Study of Genetic Variation of Tusam (*Pinus merkusii* Jungh. et de Vriese) Natural Forest in Aceh and Plantation Forest in Java Using Isozyme Analysis Method

By :
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Abstract

Isozyme analysis was applied to five natural forest populations of tusam in Blangkejeren, Aceh, namely Arul Rengit, Uning, Rikit, Kendawi, and Uring. In the other side, the result of isozyme analysis was also observed as a comparison from four-plantation forest population in Java, namely Sumedang, Kebasen, Jember and seed orchard in Jember. Genetic variation was examined using seven polimorphic loci from 3 enzyme systems, namely *Esterase* (EST), *Glutamate oxaloacetate transaminase* (GOT), and *Shikimate dehydrogenase* (ShDH).

Research result showed that genetic variation in natural population was the highest (He=0,304) comparing to plantation forest (He=0,276) and seed orchard (He=0,266). In general, the rate of expected heterozigosity (He) was 0,290. It was indicated that tusam had a moderate genetic variation.

Result from cluster analyses of tusam was divided into two main clusters, namely natural and plantation forest population. Advance research of isozyme analysis for all natural forest population in Sumatra was needed to support tree breeding program and genetic conservation for this species in the future.

Studi Variasi Genetik Tusam (*Pinus merkusii* Jungh. et de Vriese) pada Hutan Alam di Aceh dan Hutan Tanaman di Jawa dengan Metode Analisis Isozim

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Intisari

Analisis isozim diterapkan pada lima populasi hutan alam tusam di Blangkejeren, Aceh, yaitu Arul Rengit, Uning, Rikit, Kendawi, dan Uring. Di samping itu sebagai bahan perbandingan, hasil analisis isozim pada empat populasi hutan tanaman di Jawa, yaitu Sumedang, Kebasen, Jember, serta kebun benih di Jember juga diamati. Variasi genetik diteliti dengan menggunakan tujuh lokus polimorfik dari tiga sistem enzim, yaitu *Esterase* (EST), *Glutamate oxaloacetate transaminase* (GOT), dan *Shikimate dehydrogenase* (ShDH).

Hasil penelitian menunjukkan bahwa variasi genetik pada hutan alam paling besar (He=0,304), dibandingkan dengan hutan tanaman (He=0,276) dan kebun benih (He=0,266). Secara umum, rerata Heterozigositas harapan (He) sebesar 0,290 menunjukkan keragaman genetik yang moderat.

Analisis kelompok yang dilakukan membagi tusam ke dalam dua kelompok utama, yaitu kelompok populasi hutan alam dan hutan tanaman, karena jarak genetik yang lebih lebar di antara hutan alam dengan hutan tanaman. Penelitian lanjutan analisis isozim pada seluruh populasi hutan alam di Sumatra diperlukan untuk mendukung program pemuliaan dan konservasi genetik jenis ini di masa mendatang.