



NATURAL REGENERATION OF DAMAR (*AGATHIS LORANTHIFOLIA*) IN AGROFORESTRY AND PURE STANDS AT GUNUNG WALAT EDUCATIONAL FOREST

By

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Abstract

Natural regeneration of Damar in five different stand types, i.e. dense and moderate stocking of pure stands (Stand 1 and Stand 2, respectively) and three models of agroforestry in Gunung Walat Educational Forest (Model 1, Model 2 and Model 3), was investigated in this study with aims to determine with respect to stand types: 1) the extent of forest regeneration in terms of density (i.e. seedlings per hectare) and 2) preliminary spatial patterns of genetic structures of forest regeneration. Regeneration survey was carried out following line sampling technique using square plots of 2 m x 2 m and 20 m x 20 m for seedling and tree inventory, respectively. Preliminary isozyme analysis was carried out to reveal spatially genetic structures of regeneration using two enzyme systems, i.e. esterase (EST) and glutamate oxaloacetate transaminase (GOT). Results of regeneration survey showed that the highest damar seedling density was observed under Stand 2 (205,900 seedlings/ha) followed by Stand 1 (53,000 seedlings/ha), Agroforestry Model 1 (10,000 seedlings/ha), Agroforestry Model 2 (7,500 seedlings/ha), and Agroforestry Model 3 (8,200 seedlings/ha). Isozyme analysis revealed that banding patterns of EST has one polymorphic locus, while no polymorphisms were observed in GOT. Data analysis showed that there was no great difference in terms of spatial patterns of genetic structures based on EST among locations.

Keywords: *Damar, regeneration, stands density, isozyme, agroforestry*



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Introduction

Successful establishment and vigorous growth of the newly regenerated forest crop is critical to the long-term development and value of a forest stand. During the early stages of stand development, gradual temporal shifts in stand structures can occur, both in the overstory and understory community. Regeneration study is therefore important in providing valuable baseline information for managing forest stand dynamics. In this context, forest stand density might influence natural regeneration ability of many tree species by creating differences in micro-climate conditions and reproductive processes.

Reproduction system of a population consists of all elements of the genetic system related to propagation and the establishment of a new generation. Reproduction is not only required for population growth but also for the preservation of populations due to the limited life span of single plants.

The reproductive phase during the development of populations is of high interest from a genetic point of view since it is the phase of the highest dynamics of genetic structures in plant populations. Sexual reproduction results in the production of large numbers of genetically different progenies for most forest trees. This offers the potential for intense viability selection starting from the formation of zygotes. The potential for adaptive changes of genetic structures is highest during early developmental stages, i.e. seed development, germination, and the development of young seedlings.

The aim of regeneration study of Damar in pure and agroforestry stands was to determine with respect to stand types: 1) the extent of forest regeneration in terms of density (i.e. seedlings per hectare) and 2) preliminary spatial patterns of genetic structures of forest regeneration

Materials and Methods

Sampling procedure

Number of young seedlings having two leaves and putatively mother trees of Damar were observed in 5 forest stands with their different densities, namely: 1) one dense stocking of forest stand (370 trees/ha), 2) one moderate stocking of forest stand (219 trees/ha), 3) two moderately dense agroforestry stands (Model 1 and 2), and 4) one highly dense agroforestry stand (Model 3). Vegetation analysis was carried out to

estimate densities of seedlings and Damar trees. Techniques of regeneration survey was based on Kusmana (1997) using plotted line method, in which 35 square plots of 20 m x 20 m and 2 m x 2 m were made for trees and seedlings, respectively. Composite samples of young seedlings having at least two leaves of each stand type were uprooted and raised in green house for isozyme analysis.

Isozyme analysis

Young leaves from 20 seedlings from each stand type were used as material for isozym analysis. Two enzyme systems were analyzed, namely: 1) esterase (EST) and 2) glutamate oxaloacetate transaminase (GOT). The samples were run in horizontal starch gel electrophoresis following Ashton System (Ashton and Braden, 1961) with little modifications.

Result and Discussion

Vegetation analysis

Approximate numbers of seedlings and trees in each stand type are presented in Table 1. It is very clear that land use change has an impact on natural regeneration of Damar, in which reduction of mother trees has resulted in low natural regeneration rate following an exponential trend as presented in Figure 1.

Table 1 Result of vegetation analysis of Damar in pure stands and agroforestry stands

Type of Stands	Approx. density (number/ha)	
	Seedlings	Trees
Dense stocking of Damar stand	205,900	369
Moderate stocking of Damar stand	53,000	219
Agroforestry stand - Model 1 (open)	10,000	125
Agroforestry stand - Model 2 (moderate)	7,500	125
Agroforestry stand - Model 3 (closed)	8,200	82

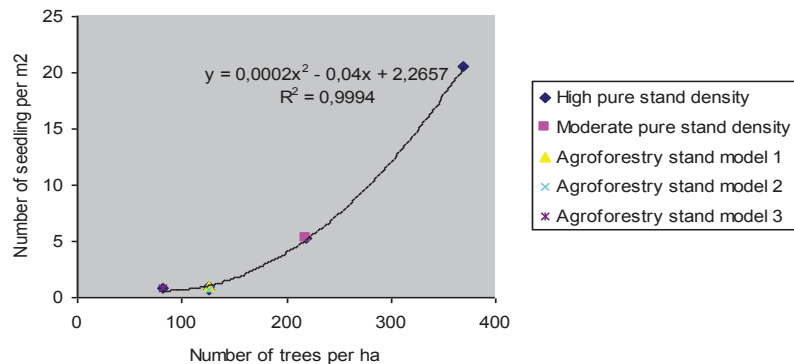


Figure 1 A trend in seedling number (per m²) as a function of mother trees number per ha

Microclimate is an important factor influencing seed germination and seedling development. High humidity, relatively low temperature as well as low to moderate sun light are optimum condition for seed germination and seedling development. In this case, it was obviously found that high density of pure Damar stands favors regeneration. On the other hand, agroforestry which is a mixture of less Damar trees and agricultural crops allow lights to penetrate more. This might cause unfavorable conditions to seed germination and seedling growth. Some wilted seedlings were observed in some plots during field observation. In addition, it is found that intensive treatments in agroforestry remove not only unwanted weeds but also natural regeneration of Damar.

Isozyme analysis

Polymorphisms were observed in esterase enzyme system, while GOT showed monomorphic banding patterns. There were no great differences in terms of isozyme band types with respects to stand types as shown in Figure 2, 3, 4 and .5. All stand types share almost similar distribution of esterase band types suggesting extensive gene flows between stand types and possible random mating among effective reproductive trees in all stands.

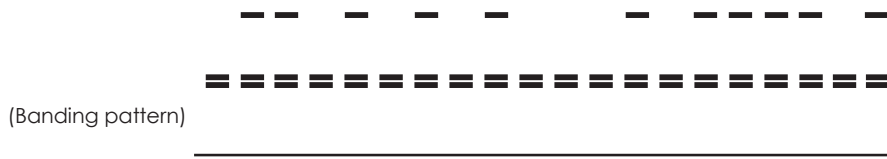


Figure 2 Esterase banding patterns in seedlings of high density of Damar stand

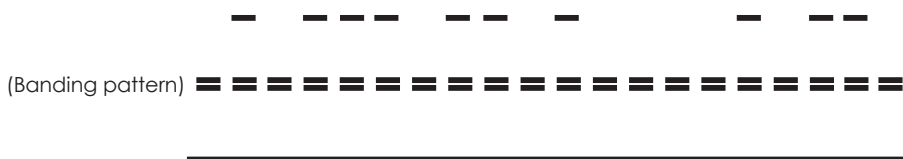


Figure 3 Esterase banding patterns in seedlings of moderate density of Damar stand



Figure .4 Esterase banding patterns in seedlings of agroforestry model 1 and 2

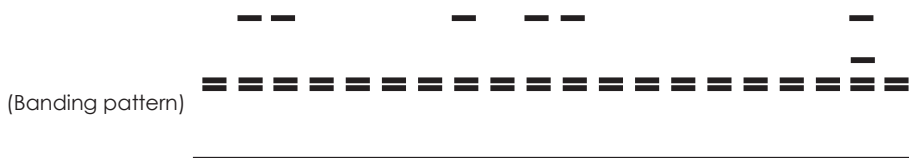


Figure 5 Esterase banding patterns in seedlings of agroforestry model 3

Detailed knowledge of the mating system is necessary for the understanding of the distribution of genetic variation within and among individuals as well as gene flow within and between stands (Boshier et al., 1995). In addition, understanding the mating system may also explain spatial and temporal patterns of genetic structure.

In wind-pollinated species such as Damar, some possible events could occur with regard to individual effective pollen clouds. Firstly, pollen of every individual might be expected to be uniformly distributed throughout the population pollen cloud, resulting in uniform distribution of effective individual pollen clouds in the population, as was for example, found in *Picea abies* (Finkeldey, 1995). Secondly, there is a variation in the pollen density released by individuals resulting in spatial heterogeneity in pollen allele frequencies for the population, for example in *P. pungens* (Gibson and Hamrick, 1991).

Conclusion

Natural regeneration rates of Damar were greatly influenced by stand density. On the other hand, spatial patterns of genetic structures were not significantly affected, due probably to extensive gene flows through pollens and relatively big effective population size of Damar in Gunung Walat Educational Forest.

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