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Comparative proteomics study of disease resistance genes expressed in *Cajanus cajan* genome employing next generations sequencing techniques tools

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Plant functional proteomics has emerged as a new and rapidly evolving scientific discipline to study the functions of genes as well as their corresponding proteins. In response to stress, plants activate a number of defense mechanisms that help the plants to alleviate the stress with enhanced tolerance. Pigeon pea (*Cajanus cajan*) is an important food legume crop of tropical and sub-tropical regions of the world. It is diploid with moderate genome size of 858 Mbp. We analyzed, nearly 13 million raw sequence reads (454 GS-FLX; N. K. Singh et al., 2012) of popular variety 'Asha'. The datasets were used for prediction of disease resistance genes such as NBS-LRR, NB-ARC, Leucine Rich etc. All predicted genes were functionally annotated following a consensus approach of either known homologous or predictive sequence signatures using CLC Genomics workbench version 6.5.1, Swiss-Prot, BLAST2GO, TrEMBL, InterPro and KEGG. After the functional analysis of predicted genes, the resistant proteins are modeled using Discovery Studio 3.5. The evolutionary relationships of the resistance genes and the existing gene-gene interactions are being studied.

Biography

Upasna Srivastava is currently working as Next-generation sequencing analyst at NBPGR, ICAR Pusa Campus New Delhi. She had been recognized and lauded for bioinformatics knowledge. She completed her Ph.D. dissertation work in bioinformatics entitled "Antibody modeling and vaccine design for cervical cancer caused by HPV type 16 E 7 Protein" from SHIATS, Allahabad University. She graduated in 2004 with a degree in Bioscience and completed my post-graduation in the area of Bioinformatics in 2007. Many of her research activities were in the field of molecular docking, Modeling, Vaccine designing, transcriptome sequencing etc.

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Molecular characterization of gut associated culturable microflora of the brown planthopper, *Nilaparvata lugens* (Stal)

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Symbiotic associations between insects and the microbes they harbor are very common. In addition to the classical nutritional symbiosis, there are reports that these symbionts play role in the fitness attributes of host such as insecticide resistance; for instance, an insecticide degrading bacteria of the genus *Burkholderia*, present in the gut of stink bugs impart protection against fenitrothion, an organophosphate. The brown planthopper *Nilaparvata lugens* (Stal) is an important pest of rice in Asia. *N. lugens* reportedly harbors numerous endosymbionts. In the present study, the culturable gut bacteria of *N. lugens* populations collected from Warangal, Nellore and Mandya in South India, were characterized by molecular technique, where insect gut is exercised under aseptic conditions, homogenized and plated on various growth media. The microbial isolates obtained were characterized using 16S rRNA gene amplification and the sequences were deposited in GenBank.

The bacterial isolates were: *Delftia acidovorans* (KF 448523), *Acinetobacter lwoffii* (KF 448525) and *Chryseomicrobium imtechense* (KF 448526) from Nellore population; *Pantoea dispersa* (KF 512549), *Acinetobacter baumannii* (KF 359493), *Acinetobacter baylyi* (KF 359494), *Bacillus cereus* (KF 359495) from mandya population; and *Enterobacter asburiae*, *Exiguobacterium mexicanum*, *Lysinibacillus* sp., *Bacillus licheniformis*, *Bacillus circulans* from Warangal population. Further, this study will be useful for finding the role of these gut bacteria in insecticide resistance.

Biography

V M Malathi has completed her M.Sc. from Mahatma Gandhi University, Kerala and presently doing Ph.D. in Biotechnology at National Bureau of Agriculturally Important Insects, Bangalore under DST- Inspire fellowship scheme.

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