

KERAGAMAN GENETIK SPASIAL DAN TEMPORAL PADA ENAM KELOMPOK TEGAKAN CENDANA DI BAGIAN BARAT DAYA, ZONA BARAT GUNUNG SEWU

Ibnu Ahmad Rizal¹, Yeni W. N. Ratnaningrum², Sapto Indrioko²

INTISARI

Raslahan cendana di Zona Selatan dan Tengah mengalami degradasi, sehingga raslahan di Zona Barat dari Geopark Gunung Sewu, diusulkan menjadi alternatif untuk sumber materi genetik. Zona Barat memiliki lanskap pegunungan aluvium yang saat ini disebut Formasi Pegunungan Batur Agung. Cendana di Zona Barat tumbuh dalam kelompok kecil sepanjang bibir tebing, jurang, atau tepian sungai; diduga terisolasi oleh barier alam. Cendana di Zona Barat diduga memiliki keragaman genetik lebih tinggi, karena terdapat raslahan Imogiri yang merupakan *center of biodiversity* di Gunung Sewu. Raslahan cendana di Zona Barat meliputi kelompok Barat Daya (Imogiri, Watu Payung, Pongol, Nglesih, Banyusumurup dan Sriharjo) dan Barat Laut (Nglanggeran dan Sriten). Penelitian ini bertujuan untuk mengetahui variasi genetik temporal (individu dewasa dan permudaan alam) serta spasial (antar kelompok tegakan) cendana di bagian Barat Daya dari Zona Barat Gunung Sewu.

Penelitian ini dilakukan pada enam kelompok tegakan cendana di bagian Barat Daya dari Zona Barat Gunung Sewu. Penelitian terbagi menjadi beberapa tahapan yaitu (1) inventarisasi individu dewasa, individu berbunga dan anakan hasil permudaan alam, (2) pengambilan sampel untuk analisis isozim, serta (3) analisis isozim; yang dilakukan pada bulan Maret hingga April 2022.

Tiap kelompok hanya memiliki sedikit individu dewasa (29-108 individu), kecuali Stone Park (494 individu), dengan tingkat klonalitas > 90% kecuali di Watu Payung (50%). Proporsi individu berbunga 6%-20,7%; sebagian besar induk berbunga adalah klonal kecuali Watu Payung. Semai generatif hanya dijumpai di Watu Payung. Di kelima lokasi selain Watu Payung, basis genetik sempit dan klonalitas tinggi menyebabkan *inbreeding* dan *genetic drift*, sehingga banyak alel langka dan alel hilang. Induk berbunga pada kelima kelompok klonal memiliki keragaman genetik rendah (H_e 0,025-0,213; H_o 0,024-0,122). Hanya Watu Payung yang memiliki keragaman genetik tinggi (H_e 0,513; H_o 0,800), dan menghasilkan semai dengan keragaman sangat tinggi pula (H_e 0,507; H_o 0,756). Nilai FIS menunjukkan *inbreeding* di kelima lokasi yang klonalitasnya sangat tinggi (FIS 0,115-0,821). Hanya induk di Watu Payung yang cenderung *outcrossing* (FIS -0,413). Nilai Heterozigositas harapan total pada seluruh individu dewasa adalah HT 0,538; dan pada individu berbunga adalah HT 0,451. Keragaman genetik antar kelompok tegakan (DST) di bagian Barat Daya cukup tinggi, baik pada total individu dewasa dan semai (DST 0,177), total individu dewasa (DST 0,201), maupun individu berbunga (DST 0,283). Proporsi keragaman genetik antar populasi terhadap keragaman total (GST) sangat tinggi, baik pada total individu dewasa dan semai (GST 32,89%), total individu dewasa (GST 37,40%), maupun individu berbunga (GST 62,65%). Dendogram menunjukkan bahwa raslahan tidak dikelompokkan berdasarkan lokasi geografis atau kedekatan jaraknya, tetapi lebih pada kesamaan basis genetik, tingkat fragmentasi, dan klonalitas.

Kata kunci: cendana, keragaman genetik spasial dan temporal, Bagian Barat Daya Zona Barat Gunung Sewu

¹Mahasiswa S1 Fakultas Kehutanan UGM

²Dosen Fakultas Kehutanan UGM

SPATIAL AND TEMPORAL GENETIC VARIATION ON SIX SANDALWOOD STANDS IN THE SOUTH-WESTERN PART OF WESTERN ZONE IN GUNUNG SEWU

Ibnu Ahmad Rizal¹, Yeni W. N. Ratnaningrum², Sapto Indrioko²

ABSTRACT

The sandalwood landraces in the Central and South Zones of Gunung Sewu are rapidly degraded, and therefore the occurrence of stands in the West Zone might be an alternative sources of genetic materials. West Zone was derived from volcanic-fluvium processes in the past, recently known as Pegunungan Batur Agung Formation. Sandalwood in West Zone grew in small group of stands, along with the verge of the cliffs, ravines, and the riparian catchment areas; possibly isolated by these natural barriers. This West Zone groups considered having higher genetic diversity, since it also included the Imogiri landrace which is the center of biodiversity in Gunung Sewu. Sandalwood stands in the West Zone consisted of the South-Western group (Imogiri, Watu Payung, Pongol, Nglesoh, Banyusumurup and Sriharjo) and the North-Western one (Nglangeran and Sriten). This study aimed to estimate the temporal (parents and progenies) and spatial (among groups) genetic diversity of sandalwood stands in the South-Western part of Western Zone in Gunung Sewu.

This study is carried out in the sandalwood group of stands in the South-Western part of Western Zone Gunung Sewu. Study was conducted from March to April 2022, and divided into several steps: (1) inventory of mature individuals, flowered parents and generative progenies, (2) isozyme samples collection, and (3) isozyme analysis.

Results found only few mature individuals in each stand (29-108 individuals), except in Stone Park which has 494 individuals. The clonality rate is >90% except in Watu Payung (only 50%). The proportion of flowering parents is 6%-20,7%; mostly were derived from clones except in Watu Payung. Seedlings were only found in Watu Payung. Five stands except Watu Payung were subjected into narrow genetic base and highly clonalized conditions, caused inbreeding which was resulted in more rare and missing alleles. Flowering parents in the five highly-clonalized stands had H_e 0,025-0,213; and H_o 0,024-0,122. The less clonalized one, Watu Payung, has H_e 0,513; and H_o 0,800, while the progenies has H_e 0,507; and H_o 0,756. The F_{IS} indicated inbreeding at flowering parents in the five highly-clonalized stands (F_{IS} 0,115-0,821). Only flowering parents in Watu Payung were outcrossing (F_{IS} -0,413). The total expected heterozygosity in mature individuals is H_T 0,538; and in the flowering parents is H_T 0,451. The genetic diversity among population in the South-Western Zone (D_{ST}) is high for the total mature individuals and progenies (D_{ST} 0,177), the total mature individuals (D_{ST} 0,201), and even higher in the flowering parents (D_{ST} 0,283). The proportion of genetic diversity among populations to the total diversity (G_{ST}) is very high for the total mature individuals and progenies (G_{ST} 32,89%), the total mature individuals (G_{ST} 37,40%), and even higher in the flowering parents (G_{ST} 62,65%). Dendrogram clearly showed that the sandalwood stands were not clustered by geographical distances, but more by the similarity on the genetic base, fragmentation level, and clonality.

Keywords: sandalwood, spatial and temporal genetic diversity, the South-Western part of Western Zone Gunung Sewu

¹Student of the Faculty of Forestry UGM

²Lecturers of the Faculty of Forestry UGM