

## FIRST GENOMIC INSIGHTS INTO THE MANDEVILLA GENUS

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Mandevilla (Apocynaceae) is a greatly appreciated genus in the world ornamental market. In this study, we attempted to address the poor genetic knowledge and the huge taxonomic gaps existing in this genus by analyzing the germplasm of 55 accessions. After cytometrically determining the triploid genome size (1,512.64 Mb) of a reference sample (variety “Mandevilla 2001”), the plastidial genome (cpDNA, 0,18 Mb) and a draft of the nuclear genome (nuDNA, 207 Mb) were assembled. While cpDNA was effective in reconstructing the phylogeny of the Apocynaceae family based on a DNA superbarcoding approach, the nuDNA assembly length was found to be only 41% of the haploid genome size (506 Mb, predicted based on the K-mer frequency distribution). Its annotation enabled the prediction of thousands of genes, of which 5,275 resulted in full CDS. Among them, we identified nine genes whose orthologs (in *Catharanthus roseus*) encode enzymes involved in the biosynthesis of monoterpene indole alkaloids (MIAs), including catharanthine, tabersonine and vincadifformine. The nuclear genome draft was also useful to develop a highly informative (mean PIC=0.62) set of 23 SSR markers that was validated on the Mandevilla collection. These results were integrated with cytometric measurements, nuclear ITS1 haplotyping and chloroplast DNA barcoding analyses to assess the origin, divergence and relationships existing among the 55 accessions object of the study. As expected, based on the scarce information available in the literature, the scenario was extremely intricate. A reasonable hypothesis is that most of the accessions represent interspecific hybrids sharing the same species as maternal parent (i.e., *Mandevilla sanderi*).