GENETIC VARIATION OF SENGON (*Paraserianthes falcataria*), AN IMPORTANT TREE SPECIES FOR AGROFORESTRY, IN WEST JAVA

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Introduction

The important role of Sengon (*P. falcataria*) in agroforestry system, which is mostly found in local community forests and its susceptibility to insect pest, has led to development of improvement program of this species by both government institution and companies. The program was started with selection of plus trees in both natural stands and plantations throughout Indonesia's islands, followed by some testing programs, i.e. provenances and progeny testing, as well as establishment of seed orchards in several locations in Java.

Any tree improvement program will need broad genetic diversity of the traits as basis for selection. Later examination on sengon genetic diversity captured in a trial plantation in West Java using isozyme (Siregar et al., 1998) gave different view as compared to findings by Seido et al. (1993). Highest genetic diversity was found from Kediri provenance of Java Island, higher than Wamena natural stands of Irian Jaya. The magnitude (He = 0.226) is comparable to other tropical species in a natural population. Other populations in this study also have on the average higher estimates of heterozygosities (He = 0.137) than previously reported. This discrepancy with previous study is probably due to different enzyme systems used and different sampling strategy (Siregar et al., 1998). This discrepancy also underlines the need for further clarification on the extent of genetic variation and population genetic structure of sengon populations in Java.

This study aimed at investigating the extent of genetic diversity of sengon populations in West Java, by examining half-sib progenies of several plus trees in several locations using isozymes.

Methodology

Seeds from 27 selected plus trees, which were located in 6 districts of West Java were collected and germinated in the greenhouse to form 27 families. The list of locations and number of plus trees is shown in Table 1. Before germinated, seeds were treated with boiled water and been immersed in it for 24 hours. After seedling reach the age of about a month leaf sample was taken for laboratory analysis of isozymes from randomly selected 6 seedling individuals of each family. Starch gel electrophoresis was done according to protocol developed by Soltis and Soltis (1989), followed by assay of 2 enzyme systems, i.e. EST (*esterase*) and PER (*peroxidase*). Detected isozyme band morphs for genetic variation were then recorded and analyzed using BIOSYS-1 and GSED programs.

Table 1. List of selected plus trees grown in six districts of West Java province.

District Name	Number of Plus Tree	Name Code
Cianjur	4	CNJ.008, CNJ.009, CNJ.010, CNJ.013
Garut	4	GRT.039, GRT.041, GRT.042, GRT.043
Kuningan	4	KUN.064, KUN.065, KUN.066, KUN.068
Subang	8	SBG.020, SBG.022, SBG.023, SBG.025, SBG.030, SBG.031, SBG.032, SBG.033
Sukabumi	4	SKB.058, SKB.059, SKB.060, SKB.061
Tasikmalaya	3	TSK.050, TSK.051, TSK.052

Results and Discussion

Seed Germination and Seedling Survival Rate

From each plus tree a number of 100 seeds were germinated. Germination percentage as well as survival rate of each family are shown in Table 2. Analysis of variance on both traits showed that differences on germination percentage was significantly high ($P>0.0001$), whereas survival rates were not. For the two traits, which could be considered as adaptive traits, Tasikmalaya population occupied the highest rank. It is interesting to note that four populations, namely Sukabumi and Cianjur versus Kuningan and Subang, were exchanged places in the ranking of the two traits. Population Sukabumi-Cianjur- which had higher germination percentage, turned out to lower survival rates than Kuningan-Subang when germinated in Bogor.

On the average, germination and survival rate across the whole populations were 73.1 $\pm$ 9.1%, and 37 $\pm$ 11.7 %, respectively. Variation in germination percentage within population was always lower than amongst population, whereas for the survival of two populations- namely Tasikmalaya and Cianjur, population variation within population was higher than amongst population variation.

Table 2. Percentage of germination and survival rate of 27 sengon families from 6 locations in West Java studied.

Location	Germination (%)	Survival (%)
Tasikmalaya	82.0 a $\pm$ 2.7	49.7 a $\pm$ 25.9
Sukabumi	80.8 a $\pm$ 6.9	34.9 abc $\pm$ 4.6
Cianjur	80.0 a $\pm$ 6.4	31.5 bc $\pm$ 12.0
Garut	76.3 a $\pm$ 9.0	25.9 c $\pm$ 4.3
Kuningan	65.5 b $\pm$ 4.7	43.5 ab $\pm$ 8.4
Subang	64.6 b $\pm$ 3.3	38.1 abc $\pm$ 4.8

Isozyme Genetic Variation

The enzyme assay for PER revealed 4 loci, i.e. PER A. PER B, PER C and PER D, of which two are polymorphic, i.e. PER C and PER D. Loci A, B and C moved anodally, while locus D moved towards cathode. From these loci, there were 11 combinations of band morphs generated, with the highest variation of Sukabumi population. Meanwhile enzyme EST detected 3 polymorphic loci, namely EST A, EST B and EST C, of which locus C only moved cathodally. Most polymorphic loci have 2 alleles, except EST A, which has 3 alleles. From EST isozyme, 17 combinations of bandmorphs were detected, of which Sukabumi population again has highest variation. Summary of isozyme data analysis is given in Table 3, together with other genetic diversity estimates.

Genetic variability

Measures of genetic variability of six investigated populations were estimated based on their progenies; the results are presented in Table 3. Computed average H_e for whole population is 0.217, which is in accordance with previous finding (Siregar et al. 1998) and comparable to estimates of other tropical tree species.

Table 3. Genetic variability measures of progenies in the investigated populations of *P. falcataria* based on a survey of 5 enzyme gene loci.

Population	Mean sample size per locus	Genetic Multiplicity		Allelic Diversity	Gametic Diversity	Heterozygosity	
	Size (N)	*A/L*	*P*	ν	ν_{gam}	H_a	$H_e=\delta_T$
Sukabumi	18.0	2.2	100	1.484	7.596	0.421	0.338
Kuningan	19.2	1.8	60	1.224	3.133	0.216	0.187
Subang	38.4	1.4	40	1.122	1.969	0.111	0.110
Cianjur	22.6	1.8	60	1.259	3.708	0.283	0.210
Garut	16.0	1.6	60	1.314	4.683	0.257	0.244
Tasikmalaya	13.4	1.6	60	1.261	3.636	0.240	0.214

Note:
A/L = Number of allele per locus
P = Percentage of polymorphic loci (among 5 loci studied)
δ_T = Total population differentiation

In general, the population of Sukabumi had higher variability than that of others. In this case, population Subang showed the lowest variability as shown by all measures. It is interesting to note that genetic diversity estimates also gave similar view with quantitative measures, i.e. germination and survival rates, of which Kuningan-Subang clustered together with lower diversity. Except Sukabumi, the other 3 remaining populations have relatively higher diversity estimates.

Cluster analysis

Patterns of clustering between the two measures are similar in which four clusters were identified very clearly as shown in Figure 1. Populations of Sukabumi (SKB), Subang (SUB) and Tasikmalaya (TSK) separated individually, while populations of Kuningan (KUN), Cianjur (CNJ) and Garut grouped together.

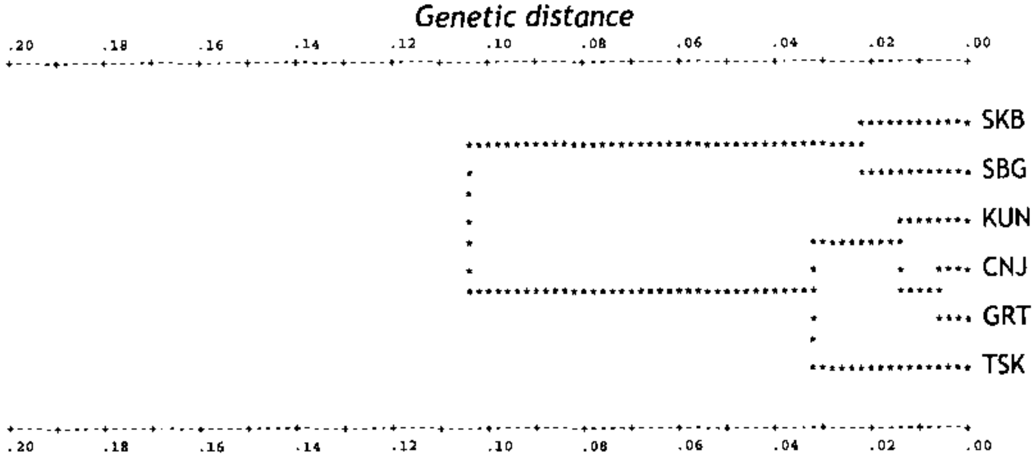

Figure 1. Dendrogram of genetic distances as estimated according to Nei (1972)

Comparisons between quantitative measures and estimation from molecular data pointed out toward similar Conclusionsss, i.e. Tasikmalaya population were differentiated from the rest of populations. Similar indirect correlation between isozyme variation and quantitative variation was also observed in other study on mahoni (unpublished data). Recently, debates on possible correlation between adaptive traits and markers, also whether quantitative measures is better in predicting differentiation at QTL loci than estimation from markers, indicated that Fst estimates from markers can work better (McKay and Latta, 2002). In this paper survival rate in nursery can be regarded as adaptive trait, albeit it is rather early. Similarity in Conclusionss between the two approaches supports the above point of view.

High genetic diversity observed from this study indicates that sengon population in West Java must have been introduced since long time ago, and therefore, it is arguable that those populations are descended from one single ancestor in Bogor Botanical Garden. Previous study indicated that West Java population is relatively closer to Wamena population, Irian Jaya (Siregar et al., 1998).

Conclusions

These findings should be very valuable for programs on conservation as well as tree improvement. For example, for conservation purposes, when only limited fund is available we can choose only three populations instead of six, since those six populations are basically derived from three ancestors. For breeding program we can choose populations with highest average on quantitative traits and at the same time have high genetic variation as base for selection. Such populations in this case are Tasikmalaya and Sukabumi populations.

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References

McKay, J.K. and R.G. Latta. 2002. Adaptive population divergence: markers, QTL and traits. Trends Ecol. Evol. 17(6):285-291.

Nei, M. 1972. Genetic distance between populations. Amer. Nat. 106:283-292.

Siregar, U.J., M. Basyuni, E. Sudarmonowati and D. Iriantono. 1998. Genetic diversity in a *Paraserianthes falcataria* provenance trial in Parung Panjang, Bogor, Indonesia. Proc. Third National Congress on Genetics, 18-19 November 1998, UKM, Bangi, Malaysia. p114-117.

Seido, K, AYPBC Widyatmoko and G. Nursinggih. 1993. Preliminary analysis of isozyme variation of *Paraserianthes falcataria* in Indonesia. Proc. Yogjakarta Workshop, 20-23 September 1993.

Soltis, D.E. and P.S. Soltis. 1989. Isozymes in plant biology, Vol. 4. Dioscorides Press. Portland, Oregon. 258p.