

## Extended Abstract

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

Sunita Singh and Mala P

D Y Patil University, India

### Abstract

Horizontal genomics drove by footprints of comparative barcode sequence analysis, agapes genological 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 apomixsis 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.