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Research Article

Stability analysis for seed yield and its attributing traits in advanced breeding lines of blackgram [*Vigna mungo* (L.) Hepper]

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Abstract

Blackgram plays a significant role in Indian food as a supplement to cereal based diet. It contains three times higher protein than cereals. In India, unavailability of stable and high yielding varieties is a major issue in blackgram. Yield is a quantitative character and is significantly influenced by environment. A study was carried out with 18 genotypes during *kharif* season (2021) at four locations (Sehore, Gwalior, Barwani and Jhabua) to determine stable genotypes of blackgram by Eberhart and Russell approach for 12 yield and its attributing traits. The genotypes RVSU 22-6, RVSU 22-8, RVSU 22-12, Indira URD 1 (C) and IU 94-1 were found to be most stable and adapted to the diverse environments and could be included in the hybridization program to converge the stability characteristics of grain yield for the development of stable cultivar adapted to a wide range of environments.

Keywords: Blackgram, Eberhart and Russell, stability

INTRODUCTION

Among the pulses, blackgram (*Vigna mungo.* L. Hepper) is one of the significant pulse crops in India after mungbean, chickpea and pigeonpea. It is native to the Indian subcontinent, belonging to the leguminaceae family, possessing somatic chromosome number of $2n = 22$. It is a self-pollinated crop with very limited percentage of out crossing (Gill *et al.,* 2017). It plays a prominent role in Indian food, as it consists of vegetable protein and supplementation to cereal based food. Blackgram is a short duration pulse crop. It contains approximately 25-28% of protein, which is nearly triple times higher than that of cereal and also consist of minerals and vitamins (Gowda *et al.,* 2015). By enhancing the physical characteristics of the soil and fixing atmospheric nitrogen, blackgram is the crop that maintains soil fertility (Nongthombam *et al.,* 2016). Blackgram is cultivated in India in approximately 4 m ha with annual production of approximately 2 million tonnes along with 598 kg/ha of productivity (Crop outlook report of Andhra Pradesh, 2023-2024). Regrettably, unlike those of cereals, the current production level of pulses does not satisfy the emerging requirement. One of the major reasons for the minimal yield of blackgram is the poor acquisition of improved varieties and their unstable performance over the range of environments. Yield along with other quantitative traits are significantly influenced by genotype, environment and their interaction. The intensity of genotype × environment interaction had put a major challenge to the breeders (Hall *et al.,* 2003). Although a number of improved cultivars in blackgram have been evolved, mostly they show unstable performance under diverse environmental circumstances because of genotype × environment interaction (Shanthi *et al.,* 2007). Consequently, it has become requisite to develop varieties with sustainable characteristics such as wider adaptability, fertilizer responsiveness, biotic and abiotic stresses tolerant so as to get yield levels comparable to other pulses. When a variety adapts its genotype and phenotypic status to fluctuating environmental conditions, it is said to be stable. To choose a stable and adaptable variety for various yield-contributing qualities, numerous studies have been conducted in the past and are still ongoing. Specific cultivar can be prescribed for specific environments to control failure of the crop. But, it is necessary to recognize the genotypes responsive towards varied locations. Therefore, the current study was taken up to identify stable genotypes for seed yield and component traits among advance lines of blackgram.

MATERIALS AND METHODS

The experimental study comprised of eighteen genotypes including four checks *i.e*., Indira URD 1 (C), KU 96-3 (C), Pratap URD 1 (C) and TPU 4 (C) (**Table 2**) of back gram. The experiment was conducted in four different locations of Madhya Pradesh namely, R.A.K. College of Agriculture Sehore, College of Agriculture Gwalior, Krishi Vigyan Kendra Jhabua and Krishi Vigyan Kendra Barwani (**Table 1**) during *kharif* 2021. All the genotypes were raised in six row plots of 4 m length adopting a randomized complete block design with three replications. The rows were spaced at 30 cm with intra row spacing between plants of 10 cm. All the prescribed level of package and practice were applied, for healthy crop growth. Observations were recorded on plot basis for The data were recorded on plot basis for days to 50 % flowering, days to maturity, biological yield per plot (g), seed yield per plot (g) and harvest index, while for plant height at maturity, number of branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight (g), biological yield per plant (g) and seed yield per plant (g), observations were recorded on five random plants. In order to explain and examine the stability of diverse genotypes for various traits under examination, stability metrics, namely mean, regression coefficient (bi), and deviation from regression (S^2di), as recommended by Eberhart and Russell (1966), were worked out. A genotype that exhibits good mean performance, a regression coefficient near unity (bi=1), and a deviation from regression (S^2di) that is almost zero is considered highly stable. The estimation of a specific genotype's linear response to a changing environment is known as linear regression. If the regression coefficient (bi) is more than unity, the genotype is assumed to be very sensitive to environmental changes but suitable for high yielding conditions. A regression coefficient (bi) of unity denotes universal adaptability and average sensitivity to environmental changes. A high mean value indicates reduced susceptibility to environmental variations in the regression coefficient (bi), which suggests that the genotype is better suited for harsh environments.

RESULTS AND DISCUSSION

Pooled analysis of variances over four environments indicated that the genotypic variance were significant for all the parameters except days to 50% flowering, days

Table 1. Location wise information

Particulars	Environments			
Location	R.A.K. College of Agriculture, Sehore	College of Agriculture, Gwalior	K.V.K Jhabua	K.V.K Barwani
Latitude	23.1876°N	26.2232°N	22.765282°N	22.052508°N
Longitude	77.0646°E	78.1909°E	74.600252°E	74.901475°E
Altitude	502 m	478 m	318m	178 m
Soil type	Black soil	Alluvial soil	Black soil	Black soil

Table 2. List of genotypes

S.No.	Genotypes	S.No.	Genotypes	S.No.	Genotypes
1.	RVSTU 22-1	7.	RVSU 22-7	13.	Indira URD 1(C)
2.	RVSTU 22-2	8.	RVSU 22-8	14.	KU 96-3 (C)
3.	RVSTU 22-3	9.	RVSU 22-9	15.	Pratap URD 1(C)
4.	RVSTU 22-4	10.	RVSU 22-10	16.	IU 92-14
5.	RVSU 22-5	11.	RVSU 22-11	17.	IU 94-1
6.	RVSU 22-6	12.	RVSU 22-12	18.	TPU 4 (C)

to maturity, number of seeds per pod, 100 seed weight, and biological yield per plant (**Table 3**). The number of seeds per pod was the only characteristic for which the environmental variances was found to be significant. The G×E interactions were non-significant for all the traits except for plant height, number of branches per plant and 100 seed weight when tested against pooled deviation (**Table 3**). When compared to the pooled error, the effects of the pooled deviation were significant for the following characters like days to 50% flowering, days to maturity, plant height, number of pods per plant, number of seeds per pod, 100 seed weight, biological yield per plant, seed yield per plant, biological yield per plot and harvest index. On comparison to pooled deviation and pooled error, environment (linear) impacts were significant for all the traits under study (**Table 3**). The trait-wise findings of the evaluation of the three stability metrics namely, mean, regression coefficient (bi), and mean square deviation from regression line (S^2di) for all the twelve traits are furnished in **table 4**. The seed yield per plant ranged from 4.02 (TPU-4 (C)) to 6.49 g (RVSU 22-6) with the population mean of 4.66 g. Six genotypes *viz.*, RVSU 22-6, RVSU 22-8, RVSU 22-10, RVSU 22-11, RVSU 22-12 and IU 94-1 showed higher seed yield per plant than population mean. Genotypes *viz.*, RVSTU 22-4, RVSU 22-6 and IU 92-14 had bi near to unity while, genotypes *viz.*, RVSU 22-5, RVSU 22-7, RVSU 22-9, RVSU 22-11, IU 94-1, Indira URD 1 (C), KU 96-3 (C), Pratap URD 1 (C) and TPU 4(C) showed bi>1 and genotypes *viz.*, RVSTU 22-1, RVSTU 22-2, RVSTU 22-3, RVSU 22-8, RVSU 22-10 and RVSU 22-12 showed bi<1. With a non-significant regression coefficient, non-significant deviation from regression and a high mean performance the genotype RVSU 22-6 displayed average stability. Similar outcomes were obtained in blackgram by Mishra *et al*. (1990), Babu *et al*. (2009), Konda *et al*. (2009), Revanappa *et al*. (2011), Senthilkumar and Chinna, (2012), Nongthombam *et al*. (2016), Sridhar *et al*. (2023) and Rajalakshmi *et al*.(2024). Eight genotypes had significant deviation from regression values revealing their unpredictability (**Table 4**). For some other yield attributing traits *viz*., number of branches per plant, ten genotypes had superior mean value than population mean. The genotypes *viz*., RVSU 22-8, RVSU 22-12 and KU 96-3 (C) had superior mean than population mean, non-significant regression coefficient close to unity with non-significant deviation from regression indicating their average stability *i.e.,* can be suitable for all environments. Genotypes IU 94-1 and Pratap URD 1 (C) had high mean and regression coefficient significantly more than unity with non-significant deviation from regression indicating below average stability *i.e*., suited for only favorable environment. Similar outcomes were recorded for number of primary branches per plant in blackgram by Pervin *et al*. (2007) and Senthilkumar and Chinna, (2012). For number of pods per plant, seven genotypes exhibited superior mean value than population mean. The genotype RVSU 22-8, recorded greater mean values, non-significant regression coefficient close to unity and non-significant deviation from regression showing average stability *i.e.*, can be suitable for all environments. The genotypes *viz*., RVSTU 22-2, RVSTU 22-3, RVSU 22-7, RVSU 22-9, RVSU 22-10, RVSU 22-11, RVSU 22-12, IU 94-1 and KU 96-3 (C) had significant value of deviation for regression showing their unpredictability. The non-linear component of GxE interaction was determined to be non-significant, indicating that it contributed least to number of pods per plant. Pervin *et al*. (2007), Senthilkumar and

Table 3. Pooled analysis of variance for stability over the four environments for eighteen genotypes

S.No.	Source	d.f.	Mean sum of squares											
			DFF	DM	PH	NB/P	NP/P	NS/P	100 SW	BY/P	SY/P	BPP	SPP	HI
1	Rep within Env.	8	1.46	2.14	0.96	0.73	2.43	0.77	0.04	0.48	0.09	30528.40	696.27	3.62
2	Varieties	17	4.82	6.93	36.68**	1.09*	34.31**	0.66	0.41**	18.51	2.84**	229238.50**	27099.10**	23.58*
3	Env. + (Var.* Env.)	54	14.41**	11.18**	196.63**	7.49**	19.71	0.79	0.11	41.75**	1.49**	264133.90**	7858.89**	13.54
4	Environments	3	171.36**	113.12**	3266.87 **	107.92**	72.44**	1.83	1.30**	497.15**	17.16**	3199954**	85053.68**	72.60**
5	Var.* Env.	51	5.18	5.19	16.03**	1.58**	16.61	0.73	0.06	14.96**	0.57	91438.58	3318.02	10.07
6	Environments (Lin.)	1	514.09**	339.37**	9800.61**	323.77**	217.33**	5.49*	2.61**	1491.46**	51.50**	9599862**	25516**	217.81**
7	Var.* Env. (Lin.)	17	5.42	6.51	32.48**	3.72**	24.35*	0.55	0.06	21.64*	0.70	100063.70	4288.47	6.187
8	Pooled Deviation	36	4.77**	4.28**	7.37**	0.49	12.03**	0.77*	0.06**	10.98**	0.48**	822285.68**	2675.42**	11.349**
9	Pooled Error	136	1.40	1.36	2.12	0.47	1.42	0.47	0.03	0.76	0.10	13422.91	641.25	2.918
10	Total	71	12.11	10.17	158.33	5.96	23.21	0.76	0.21	0.30	1.81	255778.70	12465.71	15.951

Note- * Significant at 5%, ** Significant at 1 %, DFF- Days to 50% Flowering, DM-Days to Maturity, PH- Plant Height, NB/P-Number of Branches/Plant, NP/P-Number of Pods/Plant, NS/P-Number of Seed/Pod, 100SW- 100 Seed Weight, BY/P-Biological Yield/Plant, SY/P-Seed Yield/Plant, BPP- Biological Yield Per Plot, SPP- Seed Yield Per Plot and HI- Harvest Index

Table 4. Estimates of stability parameters for all the traits under study

S.No.	Genotype	DFF			DM			PH			NB/P		
		Mean	Bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di
1	RVSTU 22-1	48.01	0.34	1.55	73.31	0.3	0.81	36.85	0.49	16.12*	6.98	0.91	0.75
2	RVSTU 22-2	47.83	0.99	1.86	75.84	0.95	13.65**	39.99	0.95	3.21	7.11	0.23*	-0.18
3	RVSTU 22-3	49.37	1.46	4.15*	73.80	1.88	1.01	37.57	0.7*	-0.5	7.56	0.47*	-0.31
4	RVSTU 22-4	48.08	0.46	0.48	74.06	0.53	2.88	39.20	0.87	6.54*	6.98	0.37	0.23
5	RVSU 22-5	49.29	0.71	6.02**	75.43	0.3	7.67**	41.62	1.09	-0.39	7.58	1.58	1.21*
6	RVSU 22-6	50.02	0.79	2.7	73.89	1.15	-0.91	43.05	1.11	-0.71	7.23	0.67	-0.35
7	RVSU 22-7	48.06	0.5*	-1.05	75.5	-0.38	4.1*	37.09	0.67	3.19	7.47	0.96	-0.45
8	RVSU 22-8	47.68	1.06	5.7**	75.6	0.82	2.94*	39.72	0.9	13.96**	7.87	0.85	-0.33
9	RVSU 22-9	50.08	0.81	4.35*	74.31	0.96	-0.79	43.88	1.16	-0.55	7.22	1.03	-0.11
10	RVSU 22-10	48.94	1.68	5.38**	75.37	1.73	10.41**	43.76	1.21	0.33	8.13	1.42	-0.14
11	RVSU 22-11	50.38	1.68	16.42**	77.07	1.12	3.25*	46.26	1.36	3.22	6.47	0.42*	-0.39
12	RVSU 22-12	47.84	0.64	1.88	73.22	0.96	-0.27	42.8	1.06	0.01	7.71	0.8	-0.18
13	IU 92-14	49.11	1.47	0.44	75.62	1.69	1.68	43.80	1.16	0.46	7.68	1.36	-0.1
14	IU 94-1	48.49	1.01	-0.98	72.87	1.09	1.63	42.88	1.17	0.84	8.28	1.65*	-0.4
15	IndiraURD 1(C)	48.10	1.09	-0.82	73.30	1.29	-0.74	35.78	0.61	14.7**	6.68	1.29	1.18*
16	KU 96-3 (C)	47.44	1.02	1.99	74.31	1.43	8.32**	41.41	1.06	19.6**	7.58	0.92	0.07
17	Pratap URD 1 (C)	50.91	1.67	6.43**	77.23	1.65**	-1.38	42.8	1.15	10.41**	7.67	1.63*	-0.23
18	TPU 4 (C)	47.17	0.63	4.15*	73.56	0.56	-0.85	44.70	1.27	5.19*	8.40	1.43	-0.25
	Mean	48.71	-	-	74.68	-	-	41.29	-	-	7.48	-	-

S.No.	Genotype	NP/P			NS/P			100SW			BY/P		
		Mean	bi	S^2di	Mean	Bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di
1	RVSTU 22-1	16.35	-0.43	0.82	6.16	1.73	-0.22	3.87	1.26	0.00	17.33	0.65	2.19*
2	RVSTU 22-2	19.79	-1.9	34.81**	6.75	2.31*	-0.48	3.65	-0.17	0.05*	18.64	0.81	6.27**
3	RVSTU 22-3	15.07	0.31	6.93**	6.66	0.99	-0.3	3.7	-0.42	0.13**	18.31	0.7	12.2**
4	RVSTU 22-4	18.46	0.1	2.13	6.41	-0.1	1.55*	3.49	-1.3**	-0.02	17.41	0.84	3.15**
5	RVSU 22-5	17.65	1.42	11.8**	5.66	0.12	-0.16	3.58	1.41	0.12**	19.07	0.72	9.1**
6	RVSU 22-6	24.58	1.73*	-1.27	5.75	1.38	0.26	3.67	0.86	0.03	21.16	-0.04	9.86**
7	RVSU 22-7	18.27	-0.84	8.59**	5.91	2.46	0.63	3.70	1.9	0.25**	19.29	0.5	21.28**
8	RVSU 22-8	24.17	0.88	0.96	5.66	-0.77	0.76	3.74	0.53	0	23.09	0.66	6.48**
9	RVSU 22-9	17.95	-0.02	13.88**	5.83	0.96	-0.13	3.74	1.25	0.6**	22.09	1.2	22.81**
10	RVSU 22-10	22.23	3.7	31.26**	6.58	2.6	-0.15	3.98	0.3	0.08**	22.37	0.89	8.3**
11	RVSU 22-11	22.46	0.14	24.55**	5.66	-0.32	0.05	4.00	1.48	0	21.09	1.5	6.59**
12	RVSU 22-12	23.55	3.23	45.32**	5.91	2.08	0.45	3.71	-1.32	0.11**	24.06	0.77	3.57**
13	IU 92-14	18.56	2.03*	-1.04	5.5	3.43	0.22	4.09	2.33	0.4**	20.48	1.04	6.98**
14	IU 94-1	20.85	1.83	3.2*	6.58	0.46	1.3*	4.15	3.04	0.1**	21.13	1.04	15.74**
15	IndiraURD 1(C)	15.55	0.68	-0.93	5.75	2.29	1.09*	3.51	0.44*	-0.02	24.04	1.26	0.23
16	KU 96-3 (C)	18.03	1.04	9.75**	6.08	0.03	0.44	3.99	2.38	0.07*	22.97	1.55*	0.57
17	Pratap URD 1 (C)	17.04	2.45*	-0.66	5.58	-0.29	-0.13	4.17	1.95	0.26*	21.43	1.76	27.49**
18	TPU 4 (C)	18.39	1.63	-0.11	6.08	-1.35	-0.06	3.69	2.07	0.1**	22.61	2.16	21.52**
	Mean	19.39	-	-	6.03	-	-	3.80	-	-	20.92	-	-

S.No.	Genotype	SY/P			BPP			SPP			HI		
		Mean	bi	S²di	Mean	bi	S²di	Mean	Bi	S²di	Mean	Bi	S²di
1	RVSTU 22-1	4.14	0.24	0.00	1939.97	0.68	-5908	386.86	1.17	2723.82**	19.97	0.67	5.21
2	RVSTU 22-2	3.59	0.15	0.45**	2054.37	0.89	8430	412.86	1.38	10446.56**	20.20	0.17	25.35**
3	RVSTU 22-3	4.11	0.67	1.68**	2116.28	0.57	176397**	460.45	1.29	2563.3**	22.08	1.06	17.75**
4	RVSTU 22-4	4.02	1.06	0.42**	1844.28	0.45	57440**	417.82	-0.74*	773.35	23.65	2.72	18.03**
5	RVSU 22-5	4.17	1.46	-0.06	2226.81	0.91	59797**	479.31	0.96	1722.2*	21.68	0.66	-2.28
6	RVSU 22-6	6.49	0.95	0.03	2472.37	0.27	88357**	637.37	0.69	814.58	26.20	0.06	5.89
7	RVSU 22-7	4.02	1.25	-0.06	2189.00	0.49	223964**	478.41	1.36	-71.75	22.62	2.08	30.48**
8	RVSU 22-8	5.30	0.29	0.89**	2562.36	0.65	15345	537.25	0.33	311.86	21.24	0.59	5.08
9	RVSU 22-9	4.24	1.22	0.76**	2371.05	1.37	90668**	445.43	1.17	5802.93**	19.32	1.42	0.66
10	RVSU 22-10	6.01	0.76	1.50**	2611.26	1.12	46130*	622.26	0.74	494.08	24.23	0.71	6.3*
11	RVSU 22-11	5.03	1.8	0.48**	2339.99	1.49	118518**	489.33	0.96	-131.16	22.07	1.89	11.98**
12	RVSU 22-12	6.08	0.31*	-0.03	2805.05	0.83	51840*	628.01	1.01	2120.55*	22.59	0.84	3.46
13	IU 92-14	4.51	1.03	0.51**	2326.39	1.3	113259**	471.49	1.9	930.98	20.57	1.3	13.61**
14	IU 94-1	5.30	1.54	0.18	2457.52	1.41	98569**	563.60	1.04	712.43	23.60	0.66	10.49*
15	IndiraURD 1(C)	4.4	1.4	-0.01	2454.81	0.86	-7469	446.99	0.96	907.48	18.35	0.28	-0.65
16	KU 96-3 (C)	4.44	1.32	0.02	2417.32	1.6*	-5698	401.28	1.41	180.96	16.72	0.58	-2.27
17	Pratap URD 1 (C)	4.02	1.12	0.11	2255.62	1.51	58294**	416.25	1.32	-339.8	18.96	0.63	-0.97
18	TPU 4 (C)	4.02	1.44*	-0.09	2218.31	1.59	34493*	390.73	1.06	6597.6**	18.22	1.68	2.9
	Mean	4.66	-	-	2314.60	-	-	482.54	-	-	21.24	-	-

Note- *Significant at 5%, **Significant at 1 %, DFF- Days to 50% Flowering, DM-Days to Maturity, PH- Plant Height, NB/P-Number of Branches/Plant, NP/P-Number of Pods/Plant, NS/P-Number of Seed/Pod, 100SW- 100 Seed Weight, BY/P-Biological Yield/Plant, SY/P-Seed Yield/Plant, BPP- Biological Yield Per Plot, SPP- Seed Yield Per Plot, HI- Harvest Index, bi –Regression coefficient and S²di – Deviation from regression.

Chinna, (2012), Sharma and Rao, (2015) and Nongthombam *et al*. (2016) recorded significant linear and non-linear components of G x E interaction in blackgram for number of pods per plant. For number of seeds per pod, eight genotypes showed mean values higher than population mean. The genotype RVSTU 22-3 had high mean value with non- significant regression coefficient near to unity and non-significant deviation from regression showing its average stability *i.e*., can be suitable for all environments. Comparable results were recorded by Babu *et al.* (2009), Konda *et al*. (2009) and Sharma and Rao, (2015) in their stability studies with blackgram. For biological yield per plant, eleven genotypes had mean values higher than population mean. The genotype Indira URD 1 (C) showed non-significant regression coefficient and non-significant deviation from regression indicating its average stability *i.e*., genotype can perform better in all environment while nine genotypes showed significant deviation from regression *i.e.,* showing unpredictability. The non-linear G×E interaction was non-significant for biological yield per plant and similar findings were observed by Gupta and Sharma (2009). For biological yield per plot, ten genotypes had mean values higher than population mean. Genotype Indira URD 1 (C) showed non-significant regression coefficient and non-significant deviation from regression indicating its average stability *i.e*., genotype can perform better in all environment while thirteen genotypes showed significant deviation from regression *i.e*., showing unpredictability for biological yield per plot. For harvest index, ten genotypes recorded mean values above the population mean. The regression coefficient was near to unity for genotypes RVSTU 22-3 and RVSU 22-12. The genotype RVSU 22-12 had high mean value with non-significant regression coefficient near to unity and non-significant deviation from regression *i.e*., showing average stability. Genotypes *viz*., RVSU 22-5 RVSU 22-6 and RVSU 22-8 had regression coefficient, significantly less than 1 with superior mean and non-significant deviation from regression. Harvest index had both the linear and non-linear G×E interaction as non-significant. Considering the above discussion, genotypes *viz*., RVSU 22-6, RVSU 22-8, RVSU 22-12, Indira URD 1 (C) and IU 94-1 were found the most stable and adapted to the diverse environments and could be included in the hybridization program to converge the stability characteristics of grain yield for the development of stable cultivar adapted to a wide range of environments.

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