GENETIC PARAMETER ESTIMATION OF RAMBUTAN SEEDLING MORPHOLOGICAL TRAITS FOR A BETTER ROOTSTOCK PERFORMANCE

PENDUGAAN PARAMETER GENETIK TERHADAP SIFAT MORFOLOGI SEMAI RAMBUTAN UNTUK MEMPERBAIKI KINERJA BATANG BAWAH

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INTISARI

Perbaikan mutu batang bawah rambutan perlu dilakukan dengan menyeleksi pohon-pohon lokal yang zuriatnya memiliki sifat-sifat baik. Variansi genetik, daya waris, serta korelasi genetik dan fenotipik dari diameter batang, tinggi tanaman, volume akar, dan panjang akar primer dari semai rambutan diduga untuk memperoleh informasi mengenai sifat yang dapat diseleksi, efektivitas seleksi tak langsung, dan macam seleksi yang sebaiknya dilakukan.

Biji-biji dari sembilan belas tanaman rambutan lokal, dipilih secara acak, yang tumbuh di Salaman, Magelang, ditanam di polibag dan disusun menurut Rancangan Acak Kelompok Lengkap berulangan tiga. Perlakuan berupa baris-baris yang masing-masing terdiri dari dua puluh semai. Pengamatan dilakukan 20 minggu setelah tanam. Selain itu, gaya berkecambah diamati pula tiga minggu setelah tanam dan diameter batang juga diamati delapan minggu setelah tanam.

Perkecambahan terjadi sepuluh hari setelah tanam, dengan gaya berkecambah 90% untuk sebagian besar famili. Daya waris tinggi tanaman dan korelasi genetiknya dengan sifat-sifat lain ternyata tinggi sehingga seleksi tidak langsung untuk memperbaiki keragaan batang bawah dapat dilakukan melalui sifat ini. Nilaiduga daya waris diameter batang pada minggu kedelapan melebihi satu. Pada saat itu, cadangan makanan pada biji diduga masih mengimbas sehingga memperbesar kemiripan dalam famili. Uji zuriat dipandang sebagai cara seleksi yang paling sesuai untuk keperluan pemilihan tetua sumber batang bawah.

Kata kunci: parameter genetik, rambutan (Nephelium lappaceum L.), famili-saudara tiri, batang bawah.

ABSTRACT

Better rambutan rootstock materials need to be established by selecting local trees which have progenies with desired characters. Genetic variances, heritability, genetic and phenotypic correlation of stem diameter, plant height, root volume, and primary root length of rambutan seedling were estimated to obtain informations on which trait selection could be practiced, how effective an indirect selection was, and what type of selection should be applied.

Seeds of nineteen randomly chosen local rambutan trees grow in Salaman, Magelang, were planted each in a polybag, arranged in randomized complete block scheme with three replicates. Each experimental unit consisted of twenty seedlings. Data were collected twenty weeks after planting. In addition, germination rate at three weeks after planting as well as stem diameter at eight weeks after planting were recorded.

Germination occured ten days after planting with the rate at above 90% after three weeks for most of

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the families. Plant height had the highest heritability and its genetic correlations with the other traits were also high, suggesting that indirect selection for better rootstock morphology may be conducted by selecting it.. Heritability estimate of stem diameter at eight weeks was greater than unity, probably due to residue of stored food contained in the cotyledon. Hence, the estimate was biased due to maternal effect. Progeny testing was considered as the most proper method of selection to be applied.

Keywords: genetic parameter, rambutan (*Nephelium lappaceum* L.), half-sib family, rootstock.

INTRODUCTION

Vegetative propagation of rambutan [*Nephelium lappaceum* L.; family S*apindaceae*; $2n = 2x = 22$ (van Welzen and Verheij, 1997)] commonly practiced in Indonesia, especially Java, is bud grafting. It requires two parents, i.e. the rootstock and the scion. A number of improved varieties have been released as scion parent (Anonymous, 1992), but any rootstock parent variety has not available yet.

Rambutan growers and nursery industry usually use seedlings from illegitimate or semilegitimate seeds as rootstocks. Since rambutan is a cross-pollinating species (Sunarjono, 1990), there will be variability in rootstocks so obtained which, in turn, will affect growth of the scion grafted on it differently. This may become a problem in a large-scale rambutan estate. Thus, selection for trees which progenies have good characters as a rootstock should be considered.

Hartmann and Kester (1960) suggested that seedlings to be used as rootstock must be vigorous and have quite uniform performance. Kalie (1994) listed five criteria of a good rootstock: good and robust rootage, resistant or tolerant to root and lower stem pest and disease, adaptable to a wide range of soil types and conditions, compatible with its upper stem tissues, and able to withstand long distance travel.

Some (see, for examples, Mahisworo *et al.*, 1991 and Sunarjono, 1990) recommend Sinyonya, Simacan, and Sitangkue as rootstock varieties due to their good rootage. Unfortunately, their clones are not widely available. However, it is known from experience that local genetic resources can give good results, too. Selecting best local trees, followed by cloning and distributing their vegetative descendants may worth consideration.

As a first step of selection is choosing characters responsive to selection, that is have high heritability. Heritability indicates relative amount of phenotypic variability attributable to genetic differences. It often determines whether individual or family selection should be applied (Falconer and Mackay, 1996). Narrow sense heritability can be estimated using one factor mating design, such as topcross or half-sib family design (Dudley and Moll, 1969).

Two other important parameters are genetic and phenotypic correlation coefficients. Since selection for a trait may change other traits it correlates, both coefficients can give justification in applying indirect selection. This type of selection should be considered as rambutan rootstock should have good rooting and thick root diameter, traits that are difficult to measure.

Southern part of Magelang Regency is known for its local rambutan gene pool. The aim of this study is to estimate certain genetic parameters of seedling morphological traits at the population, to choose traits that are effective to be selected, to judge indirect selection merit, and to suggest method of selection to be applied.

MATERIALS AND METHOD

Local rambutan stands of Salaman, Magelang Regency, was the subject population to the study. Fruits of relatively the same maturity were collected from nineteen randomly chosen trees. Fruit flesh was excluded by rubbing it to sand until the seed is totally free from the flesh. Seed was rinsed with water then wind-dried. Seeds from a single tree comprised a half sib family.

Seeds were planted in polybags filled with mixture of manure and soil, one seed each. Randomized Complete Block with three blocks as replicates was held. Each block contained randomly

allocated nineteen half-sib family rows of twenty polybags. Foliar application of plant nutrient was provided every two weeks. Pest and disease control was done whenever it is necessary.

Measurements were made on germination rate, stem diameter, primary root length, root volume, and plant height. Germination rate was recorded three weeks after planting Stem diameter at 10 cm above soil surface was measured eight and twenty weeks after planting using calipers. Other traits were taken at the end of the experiment, twenty weeks after planting. Root volume was measured with water displacement method (Böhm, 1979) with modification on its drying after cleaning the root. Instead of winddrying the root, drying was done by placing washed root on dailynews paper.

Analysis of data was based on the following model:

$$Y_{ijk} = m + F_i + R_j + \epsilon_{ij} + \delta_{ijk},$$
$$(i = 1,2, ...,f; j = 1, , ...,r; \text{ and } k = 1,2, ..., s_{ij});$$

relationship :

$$V_A = 4\,\sigma^2_f.$$

Similar relationship are used for additive genetic covariance (Cov_A). Heritability (h^2) is defined as

$$h^2 = V_A / V_p,$$

where V_p was obtained following

$$V_p = \sigma^2_f + \sigma^2_c + \sigma^2_w$$

for individual-based selection and

$$V_p = \sigma^2_f + \sigma^2_c / r + \sigma^2_w$$

for family-mean-based selection.

The latter must be added with an assumption that within family variation was entirely

Table 1. Estimates of additive genetic variance (V_A), phenotypic variance (V_p), individual-based heritability (h^2), and family-mean-based heritability (h^2_f) of traits being examined.

Trait	V_A	V_p	h^2 (%)	h^2_f (%)
Stem diameter (8 wks)	1718.04	1540.06	112	116
Stem diameter (20 wks)	2213.85	4103.38	54	56
Root volume	1.44	3.02	48	49
Primary root length	1973.05	9237.98	21	22
Plant height	3989.89	5010.53	80	83

with all sources of variation are random (Eisenhart's Model II), where

Y_{ijk} = observation from k-th plant of i-th family at j-th block;

m = grand mean;

F_i = effect of i-th family, NID(0, σ^2_f);

R_j = effect of j-th block, NID(0, σ^2_r);

ϵ_{ij} = plot to plot error, NID(0, σ^2_c); and

δ_{ijk} = plant to plant error, NID(0, σ^2_w);

f stands for family number, r for number of replication, and s_{ij} for number of survived individuals from i-th family at j-th replicate.

Under some well-known assumptions (see for examples Mayo, 1980 and Warwick *et al.*, 1990), additive genetic variance (V_A) has the following

genetically controlled.

Genetic correlation coefficient (r_A) between two traits, namely X and Y, was computed following

$$r_A = Cov_A(X,Y) / \sqrt{[V_A(X) . V_A(Y)]};$$

whereas phenotypic correlation coefficient (r_p) was computed the same way, using family-mean-based phenotypic variance and covariance.

RESULTS AND DISCUSSION

Not all individuals survived. Two family had

poor germination rate (under 20%) but most families gave germination rate over 80%. Some plants were killed by grob attack. Seedling production for most of sampled trees did not seem different.

Estimates of the variance components showed values that was mostly significant ($P < 5\%$) and Table 1 shows etimates of additive genetic and phenotypic variances together with the heritabilities for the different traits.

Genetic variability for seedling traits in Salaman rambutan population varies for different traits under consideration. Progress in selection toward plant height ($h^2 = 83\%$ for family mean based), was expected to be rapid. However, the root variables only gave moderate heritabilities (between 20% to 50%). Selection towards these ones will be more effective if we select them indirectly through highly heritable trait that is highly correlated.

Stem diameter, recorded twice, showed interesting result. Although both gave high heritabilities, the estimate for first (8 weeks) observation was higher than 100%, a value that was unrealistic. This situation occurred because changes in phenotypic variances was faster than in additive genetic one, although both changed higher. We suspect that there was an overestimated value at the first observation caused by maternal effects resulting in a too high estimate for additive genetic variance. Mather and Jinks (1977) mentioned about cellular, as well as histological, maternal nongenetic effect affecting earlier phase of plant growth which gradually diminish after a certain time. It seemed that the effect made each individual of the same family tended to be much more alike than it should.

Genetic and phenotypic correlation coefficients between each trait were presented in Table 2. All correlation coefficients were positive and phenotypic correlations were always lower than its genetic counterparts.

Values higher than 0.5 were found to all genetic correlation coefficient estimates. Although phenotypic correlation coefficients were not as high as genetic ones, the situation was condusive for indirect selection. Indirect selection needed to be considered because root characters and stem diameter were more difficult to be examined compared with other traits, such as plant height. By exploiting the correlated response, selecting higher plant height would result in better seedling performance. Falconer and Mackay (1996) mentioned that selecting a trait (target trait) via selection on another (secondary) trait would have comparative merit provided the other trait have substantially higher heritability than the target trait, both traits having high genetic correlation, higher selection intensity could be applied to the secondary trait, there was technical difficulties in measuring target trait, or the character was sex linked.

Estimates of heritability showed no significant difference between individual- and family-mean-based estimates. This means response of the trait would not be different whether selection is individual type or by any type of family selection. However, mass selection, including within family selection, can only be applied to obtain desired individuals within progeny population, not to improve a population in a short term. Mass selection can be used to improve the population but we should wait until the selected individuals bear fruits and seeds.

We then agree with what Mayo (1980) had

Table 2. Estimates of genetic (above diagonal) and phenotypic (below diagonal) correlation coefficient between traits being considered.

Trait	Stem diameter (8 wks)	Stem diameter (20 wks)	Root volume	Primary root length	Plant height
Stem diameter (8 wks)	1.00	1.00	0.94	0.79	0.85
Stem diameter (20 wks)	0.68	1.00	0.97	0.76	0.78
Root volume	0.53	0.66	1.00	0.65	0.65
Primary root length	0.27	0.24	0.29	1.00	0.90
Plant height	0.53	0.67	0.46	0.16	1.00

stated that family selection was the most appropriate selection method to be applied for perennial crops. Progeny testing, a type of family selection, could be applied to select the best rambutan trees which have good progeny performance. Selection was based on mean of seedling height. Trees having a desired progeny height then selected and vegetative propagation was applied to regenerate them rapidly.

CONCLUSION

Conclusions were that plant height was a character where selection should be applied to improve morphological performance of rambutan seedling and the method of selection which was appropriate to conduct was progeny testing.

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