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Mechanism of salt stress tolerance in Pigeon pea

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Pigeon pea (*Cajanus cajan* L), a diploid legume crop species is an important dicot crop grown largely in tropical and subtropical regions of India and is one of the main sources of dietary protein. From a food security perspective, legumes provide a highly balanced and nutritious source of calories and protein that is not provided by cereals. Salinity is one of the most widespread agricultural problems in arid and semi-arid regions around the world that makes the field unproductive. As a result, the development of improved levels of tolerance to stress has become an urgent priority and much research efforts are being applied to gain better understanding of the adaptive mechanisms of the plants to combat salt stress. Molecular mechanisms governing salinity stress induced responses in pigeon pea has far from being elucidated largely due to non-availability of genome sequence. To cope with salt stress, plants have evolved complex salt-responsive signalling and metabolic processes at the cellular, organ and whole plant levels. Being major protein source of Indian vegetarian population it is crucial to improve pigeon pea productivity under such harsh condition. Proteomic applications provide a powerful tool for the study of plant response to salt stress because it offers insights into the quantity and quality of the final gene products, that is, proteins. The functional translated portion of the genome have fundamental role in plant stress response, proteomic studies can provide a refined depiction of protein networks and metabolic pathways involved in stress tolerance mechanism. Identifying master regulator proteins that play key roles in the salinity stress response pathway is fundamental in providing opportunities for developing genetically engineered stress-tolerant crop plants.

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Molecular phylogenetics betwixt *Cucurbitaceae* spp. appraised by cpDNA and nDNA

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Horizontal genomics drove by footprints of comparative barcode sequence analysis, appraises geological relations amid genetic, species and community levels in green plants. Among the core barcode sequences proposed by CBOL, matK and ITS have been used for resolving the species delineations for several vegetal organisms. *Cucurbitaceae* are dioecious, vegetal crop species, disseminated in Asian and African continent. Every member of this family has multifarious medicinal chattels and agronomic essence. The present research endeavors to gauge evolutionary trend and phylogenetic monophyly amongst geo-edaphically divergent plant types of *Cucurbitaceae* using matK and ITS. Different types of sequences within species were observed, illuminating high frequency of gene passage during domestication apomixis or due to polyploidization events. The inter-/intra-species and inter-genus evolutionary distances were inferred from the employing Bootstrap method of UPGMA and ML using MEGA (version 6.0) and DAMBE (version 5.5.16) softwares, along Tajima's relative rate test and Nei's genetic distances. The values of genetic distances at inter-/intra species denote plausibility of occurrences of random population expansion, slow ontogenic transitions and or low consanguinity percentage among matK loci. However the marker was efficant is segregating the higher taxa betwixt *Cucurbitaceae*. Contrariwise the 'sequence types' within ITS loci revealed autapomorphy, along inconsistent inter, intraspecific & intergenus barcode gaps. Thereupon the ITS primers employed herein prevailed as neutral markers amongst *Cucurbitaceae*. Also an interspecies divergence appears to exceed intraspecies variance amidst some of the species.

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