

ASSOCIATION STUDIES OF QUANTITATIVE TRAITS IN SOYBEAN [GLYCINE MAX (L.) MERRILL] CULTIVARS

¹Jyoti Joshi, ²Brindaban Singh, ³Ayodhya Pandey, ⁴Rajbeer Singh Gaur, ⁵Neeraj Verma

Department of Genetics and Plant Breeding, Faculty of Agriculture Science and Technology, AKS
University, Satna (M.P.)

Abstract

This study investigated the correlation between various agronomic and morphological traits in twenty-two varieties/strains of soybean germplasm collected from different regions in Madhya Pradesh, India. The experiment was conducted during the Kharif season of 2022 using a Randomized Block Design with three replications. Fourteen quantitative traits were recorded from randomly selected plants, including days to 50% germination, flowering, maturity, plant height, number of branches and clusters per plant, pod characteristics, 100-seed weight, biological yield, harvest index, and seed yield per plant. Correlation coefficients were calculated at both genotypic and phenotypic levels, revealing significant associations between various traits. The findings indicated that while there existed a strong underlying connection between the examined attributes, environmental factors influenced the visible manifestation of these correlations. Genotypic correlations generally outweighed phenotypic correlations across most traits, except for specific associations. Notably, days to 50% flowering exhibited significant correlations with days to maturity, number of branches and clusters per plant, and biological yield, impacting seed yield per plant negatively. Conversely, traits such as days to maturity, number of pods per cluster, 100-seed weight, and biological yield showed positive significant correlations with seed yield per plant at both genotypic and phenotypic levels. These results underscore the importance of understanding trait correlations in soybean breeding programs to enhance yield and quality effectively. The study contributes valuable insights into selecting appropriate traits for soybean improvement strategies, aiding in the development of high-yielding and resilient soybean varieties.

Keyword: Association, Correlation coefficients, Genotypic, Phenotypic and Soybean

Introduction

Soybean, botanically known as *Glycine max* (L.) Merrill, is a remarkable crop with numerous attributes that make it highly valuable. This leguminous, self-pollinated annual plant originated in China and was introduced to India in 1968 from the United States. It belongs to the Fabales order, Leguminosae family, and Faboideae subfamily. Soybean is celebrated as a "wonder crop" due to its exceptional nutritional profile. It contains around 37-42% high-quality protein, 17-24% oil rich in unsaturated fatty acids, and essential fatty acids like linoleic and linolenic acid (Balasubramanian et al., 2003). This nutritional composition, including its abundance in lysine and tryptophan, sets soybeans apart from conventional cereal grains. Additionally, it is a valuable source of vitamins, antioxidants like ascorbic acid and beta-carotene, and isoflavones such as daidzein and genistein. The biological value of soybean protein rivals that of meat and fish. Soybean is versatile in terms of cultivation, thriving in tropical, subtropical, and temperate climates. It exhibits resilience to extreme temperatures, although its growth rate varies with temperature fluctuations. One of the

key ecological benefits of soybean is its ability to enhance soil fertility by fixing atmospheric nitrogen through root nodules and leaf decomposition. Furthermore, it aids in reducing soil erosion, weed suppression, and complements intercropping and sequential cropping patterns. Despite its low input requirements, soybean commands a high market price (Gautam et al., 2004). Soybean is the most important oilseed crop in the world in terms of acreage and production. Major soybean-cultivating countries are Brazil, the United States, Argentina, China, India, Paraguay, Canada, Ukraine, Russia, Bolivia, South Africa, Uruguay, Italy, Indonesia and others. This figure highlights the world's leading soybean development countries in 2022-23. Brazil was the top global producer of soybeans from in 2022-23. India ranks fourth in acreage and fifth in production in the world. Soybean productivity in India is very low compared to the rest of the dominant producers. Soybean production of India (2020) is estimated at 127.20 lakh tonnes as compared to 128.97 lakh tonnes in 2020-21, (Anonymous 2022). The major soybean-growing Indian states are Madhya Pradesh, Maharashtra, Rajasthan, Karnataka, and Telangana accounting for about 95 percent of the country's total area and soybean production. In India, as of 17th September 2021 area under soybean during 2021-22 was 121.76 lakh hectares as against 121.20 lakh hectares during 2020-21. Among the states, Madhya Pradesh stood first with 55.84 lakh ha followed by Maharashtra (46.01 lakh/ha), Rajasthan (10.62 lakh/ha), Karnataka (3.82 lakh/ha), Gujarat (2.24 lakh/ha) and Telangana (1.51 lakh/ha). The major constraints in production include the non-availability of adequate amounts of quality seed of improved varieties, poor adoption of improved production technology and the risks of crop cultivation in rain-fed conditions. Soybean seed is the least storable and is vulnerable to mechanical damage. Given the importance of soybean as a crop, understanding its genetic variability is crucial. While natural variation is limited in heavily self-pollinated crops like soybeans, studying genetic variations can provide insights into selecting suitable parent plants for breeding programs (Ram and Singh, 2005). Association analysis is essential for yield improvement. Character association analysis helps identify traits correlated with seed yield, aiding breeding efforts. In short, soybean's exceptional nutritional value, adaptability, and ecological benefits make it a significant crop globally. Enhancing its yield and quality through genetic variability studies and breeding efforts is vital for addressing protein based malnutrition and increasing soybean productivity.

Materials and methods

The collections of twenty-two varieties/strains of soybean [*Glycine max* (L.) Merrill] germplasm comprising indigenous genotypes, constituted the experimental materials for this study. These genotypes exhibit a wide spectrum of variability for various agronomic and morphological characters. Genotypes were collected ten from JNKVV, Jabalpur, M. P. three from RVSKVV, Gwalior, M. P., six from KVK, Indore M. P. and three genotypes from KVK, Majhgawan, Satna, (M. P.). The field experiment was carried out throughout Kharif (2022) using a Randomized Block Design with three replications. Genotypes were raised in four rows of three metres each, with a row to row spacing of 40 cm and a plant to plant distance of 15 cm between them. Fourteen characters were recorded from 5 randomly selected plants in each: days to 50% germination, days to 50% flowering, plant height (cm), days to maturity, number of primary branches per plants, number of clusters per plants, number of pods per clusters, number of pods per plants, pod length (cm), number of seed per pods, 100 seed weight (g), biological yield (gm), harvest index (%) and seed

yield per plant (g). The association between different characters at genotypic and phenotypic levels were worked out between characters as suggested by Searle, (1961).

Result and Discussions

The grain yield of a crop is determined by the complex interplay of various interconnected traits. Hence, the selection process should rely on these constituent traits, taking into account their correlation with grain yield. Character association elucidated the reciprocal connection between two characters, serving as a crucial factor in determining the appropriate selection strategy for enhancing the crop being studied. The current study calculated the correlation coefficient at both the genotypic and phenotypic levels for all fourteen quantitative traits. The results are displayed in Table 4.6. This suggests that although there is a strong underlying connection between the many attributes that were examined, the visible manifestation of this link is reduced due to the impact of the environment. The findings of Saxena and Asthana (1962) were similar. The genotypic and phenotypic connection showed a consistent direction for nearly all the characters that were investigated. Overall, the genotypic correlation was generally stronger than the phenotypic correlation for all the traits, except for the correlation between days to 50% flowering and plant height (cm), days to 50% flowering and number of pods per plant, plant height (cm) and number of primary branches per plant, plant height (cm) and number of pods per plant, plant height (cm) and biological yield (gm), plant height (cm) and seed yield per plant (g), number of pods per cluster and biological yield (gm), 100 seed weight (g) and harvest index, and harvest index and seed yield per plant (g). The number of days it takes for 50% germination to occur is significantly positively correlated, at a 5% probability level, with the biological yield (gm) (0.4525*) and seed yield per plant (g) (0.4239*) at the genotypic level only. However, at the phenotypic level, the association is not significant. Days to 50% flowering revealed extremely positive significant connection at 1% probability level with days to maturity (0.870** and 0.7344**) and biological yield (grams) (0.7369** and 0.630**) at both genotypic and phenotypic levels, respectively. It is also exhibited positive significant connection at 5% probability level with number of clusters per plants (0.5073* and 0.4397*) at both genotypic and phenotypic levels, respectively. Days to 50% flowering also demonstrated extremely negative significant connection at 1% probability level with seed yield per plant (g) (-0.8178** and -0.6646**) at both genotypic and phenotypic levels, respectively. Plant height (cm) demonstrated positive significant connection at 5% probability level with biological yield (gram) (0.4148* and 0.4894*) at both genotypic and phenotypic levels, respectively. It is also exhibited high negative significant connection at 1% probability level with harvest index (-0.564**) at genotypic level only. Days to maturity revealed extremely positive significant connection at 1% probability level with number of primary branches per plants (0.8138** and 0.7064**) and number of clusters per plants (0.7318** and 0.6687**) at both genotypic and phenotypic levels, respectively. It is also exhibited positive significant correlation at 5% probability level with biological yield (gm) (0.4399*) and seed yield per plant (g) (0.4994*) at genotypic level only. Number of major branches per plants exhibited high positive significant connection at 1% probability level with number of clusters per plants (0.7558** and 0.699**) at both genotypic and phenotypic levels, respectively. Number of pods per clusters revealed positive significant connection at 5% probability level with seed yield per plant (g) (0.4904* and 0.4719*) at both genotypic and phenotypic levels, respectively. Number of seed per pods revealed substantial

negative significant connection at 1% probability level with 100 seed weight (Seed Index) (g) (-0.6632** and -0.6523**) at both genotypic and phenotypic levels, respectively. 100 seed weight (g) revealed high positive significant connection at 1% probability level with seed yield per plant (g) (0.554** and 0.5137*) at both genotypic and phenotypic levels, respectively. Biological yield revealed highly significant positive connection with seed yield per plant (g) (0.9522** and 0.9463**) at both genotypic and phenotypic levels, respectively.

Days to 50% flowering showed highly significant positive correlation with Days to maturity and biological yield (g). Days to 50% flowering showed positive correlation with days to maturity. Days to maturity showed highly significant positive correlation with number of primary branches per plants and number of clusters per plants. Number of primary branches per plants showed highly significant positive correlation with number of clusters per plants. Biological yield (g) showed highly significant positive correlation with seed yield per plant (g). Days to 50% flowering showed highly significant but negative correlation with seed yield per plant (g). Number of seed per pods showed highly significant but negative correlation with 100 seed weight (g). The characters viz., days to maturity, number of pods per clusters, 100 seed weight (g) and biological yield (gm) showed high positive significant correlation with seed yield per plant (g) and days to 50% flowering showed high negative but significant correlation with seed yield per plant (g) at both genotypic and phenotypic levels, respectively. Similar finding of positive and significantly correlation between seed yield per plant and for days to 50% flowering Mehra et al. (2020), Balla and Ibrahim (2017), for number of pods per clusters Ningwal et al. (2023), Mehra et al. (2020), Guleria et al. (2019), Balla and Ibrahim (2017), Chavan et al. (2016), for 100 seed weight (g) Rahaman et al. (2022), Mehra et al. (2020), Guleria et al. (2019), Balla and Ibrahim (2017), Chavan et al. (2016), and for biological yield (gm) Ningwal et al. (2023), Mehra et al. (2020), Balla and Ibrahim (2017).

Conclusions

In general, genotypic correlation was higher than phenotypic ones in magnitude for all the characters except correlation between days to 50% flowering and plant height (cm), days to 50% flowering and number of pods per plants, plant height (cm) and number of primary branches per plants, plant height (cm) and number of pods per plants, plant height (cm) and biological yield (g), plant height (cm) and seed yield per plant (g), number of pods per clusters and biological yield (g), 100 seed weight (g) and harvest index and harvest index and seed yield per plant (g). The characters viz. days to maturity, number of pods per clusters, 100 seed weight (g) and biological yield (g) showed high positive significant correlation with seed yield per plant (g) and days to 50% flowering showed high negative but significant correlation with seed yield per plant (g) at both genotypic and phenotypic levels, respectively.

Competing Interests

Authors have declared that no competing interests exist.

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Table 1: Genotypic and phenotypic correlation coefficient for 14 quantitative traits in soybean

Traits		DTF G	DTFF	PH	DTM	NPBPP	NCPP	NPPC	NPPP	PL	NSPP	100-SW	BYPP	HI	SYPP
DTFG	Ge n	1.000	0.322	0.356	0.124	-0.277	-0.338	-0.263	0.038	0.070	0.211	-0.037	0.4525*	-0.102	0.4239*
	Phe	1.000	0.233	0.204	0.048	-0.174	-0.263	-0.223	0.035	0.073	0.180	-0.004	0.233	-0.145	0.185
DTFF	Ge n		1.000	0.170	0.870**	0.371	0.5073*	0.232	0.023	- 0.243	0.166	-0.190	0.7369* *	0.268	- 0.8178* *
	Phe		1.000	0.195	0.7344* *	0.318	0.4397*	0.180	0.032	- 0.199	0.151	-0.177	0.630**	0.160	- 0.6646* *
PH	Ge n			1.000	0.209	0.116	0.031	-0.072	0.198	0.056	0.290	-0.103	0.4148*	- 0.564* *	0.214
	Phe			1.000	0.178	0.120	0.030	-0.003	0.199	0.040	0.258	-0.105	0.4894*	-0.440	0.315
DTM	Ge n				1.000	0.8138* *	0.7318* *	0.212	0.123	- 0.366	0.097	0.125	0.4399*	0.189	0.4994*
	Phe				1.000	0.7064* *	0.6687* *	0.156	0.117	- 0.313	0.094	0.109	0.372	0.160	0.417
NPBP P	Ge n					1.000	0.7558* *	-0.003	-0.113	- 0.114	0.037	0.221	0.051	0.264	0.128
	Phe					1.000	0.699**	-0.003	-0.089	- 0.101	0.036	0.209	0.049	0.189	0.107
NCPP	Ge n						1.000	0.358	0.180	- 0.194	0.213	-0.058	0.265	0.188	0.315
	Phe						1.000	0.324	0.173	-	0.207	-0.058	0.231	0.156	0.270

										0.189					
NPPC	Ge n							1.000	-0.008	0.049	-0.051	0.123	0.343	0.169	0.4904*
	Phe							1.000	-0.006	0.025	-0.053	0.121	0.353	0.082	0.4719*
NPPP	Ge n								1.000	- 0.035	0.143	-0.326	0.322	-0.070	0.275
	Phe								1.000	- 0.031	0.140	-0.314	0.305	-0.036	0.265
PL	Ge n									1.000	0.379	-0.266	0.062	0.035	0.050
	Phe									1.000	0.375	-0.258	0.026	0.020	0.012
NSPP	Ge n										1.000	- 0.6632* *	0.220	0.017	0.212
	Phe										1.000	- 0.6523* *	0.183	0.017	0.174
100- SW	Ge n											1.000	-0.386	0.058	0.554**
	Phe											1.000	-0.351	0.059	0.5137*
BYPP	Ge n												1.000	-0.087	0.9522* *
	Phe												1.000	-0.048	0.9463* *
HI	Ge n													1.000	0.222
	Phe													1.000	0.275
SYPP	Ge														1.000

	n														
	Phe														1.000

*Significant at 5% probability level.

**Significant at 1% probability level.

DTFG= Days to 50% germination, **DTFF**=Days to 50% flowering, **PH**= Plant height (cm), **DTM**= Days to Maturity, **NPBPP**= Number of primary branches per plants, **NCPP**= Number of clusters per plants, **NPPC**= Number of pods per clusters, **NPPP**= Number of pods per plants, **PL**= Pod length (cm), **NSPP**= Number of Seed per pods, **100-SW**= 100 seed Weight (g), **BYPP**= Biological Yield (g), **HI**= Harvest index (%), **SYPP**= Seed yield per plant (g)