PENDUGAAN PARAMETER GENETIK DAN PARAMETER STABILITAS HASIL DAN KOMPONEN HASIL KACANG TANAH

( Arachis hypogaea (L) Merr, )

Oleh

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SUMMARY

ASTANTO KASNO. Estimation of Genetic and Stability Parameters for Yield and Yield Components of Peanut (Arachis hypogaea (L) Merr.) (Under the guidance of ABDUL BARI as chairman, AHMAD ANSORI MATTIJK, SUBANDI, SADIKIN SOMAATMADJA, and SOLEH SOLAHUDIN as members).

Genetic parameters for number of total pods, number of seeded pods, number of unseeded pods, number of seeds, 100 seed weight (gram), pod weight (gram/1.4 m²), and seed weight (yield) (gram/1.4 m²) were estimated from field trials using forty genotypes of peanut which were tested in a split plot design with 3 replications at 3 locations (Cikeumeuh, Sukamandi, and Kuningan). Three main plots were used, i.e. the peanuts were grown in monoculture and in association with maize grown at 7 and 15 days after the peanuts were planted, respectively. Three growing environments used in this study were to create a greater environmental variation. It was done because many peanut farmers are still planting this crop either in monoculture or associated with maize in Indonesia.

In the analyses of variance the effect of genotype, season, and location were considered random. The assumption of random effect of genotypes should be interpreted that the varieties included in the study were a random
sample from a population of the bunch type cultivars. The growing environments were considered fix and confounded in the location. The components of variance were estimated as linear functions of the mean squares of the combined analysis for mixed model. Phenotypic and genotypic variances were used to estimate the heritability (broad sense), expected response to selection, coefficient of genetic variability, and mean of selected lines. Genotypic correlation for yield in a pair of environments was used to estimate the correlated response of yield, and phenotypic correlation to identify the similarity of those paired environments. Whereas, correlations among mean yield in one environment with the overall mean yield and the associated heritabilities in those environments were used to evaluate the productivity of those environments. The values of the estimates for genotype x season, genotype x location, genotype x season x location, genotype x cropping pattern, and genotype x season x cropping pattern interactions, and error variance components were used to determine the maximum combination of the number of replications, seasons, and locations for future testing programmes; and to see the effect of the cropping pattern (growing environment) to the error variance of a genotype mean and its standard error for yield.
Genotypes of peanut in each growing environment were considered as a separate test with a randomized complete block design and 3 replications. Combined analyses for random model was done to compare the genetic parameters in one growing environment with the others.

Regression of mean traits (yield, pod weight, and 100 seed weight) on environmental index, and regression of genotype-environment effect on environmental index were employed for stability analyses. Compensation index was also used as a stability parameter for yield.

There were significant differences among the genotypes tested for yield and yield components, and their tolerance to the shade. The performances of genotypes in monoculture were significantly better than in intercrop with maize for all of the traits studied. However, the maize crops grown at 7 and 15 days after the peanuts did not show any significant differences in performance. Genotype x season interaction was not significant for all the traits indicating that the different effect of various genotypes were consistent among seasons, even though the weather in the growing seasons was probably different significantly. Significant interactions between genotypes and location were only found for 100 seed weight, pod weight, and yield. This indicated that for those traits the orders of various genotype
effects were different among locations. Kuningsan gave the 100 seed weight, pod weight, and yield significantly higher than Cikeumeuh and Sukamandi. Those traits, however, were not significantly different in Cikeumeuh and Sukamandi.

The genotypic variance components for number of total pods, number of seeded pods, number of seeds, and 100 seed weight were higher than the genotype x environment interaction variance components, followed by the high heritability estimates indicating that the variations of those traits were mainly caused by genetic rather than non genetic factors. On the contrary, the genotypic variance components for pod weight and yield were small relative to the variance components of the interaction of genotype an environment (season and location). The low heritability estimates for these traits suggested the variations were primarily caused by the non genetic factors. The results suggested that improving genotypes for pod weight and seed weight (yield) would not be easy.

The estimated variance components of interactions between genotype and cropping pattern \( s_{gp}^2 \) and between genotype, season, and cropping pattern \( s_{gmp}^2 \) were small relative to genotypic variance component \( s_g^2 \) for all of the traits. This could be interpreted that effects of the various genotypes were more important that those of
the interactions of genotypes with various cropping patterns and seasons. The $\hat{s}_{gm}^2$ (variance component of interaction between genotype and season) was two times greater than the $\hat{s}_{gp}^2$, however, for both variances were small relative to $\hat{s}_{gt}^2$ (variance component of interaction between genotype and location) for yield. The results suggested that improving yield for location adaptation may be more necessary than for cropping pattern adaptation. The interactions in which a plant breeder in most interested are the predictable ones. A breeding program could develop cultivars adapted to those predictable environments. The predictable interactions in this study are $\hat{s}_{gp}^2$ and $\hat{s}_{gt}^2$.

The number of unseeded pods could be ignored for its effect was not so clear and its heritability estimates was low.

Competition between peanut and corn besides affecting the means also caused large effect (upward as well as downward) on the other genetic parameters (genotypic variance, heritability, expected response to selection, and coefficient of genetic variability) for all of the traits studied. The greatest genotypic variance components for yield, 100 seed weight, number of total pods, number of seeded pods, and number of seeds in the monoculture was a good indication that improving those traits in the monoculture would be advantageous.
The correlated response for yield in the intercrop condition of certain environment (season or location) was higher than the direct response in the monoculture strongly suggests that genotype selected in the monoculture in this study could still well be grown in association with maize. The indirect selection method to find superior genotype for intercropping with maize from selection in the monoculture was better than the direct selection method, suggesting that the separate breeding program of peanut for specific adaptation is not required yet.

The closely associated between main traits (yield, pod weight, and 100 seed weight) and their stability parameters (coefficient of regression and deviation from the regression) suggested that the population of genetic materials in this study were generally homogenous, so that improving those traits of these population was not necessary.

The coefficient of correlation for mean yield between pairs of location were generally low suggesting that the levels of the highest and lowest yields in the pairs of location were not the result of the same genotype. This also suggest that the relative ranking of a set of the best genotypes for yield change the order from environment to environment.

The value of r h (r is coefficient of correlation and h is square root of heritability) in this study
indicated that Kuningan in the growing season from June to September gave an optimum environment for peanut yield testing grown in monoculture as well in intercropping. Evidence was also obtained that Kuningan had the agroclimate characters for the optimum growth and development of peanut such as recorded by Norden, Smith, and Gorbet (1982). These results suggest that Kuningan could be used as a standard environment for variety testing of peanut.

Yield and yield components stability was not always similar for a genotype in the monoculture and in the intercropping. A stable genotype for yield was not always accompanied by stable pod weight and 100 seed weight. Also, the stable genotype for one, two, or three of those traits across environment was not always stable in monoculture or in intercropping. Regression of mean yield and yield components and of the interaction effect on the environmental index give similar results. Pelanduk variety was identified as a variety with maximum stability. It suggests that Pelanduk variety could be grown in various regions in Indonesia. The stability analyses also indicated that the lines RR-4, RR-6, 26, 28, and 31 had the maximum stability. These lines could be multiplied and recommended for release. The lines 37, 38, and 39 need further improvement, especially for yield stability. These lines belong to the 11 best genotypes in the study.
The study showed that the effect of interaction between genotype and environment could eliminate 63 percents of these eleven best genotypes when selection was conducted in the low productivity or stress environment. On the contrary, selection in the high productivity or non stress environment could maintain those best genotypes. The result, suggests that under very poor environmental conditions selection intensity should be lowered in order to avoid losses of the possible prospective lines. Under rich environmental condition, however, the percent of truncation selection could probably be decreased without discarding outstanding lines seriously.

The error variance of a genotype mean and its standard error could be reduced by including the cropping pattern to the variety testing of peanut replicated in several seasons and in various locations. It suggests the need of the components of technology in advance yield trials involving various research disciplines. Thus, the release of a genotype will be supported by the components of technology of at variety.

Given 14.53 gram per 1.40 m² as being acceptable for LSD at 0.05 probability level for future testing program, the following combinations of number of replications, seasons, and locations per season may be proper:
(3, 3, 10), (3, 4, 7), or (4, 4, 6). The decision however, will be greatly affected by economic and other factors such as the availability of personal, facilities, and seeds.

The standardized Euclidean distance method used for grouping the genotypes based on the mean yield in the monoculture, and the ratio of mean yield in the intercropping and in the monoculture was also discussed.

The environment stratification based on the growing environment was efficient. The environment grouping using the standardized Euclidean distance method based on the environmental index was also reported.