INTRASPECIFIC VARIATION ON EARLY GROWTH OF *Neolamarckia cadamba* MIQ. IN PROVENANCE-PROGENY TESTS IN WEST JAVA PROVINCE, INDONESIA

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ABSTRACT

Genetic parameters on early growth of *Neolamarckia cadamba*, an indigenous species with potential as a source of wood timber, were estimated in open-pollinated provenance-progeny tests at two sites in West Java Province, Indonesia. The experiment was conducted using randomized complete block design with 12 provenances, 105 families and 5 replications of 4-tree row plots. Total height and root collar diameter were measured at the age of 18 months growth. Significant differences among the provenances and families within provenances were observed for height and collar diameter at all sites, except for the collar diameter of among provenances at Parungpanjang site. In general, Garut (GSJ) provenance performed better growth at the two sites than Kualakencana (KKP) and Nusa Kambangan (NKJ) provenances. The evaluation of component of variance at the two sites showed that the provenance effects (ranging from 0.5 to 1.7%) contributed more to total variance than family within provenance effects (ranging from 0.4 to 0.6%). Genetic correlations between height and collar diameter were weak to moderate. Heritability was low for all traits at Limbangan, while at Parungpanjang, the heritability was moderate. Estimation of genetic gain for height and diameter by proportional selected family 0.30 was 0.13 and 0.18 for Limbangan and 0.31 and 0.16 for Parungpanjang. Heritability measurement should be sustained to reach stable value. Stable heritability combined with selection of family and selection within family will improve genetic gain.

Keywords: Genetic correlation, genetic parameter, heritability, *Neolamarckia cadamba*, progeny, provenance, selection

INTRODUCTION

Neolamarckia cadamba (Roxb.) Miq. commonly known as white jabon is a native fast growing tree species playing an important role in both commercial and traditional farming systems in several sites in Indonesia (Krisnawati *et al.* 2011; Kallio *et al*. 2011). This species produces timber for pulp and light construction (Soerianegara & Lemmens 1993). Various parts of the plant also have many bioactive substances, such as antioxidant, hypoglycemic substance, hypolipidemic substance, antibacterial substance, antimicrobial substance, etc. (Acharyya *et al.* 2011; Xu *et al.* 2011; Mishra & Siddique 2011). *N. cadamba* has a very extensive natural distribution extending from India, Nepal, Burma, Sri Lanka and Malaysia across Indonesia, Philippines and Papua New Guinea (Lamprecht 1989). In Indonesia, white jabon is distributed almost across the entire country (Soerianegara & Lemmens 1993). Evolutionary theory predicts that species with large population sizes, broad geographic ranges and varying climate condition will have large inter and intraspecific variation (Rawat & Bakshi 2011). Population within plant species with wider geographic ranges has higher allozyme variation and the widely distributed species have more overall allozyme variation (Hamrick & Godt 1989). Some studies showed that genetic variation of *N. cadamba* ha been detected among provenances for quantitative

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seed and seedling morpho-physiological parameters (Sudrajat 2016), as well as among natural populations to AFLP loci (Sudrajat *et al*. 2015). Given its wide ecological amplitude and a large amount of genetic variation, *N. cadamba* is a promising species for tree improvement program to increase its productivity and quality.

Tree improvement program of *N. cadamba* is not yet running well, so that large cultivation activities of this species is not yet supported by high quality seed. The main seed sources for all kinds of plantation activities are from unknown origin, which are collected from unimproved seed sources. However, the initiation of the tree improvement program of *N. cadamba* is very important as a basic for high qualified seed procurement. The success of tree improvement efforts depends upon many factors including genetic variation, heritability of desired parameters and potential gains derived (Nebgen & Lowe 1982; Borralho 2001), so it is very important to use the genetic material from wide natural distribution of the species to establish a breeding population. In Indonesia, establishment of breeding population with open pollinated progenies of plus trees is widely applied as the first step towards tree improvement for fast growing species (Hashimoto *et al.* 1996; Soeseno 1988). It might be the most reasonable and practical way to meet an immediate demand for genetically improved seed to be used in reforestation programs in Indonesia. Traditionally, forest genetic tests have been conducted sequentially with successive species, provenance and progeny trials. In practice, however, there is strong economic pressure to reduce the testing interval between these stages in a traditional tree improvement program. The use of combined provenance-progeny test has been advocated to reduce the testing interval between provenance and progeny stages (Zheng *et al.* 1994; Sebbenn *et al*. 2003; Finkeldey 2005). It may be extended to combine provenance testing, progeny testing, seed production and *ex situ* conservation of *N. cadamba* in a single trial.

The study investigated intraspecific variation for early growth parameters in 105 families from 12 *N. cadamba* provenances originated from seven Indonesian islands. The objectives of this research were: i) to examine the distribution of genetic variation among and within provenances and families within provenances and ii) to determine the extent of genetic control for growth parameters in the form of provenance-progeny test at two different locations in West Java Province, Indonesia.

MATERIALS AND METHODS

Open-pollinated seeds of 105 families of *N. cadamba* were collected from 12 natural populations distributed in Sumatera, Java, Nusa Kambangan, Kalimantan/Borneo, Celebes, Sumbawa and Papua (Table 1, Fig. 1) from March to July 2012. The sampled trees were phenotypically average or above average with respect to stem diameter (diameter at breast height/DBH) and total height compared with surrounding trees in the population. The distance among mother trees within population was kept at a minimum of 100 m to minimize relation between seed lots. Seeds were collected by climbing the tree samples. Every seed lot was separated for each sample tree and information about location and number of samples was noted at every seed lot. The information was kept until the seed reached nursery stage to establish the provenance-progeny trials.

Seeds were sown in plastic pot filled with media consisted of sand, compost and charcoal (5:3:1, by volume). Prior to sowing, the potting mixture was treated with 0.2% a fungicide to avoid any chances of fungus infection attacking newly germinated seedlings. Pots were water-sprayed with fine sprayer to keep them wet and were maintained in greenhouse. Young four-leaf seedlings were transplanted on polythene bags (10 cm in diameter and 15 cm in height), containing media consisted of top soil, sand and compost in a ratio of 2:1:1 (volume) and were set up in nursery. Seedlings were grown at 50% light intensity using shade net for 3 months. One month afterwards the seedlings were exposed at open area for hardening off. Seedlings were irrigated based on the operational regime for the nursery. Forty vigorous and healthy seedlings were selected from each family to be planted at two trial sites.

The experiment was set up in two sites in West Java Province, i.e. site I in Limbangan, Garut (07°02'23" S, 108°00'43" E, 520 m altitude) and site II in Parungpanjang, Bogor (06°20'42" S, 106°06'15" E, 52 m altitude).

Table 1 Provenance detail of *N. cadamba* and their geographical locations

Locality	Latitude	Longitude	Altitude	Number of families (tree)	Range of stem diameter of tree samples (cm)	Range of height of tree samples (m)	Climate type (Schmidt and Fergusson)	Type of the provenances (populations)
Rimbo Panti Nature Reverse, Sumatera (RPS)	00°19' U	100°05' E	294	2	36-75	22-30	A	Primary rain forest along riverbanks.
Kampar, Riau, Sumatera (KRS)	00°18' U	100°57' E	50	14	37-80	23-33	A	Secondary forest along riverbanks, periodically flooded sites.
Ogan Komering Ilir, Sumatera (OKS)	03°12' S	104°51' E	23	11	37-77	16-31	B	Secondary forest along riverbanks, periodically flooded sites.
Garut Selatan, Java (GSJ)	07°26' S	107°42' E	628	8	30-59	16-32	B	Secondary forest in the highland, dry sloping sites.
Nusa Kambangan nature Reverse (NKJ)	07°43' S	108°55' E	40	7	59-102	22-35	D	Primary rain forest along riverbanks.
Alas Purwo National Park, Jawa (APJ)	08°38' S	114°21' E	33	11	40-91	26-30	D-E	Primary rainforest, along riverbanks.
Batulicin , Kalimantan (BLB)	03°19' S	115°41' E	47	4	47-65	33-35	B	Secondary forests along riverbanks, periodically flooded sites.
Kapuas Tengah, Kalimantan (KTB)	01°00' S	114°28' E	147	2	57-95	33-35	A	Secondary forests along riverbanks, periodically flooded sites.
Parangloe, Gowa, Sulawesi (PGC)	05°14' S	119°35' E	119	15	38-62	29-32	C	Secondary forest along riverbanks and some tree samples are growth in dry sloping sites.
Pomalaa, Sulawesi (PKC)	04°03' S	121°39' E	210	22	41-78	28-34	C	Secondary forest along riverbanks and some tree samples are growth in dry sloping sites.
Batuhijau, Sumbawa (BHS)	08°58' S	116°48' E	53	8	47-82	30-36	D	Secondary forest along riverbanks.
Kuala Kencana, Timika, Papua (KKP)	04°24' S	136°52' T	107	1	53	31	A	Secondary forests along riverbanks.

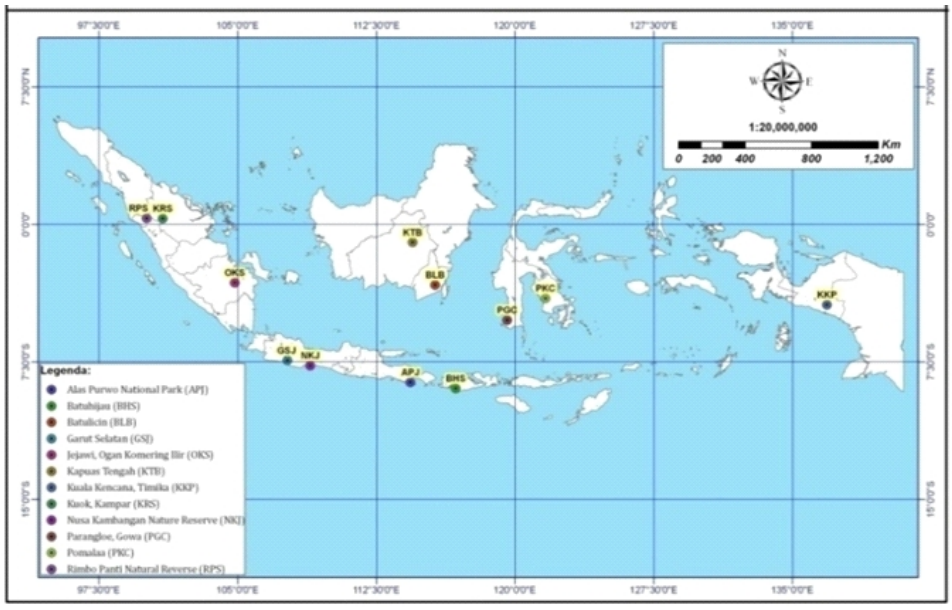

Figure 1 Geographic distribution of 12 populations was tested

Average annual rainfall and temperature were 2,580 mm and 27 °C at site I, respectively and 2,440 mm and 28 °C at site II, respectively. Soil at site I and site II had low level of N, P, K and C-organic with pH of 5.1 and 4.2, respectively. Site I was an open private land with slope ranged from 5 to 15%, having high incidence of domestic animal and was planted with irregular agricultural crops in several parts of area. Site II was an even area within state forest land covered with dense weed, that grew rapidly even after cleaning. The locations were selected based on several reasons. Limbangan was selected to represent medium to high level of elevated land where many *N. cadamba* plantations were cultivated as dominant species in forest community areas, such as in Garut District, West Java Province. Parungpanjang was selected to represent the common site condition of forest plantation industries that are generally established in podsolic soil associated with low pH and low soil nutrients.

Four-month-old seedlings were planted at the fields in February 2013 (planting hole size 40 x 40 x 40 cm) administered with 3 kg manure per seedling as basic fertilizer. The spacing between planting hole was 3 x 3 m. The experiment was conducted in randomized complete block design (RCBD) with 5 replications of 4-tree row plots (Fig. 2). Within two months after planting, 100 g of NPK fertilizer (15:15:15) was applied to each

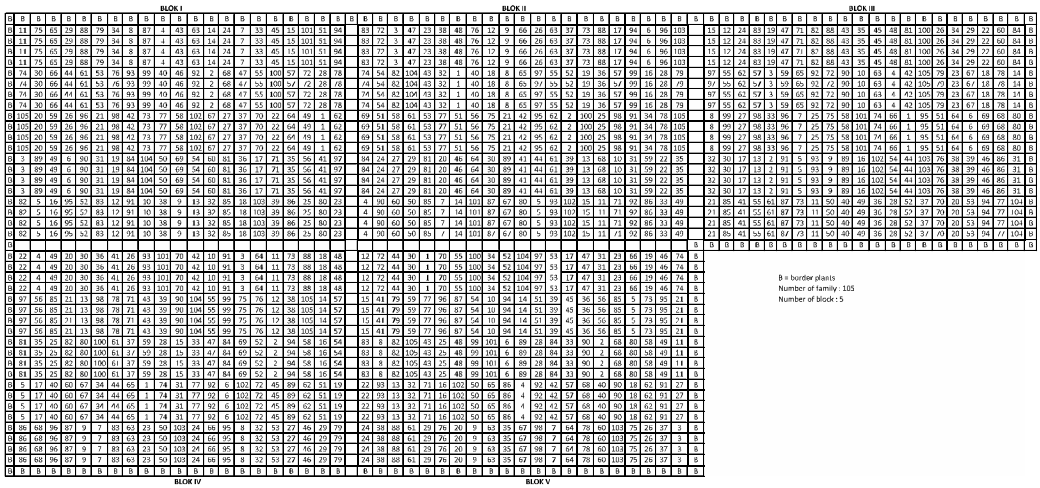

Figure 2 Design of planting test of *N. cadamba* at Parungpanjang, Bogor and Limbangan, Garut

plant. Weed competition was kept to a minimum by manual weeding. All trees in each plot constituted the measuring unit in all replications. The first assessment was carried out at the age of 6 months and subsequently after 12 months. In this paper, results of 16 months growth (4 months in nursery + 12 months in field) planting have been described. The parameters assessed are height (m), collar diameter (cm) and survival percentage.

Data Analysis

The data were analyzed for each site, to determine the provenance and family effects using two-way analysis of variance (ANOVA). Before performing the analysis, data were examined for conformity to normal distribution and homogeneity of the variance assumptions. ANOVA for all parameters was conducted using the following statistical model (Falconer & Mackay 1996; Sebbenn *et al*. 2003):

$$Yijkl = \mu + Ri + Pj + F(P)k(j) + RPij + RF(P)ik(j) + El(ijk)$$

An extra term (across site effect) was added to the model to investigate the significance of the difference of parameters across site.

Thus, the model used was:

$$Yijkl = \mu + Si + Pj + F(P)k(j) + SPij + SF(P)ik(j) + El(ijk)$$

where :

$Yijkl$ = the measurement on the l^{th} individual of the k^{th} family from the j^{th} provenance in the i^{th} replication

μ = the overall mean

Ri = the effect of i^{th} replication ($i = 1, 2, 3, .., n$)

Si = the effect of i^{th} site ($i = 1, 2$)

Pj = the effect of j^{th} provenance ($j = 1, 2, 3, \ldots, n$)

$F(P)k(j)$ = the effect of k^{th} family in j^{th} provenance ($k = 1, 2, 3, \ldots, n$)

$RPij$ = the interaction effect between I^{th} replications and j^{th} provenances

$RF(P)ik(j)$ = the interaction between i^{th} replications and k^{th} family within j^{th} provenance

$El(ijk)$ = the residual.

The SAS PROC GLM was used to obtain the coefficients of the expected mean squares for the calculation of heritability. The components of variance were calculated using VARCOMP PROC from SAS statistical program (Cary 1999).

Heritability was estimated from the variance components as described in Falconer and Mackay (1996). Narrow sense individual (h^2i) and family heritability (h^2f) for each parameter were estimated using equations:

$$h^2i = \frac{\sigma^2A}{\sigma^2U} = \frac{4\sigma^2F(P)}{\sigma^2U}\ ;\quad h^2f = \frac{\sigma^2F(P)}{\sigma^2fm}$$

where:

σ^2A = additive genetic variance

$4\sigma^2F(P)$ = between-family-within-provenance variance component

σ^2U = phenotypic variance calculated as $\sigma^2U = \sigma^2F(P) + \sigma^2RF(P) + \sigma^2e$,

where:

$\sigma^2F(P)$ = variance due to interaction between replication and family-within-provenance (experimental error)

σ^2e = variance among individual trees within family (sampling error)

σ^2fm = family phenotypic variance, calculated as $\sigma^2fm = \sigma^2F(P) + (k_2/k_3)\,\sigma^2RF(P) + (1/k_3)\,\sigma^2e$,

where:

k_2 and k_3 = respectively, coefficients for $\sigma^2RF(P)$ $\sigma^2F(P)$ and in the expected mean squares.

Phenotypic ($R_{p(xy)}$) and genetic correlations ($R_{g(xy)}$) were estimated from the component of variance and covariance (Falconer 1981) substituted into the standard equation for the product moment correlation coefficient:

$$R_{P(xy)} = \frac{COV_{P(xy)}}{\sqrt{\sigma^2{}_{P(x)}\sigma^2{}_{P(y)}}}\ ;\ R_{g(xy)} = \frac{COV_{f(xy)}}{\sqrt{\sigma^2{}_{f(x)}\sigma^2{}_{f(y)}}}$$

where:

$\sigma^2{}_{P(x)}$ and $\sigma^2{}_{f(x)}$ = components of variance of phenotypic and genotypic products of x parameter

$\sigma^2{}_{P(y)}$ and $\sigma^2{}_{f(y)}$ = components of variance of phenotypic and genotypic products of y parameter

$COV_{P(xy)}$ and $COV_{f(xy)}$ = components of covariance of phenotypic and genotypic products of x and y parameters, respectively.

Genetic gain (Δ) was calculated by Falconer's (1981) formula:

$\Delta G = h^2S = h^2\,I\,\sigma_p$

where:

I = intensity of selection taken from Zobel and Talbert (1984) with proportion selected 0.70, 0.50 and 0.30

σ_p = phenotypic standard deviation.

RESULTS AND DISCUSSION

Growth Rate and Genetic Variation

Significant differences were observed among provenances and among families within provenances for all parameters at Limbangan and Parungpanjang, except for collar diameter of among provenances at Parungpanjang (Table 2). At the Limbangan, the KKP provenance attained a maximum height followed by GSJ, PKC, PGC and NKJ provenances. Maximum collar diameter was recorded in GSJ provenance followed by KKP, PGC, RPS and NKJ. Field survival was recorded maximum in KKP provenance, followed by KRS, PGS, RPS and GSJ. The KKP provenance had the highest height growth and presented approximately 44% faster than the slowest growth provenance. For root collar diameter, the GSJ provenance was higher and presented about 59% higher growth than the least growth provenance. The range of variation at family level of irrespective provenances was large in respect to height and root collar diameter (Table 3) as proven by values of coefficient of variation. Over all KKP, GSJ and PGC provenances were better than others.

The range of family variation (irrespective provenance) at Parungpanjang was high in all growth parameters. Maximum height was recorded in GSJ provenance, which was closely followed by APJ, NKJ, KKP and BHS provenances. Maximum root collar diameter was attained by BHS provenance, however, it was at par with PKC, PGC and APJ provenances. GSJ provenance had the highest growth for height and presented about 17% higher growth than the least growth provenance. For root collar diameter, differences among provenances means were not statistically significant and the best provenance was only 10% larger than the least provenance. Ten provenances showed field survival more than 70%, except APJ and BLB provenances. Based on the values of CV and range of the family means, a wide range of variability was observed in respect of growth parameters (Table 3).

The height and collar diameter growth of *N. cadamba* were better at Limbangan than those at Parungpanjang. The plant growth at Parungpanjang was affected by heavy growth of weeds causing suppression and competition for nutrition and growth space. The factor might have led to slow growth of the plant at the site. On the other hand, survival percentage was higher at Parungpanjang. Survival percentage at Limbangan was reduced by disturbance of domestic animal and irregular agricultural crops in several parts of the area covering the main plants in early growth of seedlings. In general, growth performance in both sites is better than the other progeny test of *N. cadamba* conducted in Wonogiri, Central Java Province (Setyadi *et al.* 2013).

Differences in height and root collar diameter growth were greater among families than among provenances. At Limbangan, the best growing family exceeded the least growing family by 243% and 234% for height and root collar diameter,

Table 2 Mean square for height and collar diameter in provenance-progeny tests of *N. cadamba* at two sites in West Java Province, Indonesia

Source of variation	Degrees of freedom	Mean square					
		Limbangan, Garut			Parungpanjang, Bogor		
		Height (m)	Collar diameter (cm)	Survival (%)	Height (m)	Collar diameter (cm)	Survival (%)
Blocks	4	61.281 **	221.693 **	9,310.667ns	8.604 **	35.499 **	25,694.552**
Provenance	11	3.858 **	16.933**	3,949.994ns	0.833 *	1.6748 ns	2,902.045ns
Fam (Prov)	93	2.165 **	8.051**	2,018.897ns	0.864 **	3.428**	2,167.913ns
Block*Prov	44	1.859 **	6.208*	1,860.280ns	1.196 **	4.758**	2,799.698ns
Block*Fam(Prov)	359	1.973 **	7.498 **	2,644.036ns	1.053 **	3.897**	2,841.399ns
Error	1,044	0.740	3.353	2,153.968	0.413	1.681	1,862.556

Notes: ** = significant at $p<0.01$
* = significant at $p<0.05$
ns = not significant

Table 3 Growth performance (mean ± standard deviation) of various provenances in provenance-progeny tests of *N. cadamba* at two sites in West Java Province, Indonesia (number in parentheses are ranks)

Provenance	Limbangan, Garut			Parungpanjang, Bogor		
	Height (m)	Collar diameter (cm)	Survival (%)	Height (m)	Collar diameter (cm)	Survival (%)
RPS	2.34 ± 1.20 (8)	4.78 ± 2.77 (4)	62.5 (4)	1.97 ± 0.58 (12)	4.06 ± 1.59 (7)	77.5 (2)
KRS	2.14 ± 1.12 (11)	3.92 ± 2.26 (11)	63.9 (2)	2.08 ± 0.82 (8)	3.93 ± 1.66 (10)	75.0 (6)
OKS	2.46 ± 1.48 (6)	4.45 ± 2.53 (8)	58.6 (8)	2.04 ± 0.78 (11)	3.94 ± 1.54 (9)	70.9 (9)
GSJ	2.67 ± 1.47 (2)	5.35 ± 2.75 (1)	61.9 (5)	2.31 ± 0.79 (1)	4.11 ± 1.26 (5)	71.9 (8)
NKJ	2.47 ± 1.34 (5)	4.68 ± 2.59 (5)	50.7 (11)	2.26 ± 0.99 (3)	4.09 ± 1.73 (6)	70.7 (10)
APJ	2.17 ± 1.10 (9)	4.08 ± 2.31 (10)	53.2 (10)	2.28 ± 0.98 (2)	4.13 ± 1.78 (4)	68.2 (11)
BLB	2.17 ± 1.16(10)	4.27 ± 2.41 (9)	58.8 (7)	2.12 ± 0.78 (6)	3.78 ± 1.55 (12)	57.5 (12)
KTB	1.89 ± 1.30(12)	3.35 ± 2.45 (12)	60.2 (6)	2.05 ± 0.40 (10)	3.86 ± 1.22 (11)	73.8 (7)
PGC	2.57 ± 1.30 (4)	4.87 ± 2.61 (3)	63.7 (3)	2.06 ± 0.81 (9)	4.14 ± 1.74 (3)	76.4 (3)
PKC	2.58 ± 0.89 (3)	4.56 ± 2.72 (6)	47.5 (12)	2.11 ± 0.82 (7)	4.17 ± 1.67 (2)	78.9 (1)
BHS	2.42 ± 0.75 (7)	4.49 ± 2.07 (7)	53.8 (9)	2.21 ± 0.92 (5)	4.19 ± 1.78 (1)	76.3 (4)
KKP	2.73 ± 0.95 (1)	5.15 ± 2.06 (2)	75.0 (1)	2.25 ± 0.71 (4)	4.00 ± 1.38 (8)	75.0 (5)
Family range	1.40-4.81	2.10-7.03	35-90	1.38-2.97	2.50-5.56	40-100
Mean	2.42	4.49	59.1	2.14	4.08	72.7
CV (%)	35.50	40.76		30.06	31.76	

Notes: RPS = Rimbopanti Nature Reserve-Sumatera, KRS = Kampar-Riau-Sumatera, OKS = Ogan Komering Ilir-Sumatera, GSJ = Garut Selatan-Java, NKJ = Nusa Kambangan, APJ = Alas Purwo-Java, BLB = Batulicin-Kalimantan, KTB = Kapuas-Kalimantan, PGC = Parangloe-Sulawesi, PKC = Pomalaa-Sulawesi, BHS = Batuhijau-Sumbawa, KKP = Kuala Kencana-Papua

Table 4 Growth performance (mean ± standard deviation) of various provenances of *N. cadamba* across different sites

Provenance	Height (m)	Collar diameter (cm)	Survival (%)
RPS	2.15 ± 0.94	4.42 ± 2.16	70.0
KRS	2.11 ± 0.97	3.92 ± 1.96	69.5
OKS	2.25 ± 1.19	4.19 ± 2.10	64.8
GSJ	2.50 ± 1.22	4.77 ± 2.27	66.9
NKJ	2.35 ± 1.16	4.35 ± 2.16	60.7
APJ	2.23 ± 1.04	4.11 ± 2.04	60.7
BLB	1.97 ± 0.77	3.63 ± 1.82	58.2
KTB	2.15 ± 0.71	4.06 ± 2.19	67.0
PGC	2.30 ± 1.10	4.49 ± 2.23	70.1
PKC	2.33 ± 1.10	4.36 ± 2.08	63.2
BHS	2.31 ± 1.05	4.33 ± 2.10	61.9
KKP	2.50 ± 0.86	4.59 ± 1.83	61.3
F test: Provenance	2.80 *	3.57 **	1.43 ns
Provenance*Site	2.49 ns	2.14 ns	0.70 ns
Family*Site	1.55 ns	1.41 ns	0.84 ns

Notes: ** = significant at $p<0.01$
* = significant at $p< 0.05$
ns = not significant

respectively. At Parungpanjang, the best family exceeded the least family by 57% and 122% for height and root collar diameter, respectively (data are not shown). These results showed the potential of provenance-progeny test of *N. cadamba* for selection. Analysis of variance across the sites revealed no significant provenance against site interaction and family within provenance against

site interaction for all parameters (Table 4). In across site, a significant difference was revealed by provenances for height and diameter parameters. Among different provenances, the performance of the GSJ and KKP provenances was found significantly superior than the others. The component of variance attributed to variation among provenances ranged from 0.5% for height at Parungpanjang to 1.7% for root collar diameter at Limbangan. On the other hand, component of variance attributed to variation among families within provenances were lower than component of variance among provenance, ranged from 0.4 to 0.6% at both sites (Table 5). The higher values toward variation among provenance in relation to families within provenances suggested that provenances are isolated or gen flow is insufficient to overlap the effect of selection and/or genetic drift. Larger genetic variation among provenances than genetic variation among families within provenances were also observed in provenance-progeny test by Zheng *et al.* (1994) for *Pinus caribaea* in China, Bali-Uckas *et al*. (1999) for *Acer platanoides* in Sweden, Sebbenn *et al.* (2003) for *Araucaria angustifolia* in Brazil, Adinugraha *et al*. (2013) for *Tectona grandis* in Gunung Kidul, and Setiadi and Fauzi (2015) for *Araucaria cunninghamii* in Bondowoso, Indonesia. On the other hand, study based on AFLP loci using 4 populations of *N. cadamba* showed that variation among population (27%) was much lower than variation within population (73%) (Sudrajat *et al*. 2015). Different trend was caused by different number and distribution of *N. cadamba* population.

Genetic Parameters

Phenotypic and genetic correlations between height and root collar diameter parameters at Parungpanjang were higher than those at Limbangan (Table 6). This indicated that the possibility of selection in one parameter at Parungpanjang is more efficient than those at Limbangan. Phenotypic correlations were higher than genetic correlations among height and root collar diameter parameters (Table 5). High phenotypic correlation provided more support for combining these surveyed parameters as early selecting criteria.

Narrow sense individual (h^2i) and within families (h^2f) heritability at Limbangan were poor (ranged from 0.031 to 0.055), while the

Table 5 Components of variance and relative contribution (number in parentheses) of replications (σ^2_R), provenances (σ^2_P), interaction between replications and provenances (σ^2_{RP}), families within provenances ($\sigma^2_{F(P)}$), interaction between replications and families ($\sigma^2_{RF(P)}$) and individual within families (σ^2_e) of provenance-progeny tests at two sites in West Java Province, Indonesia

Components of variance	Limbangan, Garut		Parungpanjang, Bogor	
	Height (m)	Collar diameter (cm)	Height (m)	Collar diameter (cm)
σ^2_R	0.49330 (28.0%)	1.54578 (22.9%)	0.06746 (9.1%)	0.27601 (9.5%)
σ^2_P	0.02681 (1.5%)	0.11501 (1.7%)	0.00377 (0.5%)	0.04134 (1.4%)
σ^2_{RP}	0.00465 (0.3%)	0.04640 (0.7%)	0.01546 (2.1%)	0.07356 (2.5%)
$\sigma^2_{F(P)}$	0.01045 (0.6%)	0.03875 (0.6%)	0.00359 (0.5%)	0.01216 (0.4%)
$\sigma^2_{RF(P)}$	0.48827 (27.7%)	1.64063 (24.3%)	0.23901 (32.2%)	0.82821 (28.4%)
σ^2_e	0.74002 (42.0%)	3.35359 (49.8%)	0.41369 (55.7%)	1.68163 (57.7%)

Table 6 Genetic (upper diagonal) and phenotype (lower diagonal) correlation coefficients among traits in provenance-progeny tests of *N. cadamba* at two sites in West Java Province, Indonesia

	Limbangan, Garut		Parungpanjang, Bogor	
	Height	Collar diameter	Height	Collar diameter
Height		0.29		0.56
Collar diameter	0.799**		0.885**	

Note: ** = significant at $p<0.01$

Table 7 Estimated heritabilities in provenance-progeny tests of *N. cadamba* at two sites in West Java Province, Indonesia

	Limbangan, Garut		Parungpanjang, Bogor	
	Height	Collar diameter	Height	Collar diameter
Heritability at individual plant level - h^2i	0.034	0.031	0.093	0.114
Family heritability - h^2f	0.055	0.054	0.150	0.178

Notes : Category of heritability values according to Cotterill and Dean (1990):
heritability of <0.1 = poor
heritability of 0.1-0.3 = moderate
heritability of >0.3 = high

Table 8 Estimates of genetic gain for height and diameter by within family of in provenance-progeny tests of *N. cadamba*

Proportion selected	Garut		Parungpanjang	
	Height	Diameter	Height	Diameter
0.30	0.13	0.18	0.31	0.16
0.50	0.05	0.09	0.09	0.07
0.70	0.03	0.05	0.05	0.04

heritabilities at Parungpanjang site were moderate and ranged from 0.093 to 0.178 (Table 7). Values of heritability changed with sites with the same set of genotypes. Lower value of heritability of the trial in Limbangan could be due to high incidence of domestic animal and irregular agricultural crops covering several parts of area causing high environmental difference. Setyadi *et al.* (2013) studied 75 half-sib *N. cadamba* families explored from Java Island and found higher family heritability of approximately 0.32 for height and 0.38 for stem diameter at breast height. Poor values of heritability in this study could be due to plant age that was still young, indicating the genetic control of the parameters was still weak. For example at Parungpanjang, family heritability at 6 months old plant (0.093 for height and 0.066 for root collar diameter) was lower than family heritability at 12 months old plant (0.150 for height and 0.178 for root collar diameter), indicating heritability was not yet stable. Trend of increasing heritability with age was also reported in the studies of *Eucalyptus grandis* (Osario *et al.* 2001; Gapare *et al.* 2003), *Pinus banksiana* (Weng *et al.* 2006) and *E. urophylla* (Kien *et al.* 2009). The increased heritability with age for growth parameters could also be resulted from competitive effects occurred in later age in the stand (Kien *et al.* 2009). According to Zobel and Talbert (1984), the heritability values often change with age when the environment changes and when the genetic control of the characteristic changes as the trees reach mature age. Therefore, activities to improve site environment conditions will be very important to optimize growth and to reach stable heritability.

Heritability estimated should be interpreted carefully because of unequal number of families per provenances presented in the trials. In a multi-provenance-progeny test, the family variance is averaged across different provenances, with more information provided by the better-represented provenances (Kien *et al.* 2009). In all parameters at both sites, family heritability was found to be higher than individual heritability. Some studies in other species also revealed similar trend, such as in *Araucaria angustifolia* in Brazil (Sebbenn *et al.* 2003) and *Pinus brutia* in Turkey (Gulcu & Celik 2009). This result indicated that higher genetic gain can be achieved with family selection.

Estimation of genetic gain is determined by heritability value, selection intensity and phenotypic standard deviation. In this research, simulation to predict the genetic gain used proportional selected family of 30%, 50% and 70% and the corresponding selection intensity were 1.15, 0.79 and 0.49 (Zobel & Talbert 1984). The higher value of genetic gain estimation for height and collar diameter by proportional selected family of 30% was 0.13 and 0.18 for Limbangan and 0.31 and 0.16 for Parungpanjang (Table 8). Predictions of genetic gain from family

selection simulation revealed that height parameter showed higher values than collar diameter parameters. It was also revealed that genetic gain of height parameters at Parungpanjang was higher than genetic gain at Limbangan. Johnson *et al*. (1955) and Seghal *et al*. (1995) pointed out that heritability estimates along with genetic gain is more useful than heritability alone, because the heritability estimates indicated only the effectiveness of selection on genotype based on phenotypic performance, but fails to indicate the genetic progress. High heritability and genetic gain indicated the additive gen action on these parameters for their expression.

CONCLUSIONS

Levels of genetic variation in *N. cadamba* were found to be higher for all parameters among provenances than within provenances indicating possibility to use well performing provenances as seed sources for reforestation and regeneration practices. Estimated family heritability was higher than narrow sense individual heritability, indicating the possibility of greater gains with selection among families rather than mass selection. However, heritability was low to moderate and not yet stable for all parameters at both sites, indicating that possibility of genetic gains with selection is limited and selection should be done until the heritability reached relatively high and stable values. A combination of family and within family selection would be effective in improving growth of this species. Improving growth environment conditions with controlling the domestic animal and weed intensively should be applied immediately and continuously to optimize the plant growth, stabilize heritability and to optimize genetic gain.

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