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ELECTRONIC THESIS AND DISSERTATION UNSYIAH

TITLE

ANALISA FILOGENETIK FAMILI DIPTEROCARPACEAE BERDASARKAN DNA BARCODING MATK

ABSTRACT

Analisa filogenetik famili Diptero­carpaceae ber­das­arkan dna barcoding matK ber­tu­juan untuk menganalisa hubungan kekerabatan dari beberapa spesies famili Diptero­carpaceae dan mem­bandingkan hasil analisa ber­das­arkan nilai bootstrap dan waktu yang di­butuhkan untuk mem­bangun pohon filogenetik meng­gunak­an algoritma Neighbor-joining, Maximum Parsimony dan Maximum Likelihood. Adapun tahapan analisa terdiri dari pengumpulan data, pengubahan struktur nama sekuen, penjajaran sekuen, konstruksi pohon, evaluasi pohon dan analisa pohon. Hasil analisa kekerabatan dari ketiga metode (Neighbor-joining, Maximum parsimony dan Maximum likelihood) menunjukkan bahwa genus Diptero­carpus tidak mem­bentuk monophyletic group dengan genus lain dari tribe Diptero­carpaceae. Pohon filogenetik dengan algoritma Maximum likelihood memiliki akurasi yang lebih tinggi di­bandingkan algoritma Neighbor-joining maupun Maximum parsimony. Sedangkan waktu tercepat yang di­butuhkan untuk konstruksi pohon filogenetik secara berurutan yaitu algoritma Neighbor-joining, Maximum parsimony dan Maximum likelihood.

Kata Kunci: Filogenetik, neighbor-joining, maximum parsimony, maximum likelihood

Phylogenetic analysis of family Diptero­carps based on dna barcoding matK aims to analyze the phylogenetic relationship of some species Diptero­carps and to compare the result of the analysis based on bootstrap values and the time required to construct the phylogenetic tree using the neighbor-joining, maximum parsimony and maximum likelihood algorithm. The analysis stage consists of collecting data, changing the structure of the sequences name, sequences alignment, tree building, tree evolution and analysis of tree. The result of the analysis of all three methods (neighbor-joining, maximum parsimony and maximum likelihood) showed that the genus Diptero­carpus do not a monophyletic group with other genera of the tribe Diptero­carpeae. Phylogenetic trees with maximum likelihood algorithm has a higher accuracy then neighbor-joining or maximum parsimony and the fastest time required for construction of phylogenetic trees sequentially is neighbor-joining, maximum parsimony and maximum likelihood.

Keyword: Phylogenetic, neighbor-joining, maximum parsimony, maximum likelihood