SUMMARY

Rhynchostylis gigantea (Lindl.) Ridl. is an orchid species that exhibits variation in flower patterns and colours, specifically peach and white. Therefore, as an ornamental plant species of high economic value, this is now listed in Appendix II of CITES, mainly due to overexploitation and complicated reproduction system. Therefore, genetic conservation efforts are necessary, which should be preceded by studies on the genetic diversity. This study aims to determine the sequences of the *trnL* (UAA) – *trnF* (GAA) IGS molecular marker in two different cultivars of *R. gigantea* and to identify the existence of genetic difference between both cultivars based on the molecular marker.

The study was conducted at the Genetics and Molecular Laboratory and Teaching Laboratory III, the Faculty of Biology, Universitas Jenderal Soedirman for three months. The procedures include plant sampling, genomic DNA extraction using the CTAB method, PCR amplification of the *trnL* (UAA) – *trnF* (GAA) marker using a pair of universal primers, and sequencing the marker. The obtained sequence data were edited using Bioedit and manually checked. The sequences were then blasted to those available at NCBI database. Subsequently, sequence alignment was performed using Clustal W program to identify genetic differences between and within the two orchid cultivars.

The results indicate that the IGS *trnL*(UAA)-*trnF*(GAA) sequences of approximately 500 bp before editing and 481 bp after editing were observed. All six sequences show high similarity to the chloroplast genome sequence of *R. gigantea* available in the NCBI database. Alignment on the IGS *trnL*(UAA)-*trnF*(GAA) sequences among the six *R. gigantea* samples does exhibit some genetic difference, but these sequences could not be used to distinguish flower colour gene expression between the two *R. gigantea* cultivars.

Key words: genetic diversity, *Rhynchostylis gigantea*, *trnL* (UAA) – *trnF* (GAA) IGS