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Phylogenetic relationships of the genus *Curcuma* L. based on cytogenetical and molecular inferences

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The genus *Curcuma* L. of the family *Zingiberaceae*, is pantropical in distribution and comprises of three subgenera viz. *C.* subg. *Curcuma, C.* subg. *Hitcheniopsis* and *C* subg. Ecomatae. Of the three subgenera, the subgenus *Curcuma* (Baker) K. Schum., contains highly complex polyploid taxa with overlapping morphological characters which contributed to taxonomic perplexity in the genus *Curcuma*. A combination of classical and molecular cytogenetics as well as molecular approaches, are essential for detailed scrutiny particularly polyploid complexes which may offer a reasonable taxonomic concept. To resolve some of these issues, fifteen species belonging to the *Curcuma* subg. *Curcuma* were taken up for cytogenetical (viz. chromosome count, male meiosis and heterochromatin banding pattern) and sequence targeted (viz. nrITS and cpDNA) studies. Mitotic study in root-tip cells, could resolved the species into three groups with 2n=42 (*C amada, C aromatica, C. comosa, C haritha, C mangga* and *C montana*), 2n=63 (*C aeruginosa, C caesia, C latifolia, C longa, C leucorrhiza, C sylvatica, C zanthorrhiza* and *C zedoaria*) and 2n=105 (*C raktakanta*) with male meiotic analysis showing a varying degree of chromosome association(s) suggesting the genus might have been affected by inter-specific crosses and thus confirming their allopolyploid nature. For phylogenetic investigation, a total of 27 *Curcuma* species which included 15 species collected exclusively from India and the remaining 12 world species retrieved from GenBank, were taken up for detailed analysis with *Alpinia galangal and Globba substrigosa* as outgroups. The studies could successfully resolve the species with respect to their infrageneric groups and could deduce some of the taxonomic discrepancy related to the genus *Curcuma. C. comosa, C. montana* and *C. latifolia* with similar morphological and floral traits demonstrated a close phylogenetic relationship. *C. sylvatica* was considered a variant derived from *C. amada* due to the mango-like aroma of the rhizome, etc. However, in light of our cytogenetical data on chromosome count and male meiosis we rule out the possibility of *C. sylvatica* (2n=63) being a variant of *C. amada* (2n=42). In depth, scrutiny of the species within the *Curcuma* clade based on morphology, cytology and molecular parameters could resolve the identity of some closely resembling *Curcuma* species when there is confusion with respect to their identity. Moreover, a close relationship between species within the *Curcuma* clade suggested that hybridization and subsequent chromosome doubling has played an important role in species diversification of *Curcuma*

Biography

Rama Rao has about 30 years of teaching and research experience in the field of Plant Genetics and Molecular Biology. He has mainly focus on characterization of genetic diversity of plant resources of Indian Thar Desert regions, later the North-east regions of India with focus on Meghalaya. Over these years, he has identified novel genotypes in *Vigna, Curcuma, Citrus* and bananas. He has published more than 105 research publications in journals of international repute.

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