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Original scientific article

GENOTYPE BY ENVIRONMENT INTERACTION FOR QUALITY TRAITS IN CHILLI PEPPER (*Capsicum annuum* L.)

Tejpal Singh SRAN, S.K. JINDAL* and Neena CHAWLA

Department of Vegetable Science, Punjab Agricultural University, Ludhiana, India.

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There is a need for identifying the specific environments for the selection of adapted and stable genotypes for quality traits in chilli pepper. Among these quality traits, pungency and coloring matter are the most important ones, which need to be in stable amounts in final products. Hence, this multi-environmental evaluation of chilli pepper genotypes was done in three distinct environments, to identify the suitable environments for selection and also suitable genotypes for specific quality traits. The study includes 43 chilli genotypes tested for three distinct growing conditions for nine different quality traits at Punjab Agricultural University and data was analyzed using Eberhart & Russell's model and GGE Biplot analysis. The environmental effect accounts for more than 35% variation for the capsaicin in oleoresin and dry matter content. While the traits namely capsaicin content in red powder (3%) and capsaicin in green chili (4.73%) were least influenced by the environment. The contribution of G×E interactions was < 25% for all the studied traits except ascorbic acid. The genotype AC 101 was best for capsaicin content in green and red chilli powder across the environments. The data generated from this study help to identify the stable and superior genotypes for quality traits in early, main and late-season planting.

Keywords: chilli, capsaicin, stable, environmental, suitable.

INTRODUCTION

Chilli pepper (*Capsicum annuum* L., $2n=2x=24$) belongs to the family Solanaceae is indigenous to South America. The word 'Chilli' is Mexican origin and is still under use in India (KRAFT *et al*., 2014). Chilli crop performs well in warm humid tropical and subtropical regions

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Corresponding author: S.K. Jindal, Department of Vegetable Science, Punjab Agricultural University, Ludhiana, India. phone: +91-8968766600, E-mail: saleshjindal@pau.edu

extending from equator 45º latitude on both southern and Northern hemisphere. It can do well up to an altitude of 2000 meters above sea level. In the genus Capsicum, it is the only plant known for its pungency, which is due to the presence of capsaicinoids (the group of 15 different alkaloids). In relation to the impact of the environment on the content of the various quality traits in chilli peppers, only limited information is available. Most of the studies confined to the genotype-environmental effect on the content of capsaicinoids and flavonoids. (JUSTIN *et al*., 2012; ZEWDIE and BOSLAND, 2000). The coloring matter, ascorbic acid, oleoresin and other quality parameters were highly influenced by the environment (e.g., temperature, light intensity and humidity). The interactions between genotype and environment were also observed and indicate that different genotypes respond varyingly to changes in the environment (GURUNG *et al*., 2012). Thus, the stability of quality traits in chilli and its processed products is one of the major concerns to the processing industry. Plant breeders with taking account environmental affect develop stable cultivars, which may have certain level of pungency, coloring matter, ascorbic acid and other quality traits within a certain range. It is of huge importance because environmental conditions vary from year to year and genotype-environment (GE) interactions have a masking effect on the genotype's performance. Therefore, it is important to identify stable genotypes across the multi-environments through stability parameters. There are several techniques to evaluate the stability of genotypes over the environments and each method has its own merits and demerits. The different stability parameters explained genotypic performance differently and the popular method for stability analysis is regression analysis by EBERHART and RUSSELL (1966) model. While, GGE (Genotype-Genotype-by-Environment)-Biplot method was a more efficient tool to analyze GE interaction because it can provide the biplots and information on genotype, environment and their interaction, while the Eberhart and Russell analysis give information only on genotype evaluation (ASHRAFUL *et al*., 2017). Thus, limited information is available regarding the stability of quality traits in chilli, this investigation was undertaken over the three varied environments for selected genotypes to understand the responses and to identify the stable genotypes.

MATERIALS AND METHODS

Plant material and field experiments

Forty-three genotypes including one standard check Punjab Sindhuri (local cultivar) were planted in three different seasons for evaluation of quality traits (Table 1). The early season crop was sown during October, 2016 and transplanted on November, 2016; similarly sowing for main season crop was done on November, 2016 and nursery transplanted on February, 2017; whereas late season crop was sown on March, 2017 and transplanted on April, 2017 at Vegetable Research Farm P.A.U, Ludhiana (30.9° N and 75.85° E at 244 m above sea level). The experiment was conducted as Randomized Complete Design with three replications. The spacing between the ridges was 75cm and between plants it was 45cm with 10 plants in each row. The crop management practices was followed as describe by the university guidelines for the farmers. The experimental area was characterized by the hot and dry summer during May to June followed by the rainy season (with average annual rainfall of 750mm) and winters, especially in the month of December to February. The meteorological data of various parameters like temperature, relative humidity, sunshine hours and rainfall was presented in Figure 1 and 1a.

Table 1. List of the genotypes, their codes and source

Sr. No.	Genotypes	Codes	Source	Sr. No.	Genotypes	Codes	Source
1	PAU 115	G1	PAU, Ludhiana	22	KC 310	G22	PAU, Ludhiana
2	PAU 114	G2	PAU, Ludhiana	23	KC 311	G23	PAU, Ludhiana
3	PAU 212	G3	PAU, Ludhiana	24	ML 342	G24	Mysore, India
4	PAU 211	G4	PAU, Ludhiana	25	PP 402	G25	Pepsi Pvt. Ltd., India
5	PAU 213	G5	PAU, Ludhiana	26	PC 408	G26	PAU, Ludhiana
6	AC 102	G6	AICRP, India	27	PL 412	G27	Moga, Punjab
7	C 142	G7	PAU, Ludhiana	28	PP 414	G28	AVRDC, Taiwan
8	DL 161	G8	AICRP, India	29	PG 417	G29	PAU, Ludhiana
9	FL 201	G9	Rajasthan, India	30	AC 101	G31	PAU, Ludhiana
10	IS 262	G10	AVRDC, Taiwan	31	S 343	G32	PAU, Ludhiana
11	IS 267	G11	AVRDC, Taiwan	32	SL 466	G33	PAU, Ludhiana
12	IS 263	G12	AVRDC, Taiwan	33	SL 468	G34	PAU, Ludhiana
13	IS 261	G13	Jaipur, India	34	SL 475	G35	PAU, Ludhiana
14	KC 302	G14	PAU, Ludhiana	35	SL 473	G36	PAU, Ludhiana
15	KC 303	G15	PAU, Ludhiana	36	SU 478	G37	CSK HPKV, Palampur
16	KC 304	G16	PAU, Ludhiana	37	US 501	G38	U.S.A
17	KC 305	G17	PAU, Ludhiana	38	VR 522	G39	PAU, Ludhiana
18	KC 306	G18	PAU, Ludhiana	39	VR 523	G40	PAU, Ludhiana
19	KC 307	G19	PAU, Ludhiana	40	VR 521	G41	AICRP, India
20	KC 308	G20	PAU, Ludhiana	41	YL 581	G42	PAU, Ludhiana
21	KC 309	G21	PAU, Ludhiana	42	YL 582	G43	PAU, Ludhiana
				43	Punjab Sindhuri (check)	G30	PAU, Ludhiana

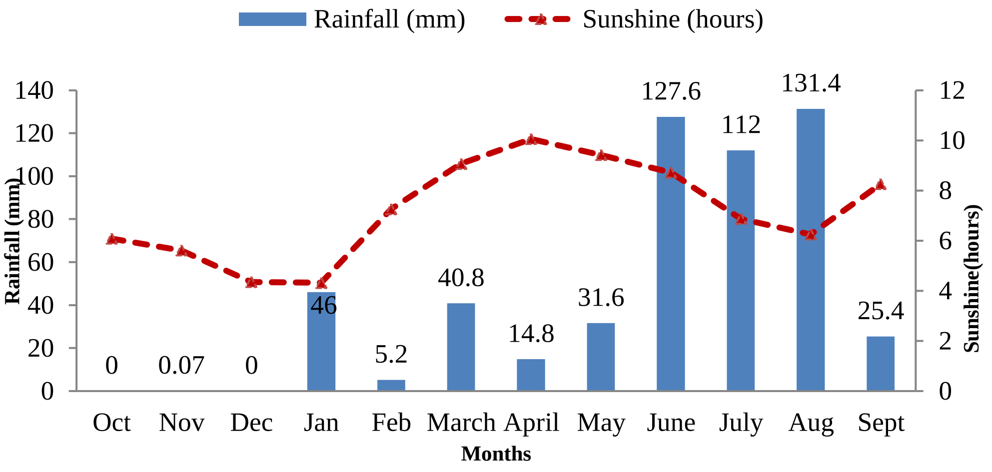

Fig.1. Graphical representation of relative rainfall and sunshine

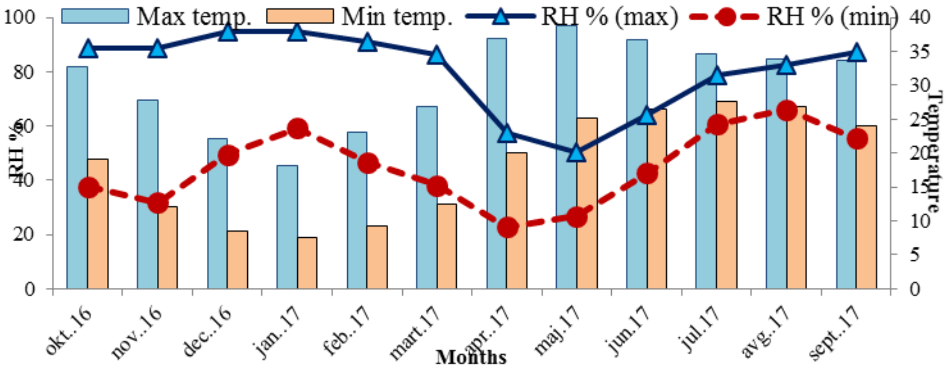

Fig.1a. Graphical representation of humidity and temperature

Sample preparation & laboratory analysis

The three subsequent harvestings was done and fruits (green and red) were dried in oven at 60°C for 24-36 hours to obtain samples for analysis of different traits. The fresh green fruits (1g sample) were utilized for the estimation of ascorbic acid by following the method suggested by BALA *et al*., (2019). The random sample of 100g dried red fruits from each replication was taken in account to calculate dry matter content (%) (by dividing the dried fruit weight with fresh weight then multiplying with 100). The powder yield was calculated in the same way as dry matter content but here total yield plant^{-1} was multiplied to calculate powder yield plant^{-1}. Capsaicin content in green and red chilli powder and in oleoresin was calculated as per method suggested by the BALA *et al*. (2019). The estimation of oleoresin content and coloring matter in red chilli powder was estimated as per method described by ARJONA *et al*. (2002).

Statistical analysis

The data of quality traits were statistically analyzed as per randomized block design using software Windowstat (version 9.3). The regression analysis proposed by EBERHART and RUSSELL'S model (1966) was used for the estimation of the analysis of variance of stability parameters (i.e. Mean across environments, linear regression coefficient b and deviation from regression Sd^2) of individual genotypes and the significance of difference was tested at 5% and 1% level of significance. The analysis of variance for randomized block design was carried out by using the following model.

$$Y_{ijk} = m + g_{ij} + b_k + e_{ijk}$$

Where,

Y_{ijk} = phenotypic value of the ijth genotype grown in the kth replication
m = general population mean
g_{ij} = effect of the ijth genotype, where I, j, = 1…..g
b_k = effect of the kth replication, where k = 1…..r
e_{ijk} = environmental effect

The G×E interaction was also visualized by using GGE Biplot. The graphical analysis helps to understands, genotype (G) and G×E interactions information therefore.

RESULTS AND DISCUSSION

Analysis of variance for genotype, environment and G×E interaction

The analysis of variance (ANOVA) of G×E interaction for quality traits are represented in Table 2. The pooled mean squares (MS) due to genotypes and environments indicated significant differences, revealing genetic variability among the genotypes and variability among the environments for all the traits. The MS due to G×E interactions were also significant for all the traits except ascorbic acid, capsaicin in red powder, capsaicin in oleoresin and coloring matter in oleoresin indicating differential performance of genotypes across the environments for the studied traits. Therefore, stability analyses for G×E interactions were carried for season specific adaptability for each genotype for the quality traits. The G×E interaction affects most of the quality traits and indicated that the genotypes showed a differential response due to the environments (LOHITHASWA *et al.*, 2001). The differential response of chilli pepper genotypes for quantitative traits through GGE Biplot and Eberhart and Russell's model was also noted by SRAN and JINDAL (2019b).

Table 2. Analysis of variance for stability of quality traits in chili

Source of variation Trait	Genotypes	Environment + G × E	Environment (Linear)	G × E	Pooled deviation	Pooled error
d.f.	42	86	1	42	43	252
Dry matter (%)	16.15**	7.48**	581.30**	1.05**	0.41	0.84
Powder yield (g plant^{-1})	1424.56**	1777.69**	126046.73**	528.07**	108.28**	63.72
Ascorbic acid (mg 100g^{-1}) in green fruit	153.17**	90.82	3828.85**	35.06	58.36**	0.80
Capsaicin content (%) in red powder	0.09**	0.01*	0.13**	0.01	0.01**	0.01
Capsaicin in green chilli (%)	0.08**	0.01**	0.17**	0.01**	0.01**	0.01
Capsaicin in oleoresin (%)	0.82**	0.51**	30.22**	0.16	0.15**	0.01
Oleoresin content (%)	5.34**	0.85**	51.86**	0.32*	0.19**	0.03
Coloring matter (ASTA)	1362.89**	100.09**	6167.41**	47.19**	10.66**	4.35
Coloring matter in oleoresin (ASTA)	43553.55**	5302.65**	260955.86**	2266.64	2322.63**	61.23

*, ** Significant at P ≤ 0.05 and 0.01 levels respectively, d.f. = Degree of freedom

Analysis of variance over environments

The ANOVA for quality traits was given to represents the relative magnitude of G, E and G×E interaction for each character in Table 3. The total sum of squares for genotype, environment and G×E interactions ranged from 28.12 to 95%, 3 to 59.25% and 2 to 27.95% interactions respectively (Table 2). The genotypes accounts large proportion (> 50%) of total variation for dry matter, capsaicin in green and red chilli, coloring matter, oleoresin content and coloring matter in oleoresin, which means that genotype, was more important factor for these traits. Similarly, a large source of variation due to the genotypes was also reported by ZEWDIE and BOSLAND (2000) and GURUNG *et al.* (2012). However, the experimental genotypes collected from various sources and grown over three different seasons and even with these diverse growing conditions, genotypes had more effect on most of the quality traits. But, there was significant G×E interactions that will lower the utility of genotype mean as alone indicator of stability parameter (PRITTS and LUBY, 1990). The environmental effect accounts more than 35% variation for the capsaicin in oleoresin and dry matter content. As the production of capsaicin in chilli is under the control of locus Pun1 and five quantitative trait loci, thus it is highly affected by the environment (BEN-CHAIM, 2006). While the traits namely capsaicin content in red powder (3%) and capsaicin in green chilli (4.73%) were least influenced by environment. The contribution of G×E interactions was < 25% for all the studied traits except ascorbic acid.

Table 3. Analysis of variance (ANOVA) for different traits of chilli genotypes

Trait	Source	d.f.	SS	Pr > F	Total variation (%)
Dry matter (%)	E	2	581.30	< .0001**	44
	G	42	678.13	< .0001**	51.33
	G × E	84	61.67	< .0001**	4.66
Powder yield (g plant^{-1})	E	2	126046.68	< .0001**	59.25
	G	42	59831.55	< .0001**	28.12
	G × E	84	26835.02	< .0001**	12.61
Ascorbic acid (mg 100g^{-1}) in green fruit	E	2	3828.8457	< .0001**	26.88
	G	42	6432.97	< .0001**	45.16
	G × E	84	3982.07	< .0001**	27.95
Capsaicin content (%) in red powder	E	2	0.12	< .0001**	3
	G	42	3.80	< .0001**	95
	G × E	84	.08	< .0001**	2
Capsaicin in green chilli (%)	E	2	0.17	< .0001**	4.73
	G	42	3.24	< .0001**	90.25
	G × E	84	0.18	< .0001**	5.01
Capsaicin in oleoresin (%)	E	2	30.22	< .0001**	38.76
	G	42	34.45	< .0001**	44.18
	G × E	84	13.29	< .0001**	17.04
Oleoresin content (%)	E	2	51.85	< .0001**	17.41
	G	42	224.25	< .0001**	75.33
	G × E	84	21.57	< .0001**	7.24
Coloring matter (ASTA)	E	2	6167.38	< .0001**	9.36
	G	42	57241.17	< .0001**	86.92
	G × E	84	2440.17	< .0001**	3.70
Coloring matter in oleoresin (ASTA)	E	2	260955.40	< .0001**	11.41
	G	42	1829249	< .0001**	80.04
	G × E	84	195072.39	< .0001**	8.53

*, ** Significant at $P \leq 0.05$ and 0.01 levels respectively, d.f. = Degree of freedom

G×E interaction with Eberhart and Russell's model analysis and GGE Biplots

The stability parameters for quality characters represented in Table 4 to Table 12. Based on the regression and mean in Table 4, the genotypes KC 302 (G14) and ML 342 (G24) had significantly higher dry matter but higher regression coefficients indicated their suitability for favorable environmental conditions. The only stable genotype with found with significantly higher dry matter across the environments was SU 478 (G37) had least regression coefficient (1.02). SHARMA *et al*. (2014) also reported the suitability of only few genotypes i.e. Suryamukhi for dry matter content in chilli under unfavorable cultivated conditions. The GGE Biplot also depicts the same result indicating SU 478 (G37) as stable genotypes with lower IPCA 1 axis score, thus it had lowest contribution towards the G×E interaction for dry matter content. The genotype KC 304 (G16) found to be generally adaptable for all three different planting conditions (Figure 2). The genotype PC 408 (G26) had the highest score on IPCA 1 axis and above average dry matter content revealed its sensitivity to environmental changes; hence this genotype had specific adaptability to favorable environments. Also, it was found that all the environments had positive interaction with the genotypes. E_1 had the highest mean dry matter as compared to E_2 and E_3 but it was suitable for selecting genotypes that were specific to this environment only, because E_1 had the higher score on IPCA 1 axis, which exhibits its unsuitability for general adapted genotypes.

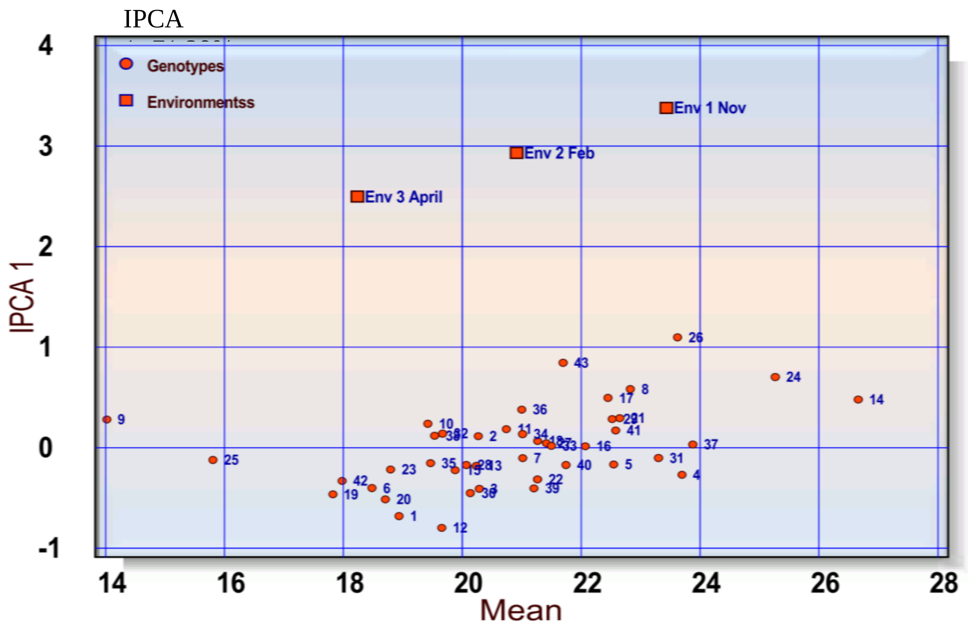

Fig 2. GGE Biplot for dry matter content (%) of 43 genotypes in 3 environments using genotypic and environmental scores

Table 4. Mean ($\bar{X}$), regression coefficient (b_i) and deviation from regression (S^2d_i) for dry matter content (%)

Codes	E_1	E_2	E_3	Overall mean ($\bar{X}$)	b_i	S^2d_i
G1	20.47	18.61	17.74	18.94	0.52	-0.64
G2	23.15	20.13	17.53	20.27	1.08	-0.78
G3	21.81	20.92	18.14	20.29	0.71	-0.30
G4	25.89	23.54	21.66	23.70	0.81	-0.78
G5	24.87	22.50	20.28	22.55	0.88	-0.82
G6	20.71	17.80	16.94	18.48	0.72	-0.05
G7	23.20	21.45	18.41	21.02	0.92	-0.62
G8	26.29	23.21	18.99	22.83	1.41	-0.70
G9	17.09	14.11	10.87	14.02	1.20	-0.84
G10	22.97	18.44	16.85	19.42	1.17	0.80
G11	23.99	20.15	18.09	20.74	1.13	-0.19
G12	20.85	19.56	18.56	19.66	0.44	-0.82
G13	22.66	19.95	18.11	20.24	0.87	-0.67
G14	29.82	27.26	22.91	26.66	1.33	-0.42
G15	22.37	19.33	17.95	19.88	0.85	-0.30
G16	25.17	21.19	19.87	22.07	1.01	0.49
G17	25.70	22.92	18.73	22.45	1.34	-0.60
G18	24.42	20.46	18.93	21.27	1.05	0.30
G19	19.21	18.52	15.75	17.83	0.67	-0.19
G20	20.09	19.24	16.79	18.71	0.64	-0.46
G21	25.98	22.28	19.69	22.65	1.21	-0.56
G22	22.97	21.87	18.96	21.27	0.78	-0.37
G23	21.03	18.74	16.62	18.80	0.85	-0.82
G24	29.08	25.39	21.33	25.27	1.49	-0.83
G25	18.13	15.91	13.38	15.81	0.91	-0.83
G26	28.64	22.83	19.40	23.62	1.77	0.34
G27	24.11	21.40	18.75	21.42	1.03	-0.83
G28	22.23	20.30	17.68	20.07	0.88	-0.78
G29	25.77	22.28	19.52	22.52	1.20	-0.69
G31	25.62	23.48	20.81	23.30	0.93	-0.81
G32	21.99	20.68	16.34	19.67	1.09	0.52
G33	23.90	21.94	18.66	21.50	1.01	-0.62
G34	23.98	20.79	18.28	21.02	1.10	-0.72
G35	21.50	20.01	16.89	19.47	0.89	-0.47
G36	24.06	21.44	17.51	21.00	1.26	-0.63
G37	26.43	24.08	21.13	23.88	1.02	0.80
G38	22.24	19.74	16.63	19.54	1.08	-0.80
G39	23.33	20.72	19.58	21.21	0.72	-0.42
G40	24.03	21.76	19.46	21.75	0.88	-0.83
G41	25.12	23.29	19.34	22.58	1.17	-0.21
G42	19.54	18.81	15.60	17.98	0.76	0.09
G43	25.24	22.82	17.03	21.70	1.59	0.78
G30 (Check)	22.17	19.65	18.59	20.14	0.69	-0.42
Range	**17.09-29.82**	**18.6-27.26**	**17.7-22.91**	**14.02-26.66**		
Mean	**23.44**	**20.92**	**18.24**	**20.87**		
LSD ($P \leq 0.05$)	2.62	2.69	2.44	1.45		
LSD ($P \leq 0.01$)	3.47	3.56	3.23	1.91		
SE of b_i	-	-	-		0.17	

*, ** Significant at $P \leq 0.05$ and 0.01 levels respectively

Table 5. Mean ($\bar{X}$), regression coefficient (b_i) and deviation from regression (S^2d_i) for powder yield (g plant^{-1})

Codes	E_1	E_2	E_3	Overall mean ($\bar{X}$)	b_i	S^2d_i
G1	99.96	79.33	64.92	81.40	0.46	-57.45
G2	195.12	165.91	102.83	154.62	1.20	140.49
G3	105.99	91.86	52.16	83.33	0.70	51.32
G4	191.41	118.21	81.07	130.23	1.44	138.28
G5	134.73	100.27	71.82	102.27	0.82	-58.44
G6	132.85	97.87	58.74	96.49	0.97	-58.88
G7	107.31	88.25	69.34	88.30	0.50	-63.07
G8	205.63	130.31	85.15	140.36	1.58	74.61
G9	98.50	76.42	53.71	76.21	0.59	-62.85
G10	182.16	102.56	54.61	113.11	1.67	88.51
G11	181.83	131.25	77.16	130.08	1.37	-59.34
G12	115.87	87.24	70.86	91.32	0.59	-40.18
G13	139.78	107.04	68.08	104.97	0.94	-54.78
G14	131.44	113.81	80.17	108.47	0.67	-17.02
G15	94.29	78.99	56.75	76.68	0.49	-53.97
G16	105.94	91.20	75.41	90.85	0.40	-62.75
G17	131.57	124.67	87.75	114.66	0.57	92.18
G18	162.97	91.80	75.09	109.95	1.15	412.82**
G19	90.47	82.21	60.56	77.75	0.39	-31.63
G20	89.39	77.73	59.07	75.40	0.40	-54.10
G21	144.26	100.93	70.62	105.27	0.96	-38.45
G22	105.96	90.87	75.08	90.64	0.40	-62.89
G23	103.70	73.81	70.37	82.62	0.44	50.08
G24	170.60	142.78	51.38	121.59	1.55	640.54**
G25	134.66	90.49	50.57	91.90	1.10	-61.31
G26	164.38	107.48	53.27	108.38	1.45	-62.76
G27	211.39	116.78	81.90	136.69	1.69	501.72**
G28	137.81	113.59	62.77	104.72	0.98	62.68
G29	166.22	124.07	91.12	127.14	0.98	-51.55
G31	154.36	112.16	70.02	112.18	1.10	-62.94
G32	223.86	174.55	109.53	169.31	1.49	-14.63
G33	165.90	122.50	50.72	113.04	1.50	84.19
G34	130.44	88.69	52.65	90.59	1.02	-59.24
G35	163.73	111.04	71.58	115.45	1.20	-38.47
G36	140.84	113.09	47.47	100.47	1.22	189.94*
G37	153.60	87.42	63.68	101.57	1.18	222.34*
G38	137.16	69.34	43.23	83.24	1.23	211.73*
G39	117.33	96.04	69.97	94.45	0.62	-58.35
G40	134.44	104.03	50.91	96.46	1.09	30.46
G41	114.65	90.30	52.87	85.94	0.81	-31.28
G42	115.29	104.65	57.29	92.41	0.76	170.06
G43	208.89	122.00	56.26	129.05	1.99	-0.62
G30 (Check)	187.61	125.29	83.44	132.11	1.36	-1.33
Range	**89.39 - 223.86**	**69.34 - 174.55**	**43.23 - 109.59**	**75.40 - 169.31**		
Mean	**143.82**	**105.09**	**67.25**	**105.39**		
LSD ($P \leq 0.05$)	29.06	21.03	15	18.15		
LSD ($P \leq 0.01$)	38.52	27.88	19.88	23.90		
SE of b_i	-	-	-		0.2	

*, ** Significant at $P \leq 0.05$ and 0.01 levels respectively

The powder yield found to be highest in genotypes S 343 (G32) and PAU 114 (G2) with significantly higher mean values (Table 5). The genotype PG 417 (G29) had higher mean value with regression coefficient close to one (0.98) and non-significant deviation indicated its stability and general adaptability across the environments. In case of environment E_2 and E_3 S 343 (G32) followed by PAU 114 (G2) had highest powder yields. On the basis of GGE Biplot (Figure 3) PG 417 (G29) was the most stable because it laid exactly on the origin with above average powder yield representing general adaptability of this genotype in all the environments. The genotype S 343 (G32) had highest mean powder yield plant^{-1} and positive interaction with the environments indicating that genotype was more sensitive to environmental changes, hence this genotype had specific adaptability to favorable environments. The Powder yield was under the direct influence of red ripen fruit yield reported by TEMBHURNE and RAO (2013). Also, the correlation and path analysis study done by SRAN and JINDAL (2019a) suggested the significant genotypic and phenotypic correlation between the powder yield and fruit yield plant^{-1} which indicates the increase in powder yield of genotypes that were either high yielder under favorable or unfavorable environments or generally adaptable for high yield performance. It was clear from the Figure 3 that variability due to environments was higher in case of powder yield, as the environment symbols were scattered on the biplot than the genotypes. E_1 was most suitable for genotype selection for high powder yield, while E_2 and E_3 poorest for selecting genotypes.

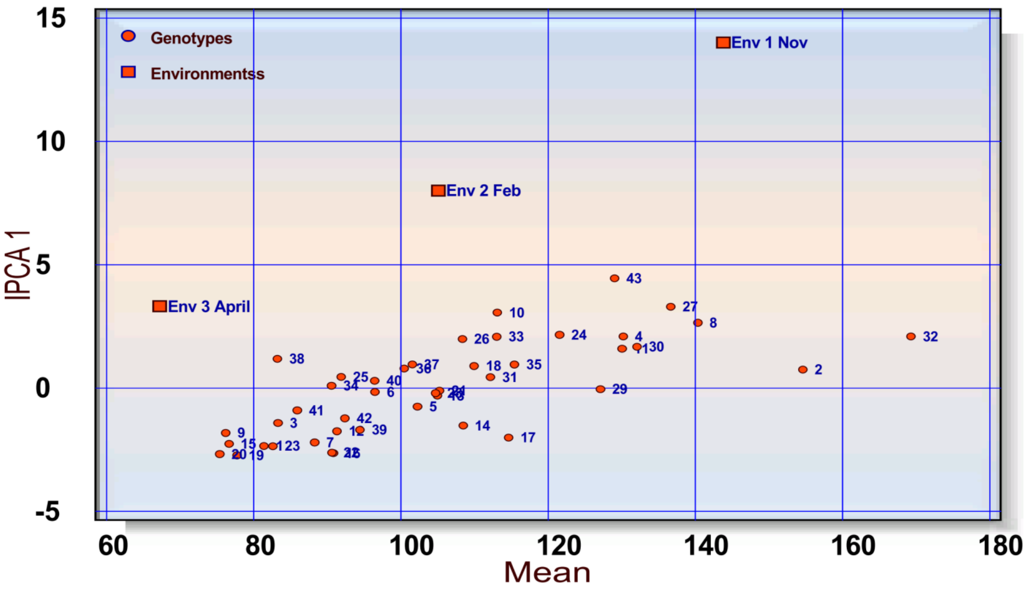

Fig 3. GGE Biplot for powder yield (g plant^{-1}) of 43 genotypes in 3 environments using genotypic and environmental scores

Table 6. Mean ($\bar{X}$), regression coefficient (b_i) and deviation from regression (S^2d_i) for ascorbic acid (m 100g^{-1})

Codes	E_1	E_2	E_3	Overall mean ($\bar{X}$)	b_i	S^2d_i
G1	38.83	65.44	55.62	53.30	2.02	-0.28
G2	42.90	53.46	51.31	49.22	0.82	2.09
G3	53.71	55.11	50.87	53.23	0.07	8.11**
G4	53.74	73.74	61.87	63.12	1.47	8.85**
G5	41.74	47.87	54.82	48.14	0.55	57.52**
G6	51.55	52.00	50.14	51.23	0.02	1.06
G7	51.88	64.45	70.42	62.25	1.05	79.21**
G8	54.20	70.43	57.92	60.85	1.17	22.79**
G9	47.75	53.71	49.11	50.19	0.43	2.39*
G10	38.83	47.78	61.93	49.51	0.85	206.46**
G11	47.32	55.47	52.28	51.69	0.62	-0.79
G12	54.53	59.90	47.45	53.96	0.30	68.89**
G13	48.30	55.50	70.03	57.94	0.71	198.94**
G14	34.09	43.10	52.30	43.16	0.80	107.49**
G15	38.83	44.23	39.07	40.71	0.38	5.09**
G16	42.98	64.23	59.66	55.62	1.64	9.57**
G17	43.06	55.92	49.94	49.64	0.96	-0.37
G18	46.48	60.12	51.51	52.70	1.00	5.62**
G19	37.00	51.67	42.40	43.69	1.07	6.69**
G20	44.23	48.03	66.26	52.84	0.48	256.03**
G21	48.22	56.49	50.10	51.60	0.59	5.37**
G22	42.40	57.04	45.56	48.34	1.05	19.83**
G23	51.46	58.11	43.76	51.11	0.39	88.98**
G24	51.06	74.14	60.40	61.87	1.70	12.30**
G25	38.16	47.08	72.49	52.57	0.95	552.55**
G26	64.27	78.66	71.01	71.32	1.07	1.50
G27	53.80	64.91	56.63	58.44	0.80	8.79**
G28	34.09	61.03	41.10	45.41	1.94	53.64**
G29	53.71	86.52	73.84	71.36	2.48	-0.62
G31	50.06	61.04	69.47	60.19	0.95	107.81**
G32	52.13	63.24	56.90	57.42	0.82	1.52
G33	42.90	54.06	47.46	48.14	0.82	2.14
G34	53.71	55.67	47.74	52.38	0.08	32.76**
G35	46.81	74.35	49.42	56.86	1.94	125.65**
G36	51.06	65.61	52.54	56.40	1.03	33.46**
G37	41.07	61.20	52.87	51.72	1.52	-0.76
G38	60.53	68.34	63.27	64.05	0.57	1.66
G39	46.65	53.85	47.06	49.19	0.50	9.17**
G40	63.27	73.04	70.93	69.08	0.75	1.37
G41	56.29	70.84	43.13	56.75	0.88	313.75**
G42	56.11	73.70	61.78	63.86	1.28	14.68**
G43	52.53	72.52	60.35	61.80	1.47	10.47**
G30 (Check)	32.26	71.09	62.73	55.36	3.00	33.82**
Range	**32.26 - 64.27**	**43.1 - 86.52**	**39.07 - 73.84**	**40.71 - 71.36**		
Mean	**47.78**	**61.04**	**55.71**	**54.84**		
LSD ($P \leq 0.05$)	2.71	2.46	2.37	5.67		
LSD ($P \leq 0.01$)	3.60	3.26	3.14	7.46		
SE of b_i	-	-	-	-	0.81	

*, ** Significant at $P \leq 0.05$ and 0.01 levels respectively

Based on the mean values, nine genotypes had significantly higher ascorbic acid content, among those PC 408 (G26) and PG 417 (G29) had highest mean values with >1.0 regression coefficient indicated their suitability under favorable environmental conditions (Table 6). The genotype C 142 (G7) had regression coefficient one and significant deviation from regression indicating that genotype had more vulnerability to unpredictable response arising from G×E interaction. The GGE Biplot identified genotype VR 521 (G41) was suitable for poor environments as it indicated negative interaction coupled with above average ascorbic acid (Figure 4). The genotypes PG 417 (G29) and PC 408 (G26) indicated general adaptability across the environments due to higher mean values coupled with almost zero score on IPCA 1 axis. The three planting conditions differ very much from each other, actually considered as three different seasons, which influences the quality characters most and congenial for selection of stable and adapted genotypes. GGE Biplot showed that all the environments had positive interaction with the genotypes. The environments E_2 and E_3 had the higher average ascorbic acid than grand mean but preferable only for selecting the genotypes that were suitable to these environments. The ascorbic acid content found to be highest in green chilli fruits under warmer condition than colder ones (KUMAR *et al*., 2012).

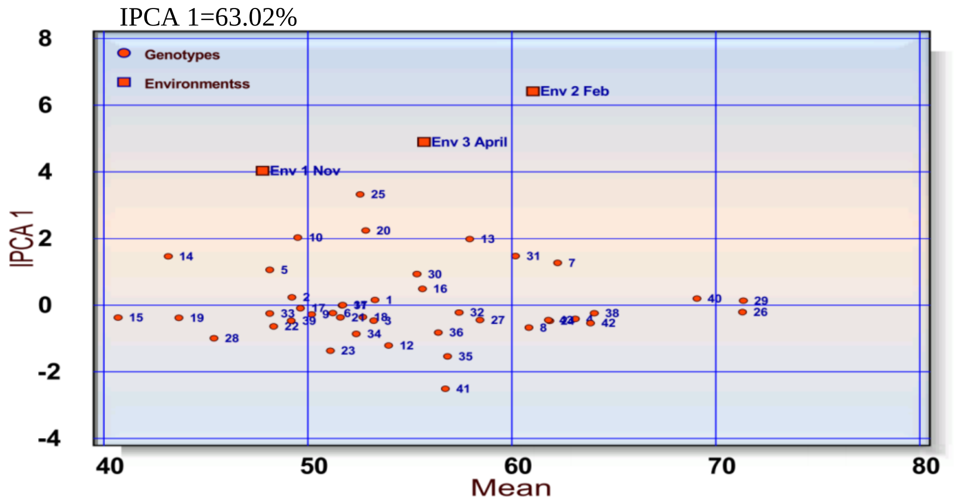

Fig 4. GGE Biplot for ascorbic acid (mg $100g^{-1}$) of 43 genotypes in 3 environments using genotypic and environmental scores

The capsaicin content in red chilli powder found to be highest among the genotypes PG 417 (G29), Punjab Sindhuri (G30), SL 473 (G36) and SL 478 (G37) that had higher mean values and regression coefficient >1.0 which indicated their suitability for favorable environment (Table 7). The genotype AC 101 (G31) had the highest capsaicin content in red chilli powder than the check Punjab Sindhuri (G30) followed by PG 417 (G29).

Table 7. Mean ($\bar{X}$), regression coefficient (b_i) and deviation from regression (S^2d_i) for capsaicin content (%) in red powder

Codes	E_1	E_2	E_3	Overall mean ($\bar{X}$)	b_i	S^2d_i
G1	0.50	0.63	0.55	0.56	2.02	0.00
G2	0.15	0.27	0.42	0.28	0.82	0.03**
G3	0.49	0.54	0.56	0.53	0.07	0.002**
G4	0.55	0.59	0.60	0.58	1.47	0.001**
G5	0.64	0.72	0.59	0.65	0.55	0.005**
G6	0.58	0.71	0.63	0.64	0.02	0.00
G7	0.47	0.58	0.59	0.55	1.05	0.003**
G8	0.43	0.51	0.47	0.47	1.17	0.00
G9	0.46	0.66	0.43	0.52	0.43	0.01**
G10	0.58	0.62	0.57	0.59	0.85	0.00**
G11	0.54	0.62	0.59	0.59	0.62	0.00
G12	0.46	0.54	0.49	0.50	0.30	0.00
G13	0.57	0.61	0.59	0.59	0.71	0.00
G14	0.40	0.48	0.44	0.44	0.80	0.00
G15	0.53	0.57	0.53	0.54	0.38	0.00
G16	0.39	0.46	0.42	0.42	1.64	0.00
G17	0.49	0.57	0.58	0.54	0.96	0.002**
G18	0.44	0.52	0.43	0.46	1.00	0.002**
G19	0.42	0.47	0.44	0.44	1.07	0.00
G20	0.41	0.48	0.44	0.45	0.48	0.00
G21	0.45	0.53	0.49	0.49	0.59	0.00
G22	0.53	0.58	0.55	0.55	1.05	0.00
G23	0.49	0.53	0.50	0.51	0.39	0.00
G24	0.46	0.54	0.53	0.51	1.70	0.001**
G25	0.34	0.42	0.39	0.38	0.95	0.00
G26	0.10	0.17	0.15	0.14	1.07	0.00
G27	0.65	0.73	0.66	0.68	0.80	0.00**
G28	0.41	0.50	0.44	0.45	1.94	0.00
G29	0.78	0.86	0.80	0.82	2.48	0.00**
G31	1.20	1.29	1.22	1.24	0.95	0.00**
G32	0.60	0.68	0.61	0.63	0.82	0.00**
G33	0.35	0.43	0.35	0.38	0.82	0.001**
G34	0.44	0.53	0.49	0.49	0.08	0.00
G35	0.55	0.63	0.57	0.58	1.94	0.00*
G36	0.72	0.80	0.73	0.75	1.03	0.00**
G37	0.67	0.75	0.73	0.72	1.52	0.00*
G38	0.38	0.46	0.43	0.43	0.57	0.00
G39	0.70	0.74	0.75	0.73	0.50	0.00**
G40	0.55	0.63	0.58	0.59	0.75	0.00
G41	0.67	0.71	0.69	0.69	0.88	0.00
G42	0.56	0.59	0.57	0.57	1.28	0.00
G43	0.51	0.57	0.55	0.54	1.47	0.00
G30 (Check)	0.91	0.99	0.93	0.95	3.00	0.00*
Range	**0.10 - 1.20**	**0.17 - 1.29**	**0.15 - 1.22**	**0.14 - 1.24**		
Mean	**0.52**	**0.60**	**0.56**	**0.56**		
LSD ($P \leq 0.05$)	0.017	0.017	0.019	0.03		
LSD ($P \leq 0.01$)	0.023	0.022	0.025	0.04		
SE of b_i	-	-	-	-	0.71	

*, ** Significant at $P \leq 0.05$ and 0.01 levels respectively

Based on the GGE Biplot performance of genotypes and environments PP 402 (G25), US 501 (G38), KC 304 (G16), KC 311 (G23), YL 582 (G43) and YL 581 (G42) had the lower coordination on the IPCA 1 axis (near the origin) thus these were stable genotypes (Figure 5). Among these genotypes KC 311 (G23), YL 582 (G43) and YL (581) had higher mean value indicated their general adaptability in all the three environments. The genotype AC 101 (G31) had negative score on IPCA 1 axis combined with above average capsaicin content in red powder, considered that it performs better under the poor environment and less sensitive to the changes in the environment for this trait. Most of the genotypes indicated stability for capsaicin content in red powder as they gathered around the origin axis of IPCA 1 but varied in their mean performance. The similar results were also reported by GURUNG *et al*. (2012), that difference in capsaicin content was not only determined by the genotypes but it was also under the great influence of the different environmental conditions. But they also reported the significant variation in capsaicin content was only accounted by the genotype itself. The higher capsaicin content was found under the warmer growing conditions. This was evident, all the environments had positive interaction with the genotypes and higher score on IPCA 1 axis but E_2 and E_3 showed above average mean value, considered suitable only for selecting genotypes that were specifically adapted to these environments. The environment E_1 had mean value lower than grand mean which resulted that it was unsuitable for selecting stable genotypes for capsaicin content in red powder.

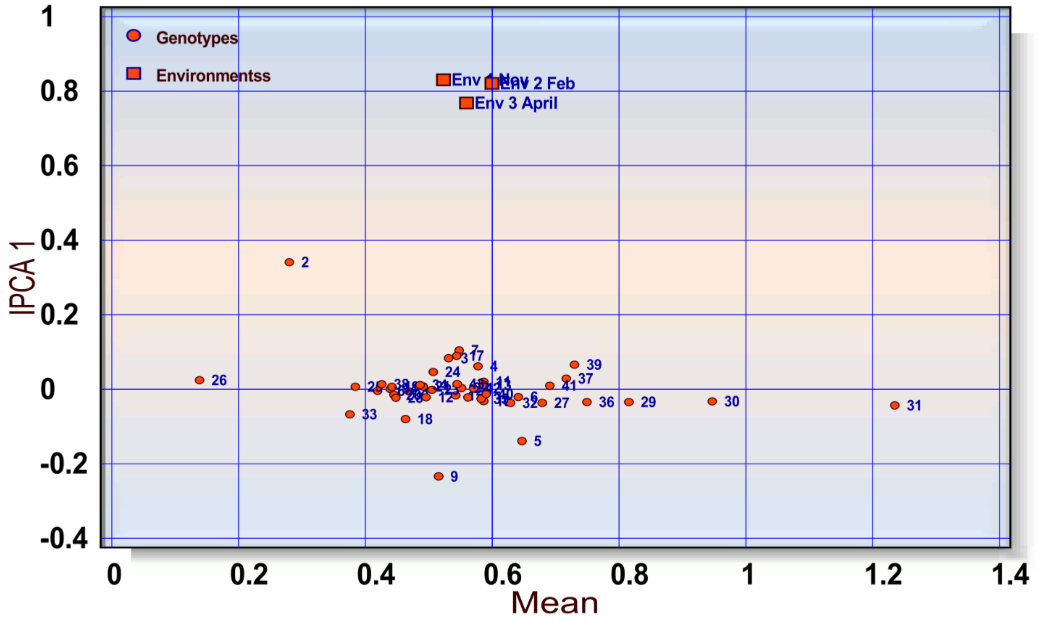

Fig 5. GGE Biplot for capsaicin content (%) in red powder of 43 genotypes in 3 environments using genotypic and environmental scores

Table 8. Mean ($\bar{X}$), regression coefficient (b_i) and deviation from regression (S^2d_i) for capsaicin content (%) in green chilli

Codes	E_1	E_2	E_3	Overall mean ($\bar{X}$)	b_i	S^2d_i
G1	0.41	0.58	0.47	0.49	1.92	0.00
G2	0.10	0.46	0.37	0.31	3.85	0.01**
G3	0.33	0.58	0.49	0.46	2.72	0.002**
G4	0.46	0.51	0.51	0.50	0.48	0.001**
G5	0.52	0.66	0.57	0.59	1.47	0.00
G6	0.54	0.65	0.56	0.58	1.25	0.00**
G7	0.42	0.52	0.51	0.49	1.06	0.002**
G8	0.39	0.45	0.38	0.41	0.70	0.00**
G9	0.41	0.56	0.33	0.44	1.85	0.01**
G10	0.45	0.58	0.53	0.52	1.41	0.00**
G11	0.50	0.52	0.53	0.52	0.19	0.00
G12	0.45	0.46	0.40	0.44	0.19	0.002**
G13	0.47	0.54	0.52	0.51	0.80	0.00*
G14	0.32	0.42	0.37	0.37	1.12	0.00
G15	0.44	0.46	0.47	0.46	0.20	0.00**
G16	0.34	0.38	0.43	0.38	0.39	0.004**
G17	0.42	0.50	0.50	0.47	0.88	0.001**
G18	0.41	0.45	0.37	0.41	0.47	0.002**
G19	0.34	0.42	0.37	0.37	0.98	0.00
G20	0.43	0.44	0.37	0.41	0.18	0.002**
G21	0.41	0.49	0.43	0.44	0.89	0.00*
G22	0.45	0.51	0.45	0.47	0.72	0.001**
G23	0.45	0.48	0.46	0.46	0.33	0.00
G24	0.41	0.63	0.46	0.50	2.45	0.001**
G25	0.28	0.38	0.31	0.32	1.13	0.00
G26	0.10	0.12	0.15	0.12	0.19	0.001**
G27	0.54	0.67	0.60	0.60	1.44	0.00
G28	0.36	0.42	0.36	0.38	0.71	0.001**
G29	0.65	0.77	0.74	0.72	1.28	0.001**
G31	1.10	1.12	1.14	1.12	0.17	0.001**
G32	0.52	0.55	0.57	0.55	0.32	0.001**
G33	0.30	0.36	0.32	0.32	0.73	0.00
G34	0.37	0.48	0.41	0.42	1.17	0.00
G35	0.46	0.70	0.50	0.55	2.70	0.002**
G36	0.66	0.75	0.66	0.69	1.12	0.001**
G37	0.61	0.67	0.65	0.65	0.66	0.00
G38	0.32	0.40	0.36	0.36	0.82	0.00
G39	0.69	0.63	0.68	0.67	-0.65	0.00
G40	0.58	0.55	0.51	0.55	-0.31	0.003**
G41	0.55	0.62	0.62	0.60	0.74	0.001**
G42	0.44	0.54	0.47	0.48	1.04	0.00
G43	0.42	0.51	0.47	0.46	0.97	0.00
G30 (Check)	0.79	1.00	0.86	0.88	2.29	0.00
Range	**0.10 - 1.10**	**0.12 - 1.12**	**0.15 - 1.14**	**0.12 - 1.12**		
Mean	**0.46**	**0.55**	**0.49**	**0.50**		
LSD ($P \leq 0.05$)	0.01	0.03	0.02	0.04		
LSD ($P \leq 0.01$)	0.02	0.04	0.02	0.05		
SE of b_i	-	-	-	-	0.57	

*, ** Significant at $P \leq 0.05$ and 0.01 levels respectively

The stability of genotypes for capsaicin content in green chilli has been presented in Table 8, it showed the highest capsaicin content in PG 417 (G29) followed Punjab Sindhuri (G30) and AC 101 (G31) in all the growing seasons. The genotype AC 101 (G31) had regression coefficient <1.0 indicated its suitability for unfavorable environments with respect to green fruit capsaicin content. The GGE Biplot resulted that the genotypes PP 402 (G25), KC 302 (G14), KC 307 (G19), C 142 (G7), YL 582 (G43), KC 305 (G17), YL 581 (G42) and SL 473 (G36) were close to the origin of IPCA 1, thus considered as the stable genotype, while AC 101 (G31) had the highest mean value and negative IPCA 1 score thus showed suitability for poor environments (Figure 6). Due to positive interaction (high score on IPCA 1 axis) genotype Punjab Sindhuri (G30) was suitable for favorable environments and sensitive to environmental changes. Based on the Biplot the variability due to genetic constitution of genotypes was higher than the environments (environment grouping on biplot). All the environments were positively related to the interaction with genotypes and higher score on IPCA 1 axis but E_2 showed above average mean value, considered suitable only for selecting genotypes that were specifically adapted to this environment. SAMNOTRA *et al*. (2011) observed that environment component was non-significant for total capsaicin content that was in lined with present study. While, GURUNG *et al*. (2012) concluded that variation in capsaicin content due to environment was 5.8%, variation due to genotypes was 74.2 % and 15.8% variation was due to G×E interaction concluded that genotypes contributed higher towards variation in capsaicin than environment.

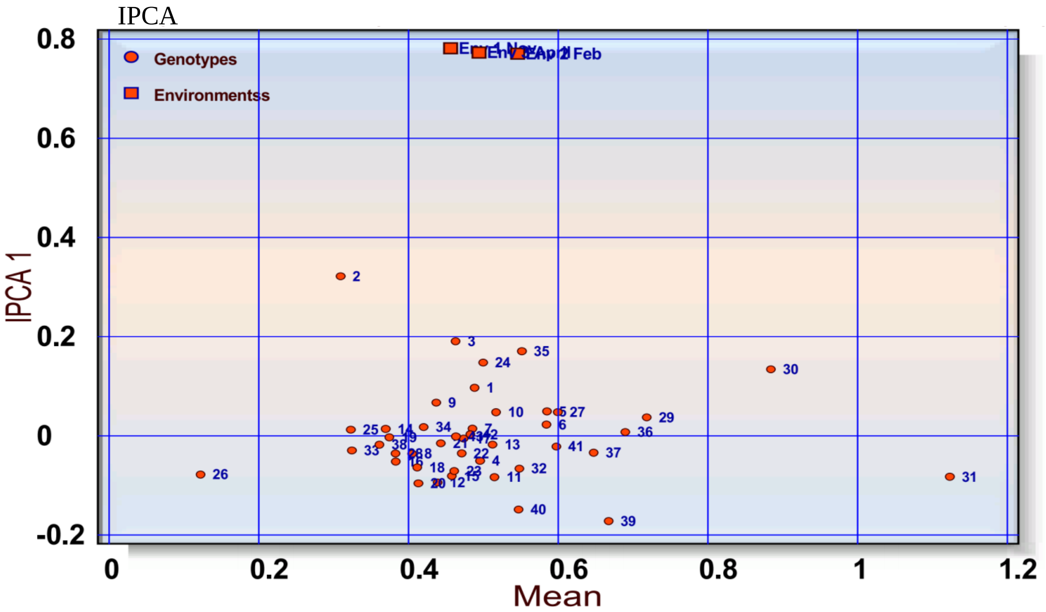

Fig 6. GGE Biplot for capsaicin content (%) in green fruit of 43 genotypes in 3 environments using genotypic and environmental scores

Table 9. Mean ($\bar{X}$), regression coefficient (b_i) and deviation from regression (S^2d_i) for capsaicin content (%) in oleoresin

Codes	E_1	E_2	E_3	Overall mean ($\bar{X}$)	b_i	S^2d_i
G1	1.56	0.32	2.09	1.32	-0.87	1.12**
G2	2.23	3.75	2.86	2.95	1.25	0.07**
G3	1.32	3.00	1.94	2.09	1.37	0.12**
G4	1.40	3.10	2.20	2.24	1.41	0.04**
G5	0.98	2.36	1.58	1.64	1.13	0.04**
G6	1.91	2.79	2.37	2.36	0.74	0.01**
G7	2.21	2.40	2.91	2.51	0.24	0.22**
G8	1.15	2.34	1.86	1.78	1.01	0.00*
G9	1.52	2.66	2.15	2.11	0.96	0.00**
G10	1.38	2.06	2.54	1.99	0.68	0.36**
G11	1.25	3.11	2.49	2.28	1.60	0.00**
G12	1.07	3.03	2.65	2.25	1.73	0.08**
G13	2.32	3.52	2.80	2.88	0.99	0.05**
G14	0.31	1.81	1.22	1.11	1.27	0.00
G15	1.97	3.12	2.48	2.52	0.95	0.03**
G16	0.74	1.27	2.89	1.63	0.71	2.15**
G17	1.20	2.90	1.87	1.99	1.39	0.10**
G18	0.49	1.97	1.06	1.18	1.22	0.08**
G19	0.84	2.94	1.99	1.92	1.76	0.02**
G20	0.42	1.56	0.95	0.97	0.94	0.02**
G21	1.31	2.53	1.84	1.89	1.01	0.04**
G22	1.00	2.03	2.94	1.99	1.06	1.11**
G23	1.41	2.97	2.19	2.19	1.30	0.02**
G24	1.53	2.43	2.11	2.02	0.78	0.00
G25	0.17	2.33	1.49	1.33	1.83	0.00
G26	1.18	2.89	2.13	2.07	1.44	0.01**
G27	1.22	3.16	2.99	2.46	1.73	0.20**
G28	1.05	2.08	1.67	1.60	0.87	0.00
G29	1.96	2.85	2.18	2.33	0.71	0.07**
G31	2.74	3.33	2.99	3.02	0.49	0.01**
G32	1.91	2.71	2.27	2.30	0.66	0.01**
G33	0.96	2.39	1.45	1.60	1.16	0.10**
G34	2.03	2.75	2.38	2.39	0.60	0.01**
G35	0.84	1.78	1.26	1.29	0.78	0.02**
G36	2.41	3.26	2.69	2.79	0.68	0.04**
G37	1.50	2.90	2.17	2.19	1.17	0.03**
G38	1.19	2.26	1.97	1.81	0.93	0.01**
G39	1.72	2.59	2.12	2.14	0.72	0.01**
G40	0.91	2.91	1.76	1.86	1.65	0.11**
G41	1.57	2.47	1.87	1.97	0.73	0.04**
G42	1.82	2.60	2.07	2.16	0.63	0.04**
G43	0.22	1.36	0.82	0.80	0.96	0.01**
G30 (Check)	2.41	3.19	2.59	2.73	0.63	0.06**
Range	**0.17 - 2.74**	**1.27 - 3.75**	**0.82 - 2.99**	**0.80 - 3.02**		
Mean	**1.38**	**2.55**	**2.11**	**2.01**		
LSD ($P \leq 0.05$)	0.04	0.05	0.04	0.32		
LSD ($P \leq 0.01$)	0.05	0.06	0.06	0.42		
SE of b_i	-	-	-	-	0.46	

*, ** Significant at $P \leq 0.05$ and 0.01 levels respectively

On the basis of regression coefficient and deviation from regression given in Table 9 there were nine genotypes that had significantly higher capsaicin content in oleoresin and among them PAU 114 (G2) and PL 412 (G27) were adapted to favorable environments for the given trait, due to >1.0 regression coefficient. In environment vise ranking AC 101 (G31) had highest capsaicin content in oleoresin followed by SL 473 (G36) and check Punjab Sindhuri (G30) in E_1, while in case of E_2 highest capsaicin in oleoresin was found in PAU 114 (G2) followed by IS 261 (G13) and AC 101 (G31). However in E_3 only the genotype AC 101 (G31) had the highest capsaicin in oleoresin than check Punjab Sindhuri (G30). On the basis of GGE Biplot (Figure 7) Punjab Sindhuri (G30) and SL 473 (G36) represented general adaptability due to higher mean values and lower IPCA 1 axis score. The genotype YL 582 (G43) was poor performer and genotypes PAU 115 (G1) and KC 304 (G16) had more sensitivity to environmental changes whereas genotypes PAU 114 (G2) and IS 261 (G13) were less sensitive to the environmental changes. As per the environmental concern all the growing environments had positive interaction with genotypes. The E_2 and E_3 environments had the higher average capsaicin in oleoresin content than E_1 and these were suitable for selecting the genotypes that were adapted to these environments growing conditions (higher score on IPCA 1 axis).

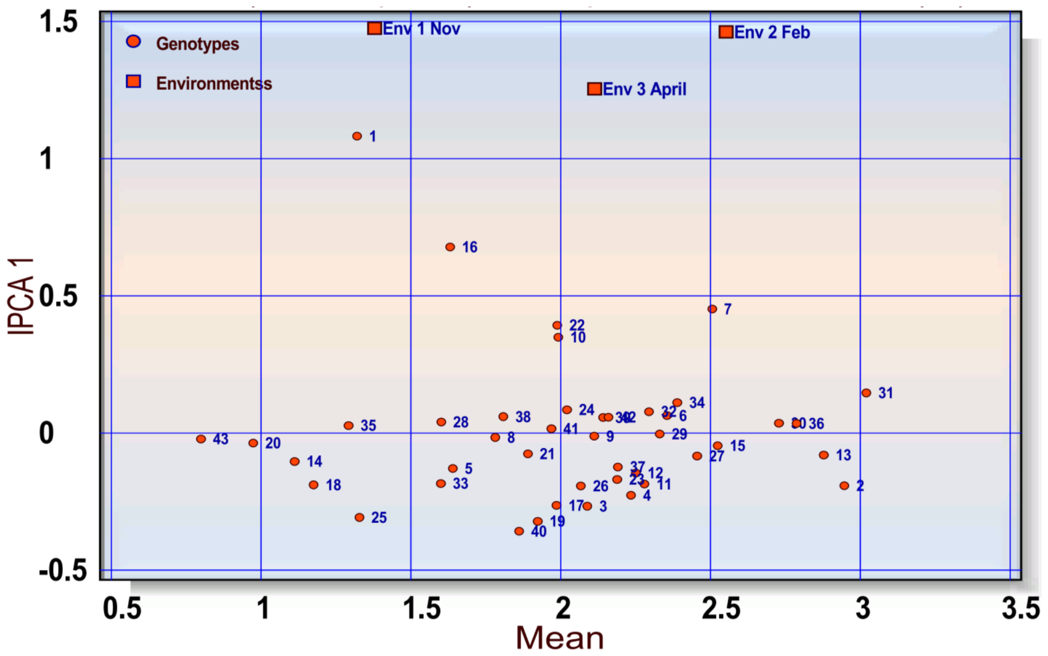

Fig 7. GGE Biplot for capsaicin content (%) in oleoresin of 43 genotypes in 3 environments using genotypic and environmental scores

Table 10. Mean ($\bar{X}$), regression coefficient (b_i) and deviation from regression (S^2d_i) for oleoresin content (%)

Codes	E_1	E_2	E_3	Overall mean ($\bar{X}$)	b_i	S^2d_i
G1	11.43	15.17	14.33	13.64	2.52	0.05
G2	10.38	13.69	12.19	12.08	2.11	0.09
G3	14.99	15.72	15.30	15.34	0.45	-0.01
G4	12.30	14.09	13.42	13.27	1.16	-0.03
G5	12.46	13.53	12.71	12.90	0.63	0.11*
G6	11.85	12.66	12.23	12.25	0.51	-0.02
G7	11.99	13.40	13.71	13.03	1.04	0.34**
G8	10.76	11.52	11.09	11.12	0.47	-0.01
G9	10.79	11.62	10.59	11.00	0.43	0.34**
G10	11.26	11.53	12.61	11.80	0.36	0.84**
G11	12.05	12.88	13.62	12.85	0.70	0.61**
G12	11.37	13.28	13.83	12.83	1.43	0.84**
G13	11.52	12.77	12.11	12.14	0.79	0.01
G14	11.32	13.31	12.22	12.28	1.24	0.10
G15	10.73	12.13	11.67	11.51	0.91	-0.03
G16	12.21	13.46	14.24	13.30	1.00	0.86**
G17	11.46	13.67	12.52	12.55	1.39	0.09
G18	10.84	12.77	11.81	11.81	1.22	0.04
G19	11.03	11.80	12.01	11.61	0.58	0.10*
G20	9.67	10.84	10.40	10.30	0.76	-0.03
G21	11.32	12.37	11.69	11.80	0.64	0.04
G22	10.49	10.85	11.93	11.09	0.42	0.88**
G23	10.56	11.30	10.91	10.92	0.46	-0.02
G24	11.57	12.81	12.31	12.23	0.80	-0.03
G25	11.11	12.18	11.49	11.60	0.65	0.04
G26	10.84	11.73	11.33	11.30	0.57	-0.03
G27	10.36	12.26	11.11	11.24	1.17	0.15*
G28	12.33	13.87	13.45	13.22	1.03	-0.03
G29	9.43	10.83	10.48	10.24	0.94	-0.03
G31	11.71	12.87	12.47	12.35	0.76	-0.03
G32	10.38	13.44	11.03	11.62	1.80	1.26**
G33	14.46	16.23	16.01	15.57	1.22	0.05
G34	10.76	12.08	11.54	11.46	0.85	-0.03
G35	14.01	15.76	15.20	14.99	1.15	-0.03
G36	11.66	13.10	12.50	12.42	0.93	-0.02
G37	16.07	17.35	16.62	16.68	0.79	0.03
G38	11.65	14.19	13.83	13.22	1.74	0.10
G39	11.57	13.97	13.10	12.88	1.56	-0.03
G40	11.58	15.05	13.51	13.38	2.22	0.08
G41	11.57	12.26	11.78	11.87	0.41	0.01
G42	11.33	13.62	13.09	12.68	1.53	-0.01
G43	11.94	12.88	12.39	12.40	0.59	-0.01
G30 (Check)	11.19	12.83	12.31	12.11	1.08	-0.03
Range	**9.43 - 16.07**	**10.83 - 17.35**	**10.04 - 16.62**	**10.24 - 16.68**		
Mean	**11.59**	**13.11**	**12.62**	**12.44**		
LSD ($P \leq 0.05$)	0.67	0.38	0.46	0.48		
LSD ($P \leq 0.01$)	0.89	0.51	0.61	0.63		
SE of b_i	-	-	-	-	0.39	

*, ** Significant at $P \leq 0.05$ and 0.01 levels respectively

The oleoresin content was found higher in genotype KC 304 (G16) combined with 1.0 regression coefficient revealed the stability of genotype across the tested environments for the given trait (Table 10). The genotype PP 414 (G28) had higher mean value with non-significant deviation and near to one regression coefficient (1.03) indicated its stability and adaptability in all the environments. The significantly highest oleoresin content was observed in the genotype SU 478 (G37) followed by and SL 466 (G33) in all the tested environments. Based on GGE Biplot scores of genotypes and environments in Figure 8, the genotypes C 142 (G7) and PP 414 (G28) had general adaptability to all the environments due to above average value and were most stable genotypes because placed exactly on the origin in Biplot. While, the genotypes PAU 212 (G3) and SU 478 (G37) performed better under poor environments and less sensitive to the environmental changes (negative IPCA 1 value). The genotypes IS 261 (G13), ML 342 (G24), AC 101 (G31) and KC 304 (G16) were laid on the same horizontal axis indicated the similar G×E interaction but varied in mean oleoresin content. All the environments were positively related to the interaction with genotypes. E_2 and E_3 laid on same horizontal axis in Biplot revealed that both the environments had the similar interaction with the genotypes and also had the higher average oleoresin content than grand mean but preferable only for selecting the genotypes that were specific to these environments, due to higher score on IPCA 1 axis. ZEWDIE and BOSLAND (2000) studied effect of different environments on the total capsaicinoids and on individual capsaicinoids, reported that warmer and hotter growing conditions increase the capsaicinoids in the chilli fruits. Similarly, the oleoresin content reacted in the same way as the capsaicinoids to different growing conditions.

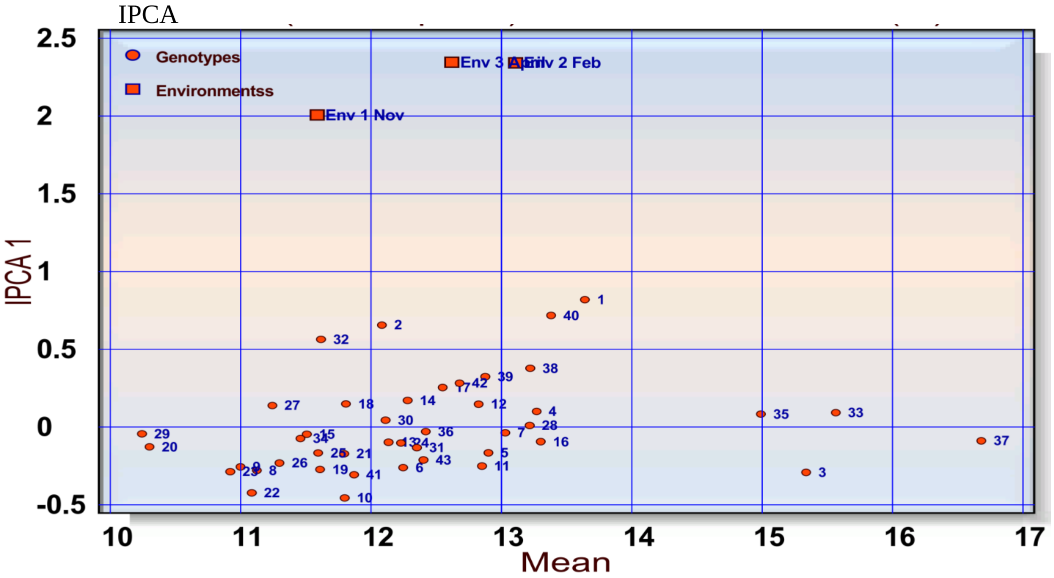

Fig 8. GGE Biplot for oleoresin content (%) of 43 genotypes in 3 environments using genotypic and environmental scores

Table 11. Mean ($\bar{X}$), regression coefficient (b_i) and deviation from regression (S^2d_i) for coloring matter (ASTA)

Codes	E_1	E_2	E_3	Overall mean ($\bar{X}$)	b_i	S^2d_i
G1	113.82	135.20	122.65	123.89	1.27	-4.34
G2	106.07	124.74	115.50	115.44	1.10	-2.56
G3	87.39	94.98	92.85	91.74	0.44	-0.87
G4	83.74	87.67	86.25	85.89	0.23	-3.85
G5	88.72	92.39	89.51	90.21	0.22	-3.98
G6	94.82	116.26	103.03	104.70	1.28	-3.99
G7	89.16	104.43	97.65	97.08	0.89	-1.34
G8	86.63	99.43	88.36	91.47	0.78	4.23
G9	87.89	103.10	95.19	95.39	0.90	-3.74
G10	98.26	106.56	104.70	103.17	0.47	1.54
G11	114.67	132.97	125.83	124.49	1.06	3.91
G12	154.79	163.68	157.52	158.66	0.53	-3.71
G13	114.32	130.41	126.06	123.60	0.92	12.36
G14	140.05	169.07	149.99	153.04	1.74	-1.28
G15	100.23	119.02	107.63	108.96	1.12	-4.22
G16	113.16	128.99	121.68	121.28	0.93	-1.91
G17	105.74	121.97	114.20	113.97	0.95	-2.45
G18	94.70	120.43	103.63	106.25	1.54	-2.23
G19	85.93	95.16	89.74	90.28	0.55	-4.34
G20	87.45	96.60	89.87	91.31	0.55	-3.05
G21	92.71	154.06	97.21	114.66	3.78	289.01**
G22	95.79	106.69	101.91	101.47	0.64	-2.71
G23	123.70	134.31	129.30	129.10	0.62	-3.44
G24	87.67	98.63	93.26	93.19	0.64	-3.66
G25	88.80	95.74	90.45	91.67	0.42	-3.32
G26	120.71	142.50	129.74	130.98	1.29	-4.34
G27	133.93	163.32	152.27	149.84	1.70	20.12*
G28	82.88	102.81	86.91	90.87	1.21	7.71
G29	111.07	121.13	117.95	116.72	0.58	0.41
G31	146.09	170.30	161.22	159.20	1.40	12.41
G32	110.21	126.99	115.05	117.42	1.01	-1.26
G33	89.47	102.26	96.54	96.09	0.75	-2.36
G34	86.64	105.04	92.18	94.62	1.11	-1.35
G35	99.94	119.72	105.69	108.45	1.19	-0.23
G36	118.37	135.46	124.71	126.18	1.02	-3.93
G37	88.07	106.82	98.87	97.92	1.09	1.55
G38	143.17	164.96	155.25	154.46	1.27	1.60
G39	104.25	124.65	116.34	115.08	1.19	4.16
G40	87.51	105.68	93.61	95.60	1.09	-2.91
G41	131.96	157.90	141.85	143.91	1.54	-3.79
G42	87.05	99.11	89.94	92.037	0.73	-1.32
G43	81.33	93.61	84.29	86.41	0.74	-1.27
G30 (Check)	89.42	98.47	94.11	94.00	0.53	-3.78
Range	**81.33 - 154.79**	**87.67 - 170.30**	**84.29 - 161.22**	**85.89 - 159.20**		
Mean	**103.45**	**120.31**	**110.48**	**111.41**		
LSD ($P \leq 0.05$)	5.44	6.46	5.66	5.21		
LSD ($P \leq 0.01$)	7.21	8.56	7.49	6.86		
SE of b_i	-	-	-	-	0.3	

*, ** Significant at $P \leq 0.05$ and 0.01 levels respectively

The coloring matter in red chilli powder found to be highest in genotypes IS 263 (G12) and AC 101 (G31). The genotype S 343 (G32) had higher mean value for coloring matter with non-significant deviation and 1.01 as regression coefficient indicated its stability and adaptability in all the three environments (Table 11). The significantly highest coloring matter across the environments was found in AC 101 (G31), IS 263 (G12) and US 501 (G38), while their ranking shuffled in different environments. The GGE Biplot (Figure 9) resulted that genotypes IS 267 (G11) and SL 473 (G36) was most stable genotypes because they were laid exactly on the IPCA 1 axis origin and also had general adaptation across the environments due to above average mean values for coloring matter. AC 101 (G31) considered suitable for favorable environment and highly sensitive to environmental changes, while the genotype IS 263 (G12) performed better under poor environment and showed resistance to environmental changes regarding coloring matter. The genotype KC 309 (G21) showed more responsiveness towards the environmental changes (highest IPCA value). All the environments were positively related to the interaction with genotypes. The growing environments named as E_2 and E_3 had the higher average coloring matter than grand mean but preferable only for selecting the genotypes that were specific to these environments, due to higher score on IPCA 1 axis. Also the study done by JINDAL *et al.* (2015) revealed the additive control for the oleoresin content, coloring matter in powder and in oleoresin both, suggested that these quality traits were more influenced by the environmental factors.

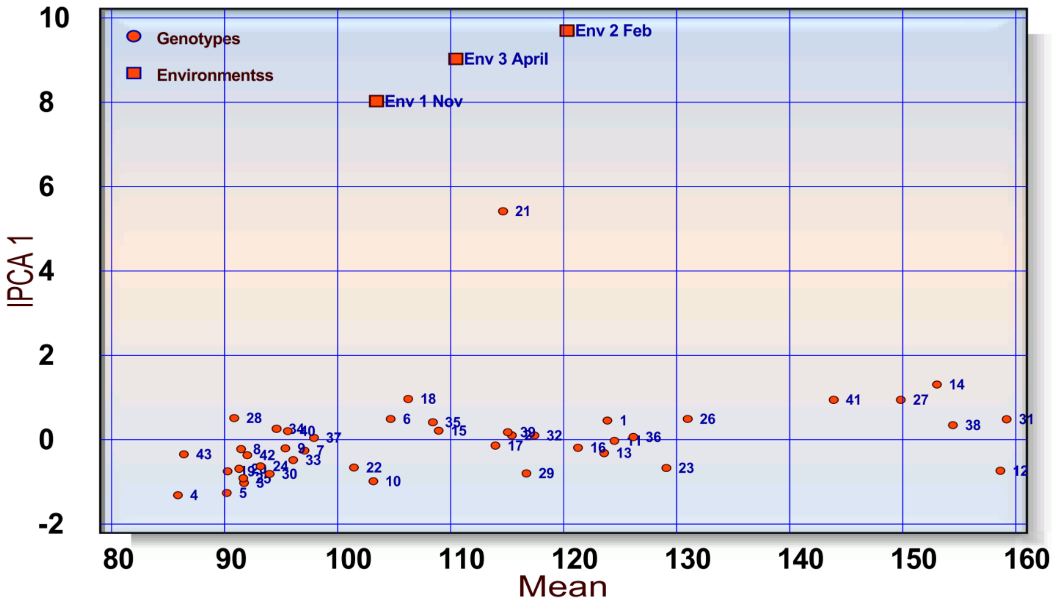

Fig 9. GGE Biplot for coloring matter (ASTA) of 43 genotypes in 3 environments using genotypic and environmental scores

Table 12. Mean ($\bar{X}$), regression coefficient (b_i) and deviation from regression (S^2d_i) for coloring matter in oleoresin (ASTA)

Codes	E_1	E_2	E_3	Overall mean ($\bar{X}$)	b_i	S^2d_i
G1	486.72	599.73	541.51	542.65	1.02	27.18
G2	434.85	527.08	478.64	480.19	0.83	-13.09
G3	332.61	433.35	392.86	386.27	0.89	248.62*
G4	271.19	348.65	311.53	310.46	0.69	14.59
G5	282.86	354.94	317.81	318.53	0.65	-24.99
G6	405.80	484.68	443.03	444.50	0.71	-28.01
G7	382.31	464.71	425.97	424.33	0.74	36.03
G8	376.14	451.68	416.37	414.73	0.68	23.49
G9	378.49	459.31	420.57	419.46	0.72	21.15
G10	411.70	494.22	454.52	453.48	0.74	22.42
G11	447.19	579.64	525.83	517.55	1.17	452.81**
G12	624.79	693.68	657.52	658.66	0.62	-33.99
G13	454.32	560.41	526.06	513.60	0.93	575.51**
G14	600.05	699.07	646.66	648.59	0.89	-10.60
G15	402.23	513.69	460.96	458.96	1.00	109.28
G16	490.16	588.99	551.68	543.61	0.87	307.98*
G17	431.41	588.97	519.85	513.41	1.40	459.93**
G18	387.87	568.43	455.93	470.75	1.66	-60.13
G19	55.93	125.16	89.74	90.28	0.62	-25.42
G20	365.24	126.60	89.87	193.90	-1.93	22135.13**
G21	383.04	683.91	428.21	498.39	2.85	3133.24**
G22	393.79	493.36	437.91	441.69	0.90	-36.77
G23	498.70	649.64	582.63	576.99	1.35	389.35**
G24	371.01	462.30	423.26	418.86	0.81	136.40
G25	358.80	457.74	407.12	407.89	0.89	11.29
G26	467.38	666.83	559.07	564.43	1.81	95.32
G27	573.93	731.99	682.27	662.73	1.38	1441.79**
G28	366.21	485.14	403.58	418.31	1.10	-17.81
G29	477.74	566.80	521.28	521.94	0.80	-1.73
G31	612.75	759.30	708.55	693.53	1.29	974.61
G32	460.21	573.66	521.72	518.53	1.01	154.45
G33	362.80	485.60	428.87	425.76	1.10	178.60*
G34	356.64	501.70	417.85	425.40	1.32	-39.12
G35	406.61	569.05	463.02	479.56	1.50	-39.57
G36	504.70	638.80	558.04	567.18	1.23	-57.93
G37	373.07	502.82	435.54	437.14	1.17	47.62
G38	609.84	730.76	670.25	670.28	1.09	70.97
G39	432.91	564.65	524.34	507.30	1.15	1043.02**
G40	359.18	492.34	93.61	315.04	1.67	65500.58**
G41	574.96	696.24	627.52	632.91	1.10	-35.59
G42	372.05	470.11	412.27	418.14	0.89	-55.86
G43	349.67	440.28	396.96	395.64	0.81	44.07
G30 (Check)	368.42	464.47	420.11	417.67	0.86	86.05
Range	**55.93 - 624.79**	**125.16 - 759.30**	**89.74 - 708.55**	**90.28 - 693.53**		
Mean	**419.91**	**529.08**	**461.65**	**470.21**		
LSD ($P \leq 0.05$)	22.42	25.17	17.79	40.20		
LSD ($P \leq 0.01$)	29.72	33.36	23.58	52.94		
SE of b_i	-	-	-	-	0.6	

*, ** Significant at $P \leq 0.05$ and 0.01 levels respectively

Based on the regression model the genotypes AC 101 (G31) and US 501 (G38) had higher mean values for coloring matter in oleoresin (Table 12). The genotypes PAU 115 (G1) and S 343 (G32) had higher mean values with non-significant deviation and close to 1.0 regression coefficient (1.01 and 1.02 respectively) indicated their stability and adaptability in all the environments. In E_1 the genotype IS 263 (G12) had significantly highest coloring matter in oleoresin followed by AC 101 (G3) and US 501(G38) while in E_2 and E_3 AC 101 (G3) had the highest value for coloring matter in oleoresin followed by the PL 412 (G27). The graphical presentation of GGE Biplot showed clustering of genotypes exhibited that most of the genotypes had similar adaptation to the environments (Figure 10). The genotypes PG 417 (G29) and KC 302 (G14) were most stable because they laid exactly on the origin axis of IPCA 1 and also had general adaptability to all the environments (higher mean values). The genotypes US 501 (G38) and AC 101 (G31) had highest mean values and were suitable for unfavorable environments (negative interaction) and were less sensitive to environmental changes. On the contrary genotype IS 263 (G12) was suitable for favorable environment (positive interaction) and it was sensitive to environmental changes. All the environments had positive interaction with the genotypes for coloring matter in oleoresin. The tested environment named E_2 had the highest average values for coloring matter in oleoresin but it was preferable only for the selecting genotypes that were specific to this environment and unsuitable for the selection of general adapted genotypes, due to higher score of E_2 on IPCA 1 axis.

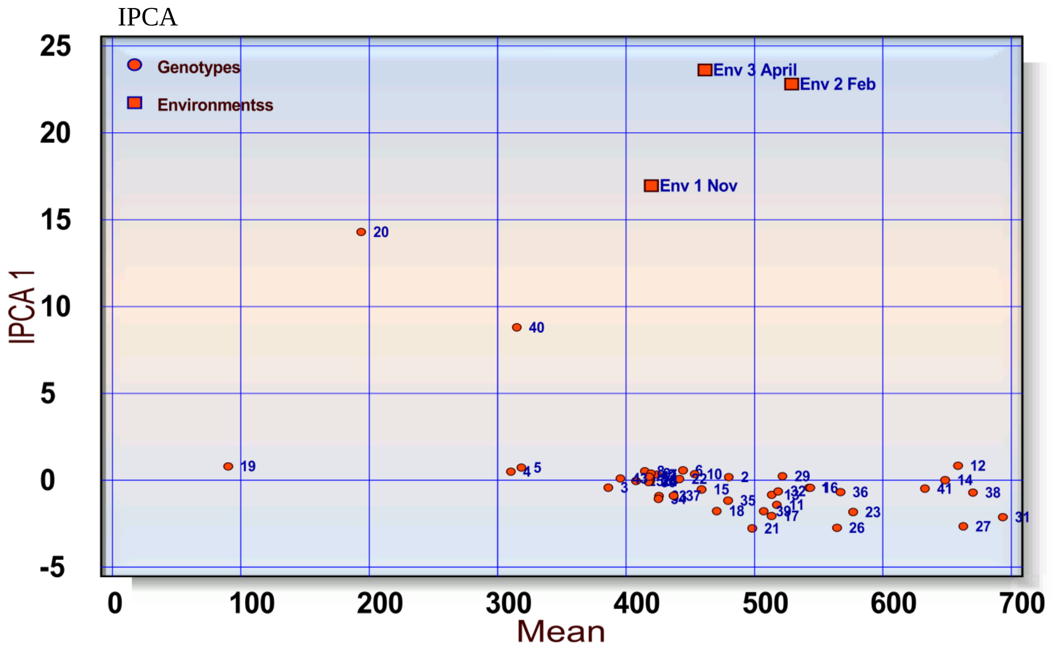

Fig 10. GGE Biplot for coloring matter in oleoresin (ASTA) of 43 genotypes in 3 environments using genotypic and environmental scores

CONCLUSION

The multi-environmental evaluation of chilli pepper genotypes for quality traits revealed the best genotypes and environments for the selection of generally adaptable, stable and superior genotypes for the three distinct growing seasons. It was evident from the study that traits like capsaicin content both in red and green chilli, the oleoresin content and coloring matter was under the great influence of the different tested environments and exhibits that warmer and hotter climate elevate the pungency in chillies. The dry matter and powder yield found to be higher in genotypes subjected to the milder climatic conditions such as E_1. As pungency is the important quality trait for most of the chilli breeding programme, the main objective of the breeder is to perform selection for uniform and stable cultivar with a specific pungency level. The genotype AC 101 (G31) had highest capsaicin content in both green and red fruits and also in oleoresin obtains from its fruits over the three environments while stability and adaptability for the capsaicinoids in red fruits and oleoresin was found in genotypes SL 473(G36) and SL 473 (G36). As the capsaicinoids has great importance for both processing and medical sector it is significant to identify the stable genotypes for this trait in local environments. Hence, this multi-environmental evaluation not only illustrate that selection of stable genotypes for pungency is possible, but also selection for other quality traits in chilli is possible.

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INTERAKCIJA GENOTIPA I SPOLJAŠNJE SREDINE ZA OSOBINE KVALITETA KOD LJUTE PAPRIKE (*Capsicum annuum* L.)

Tejpal Singh SRAN, S.K. JINDAL* i Neena CHAWLA

Departman za povrtarstvo, Pendžab poljoprivredni univerzitet, Ludijana, Indija

Izvod

Postoji potreba za identifikovanjem specifičnih sredina za odabir adaptiranih i stabilnih genotipova za svojstva kvaliteta kod paprike. Među ovim svojstvima kvaliteta najvažnija su ljutina i boja koje treba da budu u stabilnim količinama u finalnim proizvodima. Stoga je ova multi-ekološka procena genotipova ljute paprike rađena u tri različita okruženja, da bi se identifikovalo pogodno okruženje za selekciju, a I pogodni genotipovi za određene osobine kvaliteta. Studija je uključila 43 genotipa ljute paprika testirana u tri različite spoljašnje sredinea za devet različitih osobina kvaliteta na Poljoprivrednom univerzitetu Pendžab, a podaci su analizirani pomoću Eberhart - Russell-ovog modela i GGE Biplot analize. Efekat životne sredine činio je više od 35% varijacija sadržaja kapsaicina u oleoresina i suvoj materiji. Osobine sadržaj kapsaicina u crvenom prahu (3%) i kapsaicin u zelenoj paprici (4,73%) bile su pod najmanjim uticajem životne sredine. Doprinos G × E interakcija iznosio je < 25% za sva proučavana svojstva, osim za askorbinsku kiselinu. Genotip AC 101 bio je najbolji za sadržaj kapsaicina u zelenoj i crvenoj paprici u prahu u svim sredinama. Podaci dobijeni ovom studijom pomažu u identifikovanju stabilnih i superiornih genotipova za svojstva kvaliteta u ranoj, glavnoj i kasnoj sezoni sadnje.

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