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GENETIC CONSERVATION OF PINUS MERKUSII IN INDONESIA

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Abstract

INTRODUCTION

The development of successful forest management strategies requires an understanding of a wide array of topics such as the extent and diversity of forest ecosystems, the impact of forest management practices on biological diversity and tactics and strategies for gene conservation. In Indonesia, a genetic basis for rational conservation of *Pinus merkusii*, the only native pine species to this country, has not been available, although conservation efforts were initiated more than a decade ago. However, the method of dynamic conservation was carried by choosing some stands of different geographical characteristics in natural forests and a national park as well as through the establishment of seed orchard.

OBJECTIVES

In order to reveal the genetic variation of these pine species, a genetic inventory was carried out in three conservation stands. With reference to sustainable resource management, the efficiency of genetic conservation measures for this species could be greatly increased if supported by some knowledge on the geographic patterns of the genetic variation.

METHODOLOGY

Samples of trees were collected from two in situ conservation stands in the island of Sumatra and one ex situ conservation stand in the island of Java, i.e. a conservation stand in the Province of Aceh, a stand of the Kerinci-Seblat National Park in the Province of Jambi, and a seedling seed orchard in the Province of West Java, respectively. Genetic variation measures were determined using 8 isoenzyme gene loci belonging to five enzyme systems, i.e. GOT, PGM, SKDH, NDH and FDH.

RESULTS

A moderate level of genetic variation was found in the conservation stand in Aceh and the seedling seed orchard in West Java, while an absence of variation was observed in a population of Kerinci-Seblat National Park. The results of this study, especially for the non-variable population of Kerinci-Seblat, imply that the genetic conservation of this species should not only be based on information on the expression of genetically controlled adaptive phenotypic traits but requires also the results of surveys of genotypes at marker gene loci.