

Abstract

Economically important genus *Curcuma* is taxonomically critical polyploid complex. Taxa of various ploidy levels (2x, 6x, 9x, 11x, 12x and 15x) prefer different modes of reproduction (vegetative, sexual or both) and consequently exhibit different levels of morphological variability. With no recent revision and extremely complicated nomenclatoric issues incorrect identifications are very common. So far there is no suitable infrageneric classification. Moreover, concept of the genus *Curcuma* is vague, as indication exists, that *Curcuma* is paraphyletic with several closely related genera (Kress et al. 2002). Based on ongoing taxonomic revision of Indian *Curcuma* and recent extensive cytological study, that have suggested natural grouping of subgenus *Curcuma* based on differences in homoploid genome sizes, the goals of present study are: 1) to test the monophyletic character of „genome size groups“ sensu Leong-Škorničková et al. (2007) and outline phylogenetic relationships within and among these groups and 2) to assess taxonomic position of four *Curcuma*-like species often placed into separate genera: *Monolophus scaposus*, *Hitchenia caulina*, *Stahlianthus campanulatus* and *Stahlianthus involucratus*.

Two molecular markers, AFLP fingerprinting and ITS cloning and sequencing, were used. Total of 19 *Curcuma* species with representation of 115 individuals, were analysed by AFLP. By ITS cloning and sequencing 24 *Curcuma* species, 4 species belonging to *Curcuma*-related genera and 4 outgroup species were analysed. This sampling covered two currently distinguished subgenera of the genus *Curcuma* (subg. *Curcuma* and subg. *Hitcheniopsis*), three genome size groups defined within subg. *Curcuma* (Leong-Škorničková et al., 2007) and six ploidy levels detected within genus *Curcuma* in India.

Phylogenetic reconstructions based on two independent molecular markers revealed in general same pattern within genus *Curcuma*. Within subg. *Curcuma* two lineages that probably evolved independently were detected. First lineage corresponding with genome group I defined in (Leong-Škorničková et al., 2007), second lineage corresponding with genome group II and III, with only few exceptions, which are discussed. Phylogenetic relationships within particular lineages were not unambiguously resolved, however allopolyploidization, hybridization and reticulate evolution in *Curcuma* species were well documented. Complex character of evolution in ITS region and its implication for resolving *Curcuma* phylogeny is discussed. The four *Curcuma*-like species often classified to related genera (*Hitchenia caulina*, *Monolophus scaposus*, *Stahlianthus involucratus*, *Stahlianthus campanulatus*) were well supported to be a true *Curcuma* species. Therefore, previous suggestion by Ngambriabsakul et al.(2004) and by Leong-Škorničková et al. (2007), that these species should be classified as members of genus *Curcuma*, are justified by present study.

Key words: *Curcuma*, Zingiberaceae, polyploidy, phylogeny, reticulate evolution, genome size, molecular markers, AFLP, ITS