

SABRAO Journal of Breeding and Genetics
 58 (5) 2040-2047, 2026
<http://doi.org/10.54910/sabrao2026.58.5.4>
<http://sabraojournal.org/>
 pISSN 1029-7073; eISSN 2224-8978



INHERITANCE AND GENETIC VARIABILITY OF MORPHO-AGRONOMIC TRAITS IN MUNG BEAN (*VIGNA RADIATA* L. SYN. *PHASEOLUS AUREUS* L.)

L.F. UMIROVA^{1*}, S. PULATOV¹, N.M. TURSUNOVA², N.P. KHODJAYEVA³, and
 O.CH. PARDAYEV⁴

¹Tashkent Branch of the Samarkand State University of Veterinary Medicine, Animal Husbandry and Biotechnology, Tashkent, Uzbekistan

²Department of Natural Sciences, Chirchik State Pedagogical University, Tashkent, Uzbekistan

³Tashkent State Agrarian University, Tashkent, Uzbekistan

⁴Karshi State Technical University, Karshi, Uzbekistan

*Corresponding author's email: amanov.81@bk.ru

Email addresses of co-authors: lobarumirova2014@gmail.com, nilufar.azimova.85@inbox.ru, xodjayevanozigul1981@gmail.com, m-biologiya@mail.ru, pardayev.orifjon.charshamiyevich@gmail.com

SUMMARY

This research aimed to analyze the inheritance and variability of morpho-economic traits in parental lines and their F₁ and F₂ populations in mung bean (*V. radiata* syn. *P. aureus* L.). Specifically, these traits are main stem length, pods per plant, pod length, seeds per pod, and 1000-seed weight. The experiment commenced at the experimental field of Chirchik State Pedagogical University, Uzbekistan, using several mung bean's parental genotypes and their F₁ and F₂ populations. In F₁ and F₂ populations, the inheritance of main stem length primarily exhibited positive overdominance, as well as positive and negative intermediate inheritance. The pods per plant predominantly revealed overdominance, with occasional positive intermediate and negative overdominance. Pod length consistently displayed positive intermediate inheritance across all hybrids, while the seeds per pod and 1000-seed weight demonstrated instances of both positive and negative overdominance. In F₂ populations, the heritability ranges for various traits were for main stem length (53.0%–97.0%), pods per plant (66.0%–83.0%), pod length (11.0%–44.0%), seeds per pod (22.0%–66.0%), and 1000-seed weight (77.0%–89.6%). Isolation of the recombinant forms with heterotic effects occurred in F₂ populations for the above traits. The utilization of these recombinants as source material will offer significant efficacy in mung bean breeding programs.

Keywords: Mung bean (*V. radiata* syn. *P. aureus* L.), F₁ and F₂ populations, overdominance, heritability, heterosis, morpho-yield traits

Communicating Editor: Dr. Anita Restu Puji Raharjeng

Manuscript received: March 04, 2026; Accepted: June 13, 2026.

© Society for the Advancement of Breeding Research in Asia and Oceania (SABRAO) 2026

Citation: Umirova LF, Pulatov S, Tursunova NM, Khodjayeva NP, Pardayev OCH (2026). Inheritance and genetic variability of morpho-agronomic traits in mung bean (*Vigna radiata* L. syn. *Phaseolus aureus* L.). *SABRAO J. Breed. Genet.* 58 (5) 2040-2047. <http://doi.org/10.54910/sabrao2026.58.5.4>.

Key findings: The pods per plant predominantly detailed overdominance, with occasional instances of positive intermediate and negative overdominance in mung bean (*V. radiata* syn. *P. aureus* L.). Pod length consistently displayed positive intermediate inheritance, while the seeds per pod and 1000-seed weight exhibited instances of both positive and negative overdominance across all hybrids.

INTRODUCTION

According to the Food and Agriculture Organization (FAO) and World Health Organization (WHO) data, and over 840 million people worldwide suffer from undernourishment (FAO, 2023). Furthermore, more than 30% of the global population faces the challenges of malnutrition, especially characterized by the deficiency in essential micronutrients and vitamins in daily foods (Amanov *et al.*, 2022).

Among leguminous crops, mung bean is a widely used staple as an important dietary supplement in human nutrition. It serves as a valuable source of protein, vitamins, and essential minerals required for human health. Meeting the growing demand requires the primary objective of genetic improvement programs to develop new genotypes possessing economically valuable traits that are complex in nature and controlled by multiple polygenes (Suresh *et al.*, 2015; Naik *et al.*, 2020).

Mung bean (*Vigna radiata* L. Wilczek; syn. *Phaseolus aureus* L.) has its typical cultivation at low-to-medium altitudes as a rainfed crop in tropical regions worldwide. It serves as a primary crop during the dry season, ranking second to chickpea. In Uzbekistan during 2020, *Phaseolus aureus* L. cultivation occurred on 27,000 hectares, with an annual production of 54,000 tons and an average seed yield of 2,000 kg/ha. Mung bean belongs to the family Leguminosae and the subfamily Papilionoideae, taxonomically recognized as *Vigna radiata* (L.) Wilczek with a diploid chromosome number ($2n = 2x = 22$). Its synonyms are *Phaseolus radiatus* L. and *Phaseolus aureus* L. (Wilczek, 1954; Kaul, 1982). The mung bean origin likely shows a trace to India (De-Candolle, 1886; Zhukovsky, 1950; Bailey, 1970) and the Indo-Burma region (Vavilov, 1951; Atnaf *et al.*, 2013).

The Central Asian region, as proposed, has become the primary gene center for genetic diversity of mung bean, while India emerged as the established center of diversity and the probable center of domestication (Bose, 1939; Smartt, 1985). On mung bean, the conduct of most genetic research has taken place in India. According to Lukoki *et al.* (1980), *V. radiata* var. *sublobata* (Roxb.) Verdc., having recognition in wild form in India, crosses easily with *V. radiata* var. *radiata*, and therefore the regarded wild progenitor of mung bean (Lukoki *et al.*, 1980). Mung bean (*Vigna radiata* L. Wilczek) is an important annual legume crop, generally cultivated in arid regions, particularly under rainfed conditions (Karpechenko, 1925).

Overall, the mung bean attains a plant height of 0.3–1.5 meters. It grows in an erect form or suberect habit, and occasionally, the tips of the branches may be slightly twining. Mung bean possesses a deeper root system, with profuse branching and long petioles. The leaves mostly alternate and are trifoliate and range from dark to light green. The leaflets are ovate, with a width and length of 2–10 cm and 5–12 cm, respectively. The inflorescence is an axillary raceme, with peduncles ranging from two to 13 cm in length (Wilczek, 1954).

The flowers are yellow and papilionaceous, with a spirally coiled keel that features a horn-like appendage at the tip. The pods are 6–10 cm long, slender, and covered with short and soft pubescence (De-Candolle, 1886; Rachie and Roberts, 1974). The seeds are globose, weighing between 15 and 85 mg. The seeds are predominantly green, though they may occasionally be yellow, brown, black, and mottled. The hilum is white, flat, and not concave; and the germination is epigeal (Bailey, 1970; Poehlman, 1991).

Agronomic practices, such as field irrigation and mulching, intended to mitigate the effects of drought and high temperature, often

appeared cost-prohibitive and difficult to implement due to the limited economic resources of the farming community. Therefore, this applied research proceeded to evaluate mung bean genotypes with the highest yield potential and optimal agronomic traits suitable for specific agroecological zones (Shanmugasundaram, 1998). Knowledge of trait variability is a prerequisite for yield improvement.

In a biological population, the genetic variability results from the interaction between the genetic composition of its constituent genotypes and the existing environmental conditions. For genetic variability assessment, analyzing the genetic parameters, such as genotypic coefficient of variation (GCV), heritability, and genetic gain is crucial for initiating an effective breeding program (Suresh *et al.*, 2015). In the agricultural sector development, a growing interest rises among breeders in studying legume crops and improving their production horizontally and vertically. Crop diversification plays a vital role in enhancing the efficiency and sustainability of agricultural systems (Rahim *et al.*, 2010).

Mutation breeding is also a considerably effective approach for broadening genetic diversity in existing genotypes and selecting high-yielding lines and desirable mutants. The determined genetic parameters could be instrumental in developing reliable selection indices for economically important agronomic traits, thereby facilitating the development of high-yielding genotypes in mung beans (Suresh *et al.*, 2015).

MATERIALS AND METHODS

The concerned research began at the experimental field of the Faculty of Natural Sciences, Chirchik State Pedagogical University, Tashkent, Uzbekistan. The study utilized mung bean (*P. aureus* L.) accessions and cultivars as breeding materials. These include K-2 and K-338 (China), K-236 (Manchuria), K-413 and K-414 (Vietnam), K-418 (Philippines), K-489 (local cultivar, Uzbekistan), K-599 and K-255 (India), K-716 (Afghanistan), K-181 (Taiwan), and the

Uzbekistan local cultivars Turon and Durdona. The F_1 and F_2 populations derived from these lines also received analysis (Atabayeva and Xudaykulov, 2018).

In the studied F_1 hybrids, the degree of dominance calculation used S. Wright's formula (Beil and Atkins, 1965) as follows:

$$hp = \frac{F_1 - MP}{P - MP}$$

Where hp = the degree of dominance (potence ratio), F_1 = arithmetic mean value of the hybrid, MP = mid-parent value (arithmetic mean of both parental forms), and P = arithmetic mean value of the better parent.

The degree of dominance incurred classification based on the calculated Hp values as follows:

Hp = no dominance (additive gene action); $0 < hp < \pm 1.0$ = partial (intermediate) dominance; $hp = \pm 1.0$ is complete dominance, and $hp > \pm 1.0$ is overdominance (heterosis).

The heritability (h^2), defined as the ratio of genotypic variance to total phenotypic variance, entailed determination according to the formula by Allard (1956):

h^2 - heritability estimate in F_2 hybrids:

$$h^2 = \frac{\delta^2 F_2 - \frac{\delta^2 F_1 + \delta^2 P_1 + \delta^2 P_2}{3}}{\delta^2 F_2}$$

Where $\delta^2 F_1$ = variance of the F_1 generation, $\delta^2 F_2$ = variance of the F_2 generation, $\delta^2 P_1$ = variance of the parent 1, and $\delta^2 P_2$ = variance of the parent 2.

RESULTS AND DISCUSSION

In mung bean (*P. aureus* L.) parental lines, the main stem length is one of the primary biometric traits. The local cultivar Turon appeared with the tallest plants (62.0 cm)

compared with other mung bean genotypes, while the shortest plant stature was evident in the foreign accession K-2 (33.0 cm) (Table 1). Furthermore, the genotypes with moderate plant height (51.0–58.0 cm) were notable as K-181, K-236, K-414, K-418, K-255, and K-716.

The F_1 hybrids obtained through hybridization of geographically distant cultivars and accessions of mung bean (*P. aureus* L.) indicated varied inheritance patterns for the main stem length. The highest main stem length resulted in the F_1 hybrid Taiwan $\times$ Turon (70.0 ± 1.47 cm); the amplitude of variability was 41.0–50.0 cm, identifying the inheritance as overdominance ($h_p = 5.0$) (Table 1). In the F_1 hybrid Turon $\times$ K-236, the main stem length was 55.0 ± 1.95 cm with a degree of dominance ($h_p = -0.3$), while the F_1 hybrid Durdonia $\times$ K-599, recorded with a stem length of 52.0 ± 1.13 cm, had a degree of dominance ($h_p = 1$). In other F_1 populations, the inheritance recorded showed a positive overdominance and positive and negative intermediate inheritance. Reports on similar morphological observations with considerable significance have been in previous studies on various crops (Basu *et al.*, 2016).

The indicators for the main stem length also sustained analysis in the F_2 populations of mung bean (Table 1). In particular, the highest main stem length was prominent in the F_2 population Turon $\times$ K-418 (77.0 ± 0.13). In the said F_2 hybrid, the heritability coefficient (h^2) of the main stem length was 71.0%, indicating that 71.0% of the variation in the studied trait was because of the genetic makeup of the hybrid form, while 29.0% gained influences from various environmental factors (Fery, 1980; Shanmugasundaram, 1998). The F_2 population Turon $\times$ K-236 exhibited a relatively low value for the main stem length (43.1 ± 0.18), with a heritability coefficient of 53.0%, revealing the determination of more than half of the trait expression was by the genetic potential of the F_2 hybrid.

The results further revealed the pods per plant varied among the selected parental genotypes (Table 1). The highest number of pods per plant occurred in the Vietnam

accession K-414 (60.2), whereas the China accession K-338 displayed considerably fewer pods per plant (32.3). In F_1 hybrids, pods per plant expressed a predominant inheritance in an overdominance manner, while in some F_1 hybrids, the positive intermediate and negative overdominance inheritance was apparent.

The highest number of pods per plant surfaced in the F_1 hybrids derived from crosses involving the cultivated cultivars Mestniy and Turon (Table 1). The total number of pods per plant ranged from 40.03 to 62.1 pods. In the F_1 hybrid Turon $\times$ K-418, the pods per plant were 62.1, with a dominance coefficient of $h_p = 1.5$, enunciating overdominance inheritance of the said trait. The F_1 hybrid K-181 $\times$ Turon showed 55.1 pods per plant, with a positive intermediate inheritance ($h_p = 0.5$). Similar findings have also occurred in reports studying the morphological and yield-related traits in the bean genotypes (Xalikov and Negmatova, 2020). Overall, 13 F_1 hybrids exhibited heterotic inheritance for pods per plant, and especially in eight cross combinations, the said trait's inheritance was in an overdominance manner.

In F_2 populations, the pods per plant ranged from 33.67 to 61.4. In the F_2 population of Turon $\times$ K-413, the study recorded the relatively highest number of pods per plant (61.4) (Table 1). The heritability coefficient (h^2) for the said trait ranged from 66.0% to 83.0%, indicating the determination of 66.0%–83.0% of the phenotypic expression was by the genetic makeup of the hybrids, while 34.0%–17.0% of the expression bore influences from environmental factors. In particular, the F_2 population Turon $\times$ K-236, observed with a heritability coefficient of $h^2 = 83.0\%$, revealed 83.0% of the pods per plant received control from genetic factors and 17.0% from environmental conditions. Past findings also disclosed that the major portion of inheritance in yield-related traits entailed governance of the genotypes (Bangar *et al.*, 2018; Hatfield and Dold, 2019).

In parental genotypes, the highest pod length resulted in the accession K-236 (11.67 cm), whereas accession K-2 emerged with the lowest value (5.72 cm) (Table 1). In local cultivars Turon and Durdonia, the pod length

Table 1. Inheritance of morpho-agronomic traits in parental genotypes and their F₁ and F₂ populations in mung bean (*P. aureus* L.).

No.	Parental genotypes and F ₁ -F ₂ populations	Main stem length (cm)		Pods per plant		Pod length (cm)		Seeds per pod		1000-seed weight (g)	
		Mean±SE	hp	Mean±SE	hp	Mean±SE	hp	Mean±SE	hp	Mean±SE	hp
1	K-2 (China)	33.1±1.47	-	58.7±0.05	-	5.72±0.15	-	4.43±0.14	-	53.4±1.2	-
2	K-236 (Manchuria)	51.4±0.15	-	49.0±0.03	-	11.67±0.05	-	9.69±0.09	-	56.4±1.8	-
3	K-338 (China)	37.3±1.73	-	32.3±0.04	-	7.08±0.07	-	7.00±0.09	-	47.6±1.7	-
4	K-413 (Vietnam)	48.2±2.02	-	34.2±0.06	-	6.10±0.06	-	9.69±0.08	-	47.4±1.1	-
5	K-414 (Vietnam)	51.3±1.04	-	60.2±0.04	-	7.08±0.07	-	10.35±0.08	-	45.3±0.8	-
6	K-418 (Philippines)	55.7±2.70	-	41.4±0.04	-	8.85±0.08	-	9.59±0.10	-	51.6±0.5	-
7	K-489 (Uzbekistan)	44.6±1.75	-	57.4±0.04	-	7.88±0.06	-	10.40±0.10	-	59.9±0.3	-
8	K-599 (India)	52.1±1.19	-	39.9±0.09	-	6.11±0.08	-	8.74±0.11	-	55.3±0.3	-
9	K-716 (Afghanistan)	53.5±1.37	-	42.8±0.09	-	8.22±0.06	-	11.8±0.05	-	53.2±0.4	-
10	K-181 (Taiwan)	58.1±1.19	-	39.7±0.05	-	9.07±0.11	-	9.55±0.05	-	81.2±0.9	-
11	K-255 (India)	52.6±1.57	-	35.8±0.06	-	6.10±0.18	-	6.5±0.18	-	51.1±0.4	-
12	Turon (Uzbekistan)	62.3±0.93	-	59.9±0.04	-	10.8±0.10	-	10.31±0.09	-	71.6±0.4	-
13	Durdona (Uzbekistan)	47.2±1.29	-	39.1±0.05	-	9.47±0.08	-	9.41±0.06	-	63.7±0.24	-
F₁ hybrids (hp)											
1	K-338 × K-414	50.2±2.14	0.8	55.8±0.03	0.7	7.50±0.05	0.35	11.02±0.08	1.4	53.4±1.6	6.2
2	K-414 × K-489	52.4±0.26	1.2	45.0±0.06	-9.8	6.51±0.13	0.82	10.93±0.09	1.05	59.6±1.1	0.9
3	K-414 × K-413	50.6±2.02	0.3	53.3±0.07	0.5	7.07±0.07	0.49	10.80±0.09	2.4	59.6±1.1	12.6
4	K-489 × K-418	60.1±1.80	1.9	62.1±0.03	1.5	8.55±0.06	0.50	11.13±0.08	1.6	80.9±1.4	6.0
5	K-716 × K- 599	52.3±1.26	1.0	43.2±0.04	1.2	6.75±0.09	0.62	11.11±0.09	0.5	55.1±2.1	0.8
6	K-181 × K-716	68.7±1.81	5.0	40.0±0.03	2.0	9.12±0.07	0.61	10.15±0.08	-0.5	50.1±1.6	-1.2
7	K-181 × Tyron	70.2±1.47	5.0	55.1±0.05	0.5	9.65±0.05	0.45	9.74±0.08	-0.3	93.3± 0.9	3.4
8	Turon × K-413	52.3±4.07	0.73	61.7±0.03	1.2	8.72±0.07	0.59	9.54±0.10	-1.5	51.2±1.4	-0.7
9	Turon × K-418	58.5±0.10	-0.14	58.4±0.03	1.1	8.62±0.10	0.79	9.78±0.06	-0.3	56.7±2.0	0.4
10	Turon × K-226	55.4±1.95	0.27	51.4±0.04	0.6	9.13±0.10	0.88	11.20±0.07	3.8	96.6±1.7	4.3
11	Durdona × K-599	52.1±1.13	1.0	44.8±0.06	4.5	6.84±0.11	0.76	9.65±0.08	1.7	63.4±1.5	0.9
12	Durdona × K-338	60.2±0.68	2.8	56.6±0.05	6.1	9.22±0.08	0.59	11.49±0.06	2.7	55.8±1.9	0.5
13	Durdona × K-489	62.3±1.02	1.3	55.5±0.04	5.6	7.96±0.07	0.59	11.68±0.09	1.9	65.1±1.2	1.7
F₂ populations with h² (%)											
1	Turon × K-236	43.1±0.18	53.0	50.2±0.10	83.0	7.80±0.12	33.0	8.73±0.13	36.0	68.4±0.10	81.1
2	Turon × K-418	77.8±0.13	71.0	33.6±0.15	76.0	7.97±0.08	27.0	8.52±0.12	30.0	62.4±0.08	77.7
3	K-181 × Turon	54.3±2.02	93.0	58.1±0.08	72.0	7.97±0.08	15.0	9.85±0.11	53.0	77.3±0.08	87.2
4	Turon × K-413	61.5±0.13	59.0	61.4±0.07	80.0	7.32±0.08	19.0	9.39±0.12	22.0	54.9±0.10	86.8
5	Durdona × K-338	56.2±0.24	97.0	54.6±0.07	66.0	7.89±0.10	11.0	10.26±0.09	41.0	63.8±0.14	89.6
6	Durdona × K- 599	46.8±0.22	92.0	48.6±0.12	80.0	7.38±0.09	44.0	9.56±0.11	44.0	51.9±0.09	78.2
7	K181 × K-716	54.1±0.22	90.0	45.3±0.10	67.0	8.02±0.08	41.0	10.75±0.10	66.0	59.9±0.09	80.7

ranged from 9.47 to 10.8 cm. The remaining parental genotypes exhibited relatively the same pod length. Overall, in F₁ hybrids, the pod length ranged from 6.75 to 9.65 cm. However, the highest pod length (9.65 cm) was evident in the F₁ hybrid K-181 × Turon, where the degree of dominance gave characteristics of positive intermediate (hp = 0.62). A relatively low pod length was noteworthy in the F₁ hybrid K-414 × Mestniy (6.51 ± 0.13 cm), inherited with a negative overdominance manner (hp = -2.4). Generally, in F₁ cross combinations, pod length signified predominant inheritance in a positive intermediate manner (hp = 0.35 to 0.88) across most of the F₁ populations. Similar results have also appeared in reports of several

past studies (Wilczek, 1954; Rachie and Roberts, 1974).

In the F₂ population, K-181 × K-716, obtained from crosses between geographically distant cultivars of *P. aureus* L., a relatively higher average pod length (8.02 cm) appeared. The heritability coefficient for the said trait was h² = 41%, revealing the determination of 41% of the phenotypic variation was due to the hybrid genotype and 59% by environmental factors. Additionally, the F₂ population Turon × K-418 was distinct, with a pod length of 7.97 cm. In general, relatively similar pod length emerged among the studied F₂ populations. Similar results have replicates in the past studies (Poehlman, 1991; Guo et al., 2012).

Seeds per pod was one of the principal traits of the selected parental accessions. The results indicated geographically distant accessions of mung bean considerably differed in this trait (Table 1). In particular, the local cultivars Turon and Durdonia exhibited relatively more seeds per pod (9.41–10.31) than other parental sources, while the accession K-2 showed the lowest number of seeds per pod (4.43). However, recording the highest number of seeds per pod existed in the accession K-716 (11.8). Past studies also reported similar findings in newly developed *P. aureus* L. populations by comparing them with the check genotypes (Ali *et al.*, 2008).

In F_1 populations, various patterns of inheritance were evident for the seeds per pod, including positive overdominance, negative intermediate, and positive intermediate inheritance (Table 1). In the F_1 hybrid Turon $\times$ K-236, the average number of seeds per pod reached 11.20, with a dominance coefficient ($h_p = 3.8$) enunciating an overdominance inheritance. For the F_1 hybrid K-181 $\times$ Turon, negative intermediate inheritance ($h_p = -0.3$) was prominent, whereas in the F_1 hybrid K-716 $\times$ K-599, the said trait's inheritance was in a positive intermediate manner ($h_p = 0.5$). One should note that mung bean local cultivars served as maternal parents in hybridization; the seeds per pod were higher, with the trait predominantly inherited in an overdominance manner (Fahad *et al.*, 2017).

In F_2 populations, the seeds per pod is one of the key agronomic traits, receiving further evaluation. In F_2 populations, the variation range for this trait encompassed 4–5 phenotypic classes (Table 1). Particularly, positive transgressive segregation was notable in the F_2 population K-181 $\times$ Turon combination. In this combination, the heritability coefficient was $h^2 = 53\%$, revealing that 53% of the phenotypic variation had genetic factors' administration and 47% by environmental influences. Moreover, the F_2 population K-181 $\times$ K-716 exhibited a relatively high mean value for seeds per pod (10.75 ± 0.10), with a heritability coefficient of $h^2 = 66.0\%$. It demonstrated that 66.0% of the trait expression had the control of the genotype genetic makeup and 34.0% by

environmental factors (Lukoki *et al.*, 1980; Akter *et al.*, 2022).

In the cross combination Turon $\times$ K-413, the average number of seeds per pod was 9.54 in the F_1 generation and 9.39 in the F_2 generation (Table 1). The highest proportion of plants (29.5%) of this cross fell within the modal class of 10.1–11.0 seeds per pod in the F_2 population. However, the heritability coefficient for this trait was relatively low ($h^2 = 22\%$), indicating that 78% of the phenotypic variation acquired influences from environmental factors. Overall, in the studied populations, the heritability coefficient for seeds per pod ranged from 22.0% to 66.0%, suggesting that 22.0%–66.0% of said trait expression was due to genotypes, while 34.0%–88.0% was attributable to environmental effects.

According to the results, the parental accessions involved in hybridization significantly differed for 1000-seed weight (Table 1). In particular, the foreign accession K-181 had the largest seeds, with an average 1000-seed weight of 81.2 g. Three mung bean accessions, K-236, K-418, and K-599, showed characteristics of a medium-seed size, with average values ranging from 51.6 to 56.4 g. In contrast, the accession K-414 had relatively small seeds, with a 1000-seed weight of 45.3 g. For 1000-seed weight, the F_1 hybrids showed varied responses for inheritance and included overdominance, positive intermediate, negative intermediate, and negative overdominance patterns. In F_1 hybrid K-414 $\times$ K-413, the average 1000-seed weight was 59.6 g, and the degree of dominance ($h_p = 12.6$) indicated positive overdominance. In F_1 hybrid Durdonia $\times$ K-599, positive intermediate inheritance was evident ($h_p = 0.9$), whereas in F_1 hybrid K-181 $\times$ K-716, the said trait exhibited negative overdominance inheritance ($h_p = -1.2$).

In F_2 populations, on average, the 1000-seed weight ranged from 51.91 to 77.32 g. Genetic analysis of this trait revealed the heritability coefficient varied from 77.7% to 89.6%, indicating the high degree of genetic control over its expression (Table 1) (Fery, 1980; Shanmugasundaram, 1998). In particular, the F_2 population Turon $\times$ K-236

was noticeable with multidirectional transgressive segregation for 1000-seed weight, with an average value of 68.49 g. The highest proportion of hybrid plants (43.8%) fell within the modal class of 66.9–70.9 g. For 1000-seed weight, the heritability coefficient was $h^2 = 81.1\%$, demonstrating that 81.1% of the phenotypic variation entailed detection by the hybrid genetic makeup, with 18.9% influenced by environmental factors. However, in this combination, the 1000-seed weight was lower than that of the parental genotypes.

CONCLUSIONS

In the analysis of geographically distant cultivars and accessions of mung bean (*P. aureus* L.), as well as in their F_1 and F_2 populations, the inheritance and genetic variability of key morpho-agronomic traits succeeded in their investigation. In F_2 populations, the heritability coefficient for main stem length ranged from 53.0% to 97.0%, pods per plant (66.0% to 83.0%), pod length (11.0% to 44.0%), seeds per pod (22.0% to 66.0%), and 1000-seed weight (77.0% to 89.6%). The results revealed the degree of inheritance varied depending upon the hybrid populations. In F_2 populations, heterosis retention was successful, with recombinant forms selected based on main stem length, pods per plant, pod length, seeds per pod, and 1000-seed weight. The selected recombinant types were of considerable value and can be effective in their use as breeding materials in mung bean improvement programs.

REFERENCES

- Akter SE, Islam MT, Rahman MS, Khatoon M (2022). Growth analysis, nitrogen assimilation, and yield of mung bean genotypes. Green Global Foundation. *J. Sustain. Crop Prod.* 17(2): 20.
- Ali MA, Nawab NN, Rasool G, Saleem M (2008). Estimates of variability and correlations for quantitative traits in mung bean (*Vigna radiata* L.). *J. Agri. Soc. Sci.* 4(4): 177-179.
- Allard RW (1956). The analysis of genetic - environmental interactions by means of diallel crosses. *J. Genet.* (41)3: 786-792.
- Amanov B, Muminov K, Samanov S, Abdiev F, Arslanov D, Tursunova N (2022). Cotton introgressive lines assessment through seed cotton yield and fiber quality characteristics. *SABRAO J. Breed. Genet.* 54(2): 321-330.
- Atabayeva XN, Xudaykulov JB (2018). Plant Science. Tashkent. Science and Technology, pp. 408.
- Atnaf M, Mohammed H, Zelleke H (2013). Inheritance of primary yield component traits of common beans (*Phaseolus aureus* L.): Number of seeds per pod and 1000-seed weight in an 8×8 diallel cross population. *Int. J. Genet. Mol. Biol.* 5(4): 42-48.
- Bailey LH (1970). Manual of Cultivated Plants. (Rev.) MacMillan, New York. pp. 1116.
- Bangar P, Chaudhury A, Umdale S, Kumari R, Tiwari B, Kumar S, Gaikwad AB, Bhat KV (2018). Detection and characterization of polymorphic simple sequence repeats markers for the analysis of genetic diversity in Indian mung bean (*Vigna radiata* [L.] Wilczek). *Indian J. Genet. Plant Breed.* 78: 111-117.
- Basu S, Ramegowda V, Kumar A, Pereira A (2016). Plant adaptation to drought stress. F1000 Research: 5. F1000 Faculty Rev-1554.
- Beil GE, Atkins RE (1965). Inheritance of quantitative characters sorghum. *Iowa State J. Sci.* 3: 35-37.
- Bose RD (1939). Studies in Indian pulses. IX. Contributions to the genetics of mung (*Phaseolus radiatus* Linn., ph aureus Roxb.).
- De-Candolle A (1886). Origin of Cultivated Plants. Hafner Publ. Co., New York, N.Y. Reprint of 2nd Ed. 1959.
- Fahad S, Bajwa AA, Nazir U, Anjum SA, Farooq A, Zohaib A, Sadia S, Nasim W, Adkins S, Saud S, Ihsan MZ (2017). Crop production under drought and heat stress: Plant responses and management options. *Front. Plant Sci.* 8: 1147.
- FAO (2023). Food and Agriculture Organization (FAO) and World Health Organization (WHO) data. www.fao.org/statistics/mungbean
- Fery RL (1980). Genetics of Vigna. In: J. Janick (Ed.). Horticultural Reviews. Vol. 2, AVI Publishing Co., Inc., Westport, CT. pp. 311-394.
- Guo X, Li T, Tang K, Liu RH (2012). Effect of germination on phytochemical profiles and antioxidant activity of mung bean sprouts (*Vigna radiata*). *J. Agric. Food Chem.* 60: 11050-11055.

- Hatfield JL, Dold C (2019). Water-use efficiency: Advances and challenges in a changing climate. *Front. Plant Sci.* 10: 103.
- Karpechenko GD (1925). Chromosomes of *Phaseolinae*. *Bull. Appl. Bot Leningrad.* 14: 143-148.
- Kaul AK (1982). Response of mung bean cultivars to different planting date. *Sarhad J. Agric.* 5(6): 554-561.
- Lukoki L, Marechal R, Otoul E (1980). Les aneetressauva GES des haricots cultives: *Vigna radiata* (L.) Wilczek et *V. mungo* (L.) Hepper. *Bull. du Jardin Botanique National de Belgique* 50: 385-391.
- Naik MG, Panoth A, Venkatachalapathy N (2020). Mungbean. In book: Pulses: Processing and Product Development. Publisher: Springer Nature, Switzerland.
- PBS (2014). Pakistan Bureau of Statistics (PBS), Ministry for Food and Agriculture. Islamabad, Government of Pakistan.
- Poehlman JM (1991). The Mungbean. Oxford and IBH Publishing Co., New Delhi.
- Rachie KO, Roberts LM (1974). Grain legumes of the lowland tropics. *Adv. Agron.* 26: 1-132.
- Rahim MA, Mia AA, Mahmud F, Zeba N, Afrin KS (2010). Genetic variability, character association, and genetic divergence in mung bean (*Vigna radiata* L. Wilczek). pp. 1-6.
- Shanmugasundaram S (1998). Mung bean varietal improvement. Asian Vegetable Research and Development Center, Shanhua, Tainan, Taiwan. pp. 30.
- Smartt J (1985). Evolution of grain legumes. III. Pulses in the genus *Vigna*. *Exp. Agric.* 21: 87-100.
- Suresh S, Jebaraj S, Arulselvi S (2015). Analysis of genetic parameters for yield and its components in m2 generation of greengram (*Vigna radiata* [L.] Wilczek). March 14-17, 2015. pp. 14.
- Vavilov NI (1951). The origin, variation, immunity, and breeding of cultivated plants. (Translation by K.S. Chester). *Chron. Bot.* 13: 1-364.
- Wilczek R (1954). *Vigna*. In: Fiore du Congo Beige. pp. 343-393.
- Xalikov BM, Negmatova ST (2020). Mosh. Monography. Navruz Publishing House. Tashkent. pp. 1-188.
- Zhukovsky PM (1950). Cultivated plants and their wild relatives (Translation by P.S. Hudson, 1962). Commonwealth Agricultural Bureau, Farnham Royal, England, pp. 7.