



**PHYLOGENETIC ANALYSIS OF *Alocasia zebrina* complex (Araceae)
INFERRED FROM CHLOROPLAST DNA**

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ABSTRACT

Previous studies on *Alocasia zebrina* complex revealed that the taxa belonging to this group have different morphological characteristics and a subject of further investigation. The study has aimed to do molecular analyses in order to resolve the said taxonomic dilemma. Total genomic DNA of the three samples were extracted, isolated amplified and purified. The primers amplified for each of the samples were at regions of *trnL-F* and *trnK*. Alignment of DNA sequences were done through the use of CodonCode Aligner v.4.0 and for the construction of phylogenetic tree MEGA v.5.0 was used. There are 956 characters obtained for the primer *trnL-F* while 842 for the *matK*. Through the obtained base frequencies, chi-square of homogeneity and distance matrix, it was found out that the three species are exactly similar with each other. “P” values of 0.99 and 1.00 were obtained for the primers *trnL-F* and *trnK* respectively, suggests to have accepted the null hypothesis on the species’ resemblance. In addition to that the constructed phylogenetic tree has presented the three *Alocasia* taxa are monophyletic and has obtained a bootstrap percentage greater that 50%, specifically 63% and 79% for the aforementioned order of primers. The values only suggest that there is a greater plausibility in terms of their uniformity. The results proved that the taxa under the *Alocasia zebrina* complex are similar and there is no significant difference within their genomic sequences; hence, they belong to the *Alocasia zebrina*.



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