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Title: Candidate Protein identification from acid soil tolerant Rhizobium strains of Pigeon pea by using MALDI- TOF- TOF.

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Keywords: Candidate Protein identification from acid soil tolerant Rhizobium strains of Pigeon pea by using MALDI- TOF- TOF.

Abstract: Objective of this study is characterization and identification of “Candidate Proteins” identified from acid tolerant strains of Rhizobium of Pigeon pea collected from the State Of Jharkhand by utilizing MALDI-TOF-TOF approach (“Peptide Mass Fingerprinting”). We have analysed 14 unique spots by employing 2-Dimensional gel electrophoresis. These unique spots are induced in acidic conditions but not induced in neutral pH. Rhizobial cells respond to acidity by either up-regulation or down-regulation of genes that leads to the increased or decreased translation of specific proteins. To study the stress protein of Rhizobium protein profile under different pH ranges were compared. Rhizobium are the bacteria that form nitrogen-fixing symbiosis with legumes. Leguminous crops have the ability to fix nitrogen (N) biologically from the atmosphere. Bacteria of the genera Azorhizobium, Bradyrhizobium, Mesorhizobium, Rhizobium, and Sinorhizobium are able to establish an endosymbiotic association with legumes. Rhizobium – legume symbiosis is one of the ideal solutions to improve the fertility of soil and restoration of arid land. Soil acidity is one of the major problems affecting the growth of Rhizobium in the soil of Jharkhand. N₂-fixing systems under severe environmental conditions such as acidic stress, temperature stress, drought stress, salinity, oxidative stress, osmotic stress and metal stress are reviewed. These major stress factors suppress the growth and symbiotic characteristics of most rhizobia. Proteomics is an ideal tool to monitor plant-microbe endosymbioses in the rhizosphere and it provides a broad overview of proteins produced by both partners during their constant signal exchange and allows the signal transduction pathways following photophosphorylation. MALDI-TOF MS is the method for both protein identification and characterization. It is typically used to measure the masses of the peptide derived from the trypsinized parent protein spot generating “peptide mass fingerprint” (PMF). Software package then compares the peptide mass list with a predicted theoretical list of tryptic peptide fragments for every protein in the public database. In this study we have done MALDI-TOF-TOF analysis of 14 candidate spots or unique spots from the Pigeon pea. We have identified 14 genes in acid tolerance pigeon pea by the MALDI-TOF-TOF analysis. These genes play a crucial role in the acid-tolerant mechanism of Rhizobium. Future prospects of this study is analysis of candidate proteins from other crops to identify the proteins which are common to the crops in the acid-tolerant regime. That common protein has the potential to be developed as a “Protein Marker” for acid tolerance regime in the near future.

Description: Candidate Protein identification from acid soil tolerant Rhizobium strains of Pigeon pea by using MALDI-TOF-TOF.

Subject: Biotechnology

Theme: Candidate Protein identification from acid soil tolerant Rhizobium strains of Pigeon pea by using MALDI-TOF-TOF.

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