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Genetic variability of soybean pod maturity traits for environmental resilience and stress resistance using the Hayman model

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ABSTRACT

BACKGROUND AND OBJECTIVES: The ripening of soybean pods plays a crucial role in the plant's growth and development phases, as it is closely connected to the scheduling of planting practices and optimizing time efficiency in agricultural activities. Understanding the genetic factors influencing pod maturity in soybean plants is essential for the effective development of a breeding program. Diallel analysis is one of the breeding methods utilized to evaluate the effects of these genes by measuring various quantities to derive genetic estimates. This study was conducted to examine the nature and magnitude of gene action involved in the inheritance of soybean pod maturity to inform breeding strategies in the face of environmental changes. The objective of this study was to explore the characteristics and degree of gene action related to the inheritance of soybean pod maturity, aiming to offer valuable insights for the development of breeding strategies that can withstand environmental fluctuations.
METHODS: The study material for crosses is early maturing (< 80 days) soybean genotypes, namely GJ-1, GJ-2, and GJ-3, and late maturing (> 90 days), namely DL-1 and DL-2. These elders were crossed, including backcrossing (reciprocal). This diallel cross uses Griffing's 1st method. The entire study material consisted of 5 parents and 20 combinations of crosses between different parents (10 combinations of hybrids and its reciprocally), resulting in 25 treatments. Moreover, the genetic materials were planted utilizing a randomized block design, with three repetitions. The analysis of cross-diallel statistics and the estimation of genetic variant components were performed following the Hayman method.
FINDINGS: The study showed that soybean pods' maturity (GJ-1, GJ-2, GJ-3, DL-1, and DL-2) had complex gene actions, namely additive, non-additive and reciprocal effects. The imperfect dominant gene action found in genotypes GJ-1, GJ-2, GJ-3, DL-1, and DL-2 shows a small chance of getting offspring that has an earlier maturity than the early maturing parent. The genes that determine the age-related features of mature pods are interconnected, and each allele contributes to these traits. The maturity of the pods in genotype DL-2 is the parent, which has a proportion of recessive alleles, while Dl-1, GJ-1, GJ-2, and GJ-3 are the parents, which have a proportion of dominant alleles that influence character expression age of maturity of pods.
CONCLUSION: Given the important role of the additive gene action observed in the genotypes studied, selection for earlier pod maturity could be initiated in the early generations of soybean breeding programs. These results highlight crucial considerations for the advancement of soybean varieties that are more robust against environmental challenges and capable of adapting to shifting climatic circumstances. Breeding early maturing genotypes can reduce the susceptibility of soybean plants to adverse environmental factors such as short growing season drought. By emphasizing genetic characteristics that facilitate early maturity, breeders have the opportunity to create soybean varieties that are more adaptable to a range of environmental conditions, especially in regions where the growing season is limited. In addition, these early-maturing varieties can provide farmers with greater flexibility in planting schedules and increase yields, thereby enhancing food security. Leveraging these genetic insights enhance the sustainability and resilience of agricultural systems in response to the pressing global environmental challenges.

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INTRODUCTION

The maturity of soybean pods is a critical phase in the growth and development cycle, as it is directly impacts planting schedules and farming efficiency. The implementation of crop rotation leads to short cropping patterns, which in turn demand the selection of plants that have rapid growth phases. Furthermore, global climate change can lead to environmental shifts, including drought stress. These farming conditions underscore the significance of water accessibility at vital growth stages, particularly during the generative phase or pod-filling stage in soybean plants. Consequently, early-maturing soybean varieties with high productivity are in deman. Soybean pod maturity is usually evaluated from the date of planting until around 90 percent (%) of the pods have changed to yellow or brown, depending on their initial color. In Indonesia, soybean maturity is classified into five categories: very early (< 70 days), early (70–79 days), medium (80–85 days), late (86–90 days), and very late (> 90 days). The development or refinement of soybean varieties that achieve high yields and optimal maturity is vital for increasing production in challenging and stress-affected conditions. Through a soybean breeding program using single crosses between parental lines, pod maturity traits can be optimized for specific agricultural needs, for example to addresas the problem of environmentally stressed agricultural land. Understanding genetic parameters is crucial during the initial stages of improving pod maturity characteristics. Likewise, establishing a successful breeding approach is significantly tied to the understanding of gene functions that govern the traits intended for selection (Adetiloye *et al.*, 2023). A plant traits can be estimated using genetic approaches, particularly by examining gene action (Mahesh *et al.*, 2014), which is often evident in the quantitative traits (Bhor *et al.*, 2014). Grasping the genetic factors that control a trait is crucial for breeders, as it aids in the selection of effective breeding approaches (Bhor *et al.*, 2014; Sharma and Maloo, 2017). Estimating the genetic parameters of a character from the parents of the cross material is important to study before preparing a breeding program. One of the breeding methods used to determine the action of these genes is diallel cross analysis using the Hayman method, which can measure quantities to illustrate genetic predictions. Diallel crosses can be used to investigate the genetic structure of pure line populations (Virk *et al.*, 1985), making it easier to separate the components of variation from different genotypes, whether genotypic, phenotypic, or environmental variance (Chukwu *et al.*, 2016). Utilizing the Hayman method enables the confirmation of additive and non-additive effects in diallel cross populations. Additionally, it facilitates the assessment of population diversity, which is classified into components arising from additive, dominant, and reciprocal influences (Makumbi *et al.*, 2018). This method has been widely utilized to estimat the genetic parameters of various traits, such as the yield components of chili (Istiqlal *et al.*, 2014), the productivity and quality of papaya plants (Cardoso *et al.*, 2015), the maturity and yield of spring wheat (Afridi *et al.*, 2017) and several characteristics in corn (Begum *et al.*, 2018). Research on soybean plants has been carried out using various parental genotypes and traits. Bhor *et al.* (2014) demonstrated that the maturity of soybean pods is primarily influenced by predominant additive genes with an epistatic effect. Similarly, investigations into single crosses of soybean genotypes indicate that a number of traits are mainly governed by additive gene action (Soares *et al.*, 2023). In a breeding program, the significant role of additive genes in determining yield-related traits in soybean plants allows for efficient and effective traits improvement (Otusanya *et al.*, 2022). Additionally, studies on mung bean plants have shown that early maturity is controlled by both additive and dominant gene effects (Khattak *et al.*, 2001). This study aimed to examine the nature and scope of gene action associated with the inheritance of soybean pod maturity, with the intention of delivering insights that could inform the creation of breeding strategies resilient to changes in the environment. This study was conducted in Malang, East Java, Indonesia during the year 2022.

MATERIALS AND METHODS

Plant genetic material

The plant materials used in this study consisted of soybean genotypes, each exhibiting uniformity in their key characteristic, the maturity period of the pods. These genotypes were selected as parental lines for hybridization and included GJ-1 (pod maturity at approximately 76 days), GJ-2 (approximately 77 days), GJ-3 (approximately 70 days), DL-1

(approximately 92 days), and DL-2 (approximately 91 days). In this study, the soybean genotypes demonstrate uniform characteristics in pod maturity, as they have been refined to stabilized generations through prior selection processes. Each parental line was crossed, including reciprocal backcrosses, to establish a complete diallel cross population (5 × 5). The diallel cross design was based on Griffing's method 1 (Griffing, 1956). The Griffing's method 1 for diallel analysis facilitates the estimation of genetic parameters directly in the first generation (F1), eliminating the need to develop a second generation (F2) population or perform backcrossing. This study incorporated five different parental genotypes and 20 cross combinations among these lines, featuring 10 reciprocal F1 hybrids, thereby producing a total of 25 unique treatments.

Study site and experimental procedures

The study was conducted on rainfed land located at an elevation of 335 meters above sea level in Malang Regency, East Java, Indonesia in 2022. During the study period in April, May, and June 2022, the recorded rainfall was 240 millimeters (mm), 199 mm, and 136 mm, respectively. Simultaneously, the average air temperatures for these months were noted to be 25.4 degree celcius (˚C), 26.0 ˚C, and 24.6 ˚C, respectively. The soil at the site was classified as Alluvial, and the area experienced rainfall type A, according to the Schmidt and Ferguson classification system. A randomized block design was employed for the experiment, with genotype being the only factor considered. The experiment included three replications. considered to be consistent, which meant that any observed differences in treatments were ascribed to genetic diversity among the populations. The plant material included 15 individual plants per parent, F1, and reciprocal F1 populations, resulting in a total of 25 treatments × 3 replications × 15 plants, giving a total population of 1,125 plants. The planting distance was set at 40 centimeter (cm) × 15 cm, with one plant per hole. Fertilizer application involved 50 kilograms per hectare (kg/ha) of Urea, 100 kg/ha of super phosphate (SP-36), and 75 kg/ha of potassium chloride (KCl), which were distributed between the plant rows seven days after planting. Observations regarding pod maturity were conducted by tracking the number of days from planting until 90% of the pods achieved the eighth reproductive stage (R8) of soybean, characterized by the pods changing to yellow or brown, based on their original color (PCARRD, 1985). Data were collected for all individual plants.

Data analysis

An analysis of variance was carried out utilizing the Hayman method to validate the presence of additive and non-additive genetic effects in the populations resulting from the diallel cross (Mather and Jinks, 2013). This method, commonly referred to as the Jinks-Hayman diallel analysis, is widely used to assess allele dominance. The results of this analysis are graphically represented by plotting the variance of parental lines (Vr) against the covariance between parental lines and F1 progeny (Wr) (Mather and Jinks, 2013; Singh and Chaudhary, 1977). Hayman's procedure was employed to estimate the genetic variance components and statistical parameters associated with the diallel crosses (Hayman, 1954a; Hayman, 1954b; Singh and Chaudhary, 1977). The sources of variation in the Hayman diallel cross method are summarized in Table 1.

RESULTS AND DISCUSSION

The growth of soybean plants demonstrated optimal development, with no significant pest or disease attacks observed during the growth period. As noted in the reference (PCARRD, 1985), the assessment of pod maturity showed that the plants in the generative phase had achieved. The primary focus of these observation was the pod maturity period, which served as the key parameter for estimating genetic components. Consequently, the outcomes correspond with the recognized methodology and research framework. The analysis of variance using the Hayman method revealed statiscically significant differences at the 5% level for the diversity components, including additive effects (a), non-additive effects (b), maternal reciprocity (c), and non-maternal reciprocity (d) (Table 2). The results emphasize the significant contributions of both additive and non-additive effects in the regulation of soybean trait inheritance, with a particular focus pod maturity (Waly and Ibrahim, 2021). The presence of a significant additive effect shows that genes influencing pod maturity traits are interconnected, with each allele playing a role in shaping this characteristics (Mather and Jinks, 2013; Bezerra *et al.*, 2017). Soybean pod maturity is regulated

Table 1: Analysis of variance of diallel cross using Hayman method

Source of variation	Degrees of freedom	Sum of squares (SS)	Mean squares (MS)	F count (5%)
a: additive effect	n-1=4	SS_C	MS_C	MS_C/MSe'
b: non-additive effect	½n(n-1)=10	SS_D	MS_D	$MS_{D/}$ MSe'
b_1 : direction	1	SS_E	MS_E	$MS_{E/}$ MSe'
b_2 : distribution	n-1=4	SS_F	MS_F	$MS_{F/}$ MSe'
b_3 : specific combining ability	½n(n-3)=5	SS_G	MS_G	$MS_{G/}$ MSe'
c: maternal reciprocal	n-1=4	SS_H	MS_H	$MS_{H/}$ MSe'
d: non-maternal reciprocal	½n(n-1)(n-2)=6	SS_I	MS_I	$MS_{G/}$ MSe'

Remarks: n: number of elders; a: test the influence of additive effects; b: test the influence of domin ance of Genes; b1: deviation test (deviation) of the F1 average from the parent average; b2: test to determine the deviation of the average dominance of F1¬ between rows; b3: dominant deviation test specific for a particular cross; c: reciprocity test caused by maternal effects; d: reciprocity test caused by nonmaternal effects. MSe': mean square error in combined power analysis

Table 2: Analysis Hayman variance of the method of 5 x 5 complete diallel

Source of variation	Degrees of freedom	Sum of squares (SS)	Mean squares (MS)	F calculation (5%)	F table
a: additive effect	4	232.54	58.14	29.83*	2.57
b: non-additive effect	10	184.51	18.45	9.47*	2.03
b_1 : direction	1	32.1	32.1	16.68*	4.04
b_2 : distribution	4	48.88	12.22	6.27*	2.57
b_3 : specific combining ability	5	96.92	19.38	9.95*	2.41
c: maternal reciprocal	4	107.59	26.90	13.80*	2.29
d: non-maternal reciprocal	6	72.81	12.13	6.23*	2.29

Remark: ns = not significant at P 0.05, * ,** significant at P 0.05 and 0.01, respectively.

by genes denoted as *E* (late maturity) and *e* (early maturity). Research has identified the genes *e1* through *e7* as key regulators of early maturity in soybeans. These results imply that the maturity of soybean pods is regulated by a variety of genes, emphasizing the polygenic aspect and the complexity of genetic influences this traits. Nevertheless, the specific early maturity genes present in the parental lines utilized in this study have remain unidentified. Similar findings have been reported in research on kenaf plants, where the age at 50% flowering (closely linked to the harvest period) exhibited similar genetic patterns (Al-Mamun *et al.*, 2022). Concurrently, a substantial non-additive effect highlights the role of parental lines with dominant alleles in affecting the expression of traits related to pod maturity (Mather and Jinks, 2013; Waly and Ibrahim, 2021). Furthermore, the b component is further divided into three subcomponents: the mean deviation of dominance in F1 hybrids from the average of the parents (b1), differences in the distribution (number) of dominant alleles among the five parental lines (b2), and the presence of specific dominant effects associated with particular crosses (b3). This approach was also utilized to estimate gene action in soybean plants (Çınar and Ünay, 2023). The b3 component corresponds to the specific combining ability variance in Griffing's diallel analysis model (Mather and Jinks, 2013; Kearsey *et al.*, 1997). The analysis of variance related to reciprocal maternal and non-maternal effects on pod maturity demonstrated significant outcomes, highlighting the substantial impact of the female parent on the maturity traits in the oldest cross combinations.

The Jinks-Hayman analysis was used to test the suitability of the model. Results indicated that the variance of the r-th derivative (Vr) and the covariance between the parent and r-th derivative parent (Wr) across rows were homogeneous, with a F-value

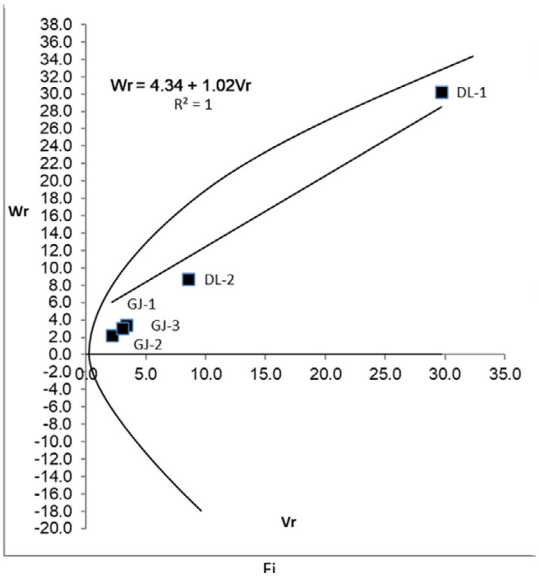

Fig. 1: Wr/Vr graphs of maturity of F_1 generation derived from a diallel cross
Remark: GJ-1: pod maturity at approximately 76 days; GJ-2: approximately 77 days; GJ-3: approximately 70 days; DL-1; approximately 92 days; DL-2: approximately 91 days; Wr: covariance; Vr: variance; R^2: R-square

of 0.18, which was not statistically significant. This observation affirms that a fundamental assumption of diallel cross analysis has been fulfilled. Furthermore, the regression coefficient test applied to the Wr/Vr graph provided additional support for the compatibility of the additive-dominance model (Fig. 1). The regression coefficient was found to be significantly different from zero (b≠0) and not significantly different from one (b=1), as shown in Table 3. These results align with those of previous studies (Bezerra *et al.*, 2017) and furhter indicate the absence of interaction effects among the genes controlling the traits (Riyanto *et al.*, 2023).

The regression line on the Vr-Wr graph showed an intercept value of 4.34 ± 1.02. The intercept was considerably above zero and positive, intersecting the ordinate at a point above the origin (0). This results suggests the involvement of incomplete dominance in gene action (Hayman, 1954a). The distribution of Vr and Wr points spread along the regression line reflects the genetic variation present for the observed traits. The analysis reveals that the location of the (Vr, Wr) values on the regression line, characterized by a slope of one, represents the dominance level of each parent. This location is established using Eqs. 1 and 2 (Singh, 2020):

$$Wr = ½D - ¼Fr,\ Vr = ¼D - ¼Fr + ¼H1 \quad (1)$$

$$Fr = 2\Sigma di\ hI\ \theta ri\ (1 - w2) \quad (2)$$

The hi θri value is positive for homozygous dominants and negative for homozygous recessive. Consequently, parents with elevated Fr values are characterized as more dominant, in contrast to those with reduced Fr values, who are considered more recessive. On the (Vr,Wr) graph, lower Vr and Wr points indicate dominant parents and points with higher values indicate recessive parents (Hayman, 1954b). Based on this relative position, genotype DL-1 is the parent with a proportion of recessive alleles, and genotypes DL-2, GJ-1, GJ-2, and GJ-3 have a proportion of dominant alleles. This study provides preliminary insights for improving the early maturing pods trait in soybean, utilizing parental lines with dominant genetic contributions (GJ-1, GJ-2, and GJ-3). Genotypes GJ-1 and GJ-3 have close (Vr, Wr) values (Fig. 1), so it is possible that the parents used have the same ancestor. Such differences can result from modifier genes or genes that have a limited impact on the specific characteristic (Nugrahaeni, 2007). The estimation of genetic parameters for pod maturity, including additive influence (D), dominant effects (H1, H2, and

Table 3: Regression of covariance (Wr) on variance (Vr) for maturitycharacter of 5 x 5 complete diallel

Wr/Vr regression	Test results
Regression equation	4.34 + 1.02 Vr
t-test for b = 0	11.47 **
t-test for b = 1	0.27 tn

Remark: ns= not significant at P 0.05, ** significant at P 0.01

Table 4: Estimation of genetic and environmental parameters in the Jinks-Hayman model for maturity of soybean pods

Parameter	Value	p<0.05	Standard deviation (SD)
D (additive effect)	38.42	*	± 1.41
H (dominan effect)			
H_1	17.99	*	± 3.81
H_2	11.48	*	± 3.46
h^2	3.29	*	± 2.33
F (gene distribution)	22.23	*	± 3.52
E (environmental effect)	1.36	*	± 0.58
$(H_1/D)^{½}$ (Mean dominant degree)	0.68		
$(H_2/4H_1)$ (Proportion of genes with + and – effects to the parents)	0.16		
h^2/H_2 (Number of gene groups that control character and indicate dominance)	0.29		
$((4DH_1)^{½}$ +F)/$((DH_1)^{½}$/-F) (Proportion of dominant and recessive genes in parents)	2.46		
0,5F/$(D(H_1-H_2)^{½}$ (dominant gene action is relatively constant between loci.)	1.14		
Narrow heritability (%)	0.89		

h2), gene distribution (F), and environmental influence (E) showed statistically significant results at the 5% level (Table 4). These genetic parameters are critical in determining trait expression (Quamruzzaman *et al.*, 2020). The significant values of D and H1 suggest that both additive and dominance genetic effects contribute to the inheritance of pod maturity traits. This result corresponds with the findings of Adetiloye *et al*. (2023), even though their investigation examined different parental lines. It was determined that the additive gene effects are more pronounced than the dominance effects, indicating that the pod maturity characteristics of the parental lines can be reliably inherited by their progeny. While the influence of dominant genes action is less pronounced, it still plays a supporting role in trait expression (Ibram *et al.*, 2024). Similar findings were reported by Silva e Souza *et al.* (2020), who observed that additive gene action predominantly controls pod maturity traits in soybean crosses between distinct parental lines. Furthermore, these genetic parameters also assess that there is no interaction between alleles at different loci.

Parameter H2 represents the degree of dominant gene influence observed in a larger set of parents. The value of H1 minus H2 is positive, indicating that the frequencies of the alleles are not the same, namely u≠v. In this case, u is the frequency of alleles that have a positive effect, and v is the frequency of alleles that have a negative effect. The H2/4H1 ratio formula produces a value of 0.16 (< 0.25) as the maximum value of the ratio and will be achieved if u=v (Mather and Jinks, 2013; Singh and Chaudary, 1977). The results of calculating the H2/4H1 ratio in accordance with the diallel variant analysis method of Hayman (1954a) are shown by a real source of b2 diversity, namely the asymmetry of allele frequencies, which shows dominance in the parents used. While the H2/4H1 ratio reflects distribution asymmetry, it does not reveal information about other allele types. The determination of the allele type can be achieved through the use of Eq. 3 based on the ratio (Singh and Chaudary, 1977):

4DH1)½+F/ DH1)½/-F or kD/kR (3)

The ratio (kD/kR) indicates the overall proportion of dominant genes compared to recessive genes among all the parent samples. With a resulting value greater than one (2.46), it can be inferred that the parents in the diallel cross carry dominant alleles. Dominant

alleles are more numerous than recessive alleles and are supported by the positive genetic parameter F (Table 3). If the value of (H1/D)½ is equal to one ((H1/D)½=1), it is an indication of perfect dominance, and if the ratio value is greater than one (H1/D)½ >1), it is an indication of over dominant gene action (Mather and Jinks, 2013; Singh and Chaudary, 1977). The average dominance level, calculated from all loci in the parents, reveals an imperfect dominance value of 0.68. The action of the imperfect dominant gene in this population is graphically shown by the intercept that intersects the ordinate above the origin on the Wr/Vr graph (Fig .1). The ratio 0.5F/(D(H1-H2))½ is around one (1.14), indicating that dominant gene action is relatively constant between loci. When the ratio is below one (<1), it indicates that the dominant gene action observed is variable between dominant loci at a particular locus and does not signify dominance at another locus (Mather and Jinks, 2013). The h2/H2 ratio estimates the number of genes involved in expressing maturity in this population. Based on the value of 0.29, it can be inferred that only a small group of genes has a minimal impact on the control of maturity in soybean plants. It appears that the maturity age of pods in the crossing pairs is governed by several minor genes, suggesting a polygenic mode of inheritance. This suggests that a tandem selection strategy could be effective in breeding programs. In this approach, individual traits are selected sequentially in each cycle, gradually accumulating genetic improvements in the desired traits over successive cycles. This is also in line with Fig. 1, where the values (Vr, Wr) are close to each other. In this instance, the gene group may not reliably represent the total count of genes (Singh and Chaudary, 1977). The heritability value of pod maturity in this study was relatively high. High heritability estimates can sometimes be overestimated when measured in a single environment, particularly if the standard error is larger than the heritability value. Such factors could hinder the dependability of heritability estimates that are essential for directing breeding efforts. As highlighted by Mertler and Reinhart (2016), smaller standard error values improve the accuracy of sample data in representing the broader population, especially when data are derivied from multiple environment. Additionally, this is due to the genetic system that regulates pod maturity in the parent group under investigation, which is determined by additive genes. Thus, selection to obtain early maturing soybean lines can be started in the early generations, and the pedigree selection method can be effectively used (Aamer and Ibrahim, 2020). In the presence of additivity characters, it is possible to select early maturity elders and combine the maturity characteristics of several elders in order to obtain a source of early maturity or to obtain zuriat (Nugahaeni, 2007). In soybean breeding programs, selection for beneficial morphological traits can be performed in the initial generations, as the dominant additive effects are evident during the segregation process (Waly and Ibrahim, 2021). This results in time savings in evaluation, contributing to greater breeding program efficiency. To ensure genetic diversity and adaptability to unforeseen environmental changes, long-term breeding strategies can utilize a range of techniques, such as hybridization, irradiation, biotechnology, or the introduction of new genetic material.

CONCLUSION

The rice-rice-soybean cropping system in Indonesia demands the development of early-maturing soybean varieties, defined as those reaching 90% pod maturity (yellow or brown pods) within 80 days after planting. Such varieties play a vital role in optimizing the restricted planting timeframe, while also delivering extra advantages by mitigating biotic and abiotic stresses. Consequently, breeding programs focused on producing early-maturing soybean varieties are critical. Attaining this aim necessitates an in-depth comprehension of the genetic factors that regulate pod maturity, enabling the selection of effective breeding strategies. This study employed diallel analysis to estimate genetic parameters, utilizing three early-maturing soybean genotypes (GJ-1, GJ-2, and GJ-3) and two late-maturing genotypes (DL-1 and DL-2) as parents. The results suggest that pod maturity in soybean plants is governed by a complex interplay of genetic factors, including additive, non-additive, and reciprocal effects, highlighting the critical role of the female parent. Additive and dominant effects are essential for effective selection in breeding initiatives, with additive gene action exerting a more substantial influence on pod maturity than dominance effects. This suggests that the traits can be effectively inheritaed, enabling the initiation of breeding programs in early generations, with methods such as pedigree selection proving effective. The challenge of developing progeny with earlier maturity than the

earliest-maturing parents arises from the presence of imperfect dominant gene action in all parental sources. A link between genes influencing pod maturity has been identified, where each allele contributes to the expression of pod maturity traits. Among the genotypes studied, DL-2 is characterized by a higher proportion of recessive alleles, while DL-1, GJ-1, GJ-2, and GJ-3 prossess dominant alleles that influence expression of pod maturity traits. These results emphasize the genetic intricacies associated with pod maturity traits in soybeans, suggesting that while dominant genes influence their expression, the primary mechanism for advancing maturity lies in additive gene action, which can be leveraged through targeted breeding strategies. The integration of morphological selection in early generations can enhance efficiency and save time in soybean breeding programs, ultimately contributing to the development of improved early-maturing lines.

AUTHOR CONTRIBUTIONS

G.W.A. Susanto conceptualized the study idea, performed data analysis, interpreted the results, and drafted the initial manuscript. A. Sulistyo was involved in data collection, drafting the initial manuscript, and finalizing the manuscript. M.J. Mejaya contributed to the study design and provided critical input during the finalization of the manuscript. F.C. Indriani carried out data analysis, interpreted the findings, and assisted in drafting the initial manuscript. Y. Prayogo supported the data collection process and contributed to drafting the initial manuscript. R.D. Purwaningrahayu was actively involved in data collection and drafting the initial manuscript. R. Budiono also contributed to data collection and drafting the initial manuscript. S.W. Indiati participated in data collection and conducted the literature review. M.S.Y.I. Bayu contributed to data collection and documentation throughout the study.

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CONFLICT OF INTEREST

The authors declare that there is no conflict of interests regarding the publication of this manuscript. In addition, the ethical issues, including plagiarism, informed consent, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy have been completely observed by the authors.

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ABBREVIATIONS

%	Percent
˚C	Degree Celcius
a	Additive effects
b	Non-additive effects
b1	Direction
b2	Distribution
b3	Specific combining ability
c	Maternal reciprocal
cm	Centimeter
d	Non-maternal reciprocal
F1	First generation
F2	Second generation
ha	Hectare
KCl	Potassium chloride
kg	Kilogram
mm	Millimeter
MS	Mean squares
n	Number of elders

R8	The eighth generative phase of soybean
SP-36	Super phosphate
SS	Sum of squares
Vr	Variance of parental lines
Wr	Covariance between parental and F1 progeny

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