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Research Note

Inter and intra cross variability analysis in F_3 generation of mung bean [*Vigna radiata* (L.) Wilczek]

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Abstract

The present investigation was conducted to evaluate 12 crosses of mungbean genotypes for 11 characters to access the extent of genetic variability and to comprehend the heritable aspect of variation for grain yield and its related characters. All the 12 crosses were raised in a compact family block design with three replications in two environments during the *kharif* season of 2022. The analysis of variance indicated significant variations among the families for grain yield and all other characters in both environments. Conversely, differences among the progenies within a family varied depending on specific trait and environment (E1) to environment (E2). Inter cross variability revealed high GCV and PCV for primary branches per plant in both environments. High estimates of PCV were recorded for pods per plant and grain yield per plant in both environments and for clusters per plant in E2. High estimates of heritability were exhibited by primary branches per plant in both the environments and plant height in E1. High estimates of genetic advance as per cent of mean were observed for primary branches per plant and plant height in both environments. Inter cross variability revealed that the highest magnitude of heritability was recorded by family C1 and C7 for grain yield per plant in E1 and E2 respectively. The highest magnitude of genetic advance as per cent of mean was exhibited by family C3 for primary branches per plant in E1 and by family C12 for clusters per plant in E2.

Keywords: Genetic variability, Inter cross variability, Heritability, Mungbean

Mungbean is a traditional and well-known tropical leguminous crop of Asia because of its nutritional value and cropping system adaptability. Mungbean, also known as moong, is the third most significant legume, next to chickpea and pigeon pea. According to Karpechenko (1925), it bears the diploid chromosomal number 2n = 2x = 22. According to Vavilov (1926) mungbean is a native of India and Central Asia. Since prehistoric times, it has been grown in these regions. The diploid mungbean (2n = 22) is a member of the Leguminaceae family, Papillionaceae subfamily, genus *Vigna* and species *radiata*. About 18.0 to 32.0 per cent protein and 1 to 5 per cent fat are both found in pulses. Chemical components include proteins, fatty acids, carbohydrates, vitamin B1, vitamin B2, beta-carotene, folic acid, calcium, phosphorus, and iron. India accounts for around 25 per cent of global production from 35 per cent of global area under pulses. In India mungbean occupied roughly 31.15 lakh hectares during 2019–20 with a production of 23.40 lakh tonnes and productivity of 798 kg/ha. States that produce a significant amount of mungbean in India include Rajasthan, Maharashtra, Karnataka, Madhya Pradesh, Odisha and Telangana (Anonymous, 2019-20). In Rajasthan, the total area planted with mungbean during 2019–2020 was 23.27 lakh hectares, with a total production of 13.04 lakh tonnes and a productivity of 561 kg/ha and it is the leading mung bean producing state in the country(Anonymous, 2019-20). It is primarily grown in the semi-arid and dry regions of Rajasthan, particularly in the districts of Nagaur, Ajmer, Jaipur, Jodhpur, Jalore,

Table 1. Details of mung bean research materials

crosses	F$_2$ plants selected	Codes in F$_3$' s	
		Family	Progeny
HUM 1 × IPM-205-07 (A_1) (A_2)	A_1A_2-1	C_1	C1P1
	A_1A_2-2		C1P2
	A_1A_2-3		C1P3
	A_1A_2-4		C1P4
	A_1A_2-5		C1P5
HUM 1 × MH 421 (A_1) (A_3)	A_1A_3-1	C_2	C2P1
	A_1A_3-2		C2P2
	A_1A_3-3		C2P3
	A_1A_3-4		C2P4
	A_1A_3-5		C2P5
HUM 1 × LGG 460 (A_1) (A_4)	A_1A_4-1	C_3	C3P1
	A_1A_4-2		C3P2
	A_1A_4-3		C3P3
	A_1A_4-4		C3P4
	A_1A_4-5		C3P5
HUM 1 × MH-2-15 (A_1) (A_5)	A_1A_5-1	C_4	C4P1
	A_1A_5-2		C4P2
	A_1A_5-3		C4P3
	A_1A_5-4		C4P4
	A_1A_5-5		C4P5
HUM 1 × RMG-975 (A_1) (A_6)	A_1A_6-1	C_5	C5P1
	A_1A_6-2		C5P2
	A_1A_6-3		C5P3
	A_1A_6-4		C5P4
	A_1A_6-5		C5P5
IPM-205-07 × MH 421 (A_2) (A_3)	A_2A_3-1	C_6	C6P1
	A_2A_3-2		C6P2
	A_2A_3-3		C6P3
	A_2A_3-4		C6P4
	A_2A_3-5		C6P5
IPM-205-07 × LGG 460 (A_2) (A_4)	A_2A_4-1	C_7	C7P1
	A_2A_4-2		C7P2
	A_2A_4-3		C7P3
	A_2A_4-4		C7P4
	A_2A_4-5		C7P5
IPM-205-07 × ML-818 (A_2) (A_7)	A_2A_7-1	C_8	C_8P1
	A_2A_7-2		C_8P2
	A_2A_7-3		C_8P3
	A_2A_7-4		C_8P4
	A_2A_7-5		C_8P5
IPM-205-07 × MH-2-15 (A_2) (A_5)	A_2A_5-1	C_9	C_9P1
	A_2A_5-2		C_9P2
	A_2A_5-3		C_9P3
	A_2A_5-4		C_9P4
	A_2A_5-5		C_9P5
IPM-205-07 × RMG-975 (A_2) (A_6)	A_2A_6-1	C_{10}	C10P1
	A_2A_6-2		C10P2
	A_2A_6-3		C10P3
	A_2A_6-4		C10P4
	A_2A_6-5		C10P5
ML-818 × RMG-975 (A_7) (A_6)	A_7A_6-1	C_{11}	C11P1
	A_7A_6-2		C11P2
	A_7A_6-3		C11P3
	A_7A_6-4		C11P4
	A_7A_6-5		C11P5
MH-2-15 × RMG-975 (A_5) (A_6)	A_5A_6-1	C_{12}	C12P1
	A_5A_6-2		C12P2
	A_5A_6-3		C12P3
	A_5A_6-4		C12P4
	A_5A_6-5		C12P5

Pali, Sikar and Jhunjhunu. Inter cross variability refers to the variation observed among different populations, which are derived from different parental crosses. Intra cross variability, on the other hand, refers to the variation observed within a single population, which is derived from a single parental cross. To genetically modify quantitative traits in any crop, a full understanding of the type and degree of variability present in the crop, as well as the heritability of the desirable attributes inherent in the breeding material, is required. For the establishment of an effective breeding plan, a study of genetic variability using several metrics such as heritability, genetic progress and phenotypic and genotypic coefficient of variation is essential. Understanding distinct genetic parameter estimations is critical for improving crop yield by better using the type and degree of genetic diversity available in the base material.

Plant material: Five single plants with high yield in F_2 generation in each of the 12 crosses were selected and advanced to F_3 generation. Each cross was considered a family, and the selected individual plants within a cross were referred to as progenies. All the twelve crosses were grown in compact family block design with three replications in conducted in two environments namely Experimental Farm of Department of GPB, SKNAU, Jobner and the ARS, Fatehpur, Shekhawati, Sikar during *Kharif,* 2022. In both the locations, the experimental plot consisted of 3 m long single rows spaced 30 cm apart, with an intra row spacing of 10 cm. Data were recorded on five randomly selected plants in each row for the traits *viz.* plant height, primary branches /plant, clusters /plant, pods/ cluster, pods/ plant, pod length, seeds /pod, 100-seed weight, grain yield /plant. Days to 50 % flowering and days to maturity were recorded on the basis of individual progeny rows.

Statistical analysis: The analysis of variance for between families and between progenies within a family was worked out using the method proposed by Panse and Sukhatme (1978). Genotypic and phenotypic coefficient of variation was estimated as per Burton (1952). Heritability in broad sense was estimated according to Burton and Devane (1953). Genetic advance and genetic advance as per cent of mean were determined as per the formula suggested by Robinson *et al.* (1949) and Johnson *et al.* (1955).

The estimates of genetic variability parameters between the families and within the families were computed for 11 traits in 12 crosses across under two environments are presented in **table 2 and table 3.**

Table 2. Estimation of variability parameters between families for yield related characters in two environments

S. No.	Characters	Env	Mean	EV	GV	PV	GCV	PCV	H(bs)	GA	GAM
1	Days to 50 per cent flowering	E1	37.72	1.06	0.37	1.43	1.61	3.17	25.70	0.63	1.68
		E2	37.94	1.09	0.33	1.43	1.52	3.15	23.41	0.58	1.52
2	Days to maturity	E1	69.28	1.95	1.90	3.86	1.99	2.84	49.35	2.00	2.88
		E2	69.63	2.10	0.86	2.96	1.33	2.47	29.07	1.03	1.48
3	Plant height	E1	69.06	38.61	71.58	110.19	12.25	15.20	64.96	14.05	20.34
		E2	45.85	39.52	42.53	82.05	14.22	19.75	51.83	9.67	21.09
4	Primary branches per plant	E1	0.89	0.03	0.14	0.17	41.41	46.29	80.03	0.68	76.31
		E2	1.96	0.05	0.17	0.21	20.92	23.63	78.40	0.75	38.16
5	Clusters per plant	E1	5.25	0.82	0.08	0.90	5.39	18.06	8.90	0.17	3.31
		E2	4.15	0.80	0.62	1.42	18.97	28.74	43.57	1.07	25.79
6	Pods per cluster	E1	3.54	0.37	0.06	0.43	7.05	18.65	14.31	0.19	5.50
		E2	4.38	0.74	0.20	0.94	10.23	22.18	21.27	0.43	9.72
7	Pods per plant	E1	17.45	9.65	4.59	14.24	12.28	21.62	32.25	2.51	14.36
		E2	16.98	7.76	4.33	12.09	12.26	20.48	35.80	2.56	15.10
8	Pod length	E1	7.52	0.57	0.17	0.74	5.42	11.43	22.49	0.40	5.30
		E2	7.46	0.62	0.09	0.71	3.96	11.26	12.36	0.21	2.87
9	Seeds per pod	E1	11.17	1.07	0.10	1.17	2.88	9.68	8.83	0.20	1.76
		E2	11.25	1.03	0.11	1.14	2.92	9.49	9.49	0.21	1.86
10	100-seed weight	E1	3.43	0.11	0.06	0.17	7.06	11.86	35.43	0.30	8.66
		E2	3.37	0.10	0.06	0.16	7.07	11.83	35.65	0.29	8.69
11	Grain yield per plant	E1	4.16	0.67	0.21	0.88	10.96	22.53	23.66	0.46	10.98
		E2	4.45	0.77	0.13	0.90	8.03	21.34	14.17	0.28	6.23

Table 3. Estimation of variability parameters in intra family progenies having significant difference in E1 and E2 environments for yield

S. No.	Characters	Env	Families	Mean	EV	GV	PV	GCV	PCV	H(bs)	GA	GAM
1	Plant height	E1	C5	71.95	23.11	25.94	49.06	7.08	9.73	52.88	7.63	10.60
			C7	60.65	18.65	26.20	44.86	8.44	11.04	58.42	8.06	13.29
			C8	60.65	55.23	55.13	110.41	12.24	17.33	49.93	10.80	17.82
		E2	C1	52.55	37.67	40.07	77.75	12.05	16.78	51.54	9.36	17.81
			C12	50.30	31.57	50.41	81.92	14.11	17.99	61.53	11.47	22.80
2	Primary branches per plant	E1	C1	1.24	0.07	0.15	0.22	30.93	37.79	66.98	0.65	52.15
			C2	0.83	0.04	0.80	0.12	34.21	41.54	67.82	0.048	58.04
			C3	0.75	0.04	0.08	0.12	38.06	46.21	67.86	0.49	64.59
			C9	0.91	0.05	0.10	0.16	36.36	43.75	69.06	0.56	62.25
			C10	1.65	0.15	0.15	0.31	23.64	33.53	49.70	0.57	34.33
		E2	C1	2.24	0.07	0.15	0.22	17.13	20.93	67.00	0.65	28.89
			C3	1.75	0.06	0.04	0.10	8.98	14.89	36.39	0.23	11.16
			C4	1.81	0.04	0.09	0.12	16.11	19.19	70.44	0.50	27.85
			C7	1.91	0.04	0.109	0.15	17.27	20.77	69.10	0.56	29.57
			C8	2.65	0.15	0.15	0.31	14.72	20.88	49.71	0.57	21.38
			C11	1.91	0.05	0.11	0.16	17.27	20.78	69.10	0.56	29.58
			C12	2.63	0.15	0.15	0.31	14.72	20.88	49.71	0.57	21.38
3	Clusters per plant	E1	C2	5.56	1.18	1.15	2.33	18.96	26.95	49.53	1.56	27.50
			C8	5.29	0.60	0.69	1.30	15.71	21.51	53.33	1.25	23.63
			C11	4.55	1.09	1.94	3.03	30.62	38.28	64.01	2.29	50.47
		E2	C4	4.73	0.79	1.19	1.98	23.08	29.78	60.09	1.74	36.86
			C8	4.52	1.76	1.69	3.45	28.78	41.13	48.95	1.87	41.48
			C12	3.70	2.30	2.32	4.62	41.22	58.13	50.28	2.23	60.21
4	Pods per cluster	E1	C5	3.80	0.42	0.71	1.13	22.12	27.91	62.84	1.37	36.13
			C6	3.79	0.34	0.37	0.72	16.09	22.29	52.12	0.91	23.93
			C8	3.62	0.39	0.84	1.23	25.36	30.60	68.67	1.57	43.29
			C9	3.61	0.51	0.80	1.31	24.76	31.69	61.07	1.44	39.86
			C10	3.59	0.49	0.47	0.96	19.05	27.27	48.83	0.98	27.42
			C12	3.17	0.53	0.25	0.78	15.86	27.92	32.27	0.59	18.56
		E2	C1	4.80	0.21	0.33	0.53	11.88	15.21	61.04	0.92	19.13
			C2	4.85	0.36	0.43	0.79	13.48	18.33	54.06	0.99	20.42
			C4	4.31	0.19	0.38	0.57	14.36	17.59	66.65	1.04	24.15
			C7	4.30	0.21	0.36	0.58	13.98	17.62	62.96	0.98	22.85

Genotypic and phenotypic coefficient of variation: Estimates of coefficient of variation indicated that the magnitude for PCV was higher than that of GCV but the difference between phenotypic and genotypic coefficient variation suggests little influence of environment on the expression of characters. High GCV and PCV was observed for primary branches per plant in both the environments. Such results were also reported by Gadakh *et al.* (2013). Moderate GCV and high PCV was recorded for pods per plant in both the environments, clusters per plant in E2, pods per cluster in E2, grain yield per plant in E1. This agrees with the results reported by Narasimhulu *et al.* (2013). Low GCV & moderate PCV were observed for pod length, 100-seed weight in both the environments, clusters per plant and pods per cluster in E1. This was also reported by Lakshminarayanareddy *et al.* (2003). Days to 50 % flowering, days to maturity, seeds per pod in both the environments exhibited low GCV & PCV, which were in accordance with the findings of Makeen *et al.* (2007), Tabasum *et al.* (2010), Nand and Anuradha (2013), Jeberson *et al.* (2015), Yadav *et al.* (2017), Mehandi *et al.* (2018), Sirohi *et al.* (2018), Susmitha and Jayamani (2018), Anuradha *et al.* (2019), Pavan *et al.* (2019). Low GCV & high PCV was observed only for grain yield per plant in E2. Moderate GCV and PCV were observed for plant height in both the environments. Among the above discussed superior families in E1, C3, C1, C7 recorded high GCV and PCV, C4 recorded high PCV and moderate GCV while C2 and C11 recorded moderate GCV and PCV for grain yield per plant. However, in E2 C1 and C10 recorded high GCV and PCV, C2, C11 and C12 recorded high PCV and moderate GCV while C7 recorded moderate GCV and PCV. Similar trends were reported by Pawar *et al.* (1988), Kumar *et al.* (1996), Pawar *et al.* (2001), Ramasamy and Jehangir (1998) and Nivethitha *et al.* (2023).

Heritability and Genetic advance: High heritability was observed for primary branches per plant in both the environments and plant height in E1. Similar finding was also reported by Gadakh *et al.* (2013). Moderate heritability and high genetic advance were observed for plant height and clusters per plant in E2. Moderate heritability coupled with moderate genetic advance was observed for pods per plant in both the environments. Moderate heritability coupled with low genetic advance was observed for 100-seed weight in both the environments and days to maturity in E1. Similar findings were reported by Kumar *et al.* (2010), Ramachandra and Lavanya (2017), Pavan *et al.* (2019), Yoseph *et al.* (2022) and Prajapati *et al.* (2023). Low heritability coupled with low genetic advance were observed for days to 50 per cent flowering, seeds per pod, pods per cluster and pod length in both the environments, days to maturity and grain yield per plant in E2, clusters per plant in E1. Low heritability coupled with moderate genetic advance were observed only for grain yield per plant in E1.

Among the above discussed superior families in E1 C1 and C2 recorded high heritability while C3, C4, C7 and C11 recorded moderate heritability for grain yield per plant. High genetic advance as per cent of mean was observed for C1, C3, C4 and C7 while C2 and C11 recorded moderate genetic advance as per cent of mean for grain yield per plant. High heritability coupled with high genetic advance was observed for C1. This shows the preponderance of additive gene action and heritability is due to additive gene effect and selection in this family for yield and component traits will be effective. Moderate heritability coupled with high genetic advance was observed for C3, C4 and C7. This indicates the presence of additive gene effect and heritability is due to high environmental influence. Selection within these families may be effective. High heritability coupled with moderate genetic advance was observed for C2. This indicates the presence of non-additive gene effect and heritability is due to unfavourable environmental effect. Simple selection within these families may not be effective. Moderate heritability coupled with moderate genetic advance was observed for C11. This indicates that the character is highly influenced by environmental effects. Selection within this family may not be rewarding.

On the other hand, in E2 C1, C2 and C7 recorded high heritability while C10, C11 and C12 recorded moderate heritability for grain yield per plant. High genetic advance as per cent of mean was observed for C1, C2, C7 and C10 while C11 and C12 recorded moderate genetic advance as per cent of mean for grain yield per plant. High heritability coupled with high genetic advance was observed for C1, C2 and C7. This shows the preponderance of additive gene action and heritability is due to additive gene effect and selection in these families for yield and component traits will be effective. Moderate heritability coupled with high genetic advance was observed for C10. This indicates the presence of additive gene effect and heritability is due to high environmental influence. Selection within these families may be effective. Moderate heritability coupled with moderate genetic advance was observed for C11 and C12. Selection within this family may not be rewarding. These are in accordance with the findings of Idress *et al.* (2006), Narasimhulu *et al.* (2013), Tiwari *et al.* (2014), Aravintha *et al.* (2023) and Sofia *et al.* (2017). This indicates that the character is highly influenced by environmental effects.

Thus selection in the families C1 and C2 which were found to possess high heritability and genetic advance for grain yield per plant in both the environments could yield desirable results.

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