransformation process is eco-friendly and does not cause further pollution. It has been widely reported that biopolymers like lipopeptides, glycolipids, proteins, carbohydrates, lipids etc enhance the degradation of the toxic compounds when supplied to the reaction system. They are effective in tiny amounts as they have both hydrophobic and hydrophilic domains in the molecule. Some of these polymers act as excellent emulsifiers that are stable for long periods. This property generates micro-aggregates of the pollutants that are bio-available for biodegradation by the microorganisms. Bacterial reduction of toxic Se oxyions selenate Se (IV) and selenite (IV) to nontoxic insoluble elemental state Se (0) is an important biological process involved in biogeochemical cycling of selenium in the environment. A bacterial strain (S-5) characterized as *Ochrobactrum intermedium* isolated from seleniferous agricultural soil is tolerant to high concentrations of selenite (250mM), the most toxic form of selenium. The effect of selenite on the growth kinetics of *Ochrobactrum intermedium* was studied in oxic conditions. It transformed about 50% of selenite to nontoxic red elemental Se (0) form in 72 hours. There was no change in growth characteristics of the strain even at 5mM concentrations of selenite. Electron microscopic studies show that there is aggregation of cells in the presence of selenite due to EPS production. Accumulation of elemental selenium in the cells is revealed by the increase in the buoyant density of the cells as the transformation takes place. This is the first report of selenite transformation by a member of genus *Ochrobactrum*. This strain can be of potential use for bioremediation process of selenium contaminated soils and understanding selenium speciation in the environment in toxic conditions.

Potential Application of Pigeon Pea Proteinase Inhibitors in the Management of Lepidopteran Insects

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Plant proteinase inhibitors (PIs) have been established as defense proteins against insect and microbial pests. In the present study, the seeds of pigeonpea (*Cajanus cajan* and *C. platycarpus*) were evaluated for the presence of potential PIs active against larval gut proteinases of lepidopteran insects *Spodoptera litura*, *Helicoverpa armigera* and *Achaea janata*. Red gram is a host plant to *S. litura* and *H. armigera* and nonhost plant to *A. janata*. The cultivars of *C. cajan* showed highest inhibitory activity towards the *A. janata* midgut trypsin-like proteinases. Conversely, the wild relatives of *C. cajan* and *C. platycarpus* accessions showed significant inhibitory activity against gut proteinases of *S. litura*

and *H. armigera*. The PIs from different tissues showed differential activity on the larval midgut trypsin-like proteinases of *H. armigera*. The PI activity against the midgut trypsin-like proteinases of *H. armigera* was highest in the seeds, followed by flower, pod and leaf. The PIs purified from red gram (RgPI) cultivar ICP 14770 (Abhaya) seeds by ion-exchange, affinity and gel-filtration chromatography showed remarkable inhibitory activity towards midgut trypsin-like proteinases of *A. janata* and *S. litura* compared with *H. armigera*. The *in vivo* feeding assays using *A. janata* and *S. litura* larvae further confirmed the remarkable insecticidal potential of RgPI. The biochemical characterization and N-terminal sequence homology studies clearly suggested that RgPI belongs to Bowman-Birk inhibitor (BBI) family. The cDNA sequence obtained from the leaf tissues showed high homology to double headed Bowman-Birk inhibitor from leguminous species. Further, 2-D gel electrophoresis revealed that RgPI existed in different isoform forms. MALDI-TOF mass spectrometry as well as SDS-PAGE clearly revealed the existence of self-association pattern in RgPI, leading to the formation of oligomers. Studies involving amino acid modification suggested that lysine present in the reactive site of PIs is responsible for their inhibitory activity against trypsin or trypsin-like proteinases. Thus, this study clearly demonstrates the potential of Bowman-Birk type of PIs isolated from pigeon pea in the management of both host and nonhost insects.

Development of Polymorphic Microsatellite Markers for *Fusarium* Wilt Pathogens of *Psidium guajava* L.

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Wilt of *Psidium guajava* L. is very serious problem in India. *Fusarium oxysporum* f. sp. *psidii* and *Fusarium solani* are the main causal agents for this disease. Microsatellite markers are currently used as marker of choice for genetic analysis for fungal pathogens. In the present investigation, DNA sequence of 27 different strains of *Fusarium oxysporum* f. sp. *psidii* and *Fusarium solani* isolated from wilted *Psidium guajava* L. root, were submitted to gene bank and their respective sequencing data was released by NCBI, USA. On the basis these sequence, we developed and characterized 13 polymorphic microsatellite markers, present in the genome of *Fusarium oxysporum* f. sp. *psidii* and *Fusarium solani*. Out of 13 newly developed microsatellite marker, 8 microsatellite primer pairs were successfully amplified DNA fragments from 21 isolates each of *Fusarium oxysporum* f. sp. *psidii* and *Fusarium solani* with average ranged of 2.5 alleles. The polymorphic information content (PIC) of developed markers was ranged 0.10 to 0.92. Since the observed heterozygosity values were significant, therefore, microsatellite marker developed in present investigation can be useful for population genetics study of the *Fusarium* wilt pathogens of *Psidium guajava* L.