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Estimation of gene action through skewness and kurtosis analysis in soybean population [*Glycine max* (L.) Merr] F5 generation resulting from three-parent cross

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Abstract. Soybean productivity can be increased by planting superior varieties. In obtaining superior varieties, many techniques can be used, such as crossing. The cross of Grobogan x Anjasmoro x Dega 1 is anticipated to enhance soybean production in Indonesia. This study aims to see the estimation of gene action through skewness and kurtosis analysis in F5 soybean population resulting from three-parent cross. The study was conducted in a field located in Tanjung Sari Village, Medan Selayang District. Plant height, flowering age, number of seeds, and weight of 100 seeds were observed in this study. The results of skewness and kurtosis analysis in the F5 generation resulting from three-parent cross in plant height, number of seeds, and weight of 100 seeds were controlled by additive gene action and influenced by many genes with a platykurtic graph form. Meanwhile, the character of flowering age was controlled by complementary epistatic gene action and influenced by a few genes with a leptokurtic graph form.

1. Introduction

Soybeans [*Glycine max* (L.) Merr] is the main food commodities after rice and corn, playing an important role in meeting food, feed, industrial material, and human nutritional needs. Soybeans are a major source of vegetable protein, which is relatively more economical than animal proteins such as meat, fish, and milk [1]. National soybean productivity in 2023 was recorded at an average of 14.56 quintals per hectare [2].

Soybean productivity can be increased by using superior varieties, which are developed through plant breeding activities aimed at improving and increasing genetic diversity, thereby producing superior soybean varieties with high quality and productivity [3]. The development of superior varieties can be done through crossing techniques. The success rate of crossing ranges from 42.9% to 80% [4].



Plant crossing aims to increase genetic diversity, which is used to form the base population in plant breeding activities [5]. The estimation of gene action in plant breeding that controls a trait and the relationship between component traits and crop yield can be calculated using skewness and kurtosis values. Skewness values are used to identify patterns of gene action on a trait, while kurtosis is used to assess the level of sharpness of data distribution in research [6].

Crossing of soybeans between the Grobogan X Anjasmoro varieties achieved a success percentage of 57.14% [7]. The F1 cross between Grobogan X Anjasmoro was then crossed again with the Dega 1, achieved a success percentage of 35.37%. The development of superior varieties through three-way crossing has the potential to create broad genetic diversity with maximum production potential, earlier ripening, and large seed size [8].

The research of F1 generation derived from three-parent cross based on the results of heterosis and heterobeltiosis analysis showed better performance than the three parents, particularly in terms of seed weight and 100-seeds weight, namely 26.856%, 5.676%, 16.889% and 5.689% [9]. The estimation of genetic parameters and the selection of promising individuals in the F2, F3, and F4 generations derived from the three-parent cross showed that the F3 generation had a faster flowering time and higher productivity than its parents [10].

Based on the above description, study was conducted on gene action estimation through skewness and kurtosis in the F5 generation soybean population [*Glycine max* (L.) Merr] resulting from three-parent cross.

2. Materials and methods

2.1 Location and times

This study was conducted in Tanjung Sari Village, Medan Selayang District, Medan, North Sumatra from October to December 2024.

2.2 Research materials

This study uses materials including seeds of Anjasmoro, Grobogan, Dega 1, F5 generation resulting from three-parent cross ([Grobogan X Anjasmoro] X Dega 1), KCl, TSP, Urea, bamboo sticks, fungicide, and insecticide.

2.3 Research methods

This study was carried out by cultivating three parent varieties and F₅ generation obtained from three-parent cross [(Grobogan × Anjasmoro) × Dega 1], then observing each individual within the plant population. There were 90 plants from the three parent varieties, 30 plants per parent variety, while the F5 population consisted of 570 plants, bringing the total to 660 plants. The seeds were planted in plots (140 cm × 200 cm) with a spacing of 50 cm between plots. Planting was carried out by making planting holes ±2 cm deep with a planting distance of 20 × 40 cm. Each hole was filled with one seed and then covered with soil.

The data were obtained through observations of agronomic characters in the F5 generation resulting from three-parent cross. The observed characters included plant height, flowering age, number of seeds.plant⁻¹, and weight of 100 seeds.plant⁻¹. The data were analyzed using Microsoft Excel and Statistical Product and Service Solutions (SPSS).

The mechanisms of gene action and gene number controlling each character were estimated using skewness and kurtosis analysis in the F5 generation. The skewness and kurtosis formulas are used referring to the Roy method [11] as follows:

$$Skewness = \frac{\sum_{i=1}^n (Y_i - \bar{Y})^3}{(n-1)s^3}$$

$$Kurtosis = \frac{\sum_{i=1}^n (Y_i - \bar{Y})^4}{(n-1)s^4}$$

Y_i represents the value of genotype i , $\bar{Y}$ indicates the mean value, S is the standard deviation, and N describes the number of genotypes observed. The skewness and kurtosis values were tested using standard error through statistical analysis [12].

$$ZS = \frac{S}{SEs}$$

$$ZK = \frac{S}{SEk}$$

where,

SES = standard error of skewness, SEK = standard error of kurtosis, S = skewness, K = kurtosis, the critical test values for ZS are $Z_{0.05/2} = 1.96$ and ZK are $Z_{0.01/2} = 2.75$

Skewness describes the influence of epistasis on a character, while kurtosis reflects gene number that controlling the character. Both analyses explain that:

- If skewness = 0 indicates no epistatic influence. A skewness > 0 indicates the presence of complementary epistatic gene action, while a skewness < 0 indicates that a character is controlled by the action of duplicate epistatic genes.
- If kurtosis is > 3 and positive value, then a character is controlled by several genes. If the kurtosis is < 3 and negative value, then a character is controlled by many genes.

3. Results and discussion

Estimates of gene expression patterns based on skewness analysis and the Z-skewness test at the 1% significance level are shown for plant height, flowering age, number of seeds, and 100-seed weight (Table 1).

According to Samak et al [13], analysis of skewness and kurtosis can reveal the fundamental patterns of gene activity and estimate gene number that regulate character. Table 1 shows the F5 skewness value of the cross between 3 soybean parents. In plant height, number of seeds, and weight of 100 seeds in the F5 cross of 3 parents showed no significant difference where additive gene action controls these characters. Meanwhile, the flowering age character showed a very significant difference at the 1% level where this character is controlled by complementary epistatic gene action. According to Jayaramachandra et al [14] and Roy [11], negative or positive skewness values, respectively, indicate the presence of complementary epistatic and duplicate epistatic genes in the population.

Table 1. Gene action on the characteristics of the F5 generation resulting from three-parent cross

Character	Skewness $\pm$ SE	Z-Skewness Test	Gen Axin
Plant height	-0.19 $\pm$ 0.10	-1.83 ns	Additives
Flowering age	2.90 $\pm$ 0.10	27.89 **	Ad + EK
Number of seeds.plant ⁻¹	-0.04 $\pm$ 0.10	-0.40 ns	Additives
Weight of 100 seeds.plant ⁻¹	-0.04 $\pm$ 0.10	-0.36 ns	Additives

Note: SE = standard error, Ad+EK = additive with complementary epistasis, ns = not significant, ** = significant at the 1% level.

Skewness and kurtosis analyses provide information on gene action mechanisms and estimate gene number involved in controlling character [13]. Skewness analysis can determine the presence or absence of epistasis in offspring resulting from crossing. If the epistasis value obtained is very small, it can be ignored, but when a sufficiently large value is detected, it will affect the phenotype of the plant. This indicates that there is a role for gene action from the results of crossing.

Table 2 shows the estimated gene number for F₅ derived from the three-parent cross, including plant height, flowering age, number of seeds, and 100-seed weight, analyzed at the 1% significance level.

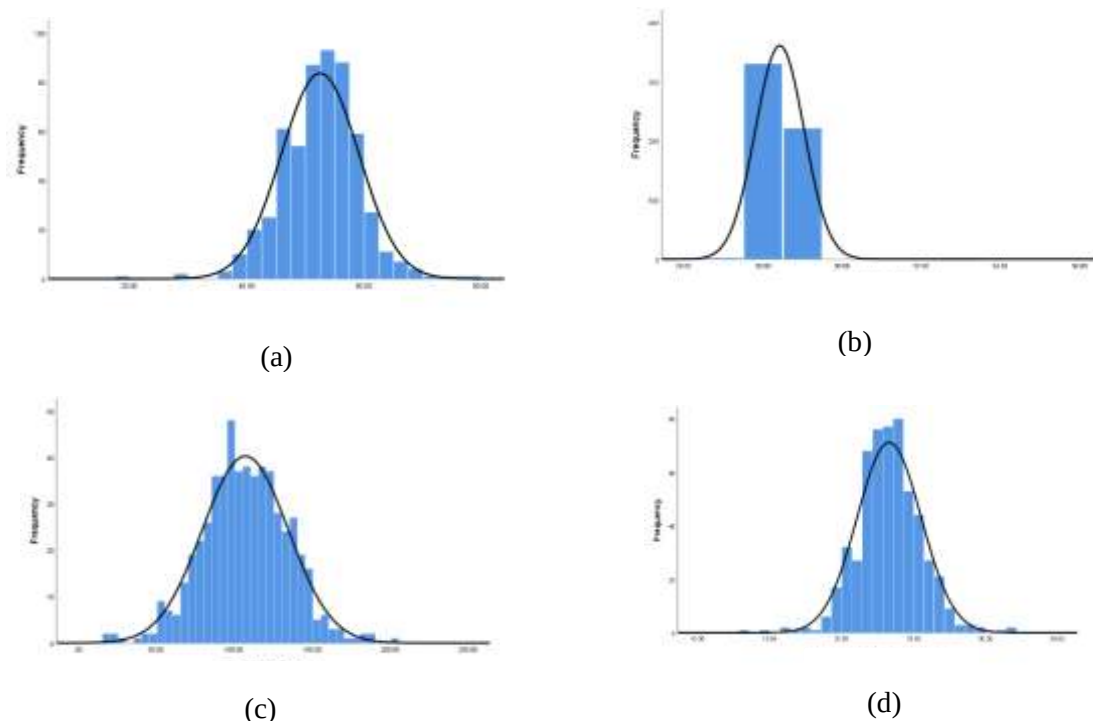


Figure 1. Distribution diagram of the F₅ population based on observed characters, a) plant height, b) flowering age, c) number of seeds, d) weight of 100 seeds

Population distribution patterns can be estimated through the activity and number of genes responsible for regulating a character, namely based on the skewness value (curve bulge) for gene action and the kurtosis value (curve sharpness) to see the number of genes [11]. Figure 1 shows that the analysis of the distribution pattern of the F₅ population for plant height, number of seeds.plant⁻¹, and weight of 100 seeds.plant⁻¹ has a platykurtic graph shape. Plant characteristics with platykurtic graphs are controlled by many genes. The flowering age characteristic has a leptokurtic graph shape. Characteristic with leptokurtic graph is controlled by a small number of genes [15].

Table 2. Gene number on the characteristics of the F₅ population resulting from three-parent cross

Character	Kurtosis±SE	Z-Kurtosis Test	Gene Number
Plant height	1.93±0.21	9.28**	Many
Flowering age	20.39±0.21	98.14**	Few
Number of seeds.plant ⁻¹	0.48±0.21	2.33*	Many
Weight of 100 seeds.plant ⁻¹	1.94±0.21	9.32**	Many

Note: SE = Standard error, * = significant at the 5% level, ** = significant at the 1% level.

According to Sayurandi [16], the kurtosis value is used to estimate the number of gene functions to see the control of the observed quantitative characters. The division in the kurtosis value is that if the kurtosis value > 3, then the population distribution is called leptokurtic, and few genes influence this character, whereas if the kurtosis value < 3, then the distribution pattern is called platykurtic, with the character being influenced by many genes. Table 2 presents the results of the kurtosis test analysis for plant height, number of seeds.plant⁻¹, and weight of 100 seeds.plant⁻¹, which are influenced by many genes with a

platykurtic graph form. Meanwhile, the character of flowering age is influenced by a few genes where the graph is leptokurtic.

The Z-kurtosis test analysis revealed a significant effect on the number of seeds at the 5% level, while plant height, flowering age, and weight of 100 seeds.plant⁻¹ showed highly significant differences at the 1% level. Positive or negative kurtosis values can each describe the number of additive genes or the small gene number involved in regulating an individual plant character [17].

4. Conclusions

The F5 population resulting from a cross between 3 parents has skewness and kurtosis analysis results, that the plant height, number of seeds, and weight of 100 seeds are controlled by additive genes and are influenced by many genes with a platykurtic graph form. Meanwhile, the flowering age is influenced by complementary epistatic genes and is influenced by a few genes with a leptokurtic graph form. Analysis of skewness and kurtosis is used to reveal information on the basic nature of action and number of genes governing plant character.

5. Acknowledgments

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