

POLA KERAGAMAN GENETIK PADA PERMUDAAN ALAM CENDANA DI
KAWASAN DESA WISATA BEJIHARJO, KARANGMOJO, GUNUNGKIDUL

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Intisari

Saat ini cendana (*Santalum album* Linn.) termasuk *Critically Endangered Species* karena degradasi atau hilangnya habitat pada populasi alamnya di seluruh dunia. Sejak tahun 2004, cendana dinyatakan *Extinct in The Wild* di sebaran alamnya di NTT; bahkan Pemerintah Daerah NTT harus mendatangkan kembali bibit dari Gunungkidul, DIY untuk kegiatan re-introduksi. Berkembangnya cendana di Kabupaten Gunungkidul, Propinsi DIY yang bukan habitat alamnya, menjadi fenomena yang menarik. Selain di Hutan Wanagama yang terletak di Kecamatan Gading, cendana dijumpai pula di beberapa lokasi yang tersebar di Gunungkidul; antara lain di Kawasan Desa Wisata Bejiharjo, Kecamatan Karangmojo. Penelitian ini dilakukan berbasis analisis isozim dan uji keberhasilan reproduksi generatif untuk mengetahui pola keragaman genetik pada permudaan alam, dan pola pewarisan dari induk kepada keturunannya, pada tegakan cendana hasil permudaan alam yang terlokalisir di 2 sub-populasi yaitu di perbukitan bagian timur laut dan barat daya Kawasan Desa Wisata Bejiharjo.

Hasil penelitian memperoleh keragaman genetik yang bervariasi pada level spasial (antar sub-populasi) maupun temporal (antar fase hidup). Sub-populasi 1, yang seluruhnya terdiri dari fase reproduktif, memiliki variasi genetik yang rendah, dengan level *inbreeding* yang lebih tinggi, dan dijumpai banyak alel langka. Pada sub-populasi 2, fase reproduktif memiliki variasi genetik yang cukup tinggi, dengan sistem perkawinan cenderung *crossing*. Pada fase-fase selanjutnya, terjadi penurunan heterozigositas, penambahan jumlah alel langka, dan sistem perkawinan cenderung *inbreeding*. Pada fase semai bahkan dijumpai *missing allele*. Teramati indikasi *inbreeding* dan *random genetic drift*, yang dimungkinkan merupakan akibat sempitnya basis genetik dan ukuran populasi, dan banyaknya pembiakan vegetatif berupa trubusan dari perakaran (*root suckers*). Variasi genetik antar populasi yang rendah ($D_{ST} = 0,009$) mengindikasikan kekerabatan sangat erat antar sub-populasi. Proporsi keragaman genetik antar populasi terhadap total keragaman genetik (G_{ST}) sebesar 0,023. Dari total keragaman genetik ($H_T = 0,396$), hanya 2,3 % yang berasal dari keragaman antar populasi. Penghitungan rerata migrasi menunjukkan bahwa sekitar 10 hingga 11 individu bermigrasi per generasi ($N_e m = 10,62$). Sebagian besar alel langka dan *missing allele* pada kedua sub-populasi adalah alel "a". Permudaan alam cendana yang tumbuh pada dua sub-populasi di Kawasan Desa Wisata Bejiharjo ini memiliki kemampuan reproduksi generatif yang rendah.

Kata kunci: keragaman genetik, pola pewarisan, cendana, permudaan alam, Bejiharjo

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**GENETIC VARIATION OF NATURAL REGENERATION OF SANDALWOOD
GROWN IN BEJIHARJO, KARANGMOJO, GUNUNGKIDUL**

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Abstract

Recently sandalwood is categorized as Critically Endangered Species due to degradation and habitat loss in its natural population all over the world. Since 2004, it was stated to be Extinct in the Wild in its natural population in NTT; even the local government has had to re-introduce genetic materials from Gunungkidul, Yogyakarta for replanting program. Regarding to this, the occurrence of sandalwood in Gunungkidul District, Yogyakarta Province is found interesting since that site is not its natural habitat. Beside Wanagama that is located in Gading Sub-district, sandalwood is distributed also in some parts of Gunungkidul; such as in Bejiharjo Village, Karangmojo Sub-district. Research based on isozyme analyses and generative reproductive tests was conducted to estimate genetic variation and inheritance pattern from parents to its off-springs, on two sub-population of sandalwood natural regeneration grown in Bejiharjo Village.

Result showed various level of genetic variation both spatially and temporally. Sub-population 1, all consisted of individual in reproductive phase, was performing low genetic variation with higher level of inbreeding and more rare alleles. Reproductive phase in sub-population 2 performed higher genetic variation with the preference for outcrossing mating system. However, the next phases such as juvenile and seedling shown the decrement of heterozygosity, increment of rare alleles, and the alteration of mating system to be inbreeding. There was also indication of inbreeding and random genetic drift that was supposed to be the effects of small population, narrow genetic base, and the occurrence of vegetative propagation by root suckers. A low genetic variation between population ($D_{ST} = 0,009$) indicated closer inheritance. Proportion of genetic variation between population to total genetic variation (G_{ST}) is 0,023, implying that only 2,3% of total genetic variation ($H_T = 0,396$) was contributed by variation between population. Migration rate was 10 to 11 individual for each generation ($N_e m = 10,62$). Most of rare and missing allele in both of sub-population was allele "a". The reproductive fitness of sandalwood was very low.

Keywords: genetic variation, inheritance pattern, sandalwood, natural regeneration, Bejiharjo village

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