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Appraisal of molecular phylogeny of *Coccinia* species employing chloroplast markers

Mala Parab and Sunita S
D Y Patil University, India

Acumen of green plant phylogeny using chloroplast DNA molecular fingerprints has enlightened the liaison between character evolution and diversification at various levels of plant taxa. Among an array of chloroplast conserved core barcode sequences proposed by CBOL, *rbcL*, *ycf5* and *trnS-trnG* have been used for inferring plant phylogenies. *Coccinia* spp. being dioecious, facultative apomictic, vegetal crops disseminated in Asian and African continent. It has multifarious ethno-medicinal assets and is agronomically imperative crop. The present study attempts to resolve inter-/intra-phylogenetic relations, evolutionary trend and speciation pattern *betwixt* *Coccinia* spp. using few chloroplastid loci. Inconsequential genetic/evolutionary distances within *Coccinia* spp. allude to possibility of reversal monophyly and high consanguinity percentage amid *Coccinia* within both the CpDNA loci i.e., *trnS-trnG* and *rbcL*. The *rbcL* and *trnS-trnG* loci, thus demonstrated chloroplast homoplasmy, reticulate speciation pattern, LBAs and LDDs. However the *trnS-trnG* loci could cluster all *Coccinia* species in to one clade. A similar plesion group amidst *Coccinia* was reported from our previous study using phenetic and MLSPAP based genetic differentiators. Thereupon we conclude that *rbcL* are symplesiomorphic traits amid Cucurbitaceae members, while *trnS-trnG* are synapomorphic traits that can be used for resolving higher phylotaxas among Cucurbits. The *ycf5* marker locus was efficant in resolving phylogeny at both infraspecies and infrageneric levels. We also propose that *Coccinia* spp. descendants of neutral theory of evolution, were observed to get enrouted towards parallel evolution and exhibit paternal inheritance.

Biography

Mala Parab is currently pursuing her PhD at the School of Biotechnology and Bioinformatics, D Y Patil University, India. She is also being associated with the school as Assistant Professor since 9 years. She has also worked as an Associate Faculty, BSc (Biomedical Sciences and Molecular Biology), University of Central Lancashire, United Kingdom for two years She has published more than 5 papers in reputed journals and over 20 sequences to NCBI during her PhD.

malaparab@gmail.com

Sequence and recombination analysis of the *AC1* gene of Mungbean yellow mosaic virus isolates

Meenakshi Sindhu and P K Jaiwal
Maharshi Dayanand University, India

Mungbean yellow mosaic virus belongs to the family *Geminiviridae* possessing bipartite genome. It is a menace in legume production being responsible for yellow mosaic disease transmitted by the whitefly *Bemisia tabaci*. The DNA 'A' component encodes for the information related to viral DNA replication, transcription and encapsidation, whereas DNA 'B' encodes for movement proteins which are responsible for virus translocation. As *AC1* gene codes for a replication-associated protein (Rep) which is essential for replication of virus, it is an important target for various strategies to develop virus resistance in legumes. Evolutionary relationship among *AC1* genes of different MYMV isolates was studied using MEGA6. Phylogenetic trees obtained from different methods gave different results revealing a pattern in diversity among these isolates. Regions of recombination in the *Rep* gene of different MYMV isolates were detected using Recombination Detection Program (RDP4). There are greater chances for a recombinant virus to emerge by increasing host range and to provide sources of variation having unpredictable effects on the viral pathogenicity.

Biography

Meenakshi Sindhu is currently pursuing her PhD from Maharshi Dayanand University under the supervision of Dr. P K Jaiwal. She has been awarded DST-INSPIRE JRF by DST, New Delhi and currently working as DST-INSPIRE SRF fellow. She has a publication from her Master's dissertation work and she is member of reputed scientific societies so as to excel her interdisciplinary research interests as well.

meenakshisindhu23@gmail.com