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Genotype × Environment Interaction for Yield and Yield Determining Traits in Green Gram (*Vigna radiata* (L.) Wilczek)

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ABSTRACT: Twenty-five green gram (*Vigna radiata*) genotypes representing diversity in characters were assessed with 3 replications in Randomized Block Design (RBD). Environment wise data on each character for all the genotypes had been subjected to pooled analysis of variance and joint regression analysis was done for each genotype in each environment to assess the environment + (genotypes × environment) effects. The pooled analysis of variance showed highly significant differences among genotypes for all the characters. The environmental effects were highly significant for all the characters and genotype × environment (G × E) interactions were significant for all the characters except pods per plant. Analysis of variance for each character was done in each environment. The replication mean sum of squares was non-significant in all the three environments for all the characters. The significant difference between genotypes was observed for all the characters in each environment. As per environmental indices, E_3 (-1.92) was most favorable and E_1 (2.45) was least favorable for days to 50% flowering and days to maturity. Remaining characters, like plant height, branches per plant, clusters per plant, pods per cluster, pods per plant, pod length, seeds per pod, seed yield per plant and test weight the most favorable environment was E_1 and least favorable environment was E_3. The environment (linear) became significant for all the characters except clusters per plant. The genotypes × environment (linear) component were significant for days to 50% flowering, pods per cluster, seed yield per plant and test weight. Pooled deviation was significant for days to 50% flowering, days to maturity, plant height and clusters per plant.

Keywords: Green gram, Environment, Genotype × Environment interaction, Yield, Variance.

INTRODUCTION

Green gram (*Vigna radiata* (L.) Wilczek) is a self-pollinating crop with chromosome number 2n=2x=22, belongs to family *Leguminaceae,* subfamily *Papilionoideae* and native to India. It is also called as mung bean, mung and moong in India (Morton *et al.*, 1982). It is an important pulse crop with high protein which is grown majorly in semiarid to sub-humid lowland tropics and subtropics with 700 to 1000 mm rainfall annually. It is a crop grown in warm season with temperature range of 25°C to 45°C (Morton *et al.*, 1982). It can mature in 55–65 days and can yield up to 2500 kg/ha (Azab, 1997; Shil and Bandopadhya 2007; Gebrelibanos and Fiseha 2018).

The nutritive value of green gram is rich with digestible protein which is nearly 25–30%, 1.5.0% oil, 4–5% fiber, 5–6% ash and 60–67% carbohydrates on weight basis. Green gram is reservoir of antioxidants like phenolic acids, flavonoids, caffeic acid, cinnamic acid etc. which deceases chronic diseases risk like heart disease, diabetes and cancers (Delfin *et al.,* 2008; Baraki *et al*., 2020).

India covers green gram cultivation up to 60% of the total world area and 50% of overall production (Rishi, 2009; Singh *et al*., 2013). It ranks third among pulses after chickpea and pigeon pea in area and production. Approxiately 32.00 lakh ha area was covered by green gram with total production of 23.40 lakh tonnes and productivity of 751 kg/ha during 2019-2020 in India. The states of Rajasthan (23.28 lakh ha), Maharashtra (3.29 lakh ha), Karnataka (2.70 lakh ha), Madhya Pradesh (1.84 lakh ha), Orrisa (1.65 lakh ha) and Telangana (0.67 lakh ha) are the main producing states of green gram in India (Anonymous, 2019-20).

The identification of high yielding and stable genotype of green gram under varied environments is difficult because of the occurrence of genotype × environment interaction (GEI). In wide variable environments, the presence of significant genotype × environment interaction is highly possible. Presence of significant genotype × environment interaction in crop improvement is challenge and also chance for plant breeders (Eberhart and Russell 1966; Baraki *et al*., 2014). Hence, deeper insight of the pattern and degree of GEI is of key importance for breeder's scientist to reduce price of genotypic evaluation. The stability of genotypes completely relies on expression of morphological and physiological traits resulting in GEI. G × E interaction has a masking impact on the production of genotype and the ranking of the genotype change over numerous environments.

MATERIAL AND METHODS

The experimental material for study comprises of twenty-five genotypes of green gram (*Vigna radiata*) representing diversity in adaptability and variability in characters. The experiment was conducted during the *kharif*, 2020 in three environments (E_1, E_2 and E_3) by keeping 15 days intervals between the dates of sowing. Each genotype was planted in a plot size of 3.0×0.3 m^2 in each environment and each replication. The spacing was maintained as 30 cm between row to row and 10 cm between plants to plant. The field experiment was carried out in Randomized Block Design with three replications at the Research Farm, S. K. N. College of Agriculture, Jobner. Observations were recorded on yield and yield determining traits *viz*., days to 50 per cent flowering, days to maturity, plant height, branches per plant, clusters per plant, pods per cluster, pod length, seeds per pod, pods per plant, and seed yield per plant and test weight. The environment wise data on each character for all the genotypes had been subjected pooled analysis of variance (Singh and Choudhary 1985). The joint regression analysis was done to determine the significance of each parameter. Detailed analysis of variance (ANOVA) for the joint regression analysis along with the formula used to obtain sum of squares for each source using the means over replication. The significance of the variance due to genotypes, environments, environments + (genotypes x environments), environmental (linear), genotypes × environments interactions, genotypes × environments (linear) was tested against pooled deviation, if it is significant, otherwise pooled error is used for significance test.

RESULT AND DISCUSSION

Pooled analysis of variance. The pooled analysis of variance was estimated from pooled data for three replications of three environments for all the genotypes. It showed highly significant differences among genotypes for all the characters. The environmental effects were highly significant as well for all the characters *viz*., days to 50% flowering, days to maturity, plant height (cm), branches per plant, clusters per plant, pods per cluster, pods per plant, pod length (cm), seeds per pod, seed yield per plant (g) and test weight (g). While genotype × environment (G × E) interactions were significant for all the characters except pods per plant. It specifies the differential influence of environment on the genotypes with respect of all the characters (Table 1).

Environment-wise analysis of variance. Significant genotype x environment (G × E) interactions for pooled data indicated requirement of analysis of variation in each of the environment separately. Analysis of variance for each character was done in each environment to know the differences amongst genotypes. The replication mean sum of squares was non-significant in all the three environments for all the characters. The significant difference between genotypes were observed for all the characters as for example, days to 50% flowering, days to maturity, plant height (cm), branches per plant, clusters per plant, pods per cluster, pods per plant, pod length (cm), seeds per pod, seed yield per plant (g), test weight (g) in each environment (Table 2). The significant differences among genotypes indicated the genotypic differences were factual and well expressed in all three environments.

Estimation of range and mean. After comparing the mean (over the genotypes and replications) for different yield and yield attributing traits in all three environments, it was specified that the means were highest in environment-I for all the characters *viz*., days to 50% flowering (42.17), days to maturity (63.44), plant height (46.81), branches per plant (4.43), clusters per plant (5.56), pods per cluster (3.96), pods per plant (21.26), pod length (7.73), seeds per pod (12.16), seed yield per plant (5.37) and test weight (34.67), whereas none of the character showed highest mean in environment-II and environment-III. Comparison of means across environments stipulates that days to 50% flowering, days to maturity, plant height (cm), seeds yield per plant (g) and test weight were highly affected across environment. Environment-I had highest mean for greater number of characters which were moderate in environment-II and lowest in environment-III. Thus, environment-I was indicated as suitable for most of the characters under study (Table 3).

The range for different characters decreased linearly with change in environments. Comparison of ranges of different characters for three environments says that environment-I (E_1) had widest range for days to 50% flowering (37.67-48.00), days to maturity (58.67-68.00), branches per plant (3.64-5.24), clusters per plant (3.87-6.48), pods per cluster (2.81-5.95), pods per plant (15.60-27.49), seeds per pod (11.29-14.44) and seed yield per plant (3.81-6.61), whereas, broad range was found for plant height (35.63-55.71) and pod length (6.93-8.52) under second environment (E_2) and single character *viz.*, test weight (26.47-33.89) had highest range in environment-III (E_3). Environment-I had lowest range for test weight (33.85-35.78), while environment-II had lowest range for pods per plant (17.04-26.79), seeds per pod (10.25-12.09) and environment-III had lowest range for days to 50% flowering (35.67-40.00), days to maturity (57.33-66.00), plant height (34.25-43.10), branches per plant (1.95-3.30), clusters per plant (4.46-6.27), pods per cluster (2.51-4.47), pod length (6.62-7.54), and seed yield per plant (3.09-4.12). Results divulges that the environment-I had widest range for most of the characters (eight out of eleven characters) thus, first environment poses as perfect and most favourable and third environment was least favorable for screening of the genotypes of green gram amongst all the three environments (Table 3).

Grading of environments. Environmental index is used to grade the environment based on overall mean performance of the genotypes. It is calculated through estimating difference between the mean of characters at the environment of interest and the grand mean and resulting in identification of suitable environment for each of the character. It was found in the present investigation that most suitable environment was different for different characters. As per environmental indices, E_3 (-1.92) was most favourable and E_1 (2.45) was least favourable for days to 50% flowering. Similarly, for days to maturity the most favourable environment was environment-III (-1.14) (late sown condition) and the least favorable was environment-l (1.83) (early sown condition). Days to 50% flowering and days to maturity are negatively correlated with yield traits as earliness is desirable for these characters. Remaining characters, like plant height, branches per plant, clusters per plant, pods per cluster, pods per plant, pod length, seeds per pod, seed yield per plant and test weight the most favorable was E_1 and least favourable environment was E_3 (Table 4).

Joint regression analysis of variance. The joint regression analysis was performed according to Eberhart and Russell (1966). The joint regression analysis was done using the means over replications for each genotype in each environment. The environment + (genotypes × environment) interaction were non-significant for all the characters (Table 5). The environment (linear) became significant for all the characters except for clusters per plant. This indicated that the effect of environment on the genotypes were significant and can be categorized and predictable. The genotype x environment (linear) component were significant for days to 50% flowering, pods per cluster, seed yield per plant and test weight, indicating that the genotype differed in their linear response to the environment. Pooled deviation was significant for days to 50% flowering, days to maturity, plant height and clusters per plant which indicates the nature of the genotype over environments was unpredictable. The pooled deviation was further partitioned into components associated with each genotype (Table 5).

Table 1: Pooled analysis of variance for yield and yield determining traits in Green gram.

Source	d.f.	DFF	DM	PH	BPP	CPP	PPC	PP	PL	SPP	SY/P	TW
Genotypes	24	14.81**	26.84**	75.09**	0.56**	1.38**	2.09**	54.68**	0.38**	1.23**	0.76**	4.36**
Environments	2	374.61**	192.46**	1615.08**	65.00**	1.93**	13.09**	98.60**	6.21**	68.75**	63.97**	509.30**
Rep. in Environment	6	7.80	22.27	5.45	0.51	0.70	0.76	16.04	0.43	0.67	0.58	5.18
G × E Interaction	48	9.86**	11.79**	25.13**	0.41**	0.91**	1.14**	8.33	0.18**	1.14**	0.75**	4.52**
Pooled Error	144	3.03	7.01	8.11	0.32	0.46	0.41	9.45	0.17	0.55	0.22	1.87

*, **: Significant at 5% and 1% levels, respectively

DFF	Days to 50% flowering	PP	Pods per plant	CPP	Clusters per plant
DM	Days to maturity	PL	Pod length (cm)	TW	Test weight (g)
PH	Plant height (cm)	SPP	Seeds per pod	PPC	Pods per cluster
BPP	Branches per plant	SY/P	Seed yield per plant		

Table 2: Environment wise analysis of variance for 25 genotypes tested under three environments.

Environments	Source	df	DFF	DM	PH	BPP	CPP	PPC	PP	PL	SPP	SY/P	TW
E_1	Replication	2	8.49	16.12	2.80	0.13	0.03	0.73	2.47	0.70	0.18	0.64	2.11
	Genotypes	24	18.39**	19.21**	36.19**	0.64**	1.19**	1.76**	32.22**	0.23**	1.42**	1.55**	0.68**
	Error	48	3.51	4.98	5.79	0.33	0.18	0.70	10.83	0.24	0.31	0.27	0.76
E_2	Replication	2	12.33	27.64	11.23	0.96	0.79	1.50	23.28	0.56	1.60	0.91	6.94
	Genotypes	24	11.20**	18.84**	72.33**	0.44**	1.32**	1.57**	19.88**	0.35**	0.83**	0.37**	2.96**
	Error	48	2.79	7.54	11.79	0.45	0.70	0.48	9.00	0.22	0.71	0.31	2.66
E_3	Replication	2	2.56	23.05	2.32	0.45	1.29	0.04	22.37	0.01	0.24	0.17	6.51
	Genotypes	24	4.94**	12.36**	16.83**	0.30**	0.69**	1.03**	19.24**	0.16**	1.26**	0.33**	9.77**
	Error	48	2.80	8.50	6.75	0.18	0.50	0.06	8.52	0.06	0.63	0.07	2.17

*, **: Significant at 5% and 1% levels, respectively

Table 3: Range and mean for yield and yield determining traits in green gram genotypes over environments.

S. No.	Characters	Range			Mean		
		E_1	E_2	E_3	E_1	E_2	E_3
1.	Days to 50% flowering	37.67-48.00	35.67-42.67	35.67-40.00	42.17	39.19	37.80
2.	Days to maturity	58.67-68.00	56.67-65.67	57.33-66.00	63.44	60.92	60.47
3.	Plant height	41.56-54.44	35.63-55.71	34.25-43.10	46.81	42.50	37.54
4.	Branches per plant	3.64-5.24	2.73-4.25	1.95-3.30	4.43	3.43	2.57
5.	Clusters per plant	3.87-6.48	4.63-6.67	4.46-6.27	5.56	5.54	5.27
6.	Pods per cluster	2.81-5.95	2.75-5.35	2.51-4.47	3.96	3.81	3.17
7.	Pods per plant	15.60-27.49	17.04-26.79	14.84-25.19	21.26	20.76	19.07
8.	Pod length	7.12-8.34	6.93-8.52	6.62-7.54	7.73	7.54	7.16
9.	Seeds per pod	11.29-14.44	10.25-12.09	8.72-11.67	12.16	11.33	10.25
10.	Seed yield per plant	3.81-6.61	3.71-5.00	3.09-4.12	5.37	4.36	3.52
11.	Test weight	33.85-35.78	30.97-34.45	26.47-33.89	34.67	33.03	29.56

Table 4: Environment indices for different traits of green gram genotypes.

Environments	DFF	DM	PH	BPP	CPP	PPC	PP	PL	SPP	SY/P	TW
E1	2.45	1.83	4.53	0.95	0.10	0.32	0.90	0.25	0.91	0.95	2.25
E2	-0.53	-0.69	0.21	-0.04	0.09	0.16	0.39	0.06	0.08	-0.06	0.61
E3	-1.92	-1.14	-4.74	-0.91	-0.19	-0.47	-1.29	-0.31	-1.00	-0.89	-2.86

Table 5: Joint regression analysis for different traits tested over three environments showing mean sum of squares for yield and its determining traits in green gram.

Source	d.f.	DFF	DM	PH	BPP	CPP	PPC
Genotypes	24	4.94**	8.95**	25.03**	0.19	0.46	0.70**
E+ G × E	50	8.15	6.34	29.58	1.00	0.32	0.54
E (linear)	1	249.74**	128.31**	1076.72**	43.33**	1.29	8.73**
G X E (linear)	24	4.44**	3.22	8.91	0.15	0.22	0.58**
Pooled deviation	25	2.05**	4.45**	7.53**	0.12	0.37**	0.17
ML 24-59	1	0.05	2.37	6.20	0.00	0.09	0.04
IGKM-06-10-7	1	2.40	6.06	0.17	0.01	0.11	0.00
PM-1618	1	0.02	2.98	6.67	0.02	0.23	0.04
JLPM-504-20	1	0.21	2.17	10.31	0.00	0.66	0.44
DGGV-80	1	2.27	0.04	9.40	0.00	0.93	0.00
MH-1703	1	0.35	0.15	20.00	0.26	1.52	0.39
MH-1421	1	1.19	0.01	11.75	0.04	0.17	0.05
ML-818	1	1.91	3.55	57.60	0.00	0.06	0.07
Pusa-BM-5	1	0.45	1.99	50.84	0.51	1.00	0.08
MH-2-15	1	5.65	2.08	8.44	0.00	0.01	0.05
PUSA M-1972	1	0.84	7.81	5.13	0.00	0.01	0.80
VGG-17-04	1	0.26	1.76	4.27	0.00	0.69	0.03
ML-2482	1	0.45	1.41	9.54	0.08	0.16	0.02
IPM-312-394-1	1	3.80	0.22	9.61	0.00	0.01	0.68
PUSA-M-1971	1	0.10	6.18	18.31	0.18	0.25	0.01
IPM-02-03	1	0.57	1.94	0.79	0.00	0.04	0.00
IGKM-05-18-02	1	2.06	12.31	4.63	0.18	0.56	0.12
OBGG-103	1	0.14	2.75	0.66	0.00	0.12	0.02
BGG-17-043	1	4.40	0.51	33.03	0.09	0.02	0.06
MGG-389	1	4.46	13.78	10.46	0.23	0.01	0.73
VGG-17-038	1	3.43	0.26	8.24	0.01	0.05	0.09
PM-16-23	1	5.22	34.36	0.21	0.55	1.59	0.20
IPM-14-49-5	1	4.32	0.69	8.18	0.00	0.32	0.26
NDMK-17-07	1	2.47	6.24	4.67	0.67	0.10	0.07
IPMD-14-10	1	4.19	22.43	0.09	0.17	0.63	0.00
Pooled error	144	3.03	7.01	8.10	0.32	0.46	0.41
Total	224	2061.38	4052.75	42781.56	212.16	150.97	194.92

Source	d.f.	PP	PL	SPP	SY/P	Tw
Genotypes	24	18.23**	0.13**	0.41	0.25**	1.45
E + G × E	50	3.99	0.14	1.28	1.09	8.24
E (linear)	1	65.74**	4.14**	45.83**	42.65**	339.53**
G X E (linear)	24	2.68	0.08	0.50	0.43**	2.03**
Pooled deviation	25	2.76	0.04	0.26	0.07	0.94
ML 24-59	1	0.14	0.02	0.04	0.04	0.07
IGKM-06-10-7	1	6.36	0.00	0.03	0.00	0.20
PM-1618	1	0.61	0.04	0.01	0.08	0.36
JLPM-504-20	1	2.39	0.08	0.07	0.00	1.11
DGGV-80	1	2.52	0.00	2.06	0.08	1.65
MH-1703	1	2.28	0.00	0.09	0.04	0.23
MH-1421	1	20.65	0.02	0.12	0.05	3.99
ML-818	1	2.32	0.01	0.26	0.01	0.02

Pusa-BM-5	1	0.66	0.03	0.01	0.01	3.41
MH-2-15	1	1.72	0.01	0.17	0.31	0.61
PUSA M-1972	1	12.48	0.05	0.74	0.02	0.08
VGG-17-04	1	0.02	0.01	0.35	0.01	2.28
ML-2482	1	0.05	0.00	0.37	0.16	0.08
IPM-312-394-1	1	3.35	0.01	0.40	0.04	4.16
PUSA-M-1971	1	0.45	0.07	0.16	0.09	0.09
IPM-02-03	1	0.59	0.21	0.14	0.15	0.59
IGKM-05-18-02	1	1.24	0.05	0.62	0.01	1.08
OBGG-103	1	10.39	0.00	0.01	0.24	1.15
BGG-17-043	1	0.71	0.01	0.09	0.15	0.32
MGG-389	1	1.76	0.23	0.35	0.00	0.43
VGG-17-038	1	0.45	0.01	0.01	0.10	0.55
PM-16-23	1	17.23	0.00	0.00	0.00	0.65
IPM-14-49-5	1	3.05	0.09	0.04	0.03	0.04
NDMK-17-07	1	0.02	0.05	0.03	0.02	0.40
IPMD-14-10	1	0.04	0.05	0.22	0.00	0.02
Pooled error	144	9.45	0.17	0.55	0.22	1.87
Total	224	5102.66	57.67	305.24	216.92	1640.58

*, **: Significant at 5% and 1% levels, respectively

CONCLUSION

Stability analysis in green gram was done to find the widely adapted genotypes in various environments where environment I was most suitable and environment III was least. The environmental effects were highly significant for all the characters and genotype × environment (G × E) interactions were also significant for most of the characters. This study was helpful in finding stable genotypes of green gram for yield and yield determining characters.

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Conflict of Interest. None.

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