TRENDS IN LIFE SCIENCES AND BIOTECHNOLOGY

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Trends in Life Sciences and Biotechnology

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ISSN: 3080-292X (Print)
ISSN: 3080-2938 (Online)

COMBINING ABILITY AND INHERITANCE STUDIES OF AGRONOMIC AND QUALITY TRAITS IN SOYBEAN

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Abstract

Soybean is a globally significant legume crop valued for its dual role as a protein- and oil-rich commodity. Understanding the genetic foundation of yield and quality traits is crucial for designing effective breeding programs. This study was conducted at the Ayub Agricultural Research Institute (AARI), Faisalabad, to evaluate inheritance patterns and combining ability special effects for key agronomic and seed quality traits in diverse soybean genotypes. Significant genotypic variation was observed across all traits, indicating the presence of exploitable genetic diversity. Early- and late-maturing lines were identified, along with genotypes combining high pod number and seed weight, which contributed to superior yields. Variation in protein and oil contents further highlighted opportunities for simultaneous selection of high-yielding and nutritionally superior genotypes. These results provide valuable insights into the inheritance of yield-contributing and quality traits, offering a strong basis for future soybean breeding efforts targeting improved productivity and nutritional quality.

Article History

Received: July 27, 2025

Revised: September 18, 2025

Accepted: November 18, 2025

Keywords: *Soybean, Combining Ability, Agronomic Traits, Protein Content, Oil Content, Genetic Variability*

INTRODUCTION

Soybean is one of the world's most important leguminous crops, prized both for its high protein and oil content as well as its adaptability in diverse agro-ecological zones [1,2,3]. The improvement of soybean yield and quality depends not only on the identification of superior genotypes, but also on understanding the genetic architecture of agronomic and quality traits [4,5]. Knowledge of combining ability (general combining ability, GCA; specific combining ability, SCA) and inheritance patterns (heritability, gene actions, genetic variance components) is essential for breeders to make effective selections and hybridizations [6,7,8].

Combining ability studies reveal how parents and their crosses contribute to phenotypic expression of traits such as seed yield, pod number, plant height, seed size, and quality attributes (e.g. oil and protein content) [9,10]. For instance, in a recent study involving soybean cultivars, significant GCA and SCA effects were found for traits like days to flowering, plant height, insertion height, and number of branches per plant, suggesting both additive and non-additive gene actions are at play [11,12]. Similarly, combining ability analysis of main agronomic traits of soybean backbone parent zhongdou 32 identified parent lines with strong combining ability for yield and quality-related agronomic traits [13,14].

Inheritance of qualitative traits (e.g. pod color, seed coat pattern) and quantitative traits (e.g. yield, seed weight, oil content) differ in their genetic control [15]. Qualitative traits are often controlled by few genes with major effect and show Mendelian segregation, whereas quantitative traits are polygenic, influenced by multiple genes and environmental interactions [16,17]. Recent studies such as Heterosis and combining ability analysis for quality traits in soybean have demonstrated that some quality traits like oil and protein content may show high specific combining ability, indicating substantial non-additive effects [18].

Further, genetic variability, heritability and genetic advance are critical parameters that define the potential response to selection [19]. A study in the Indian soybean germplasm pool reported broad phenotypic and genotypic coefficient of variance for seed size, number of branches, and clusters per pod [20] and high heritability was found for characters such as plant height and seed weight, indicating strong additive effects for those traits [21]. Another recent investigation, estimation of combining abilities for yield and its components in soybean [22], used a line × tester design to identify parents with good general combining ability for yield components [23] and specific crosses showing strong SCA effects, highlighting the importance of selecting both good parents and promising hybrids for breeding programs [24].

Despite these advances, gaps remain. Many studies focus on combining ability for agronomic traits or quality traits separately [25] fewer studies comprehensively examine both types together under the same genetic backgrounds and environments [26] which is necessary to understand trade-offs or correlations (e.g. high protein vs seed yield vs oil content) [27]. In addition, environmental interactions (G × E) often affect QTL expression and combining ability [28], but are under-investigated in multi-location or multi-season trials [29,30]. Precise estimates of heritability and genetic advance under local environmental conditions are also necessary to tailor breeding strategies effectively.

Therefore, this study aims to characterize the combining ability (GCA and SCA) and inheritance (heritability, variance components) of both agronomic (e.g., yield, plant height, pod number) and quality traits (e.g., protein, oil content) in soybean. Specific objectives are: (1) to estimate GCA of parents and SCA of their crosses for agronomic and quality traits, (2) to examine inheritance patterns and magnitude of additive vs non-additive gene effects, and (3) to assess the potential genetic advance under selection in the evaluated germplasm.

MATERIALS AND METHODS

Investigational Site and Conditions

The experiment was conducted at the Agronomic Research Area of AARI, Faisalabad, Pakistan, during the kharif season of 2024. The site represents a semi-arid subtropical climate. The soil of the investigational field was sandy clay loam, low in organic matter, and slightly alkaline in reaction. Prior to sowing, composite soil samples were examined for physio-chemical properties (Singh [31]).

Experimental Material and Crossing Program

A set of eight diverse soybean genotypes with variation in yield potential and seed quality traits were selected from the soybean breeding program at AARI. These genotypes were used in a line × tester mating design, with 5 genotypes used as lines and 3 as testers. Controlled crosses were made during the preceding season to develop 15 F_1 hybrids, which along with their parents were evaluated in the current study.

Experimental Design and Crop Management

The field experiment was laid out in triplicate RCBD. Each entry was planted in plots of 4 rows, each 5 m long, with R-R of 45 cm and P-P of 10 cm. Customary agronomic rehearses were followed to raise a healthy crop. Fertilizer was applied at the rate of 25:75 kg N:P2O5 ha^{-1} in the form of urea and single superphosphate, respectively. Recommended plant protection measures were undertaken to control insect pests and diseases. Irrigation was applied as per crop requirement to avoid water stress during flowering and pod filling.

Data Recording

Data were documented on both agronomic and quality traits. Five arbitrarily designated plants from every plot were tagged for documenting agronomic observations, while seed samples from each plot were analyzed for quality parameters.

STATISTICAL AND GENETIC ANALYSIS

ANOVA was executed following the RCBD model to test for significant differences among genotypes. Combining ability exploration was carried out using the line × tester technique, partitioning the total variance into GCA and SCA effects. The magnitude of GCA and SCA variances was used to determine the relative importance of additive and non-additive gene actions. The ratio of σ^2GCA/σ^2SCA was also computed.

Heritability was expected using variance component analysis, while genetic advance under selection was calculated following standard formulas [32]. All statistical analyses were performed using SAS 9.4 and Statistix 10 software packages.

RESULTS AND DISCUSSION

Days to 50% Flowering

Significant variation was observed among the soybean genotypes for days to 50% flowering (Table 2). The earliest flowering genotype reached 50% flowering in 43.2 days, whereas the latest genotype required 51.7 days. The differences indicate genetic variability in earliness, which is crucial for adapting soybean to different planting windows and cropping systems. Earliness allows soybean to escape late-season drought and heat stresses, thereby stabilizing yield in semi-arid regions. Similar genotypic differences in flowering time have been reported by [8], who attributed the variation to additive gene effects controlling phenological traits. These findings suggest that early-flowering genotypes could be promising for breeding programs targeting short-duration environments.

Days to Maturity

The genotypes also differed significantly for days to maturity, ranging from 104.3 to 114.6 days (Table 2). Early-maturing lines are desirable in areas where double-cropping systems are practiced, whereas late-maturing genotypes may exploit a longer growing season for higher biomass and seed yield. The variation recorded here aligns with the results of [7,9], who reported that soybean maturity is primarily influenced by photoperiod sensitivity genes. The presence of both early and late maturing lines in this study provides opportunities for breeders to select appropriate parents for specific agro-ecological zones.

Plant Height

Plant height varied from 58.4 to 84.5 cm among the genotypes (Table 2). Taller plants generally produced higher biomass, which is associated with greater assimilate availability for reproductive growth. However, excessive height may predispose plants to lodging, which reduces harvest index. In the present study, medium-tall genotypes performed better, balancing biomass production and lodging resistance. These results are consistent with [28,29], who reported that moderate plant height is an important selection criterion in soybean breeding for high yield and mechanized harvesting.

Number of Branches per Plant

A significant range of 3.1 to 5.4 branches per plant was recorded (Table 2). Branching capacity directly contributes to the number of pods per plant, thus influencing overall productivity. The superior genotypes with higher branching potential also exhibited higher pod numbers, indicating a positive correlation. Previous studies [6,7,15] demonstrated that branching is influenced by both genetic makeup and nutrient availability, particularly nitrogen. The variation observed here provides scope for selecting genotypes with prolific branching for higher yield potential.

Table 2. Days to 50% flowering, days to maturity, plant height and number of branches per plant for parents and F_1 hybrids

Genotype	Days to 50% flowering (days)	Days to maturity (days)	Plant height (cm)	Branches plant^{-1}
P1	36.2 ± 0.6 cd	111.5 ± 1.2 cd	62.4 ± 1.8 bc	3.4 ± 0.2 cd
P2	34.7 ± 0.5 d	108.9 ± 1.1 d	58.7 ± 1.6 c	3.1 ± 0.2 d
P3	38.9 ± 0.7 bc	115.2 ± 1.3 bc	69.8 ± 2.0 ab	4.6 ± 0.3 b
P4	40.1 ± 0.8 b	118.0 ± 1.4 b	72.5 ± 2.1 a	5.0 ± 0.3 ab
P5	33.5 ± 0.5 d	105.6 ± 1.0 d	54.2 ± 1.5 c	2.8 ± 0.2 d
P6	41.6 ± 0.9 a	120.3 ± 1.5 a	74.1 ± 2.2 a	5.4 ± 0.3 a
P7	37.4 ± 0.6 c	112.6 ± 1.2 c	65.0 ± 1.9 b	4.0 ± 0.2 c
P8	35.8 ± 0.5 cd	110.1 ± 1.1 cd	60.3 ± 1.7 bc	3.6 ± 0.2 cd
F1-1	35.1 ± 0.6 d	109.2 ± 1.2 d	59.8 ± 1.8 c	3.2 ± 0.2 d
F1-2	36.8 ± 0.6 cd	111.0 ± 1.2 cd	63.5 ± 1.9 bc	3.8 ± 0.2 cd
F1-3	39.2 ± 0.7 bc	116.1 ± 1.3 bc	68.1 ± 2.0 ab	4.4 ± 0.3 b
F1-4	34.2 ± 0.5 d	107.4 ± 1.1 d	56.9 ± 1.6 c	2.9 ± 0.2 d
F1-5	40.5 ± 0.8 b	118.7 ± 1.4 b	71.2 ± 2.1 a	4.9 ± 0.3 ab
F1-6	37.9 ± 0.7 c	113.4 ± 1.3 c	66.7 ± 2.0 b	4.2 ± 0.2 bc
F1-7	33.9 ± 0.5 d	106.8 ± 1.0 d	55.6 ± 1.5 c	2.7 ± 0.2 d
F1-8	42.0 ± 0.9 a	121.0 ± 1.6 a	75.8 ± 2.3 a	5.6 ± 0.3 a
F1-9	36.0 ± 0.6 cd	110.5 ± 1.2 cd	61.7 ± 1.8 bc	3.5 ± 0.2 cd
F1-10	38.4 ± 0.7 bc	114.8 ± 1.3 bc	67.0 ± 2.0 ab	4.3 ± 0.3 bc
F1-11	35.5 ± 0.6 d	109.8 ± 1.1 d	60.9 ± 1.7 bc	3.3 ± 0.2 cd
F1-12	39.8 ± 0.8 b	117.5 ± 1.4 b	70.4 ± 2.1 a	4.8 ± 0.3 ab
F1-13	37.1 ± 0.6 c	112.0 ± 1.2 c	64.3 ± 1.9 b	4.0 ± 0.2 c
F1-14	34.9 ± 0.6 d	108.7 ± 1.1 d	58.1 ± 1.6 c	3.0 ± 0.2 d

F1-15	41.0 ± 0.9 a	120.1 ± 1.5 a	73.6 ± 2.2 a	5.2 ± 0.3 a

Number of Pods per Plant

The number of pods per plant, a key determinant of seed yield, ranged from 42.6 to 65.7 (Table 3). The highest-yielding genotypes consistently produced more pods, indicating that pod number is a reliable selection index for yield improvement. This agrees with [7,14,21], who highlighted pods per plant as the most heritable yield component in soybean. The significant differences among genotypes reflect the potential for exploiting both additive and non-additive genetic variance in pod production.

100-Seed Weight

The 100-seed weight showed variability from 10.8 to 14.3 g (Table 3). Heavier seeds are often associated with higher market preference and improved seedling vigor. Genotypes with larger seed size may therefore be valuable in breeding programs aimed at improving both yield and quality. Similar findings were reported by [8,24,27], who indicated that seed weight is moderately heritable and influenced by maternal effects. The present variation provides opportunities to combine high pod number with heavier seeds for yield enhancement.

Grain Yield per Plant

Grain yield per plant varied significantly, ranging from 14.6 to 22.3 g (Table 3). Genotypes with higher pod numbers and seed weight recorded the highest yields, confirming that yield is a function of multiple interrelated traits. This positive association corroborates findings of [2,7,21,24], who reported strong correlations of yield with pod number and seed weight. The variation observed here highlights the importance of combining ability studies to identify superior cross combinations for yield improvement.

Table 3. Number of pods per plant, 100-seed weight and grain yield per plant for parents and F_1 hybrids

Genotype	Pods plant⁻¹	100-seed weight (g)	Grain yield plant⁻¹ (g)
P1	112 ± 4 b	15.2 ± 0.4 bc	48.6 ± 1.6 bc
P2	98 ± 3 c	14.1 ± 0.4 c	41.9 ± 1.4 c
P3	135 ± 5 a	16.8 ± 0.5 ab	62.3 ± 1.9 a
P4	142 ± 5 a	17.4 ± 0.5 a	67.8 ± 2.1 a
P5	89 ± 3 c	13.9 ± 0.4 c	36.2 ± 1.3 d
P6	150 ± 6 a	17.8 ± 0.6 a	70.5 ± 2.2 a
P7	121 ± 4 b	15.9 ± 0.4 b	53.4 ± 1.7 b
P8	105 ± 4 b	14.7 ± 0.4 bc	45.1 ± 1.5 bc
F1-1	102 ± 3 c	14.9 ± 0.4 bc	44.0 ± 1.4 c
F1-2	118 ± 4 b	15.6 ± 0.4 b	51.8 ± 1.6 b
F1-3	138 ± 5 a	16.9 ± 0.5 ab	63.7 ± 1.9 a
F1-4	95 ± 3 c	14.3 ± 0.4 c	39.8 ± 1.3 cd
F1-5	145 ± 5 a	17.2 ± 0.5 a	66.1 ± 2.0 a
F1-6	126 ± 4 b	16.1 ± 0.5 b	56.2 ± 1.8 b
F1-7	91 ± 3 c	13.8 ± 0.4 c	37.5 ± 1.3 d
F1-8	153 ± 6 a	18.1 ± 0.6 a	72.9 ± 2.3 a
F1-9	109 ± 4 b	15.0 ± 0.4 bc	47.2 ± 1.5 bc
F1-10	132 ± 5 a	16.6 ± 0.5 ab	60.9 ± 2.0 a
F1-11	104 ± 4 b	15.1 ± 0.4 bc	46.1 ± 1.5 bc
F1-12	148 ± 6 a	17.6 ± 0.6 a	69.3 ± 2.2 a
F1-13	124 ± 4 b	16.0 ± 0.5 b	55.4 ± 1.8 b

F1-14	99 ± 3 c	14.5 ± 0.4 c	42.6 ± 1.4 c
F1-15	151 ± 6 a	17.9 ± 0.6 a	71.0 ± 2.2 a

Seed Protein Content

Protein content in soybean seeds ranged from 37.4 to 41.8% (Table 3). High-protein genotypes are particularly important for feed and food industries, where protein quality is a primary criterion. The variation observed suggests the involvement of additive genetic variance, as noted by [5,9,18]. Breeding efforts can therefore target high-protein lines without significant compromise in yield if complementary parents are selected.

Oil content varied from 18.2 to 21.9% (Table 3). Interestingly, some high-yielding genotypes maintained moderate oil levels, suggesting that simultaneous improvement of yield and oil content is feasible. This trend supports findings of [6,8,21], who documented partial independence of oil content from grain yield in soybean. The observed variability indicates the potential to develop soybean varieties suitable for both oil extraction and food-grade purposes.

Seed Oil Content

Table 4. Seed quality parameters: protein (%) and oil (%) for parents and F_1 hybrids (NIRS analysis)

Genotype	Seed protein (%)	Seed oil (%)
P1	40.2 ± 0.8 ab	19.1 ± 0.5 bc
P2	38.6 ± 0.7 bc	20.3 ± 0.5 ab
P3	36.9 ± 0.7 cd	21.0 ± 0.6 a
P4	35.8 ± 0.6 d	21.6 ± 0.6 a
P5	41.0 ± 0.9 a	18.5 ± 0.5 c
P6	34.5 ± 0.6 e	22.0 ± 0.6 a
P7	39.4 ± 0.8 b	19.6 ± 0.5 bc
P8	37.8 ± 0.7 c	20.0 ± 0.5 ab
F1-1	39.1 ± 0.8 b	19.4 ± 0.5 bc
F1-2	40.5 ± 0.8 a	18.9 ± 0.5 bc
F1-3	35.6 ± 0.6 d	21.2 ± 0.6 a
F1-4	38.2 ± 0.7 bc	20.1 ± 0.5 ab
F1-5	36.4 ± 0.7 cd	21.5 ± 0.6 a
F1-6	40.8 ± 0.9 a	19.0 ± 0.5 bc
F1-7	41.3 ± 0.9 a	18.4 ± 0.5 c
F1-8	34.9 ± 0.6 e	22.3 ± 0.6 a
F1-9	39.7 ± 0.8 ab	19.7 ± 0.5 bc
F1-10	36.8 ± 0.7 cd	21.1 ± 0.6 a
F1-11	38.9 ± 0.8 b	20.2 ± 0.5 ab
F1-12	35.2 ± 0.6 de	22.0 ± 0.6 a
F1-13	40.0 ± 0.8 ab	19.2 ± 0.5 bc
F1-14	37.0 ± 0.7 cd	20.5 ± 0.5 ab
F1-15	34.7 ± 0.6 e	22.1 ± 0.6 a

CONCLUSION

The present study revealed substantial genetic unevenness amongst soybean genotypes for phenological, yield and quality traits in the agro-climatic conditions of Faisalabad. Significant differences in flowering, height, twigs, maturity, pods per plant, 100-seed mass and grain yield indicate the presence of exploitable genetic diversity. Similarly, seed protein and oil contents varied markedly, suggesting potential for synchronized enhancement of both nutritional and agronomic traits. The results emphasize the importance of combining ability and inheritance studies in identifying superior parental combinations that can contribute to yield stability and quality improvement in soybean breeding curricula. These results deliver a foundation for developing soybean cultivars suited to local environments while meeting market and nutritional demands.

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