

## G × E Interaction Analysis for Yield and Major Diseases in Chickpea under Rice Fallow Land of Bihar

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**Abstract** The present experiment was conducted to analyze G × E interaction and characterization of twelve chickpea genotypes of diverse origin during three consecutive years with three replications under rice fallow land. Plot yield was negatively associated with dry root rot (-0.66\*) and stunt disease (-0.53\*). Based on mean yield performance, GCP 105 (2771.11 g) produced highest yield over environment followed by JG 14 (2744.44 g) and DCP 92-3 (2716.67 g). Based on ranking using plot yield regression coefficient, Shubhra was found stable genotypes followed by Rajas and JG – 11 however Pant G186 was found more stable in reference to mean square deviation from regression followed by Shubhra and BG 372. The genotypes BG 372, Pant G 186, GCP 105 and DCP 92-3 had regression coefficient (bi) greater than one and mean value more than their population mean for plot yield and minimum incidence of DRR and stunt disease. So, our recommendation would be to promote genotypes, i.e. BG 372, Pant G 186, GCP 105 and DCP 92-3, under rice fallow areas of Bihar state.

**Keywords** Chickpea (*Cicer arietinum* L.), Correlation, Dry root rot, Environmental index, Regression coefficient.

### Introduction

Chickpea (*Cicer arietinum* L.) is the third most important pulses in the world and a predominant pulse of India in terms of both area and production. In India area under chickpea cultivation is steeply rising. However, in Bihar State total acreage is 0.061 million hectares, production 0.087 million tonnes with productivity 1.43 t/ha [1]. Rice fallow lands are major area for chickpea and wheat cultivation under Indo – Gangetic plains. About 11 mha of eastern Uttar Pradesh and central India (Madhya Pradesh) are available for chickpea cultivation after *kharif* rice. So, our aim was to popularize chickpea under rice fallow areas [2]. However, two major diseases dry root rot and stunting disease are most prevalent in Indo-Gangetic plains. Dry root rot caused by *Rhizoctonia bataticola* is most devastating among soil borne disease under rainfed condition. These diseases appear at late flowering and pod developing stage and characterized by yellowing, sudden drying of infected plants and browning of tap root followed by destroying lateral roots [3]. Plants infected by stunt disease exhibit yellow orange or brown discoloration and stunted growth which is caused by bean leaf roll virus [3, 4].

Information about yield stability and G × E interaction is prime objectives for developing new cultivars with advance acclimation potential to major environmental constraints [5]. Partitioning of the G × E interaction is essential to determine the nature of the interaction. Considering this view, an experiment was conducted to analyse G × E interaction to identify suitable genotype performing well under rice fallow land.

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**Table 1.** Genotypic correlation (rg) and phenotypic correlation (rp) of twelve chickpea genotypes for studied characters. \*, \*\* indicate significant at  $p < 0.05$  and  $< 0.01$  respectively. Days in 50% flowering (DF); Number of pods per plant (NPP); Plant height (PH); Plant stand at harvest (PSH); Seed index (SI); yield (PY); Days to maturity (DM) and Dry root rot (DRR).

Traits		DF	NPP	PH	PSH	SI	PY	DM	DRR (%)	Stunt (%)
DF	rg	1.00	0.40*	0.23	0.55**	-0.31*	0.29	0.85**	-0.15	-0.20
	rp	1.00	0.31*	0.19	0.34*	-0.30*	0.22	0.76**	-0.13	-0.18
NPP	rg		1.00	0.45*	0.33*	0.06	0.18	0.21	-0.44*	-0.77**
	rp		1.00	0.32*	0.26	0.07	0.06	0.14	-0.33*	-0.56**
PH	rg			1.00	0.56**	0.52**	0.40**	0.11	0.08	0.16
	rp			1.00	0.18	0.47**	0.33*	0.10	0.08	0.16
PSH	rg				1.00	-0.49**	0.83**	-0.02	-0.79**	-0.72**
	rp				1.00	-0.30*	0.43**	-0.05	-0.74**	-0.66**
SI	rg					1.00	-0.38*	0.02	0.75**	0.73**
	rp					1.00	-0.31*	0.02	0.71**	0.70**
PY	rg						1.00	-0.11	-0.66**	-0.53*
	rp						1.00	-0.04	-0.61**	-0.50*
DM	rg							1.00	-0.07	-0.07
	rp							1.00	-0.06	-0.06
DRR (%)	rg								1.00	0.97**
	rp								1.00	0.94**
Stunt (%)	rg									1.00
	rp									1.00

search, Kanpur, India for providing the material to promote chickpea cultivation under rice fallow areas of Bihar, India).

### Materials and Methods

The present investigation was carried out at Pulse Research Center (PRC), Mokama, Bihar Agricultural University, Sabour (Bihar) during three consecutive year 2010-11, 2011-12 and 2012-13 to evaluate twelve chickpea genotypes of diverse origin for  $G \times E$  interaction under rice fallow land with three replications. Date of sowing was 15<sup>th</sup> November of every year. The plot size was 5 m (row length)  $\times$  3.6 m (12 rows and 30 cm apart each). The fertilizers were applied as basal dose at the rate of 20 kg N, 40 kg  $P_2O_5$ , 20 kg  $K_2O$  along with 20 kg zinc sulfate per hectare. Other agronomic practices were applied to raise a good and healthy crop. Seed was soaked in water for 4-5 hours before sowing as seed priming to avoid moisture stress for better seed germination. The experimental site is located at 25°30'N latitude and 85°15' E longitude at 144 MSL. The site under sub humid climate and zone IIIB of Bihar state under Indo – Gangetic plains of India. Annual average rainfall is 1100 mm. Wide fluctuation in temperature throughout the year has been reported. It varies from around 44° C (maxi-

imum temperature) in May – June to around 10° C (minimum temperature) in December – January. Soil of experimental site is loamy in texture and pH 7.2. Soil possess 0.5–0.6% organic carbon, 25kg/ha available  $P_2O_5$  and available  $K_2O$  is 330 kg/ha. The statistical analysis was preferred by Windostat version 8.6 from indostat services. Field observations were recorded using mean data of ten plants from each plot replication wise for yield and other six yield components viz. days to 50% flowering, number of pods per plant, plant height, plant stand at harvest, seed index and days to maturity. Two major diseases i.e. dry root rot (DRR) and stunt disease were of economic importance and consider for present experiment. The disease data was recorded by estimating percent disease incidence (PDI) as per Nene et al. [3]. The data were statistically analyzed for correlation according to Robinson et al. [6] and  $G \times E$  interaction according to Eberhart and Russell stability model [7].

$$\text{Percent disease incidence (PDI) (\%)} = \frac{\text{Number of disease infeted plants}}{\text{Total number of plants}} \times 100$$

### Results and Discussion

The genotypic correlation coefficients were higher than their corresponding phenotypic correlation (Table

**Table 2.** Pooled analysis of variance for stability analysis as per Eberhart and Russell Model. \*, \*\*Indicate significance  $p < 0.05\%$  and  $0.01$  respectively. Days to 50% flowering (DF); Number of pods per plant (NPP); Plant height (PH), Plant stand at harvest (PSH); Seed index (SI); Plot yield (PY); Days to maturity (DM) and Dry root rot (DRR).

Genotypes Source of variation	Days to 50% flowering			No of pod per plant		Plant height		Plant stand at harvest		Seed index	
	df	DF	NPP	PH	PSH	SI	DM	PY	DRR	Stunt	
Rep within											
Env	6	0.13	5.85	9.66	3.07	0.45	9.79	54360.80	0.97	1.32	
Genotypes	11	40.71**	63.42	69.81**	118.09*	87.32*	14.29	1298125.88**	48.34**	66.38*	
Env +											
(Var* Env)	24	25.64*	203.16*	165.14**	18.48	0.94**	21.10	346376.63	96.28*	87.65*	
Environments	2	122.91**	1504.11**	1713.11*	1.19	2.13**	76.83	986617.56*	214.26*	158.28	
Var* Env	22	16.79	84.89	24.41	20.05	0.83**	16.04	288171.81	45.08	23.04	
Environments											
(Lin)	1	245.82**	3008.22**	3426.19*	2.39	4.25**	153.65*	1973235.13**	106.72*	188.56*	
Gen*											
Env (Lin)	11	25.49*	103.56	32.37	18.33	1.45**	9.34	418433.75*	18.56	10.76	
Pooled											
deviation	12	7.42**	60.70**	15.09**	19.95**	0.20	20.83**	144750.69	12.86*	30.45	
Pooled error	06	0.08	6.70	5.07	6.50	0.32	5.93	96333.20	16.76	8.95	
Total	35	30.37	159.24	135.18	49.78	28.09	18.96	645497.13	23.47	18.52	

1) in all cases except both diseases. It indicated that the association was primarily due to genetic reasons [8]. Days to 50% flowering has positive significant genotypic correlation with number of pod per plant (0.40\*), plant stand at harvest (0.55\*\*) and days to maturity (0.85\*\*) however significant negative genotypic correlation with seed index (-0.31\*) as similar with Shukla et al. [9]. Number of pod per plant expressed significant positive genotypic correlation with plant height (0.45\*) and plant harvest at harvest (0.33\*)

however negative genotypic correlation with dry root rot (-0.44\*) and stunt disease (-0.77\*). Plant height is positively associated with plant stand at harvest (0.56\*\*), seed index (0.52\*) and plot yield (0.40\*\*) at genotypic level in consonance with Kan et al. [10]. It means the genotype having higher plant height would produce good plant population, bold seed and good yield also. Plant stand at harvest exhibited significant negative genotypic correlation with seed index (-0.49\*\*), dry root rot (-0.79\*\*) and stunt (-0.72\*\*) how-

**Table 3A.** Stability parameters for various morphological traits in chickpea.

	X	bi	s <sup>2</sup> di	X	bi	s <sup>2</sup> di	X	bi	s <sup>2</sup> di	X	Bi	s <sup>2</sup> di	X	bi	s <sup>2</sup> di
JG-11	80.56	0.04	2.17	50.22	1.37	42.93	42.78	1.24	-1.57	81.33	-20.09	-5.70	25.41	5.46	0.57
Rajas	79.67	0.39	31.64	48.33	1.40	23.02	46.22	1.76	-0.83	86.78	11.12	21.70	20.89	-1.05	-0.17
BGM 547	82.89	-0.23	-0.02	45.89	1.71	187.51	42.56	1.11	26.22	78.44	7.35	47.55	22.91	1.18	-0.33
JG-16	81.67	1.33	0.16	53.78	1.15	-4.05	39.67	0.92	7.52	90.00	3.21	-3.60	16.16	0.62	-0.31
JAKI 9218	83.22	0.87	25.67	51.78	0.70	40.17	47.56	1.01	7.82	77.67	6.00	15.28	24.44	1.16	0.28
JG-14	75.89	3.27	-0.06	39.44	1.21	-6.24	47.56	0.79	5.29	88.22	6.88	-0.24	23.06	0.84	-0.33
BG 372	83.67	0.23	19.04	50.33	1.36	142.29	44.44	0.84	42.89	92.56	6.19	-6.21	13.29	-1.69	-0.27
Pant															
G186	85.78	1.48	0.23	49.56	0.87	97.95	49.00	1.05	7.99	96.00	5.72	-5.85	16.79	-0.51	-0.22
Vaibhav	85.67	-0.25	4.82	40.22	0.37	50.07	48.22	0.39	4.03	81.56	-10.98	56.31	22.54	0.12	-0.27
GCP105	76.89	0.47	0.17	52.89	1.91	1.29	48.00	1.17	20.72	94.44	-6.05	36.58	17.55	0.97	-0.30
DCP92-3	77.89	2.37	4.02	45.33	0.17	-5.81	42.78	1.06	-0.72	90.56	-6.37	13.33	13.68	0.66	-0.33
Shubhra	75.11	2.03	0.11	46.22	-0.23	79.68	58.67	0.65	-3.74	91.78	9.02	-4.35	31.67	4.23	0.06
Mean	80.74			47.83			46.45			87.44			20.70		

**Table 3B.** Stability parameters for various morphological traits in chickpea.

Genotypes	Days to Maturity			Plot yield			Dry root rot			Stunt		
	X	bi	s <sup>2</sup> di	X	Bi	s <sup>2</sup> di	X	Bi	s <sup>2</sup> di	X	Bi	s <sup>2</sup> di
JG-11	127.22	0.85	-6.24	1516.67	0.43	108270.80	9.44	1.38	2.93	11.22	1.64	-1.57
Rajas	122.11	0.65	14.18	2450.00	1.35	150389.97	10.22	1.17	1.02	13.33	1.26	0.82
BGM547	123.56	1.52	1.11	1088.89	-0.78	-84090.84	9.67	1.13	0.51	13.56	1.41	0.63
JG-16	125.67	0.03	-3.37	2255.56	-0.89	132263.31	8.44	0.75	-1.05	10.44	0.89	1.16
JAKI 9218	128.78	0.35	19.18	1125.56	-0.23	-82610.08	9.89	1.54	2.17	13.44	1.21	1.65
JG-14	124.22	-0.08	111.51	2744.44	3.89	335552.34	9.44	0.21	-0.24	17.78	1.08	0.29
BG372	123.67	0.85	-5.86	2694.44	2.38	-29841.51	4.44	1.75	1.30	5.00	1.61	1.89
Pant G186	127.78	1.14	16.23	2538.89	1.74	10540.96	2.67	1.87	0.95	3.22	1.18	0.88
Vaibhav	127.33	1.00	21.18	1386.67	-1.12	211633.34	9.33	0.73	2.07	14.89	1.34	2.03
GCP105	123.44	3.19	16.86	2771.11	1.64	-51328.52	3.33	1.22	1.82	4.11	1.12	2.72
DCP 92-3	125.56	1.05	-5.75	2716.67	2.87	-92309.32	4.89	1.17	-1.05	5.67	1.42	-1.16
Shubhra	122.89	1.47	-4.07	2177.78	0.72	14511.84	9.89	-1.23	0.68	13.56	0.83	-0.17
Mean	125.19			2122.22			7.64			10.52		

ever significant positive association showed by plot yield (0.83\*\*) in consonance with Kan et al. [10]. It revealed that higher plant population at harvest results good plot yield due to reduced disease infestation. Negative significant genotypic correlation was observed for seed index with plot yield (-0.38\*) and Positively associated with dry root rot (0.75\*\*) and stunt (0.73\*\*) as similar with finding of Nene et al. [3]. It means seed boldness caused less number of seed per pod (quasi-quantitative trait) causing reduced yield and more disease infestation. Plot yield was negatively associated with dry root rot (-0.66\*) and stunt disease (-0.53\*) however, dry rot highly significantly correlated with stunt disease (0.97\*\*) at genotypic level (Table 2).

As per Eberhart and Russell Model [7], pooled analysis for variance of nine studied traits against pooled error indicated that significant differences among chickpea genotypes representing vast genetic variability (Table 2). All studied traits except number of pod per plant and days to maturity showed significant variance due to genotypes. Highly significant variance due to environments was observed for all studied traits except plant stand at harvest, days to maturity and stunt disease revealed sufficient differences among the studied environments in consonance with Bose et al. [11]. Highly significant variation due to environment (linear) was observed for all studied traits except plant stand at harvest as per finding of Chaturvedi et al. and Shukla et al. [12, 9].

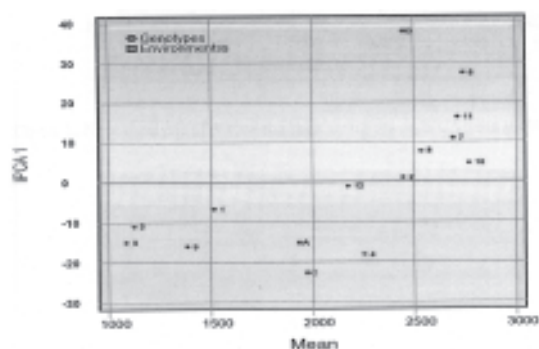
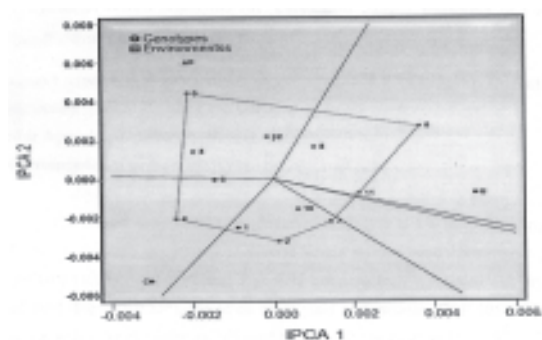
However pooled deviation was found highly significant for all studied traits except seed index, plot yield and stunt disease (Table 2). Regression coefficient and mean square deviation from regression for days to 50% flowering ranges from (-0.23 to 2.37 and -0.06 to 31.64), number of pod per plant (-0.23 to 1.91 and -6.24 to 187.51), plant height (0.39 to 1.76 and -3.74 to 42.89), plant stand at harvest (-20.09 to 11.12), seed index (-1.69 to 5.46 and -0.33 to 0.57), days to maturity (-0.08 to 3.19 and -6.24 to 111.51), plot yield (-1.12 to 2.87 and -92309.32 to 335552.34), dry root rot (-1.23 to 1.54 and -1.05 to 2.93) and stunt disease (0.81 to 1.64 and -1.57 to 2.72) respectively in consonance with Chaturvedi et al. and Bose et al. [11,12] (Tables 3A and 3B). Out of twelve chickpea genotypes, eight genotypes (JG-11, Rajas, JG-14, BG372, Plant G186, GCP105, DCP92-3 and Shubhra) produced higher yield in E<sub>2</sub> (2011-12) followed by five genotypes (JG-11, Rajas, BGM547, JG-16 and JAKI 9218) in F<sub>3</sub> (2012-13) similar with Chaturvedi et al. and Bose et al. [11, 12] as indicated by environmental index of E<sub>2</sub> (330.28 g) (Table 4). Based on mean yield performance GCP 105 (2771.11 g) produced highest yield over environment followed by JG 14 (2744.44 g) and DCP 92-3 (2716.67 g) in accordance with Shukla et al. [9] (Figs . 1 and 2). Based on ranking using plot yield regression coefficient revealed that Shubhra was stable genotypes followed by Rajas and JG – 11 however Pant G186 was found stable in performance as per mean square deviation from regression followed by Shubhra and BG 372 in consonance with Kan et al. [10] (Tables 3A and 3B).

**Table 4.** Environmental mean yield and stability parameters for various chickpea genotypes.

Genotypes	Env 1 (Plot yield in g)	Env 2 (Plot yield in g)	Env 3 (Plot yield in g)	Mean yield (g)	S <sup>2</sup> di	Rank	Bi	Rank
JG-11	1133.33	1633.33	1783.33	1516.67	108270.79	8	0.43	3
Rajas	1866.67	2866.67	2616.67	2450.00	150389.97	10	1.35	2
BGM547	1296.67	836.67	1133.33	1088.89	-84090.84	6	-0.78	8
JG-16	2100.00	1933.33	2733.33	2255.56	132263.31	9	-0.89	10
JAKI 9218	1100.00	1043.33	1233.33	1125.56	-82610.08	5	-0.23	6
JG-14	2466.67	4066.67	1700.00	2744.44	335552.36	12	3.89	12
BG 372	2083.33	3466.67	2533.33	2694.44	-29841.51	3	2.38	7
Pant G186	2433.33	3133.33	2050.00	2538.89	10540.96	1	1.74	5
Vaibhav	1966.67	1050.00	1143.33	1386.67	211633.34	11	-1.12	11
GCP105	2330.00	3300.00	2683.33	2771.11	-51328.52	4	1.64	4
DCP92-3	2200.00	3666.67	2283.33	2716.67	-92309.32	7	2.87	9
Shubhra (Kabuli)	2266.67	2433.33	1833.33	2177.78	14511.84	2	0.72	1
Envir index	-185.28	330.28	-145.00					
Mean	1936.94	2452.50	1977.22	2122.222				
CV	17.58	23.53	32.70					
SE of difference	278.00	471.18	527.93					
CD 95%	576.53	977.16	1094.85					
CD 99%	783.60	1328.14	1488.10					

Most of the genotypes exhibited different degree of stability for studied traits. The genotype JG 11 with regression coefficient (bi) less than one and mean value less than their population mean exhibited above average stability for days to 50% flowering, plant stand at harvest and plot yield however genotype Rajas for days to 50% flowering, seed index and days to maturity while genotype Vaibhav for number of pod per plant, plant stand at harvest and plot yield exhibit the same. The genotype BGM 547 with regression coefficient (bi) greater than one and mean value

less than their population mean exhibited below average stability performance for number of pod plant, plant height, plant stand at harvest and days to maturity however GCP 105 for days to maturity, dry root rot and stunt disease similar with Chaturvedi et al. [12]. Consequently, these genotypes should be grown under poor environmental conditions. Similarly, genotype JG-16 showed specific adaptation since it had regression coefficient (bi) greater than one and mean value more than its population mean for days to 50% flowering, number of pod per plant and plant stand at

**Fig. 1.** Yield performance of studies 12 chickpea genotypes over the environment.**Fig. 2.** Biplot analysis of twelve chickpea genotypes on IPCA1 and IPCA2 axis.

harvest as similar with Chaturvedi et al. [12] and Shukla et al. [9]. The genotypes BG 372, Pant G 186, GCP 105 and DCP 92-3 had regression coefficient (bi) greater than one and mean value more than their population mean for plot yield and less than their population mean for dry root rot and stunt disease (Tables 3A and 3B; Fig. 1). Therefore, these genotypes should be exploited under optimal favorable environmental condition. The genotype BGM 547 (for days to 50% flowering), Vaibhav (for plant height and seed index) and Shubhra (for plant height, plot yield and dry root rot) with regression coefficient (bi) less than one, mean value more than their population mean and deviation from regression ( $S^2_{di}$ ) minimum were less influenced by the environment and showed high stability (Tables 4) in accordance with Shukla et al. [9]. Biplot analysis revealed that the genotypes JG – 14 and DCP 92-3 performed excellent in  $E_2$  (2011-12) in comparison to other genotypes under overall environment (Fig. 2). Hence, out of twelve genotypes, these genotypes may be grown under wide range of environments particularly under rice fallow land.

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