ABSTRACT

This master thesis focuses on the phylogeny of hybridogenous and polyploid genus *Curcuma* from family *Zingiberaceae* using Next-Generation Sequencing data from hundreds to thousands nuclear loci. This approach seems to be better than widely used cpDNA and ITS sequencing especially in the case of hybridogenous and polyploid groups.

Data for phylogeny reconstruction were generated using Hybridization-based sequencing (Hyb-Seq) method which combines target enrichment and genome skimming strategies. Data analysis was performed primarily using pipeline HybPhyloMaker especially created for Hyb-Seq data analysis.

Twenty-seven species from the genus *Curcuma* and three outgroup species were sequenced in this work. Phylogenetic trees based on all 1 154 and 811 selected nuclear low-copy genes show high support values of all nodes which is in contrast to plastome and rDNA phylogeny with lower support values in some nodes and incongruences in topology compared to low-copy genes phylogeny. Phylogenetic networks inferred from low-copy genes, lineage movement analysis and monophyly tests agree with published hypotheses of interlineage hybrid origin of three species – *C. vamana*, *C. myanmarensis* and *C. roscoeana.* These analyzes show likely hybrid origin of *C. candida* too with parents from the group *Curcuma I* and basal species of the subgenus *Curcuma*.

KEY WORDS

Next-generation sequencicng, Hyb-Seq, turmeric, phylogeny, polyploidy, hybridisation, nuclear low-copy genes, plastome, ribosomal DNA