ABSTRAK

Penelitian Ini Berjudul "Variasi Genetik Mangrove *Rhizophora Mucronata* Di Segara Anakan Cilacap Berdasarkan DNA Barcoding Gen ITS". Variasi mangrove sulit dibedakan dengan identifikasi morfologi karena adanya perubahan kualitas kondisi lingkungan. Penelitian ini bertujuan untuk mengetahui variasi genetik dan mengetahui kekerabatan filogenetik mangrove *Rhizophora mucronata* berdasarkan gen *Internal Transcribed Spacer* (ITS) di Segara Anakan, Cilacap. Metode isolasi DNA dengan *GeneJET Plant Genomic DNA Purification Mini Kit*. Amplifikasi gen ITS menggunakan primer ITS, analisis sekuen gen *Internal Transcribed Spacer* ITS menggunakan *Basic Local Alignment Search Tool* (BLAST), pensejajaran sekuen dengan multalin dan konstruksi pohon filogenetik menggunakan *software* MEGA 10.1.7 dengan metode *neighbor-joining tree*. Hasil penelitian menunjukkan bahwa amplifikasi memperoleh produk berukuran 400-500 bp dengan nilai similaritas berkisar berkisar 98,01-100% dengan *No. Accesion* MH243991.1 dan adanya variasi intraspesies yang ditunjukkan dengan adanya perbedaan 8 pasang basa nukleotida pada urutan sekuens. Analisis filogenetik menunjukkan nilai bootstrap 100% yang menunjukkan memiliki kekerabatan yang dekat dan percabangan yang dapat dipercaya.

***Kata kunci** : Variasi genetik; DNA Barcoding (Gen ITS); Rhizophora mucronata; Segara Anakan Cilacap.*

ABSTRACT

This research entitled "Genetic Variation of *Rhizophora Mucronata* Mangrove in Segara Anakan Cilacap Based on DNA Barcoding ITS Genes". Mangrove variation is difficult to distinguish from morphological identification due to changes in the quality of environmental conditions. This study aims to determine genetic variation and determine the phylogenetic relationship of *Rhizophora mucronata* mangroves based on the Internal Transcribed Spacer (ITS) gene in Segara Anakan, Cilacap. DNA isolation method with the GeneJET Plant Genomic DNA Purification Mini Kit. ITS gene amplification using ITS primers, analysis of Internal Transcribed Spacer ITS gene sequences using Basic Local Alignment Search Tool (BLAST), sequence alignment with multalin and phylogenetic tree construction using MEGA 10.1.7 software with the neighbor-joining tree method. The results showed that the amplification obtained a product measuring 400-500 bp with similarity values ranging from 98,01-100% with No. Accession MH243991.1 and the presence of intraspecies variations as indicated by the difference in 8 pairs of nucleotide bases in sequence. Phylogenetic analysis showed a bootstrap value of 100% which showed a close kinship and a reliable branching.

Key words : *Genetic variation; DNA Barcodes (ITS Genes); Rhizophora mucronata; Segara Anakan Cilacap.*