Keragaman Genetik Cendana (*Santalum album* Linn.) Pada Tegakan Benih dan Tegakan Rehabilitasi di Nusa Tenggara Timur Berdasarkan Penanda Isozim

INTISARI

Cendana (*Santalum album* Linn.) merupakan tanaman endemik Nusa Tenggara Timur yang mempunyai nilai ekonomi tinggi. Potensi ekonomi yang tinggi ini mengakibatkan tingginya eksploitasi oleh masyarakat, yang tidak dibarengi upaya perbanyakan dan penanaman secara memadai. Eksploitasi berlebihan juga berdampak pada menurunnya populasi cendana serta berpotensi menurunkan keragaman genetiknya, sedangkan upaya rehabilitasi terkendala ketersediaan benih berkualitas dan keberhasilan tanaman yang rendah. Hal ini dikarenakan eksploitasi menyisakan tanaman cendana yang secara genetik kurang berkualitas dan terbatas secara kuantitas.

Penelitian ini bertujuan untuk mengetahui keragaman genetik cendana pada tegakan benih dan tegakan rehabilitasi di Nusa Tenggara Timur dengan menggunakan isozim sebagai penanda. Penelitian dilakukan menggunakan sampel yang diambil dari 3 tegakan yaitu Areal Produksi Benih (APB) yang mewakili tegakan benih, tegakan rehabilitasi KHDTK dan tegakan rehabilitasi CSR yang mewakili tegakan rehabilitasi. Sampel berupa daun juvenil cendana diambil secara random dari masing-masing lokasi. Dari tegakan APB sebanyak 57 sampel sedangkan dari tegakan rehabilitasi KHDTK dan CSR masing-masing 25 sampel. Analisis isozim dilakukan di laboratorium menggunakan 3 macam sistem enzim yaitu *Esterase* (EST), *Diaphorase* (DIA) dan *Shikimate Dehydrogenase* (SHD).

Untuk parameter keragaman genetik dalam tegakan, teramati rerata lokus polimorfik sebesar 88,89%, dengan rerata jumlah alel per lokus 2,1667 dan rerata alel efektif 1,2103. Untuk heterozigositas harapan (H_S) dalam tegakan diperoleh nilai 0,1558 dengan rerata heterozigositas teramati (H_O) sebesar 0,1402 dan rerata indeks fiksasi sebesar 0,1118. Pada pengamatan parameter keragaman genetik antar tegakan diperoleh nilai D_{ST} = 0,0090 dan G_{ST} = 0,0545, sedangkan heterozigositas harapan total ketiga tegakan cendana yang diobservasi (H_T) sebesar 0,1648. Untuk mengantisipasi penurunan keragaman genetik cendana dapat dilakukan identifikasi dan inventarisasi keberadaan populasi cendana yang masih tersisa, untuk kemudian dilakukan upaya konservasi bagi alel-alel langka baik secara *in-situ* maupun *ex-situ*.

Kata kunci : Cendana, Areal Produksi Benih, tegakan rehabilitasi, keragaman genetik, isozim

Genetic Diversity of Sandalwood (*Santalum album* Linn.) on Seed Stands and Rehabilitation Stands in East Nusa Tenggara based on Isozyme Marker

ABSTRACT

Sandalwood (*Santalum album* Linn.) is a species with high economic value endemic to East Nusa Tenggara. High economic potential of this results in a high exploitation by society, which is not accompanied by efforts to adequately propagation and planting. Excessive exploitation would lead to sandalwood population decrease in its natural distribution and this condition could potentially reduce its genetic diversity. While rehabilitation programs on sandalwood were constrained by the lack of quality seeds and low success. These happen because exploitations have left only sandalwood plants that are genetically less qualified and limited in quantity.

This study aims to analyze the genetic diversity of sandalwood on seed stands and rehabilitation stands in East Nusa Tenggara by using isozymes as a marker. Research was conducted by using samples taken from three stands, i.e. Seed Production Area (APB) representing seed stands, KHDTK rehabilitation stand and CSR rehabilitation stand representing rehabilitation stands. Sample materials taken were juvenile leaves collected randomly from each stand. There were 57 samples taken from APB, while each 25 samples were collected from rehabilitation stands of KHDTK and CSR. Isozymes analyses were carried out in the laboratory using three kinds of enzyme systems i.e *Esterase* (EST), *Diaphorase* (DIA) and *Shikimate Dehydrogenase* (SHD).

The results showed that for genetic diversity within stands, the mean of polymorphic loci was 88,89%, with a mean number of alleles per locus 2,1667 and a mean of effective alleles 1,2103. The expected heterozygosity within stands (H_S) was 0,1558, with the observed heterozygosity (H_O) of 0,1402, while the mean index of fixation was 0,1118. On genetic diversity among stands, D_{ST} and G_{ST} values were 0,0090 and 0,0545 respectively, while total expected heterozygosity of the three stands (H_T) was 0,1648. To anticipate sandalwood genetic diversity decline e.g. identify and record the remaining sandalwood populations, then conserve rare alleles either through in-situ or ex-situ conservation programs.

Keywords: sandalwood, Seed Production Area, rehabilitation stands, genetic diversity, isozyme