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Original scientific paper

MULTI-ENVIRONMENTAL EVALUATION OF CHILLI GENOTYPES FOR YIELD AND YIELD COMPONENTS

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Forty three chilli genotypes including one check Punjab Sindhuri were evaluated for yield and its related attributes to determine stability and adaptability under three different environments (November transplanted 2016, February transplanted 2017 and April transplanted 2017) at Punjab Agricultural University, Ludhiana. The mean square (MS) due to genotypes was significant for all the traits studied except primary number of branches. The MS due to genotype × environment interaction was also found significant for all the traits studied. The genotype S 343 was identified as promising for fruit yield plant^{-1} and plant height in all the three environments followed by PG 417 and PL 412 while on the basis of regression, the genotype PAU 114 was found adaptable across the environments for fruit yield and fruit weight. It was observed that the genotype FL 201 had the longest fruit, more fruit width and thicker pericarp over all the environments. The promising genotypes found in the study could have the potential of being commercially exploited at farmer's field especially for early and late season.

Keywords: Chilli, genotypes × environment, mean square, significant, fruit yield

INTRODUCTION

In north India, chilli is mainly cultivated in Kharif season; however summer and Rabi seasons are also being grown for green fruits in many regions of the country. February is the main planting time for chilli cultivation in Punjab region, and most of the available cultivars have been developed for this season. However, sowing early/late chilli crop is a worthwhile alternative to improve farmer's income and an excellent option for crop rotation in the region (BALKAYA and KARAAGAC, 2009).

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Most of the economic traits in chilli are vulnerable to environmental fluctuations (WANI *et al.,* 2012). The major effect of interaction would directly lower the contribution of genetic components to the final appearance of plants (ANNICIARICO, 2002), so this suggests to access genetic-environment interaction of desirable genotypes under variable environmental conditions. Multi-environmental or Multi-locational testing of genotypes provides an opportunity to plant breeders to identify the adaptability of a genotype to a particular environment and also stability of genotype over different environments (RAGHAVENDRA *et al.,* 2017).

Phenotypic expression of the genotype is variable when grown in different environments. The basic reason for difference in the performance of genotypes across the environments is the presence of genotype-environment interaction (GEI). It is observed that genotype × environment (G×E) interaction is widely present and contributes substantially to the non-realization of expected gain from selection (COMSTOCK and MOLL, 1963). To overcome GEI problem; trials are usually conducted across several environments to ensure that the selected genotypes have high and stable performance over a wide range of environments. It has been found that the performance of different genotypes of a crop usually differs from location to location and even more effectively from season to season. In the case of vegetable crops, it is considered important, because they are often cultivated under varying agro-climatic, management and edaphic conditions. To identify the genotypes which are high yielding and stable in performance, it is therefore considered necessary to evaluate genotypes across the environment before they are made available for commercial cultivation**.**

MATERIALS AND METHODS

Experimental area and Climate

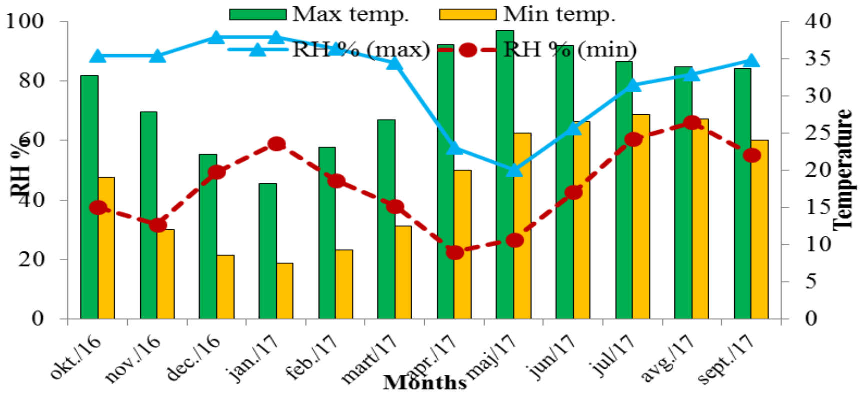

Figure 1. Maximum and minimum temperature and relative humidity during the three growing seasons.

The present research was carried at Vegetable Research Farm of Punjab Agricultural University, Ludhiana, Punjab. Ludhiana is geographically situated at 30.9° N latitude and 75.85° E longitudes and at an altitude of 244 meters above the sea level. The experimental area is characterized by hot and dry summer season during May-June followed by the rainy season and the winters, especially the months of December-February are severely cold. The mean maximum and minimum temperature show considerable fluctuation during different periods of the year. The day temperature of 40˚C and above during summer is common. The annual average rainfall of the area is 750 mm, most of which is received during July and August. The meteorological data collected from the university agro meteorological department during the crop season presented in Figure 1.

Experimental design and Morphological characterization

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

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

The experimental material comprised 43 entries (42 chilli genotypes and 1 standard check) from different sources (Table 1) and evaluated at Vegetable Research Farm, in Randomized Complete Block Design (RCBD) with split plot arrangement using three replications. The experiment was conducted with three dates of sowing on 11 October 2016 (E_1), 22 November 2016 (E_2) and 4 March 2017 (E_3) and transplanting on 11 November 2016, 28 February 2017 and 5 April 2017, respectively.

Each plot measures 3.75 m^2 with 10 plants in each row. The seedlings were planted on ridges at row to row apart 75 cm and plant to plant spacing of 45 cm. The experimental material was fertilized with a basal doze 12.5 kg N in the form of urea, 12 kg P_2O_5 as DAP and 12 kg K_2O as Muriate of Potash at the time of transplanting and 12.5 kg N in the form of urea was applied as topdressing after first picking. Weeding was done a few days after the application of basal doze of fertilizers to ensure proper development of seedlings and afterwards done when necessary. For the control of thrips, mites, aphids, and whitefly preventive measures were taken accordingly with the application of Tracer 480 SC (spinosad) for thrips and fruit borer @ 0.3-0.5 ml per liter of water, Omite (propargite) for mites @ 3ml per liter of water, Malathion 50 EC @ 4ml per liter for aphid and whitefly.

The traits evaluated are: a) Plant height (cm)- measured up to tip of the five randomly selected fully mature plants and then average was taken; b) Plant spread (cm)- measured in both directions and then average was taken; c) Primary branches plant^{-1}- counted from the base of the plant; d) Days to first picking- days counted from the transplanting to first picking; e) Number of fruits plant^{-1}- red ripe fruits from each picking counted from five plants and then average was taken; f) Fruit weight (g), length (cm) and width (mm)- data was taken from ten representative fruits and the average was noted; g) Fruit yield plant^{-1}-red ripe fruits in each picking was added to calculate total fruit yield in grams plant^{-1}; h) Pericarp thickness (mm)- the same ten fruits used to calculate the thickness of fruit pericarp.

Data analysis

The data was analyzed as per randomized block design using computer programme Windostat Version 9.3. The regression analysis proposed by Eberhart and Russell's model (1966) was used for computing analysis of variance for phenotypic stability and estimates of stability parameters of individual genotypes and the significance of difference was tested at 5% and 1% level of significance.

RESULTS AND DISCUSSION

In the present experiment, the analysis of variance (ANOVA) of G×E interaction for yield and its related traits was represented in Table 2. The pooled mean squares (MS) due to genotypes for all the studied traits in the three environments were significant except a number of primary branches, where MS was non-significant, revealing genetic variability among the genotypes. The ANOVA showed that the MS due to environments were also significant for all the traits which mean that the environments in three seasons were different from one another. The MS due to G×E interactions were also significant for all the traits except a number of primary branches indicating the 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 in this study.

Table 2. Analysis of variance for stability of yield and its related traits in chilli

Source of variation / Trait	Genotypes	Environment + G × E	Environment (Linear)	G × E	Pooled deviation	Pooled error
d.f.	42	86	1	42	43	252
Plant height (cm)	199.37**	273.31**	19020.1**	74.04**	31.98	30.88
Number of primary branches	0.73	0.85*	26.51**	0.59	0.52**	0.10
Plant spread (cm)	73.14**	179.87**	14302.05**	20**	7.60	10.21
Days to first picking	352.55**	834.53**	64510.21**	117.15**	54.39*	35.61
Number of fruits plant^{-1}	27673.65**	1805.71**	91087**	1226.34**	295.29**	107.40
Fruit yield (g plant^{-1})	28428.12**	19400.17**	1262917.5**	7566.24**	2039.89**	530.90
Fruit weight (g)	6.50**	0.70**	41.73**	0.36**	0.08**	0.03
Fruit length (cm)	4.93**	0.34**	17.93**	0.23**	0.04	0.11
Fruit width (mm)	12.22**	2.75**	195.83**	0.76**	0.20	0.26
Pericarp thickness (mm)	0.19**	0.07**	3.62**	0.03*	0.02**	0.00

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

Trait	Source	d.f.	SS	Pr > F	Total variation (%)
Plant height (cm)	E	2	19020.09	< .0001**	59.77
	G	42	8373.58	< .0001**	26.31
	G × E	84	4424.93	< .0001**	13.90
Number of primary branches	E	2	26.51	< .0001**	25.50
	G	42	30.53	0.1520	29.37
	G × E	84	46.89	< .0001**	45.11
Plant spread (cm)	E	2	14302.04	< .0001**	77.13
	G	42	3071.94	< .0001**	16.56
	G × E	84	1166.63	< .0001**	6.29
Days to first picking	E	2	64510.21	< .0001**	74.51
	G	42	14807.02	< .0001**	17.10
	G × E	84	7259.04	< .0001**	8.38
Number of fruits plant^{-1}	E	2	91087.04	< .0001**	6.91
	G	42	1162293.25	< .0001**	88.21
	G × E	84	64203.64	< .0001**	4.87
Fruit yield (g plant^{-1})	E	2	1262917.62	< .0001**	44.12
	G	42	1193981	< .0001**	41.71
	G × E	84	405496.87	< .0001**	14.16
Fruit weight (g)	E	2	41.72	< .0001**	12.53
	G	42	272.85	< .0001**	81.95
	G × E	84	18.37	< .0001**	5.51
Fruit length (cm)	E	2	17.92	< .0001**	7.59
	G	42	206.98	< .0001**	87.67
	G × E	84	11.17	< .0001**	4.73
Fruit width (mm)	E	2	195.83	< .0001**	26.11
	G	42	513.29	< .0001**	68.45
	G × E	84	40.70	< .0001**	5.42
Pericarp thickness (mm)	E	2	3.62	< .0001**	26.36
	G	42	7.95	< .0001**	57.90
	G × E	84	2.16	< .0001**	15.73

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

Table 4a. Mean ($\bar{X}$), regression coefficient (b_i) and deviation from regression (S^2d_i) for plant height (cm)

S. No.	Codes	E1	E2	E3	Overall mean ($\bar{X}$)	b_i	S^2d_i
1	G1	88.85	81.90	81.11	83.95	0.27	-27.12
2	G2	128.37	107	87.34	107.57	1.37	-20.38
3	G3	133.88	107.77	76.23	105.96	1.90	27.22
4	G4	111.78	85.88	78.89	92.18	1.14	-9.25
5	G5	90.76	82.56	75.34	82.88	0.51	-29.17
6	G6	86.34	86.45	80.56	84.45	0.17	-21.46
7	G7	116.80	93.45	85.78	98.68	1.07	-18.34
8	G8	113.40	99.45	70.56	94.47	1.39	70.63
9	G9	102	96.78	75.11	91.30	0.85	53.74
10	G10	132.42	108.87	82.08	107.79	1.66	5.85
11	G11	122.78	102.89	87.45	104.37	1.18	-28.00
12	G12	116.78	104.67	95.22	105.56	0.72	-29.38
13	G13	125.96	109.84	84.45	106.75	1.36	27.92
14	G14	123.87	104.88	84.56	104.43	1.30	-12.51
15	G15	127.01	98.82	84.29	103.37	1.45	-27.87
16	G16	103.80	95.44	90.96	96.73	0.43	-30.11
17	G17	119.23	94.67	79.71	97.87	1.34	-30.22
18	G18	110.23	104.17	84.11	99.51	0.83	35.38
19	G19	114.20	99.34	77.11	96.88	1.21	11.25
20	G20	126.12	94.97	81.84	100.98	1.52	-20.31
21	G21	116.41	102.45	84.95	101.27	1.04	-11.15
22	G22	108.27	88.45	72.11	89.61	1.21	-26.38
23	G23	131.45	94.72	88.34	104.84	1.51	37.81
24	G24	103.34	91.67	80	91.67	0.77	-25.50
25	G25	102.65	91.09	75	89.58	0.91	-10.79
26	G26	116.93	103.56	81.45	100.65	1.16	16.66
27	G27	115.70	102	101.89	106.53	0.49	-12.56
28	G28	108.67	90.14	79.56	92.79	0.99	-30.01
29	G29	115.85	91.44	89.78	99.02	0.92	15.54
30	G31	108.06	98.67	82.89	96.54	0.82	-5.91
31	G32	132.67	124.29	120.78	125.91	0.40	-29.51
32	G33	108.20	87.67	75.67	90.51	1.10	-30.08
33	G34	95.16	85.	77.56	85.91	0.59	-29.95
34	G35	111.34	86.67	91.22	96.41	0.74	68.71
35	G36	113.38	89.32	101.34	101.35	0.49	151.30*
36	G37	125.90	90.67	89.11	101.89	1.31	73.58
37	G38	125.93	89.37	77.23	97.51	1.68	-1.79
38	G39	110.87	107.35	95.78	104.67	0.48	-8.46
39	G40	112	84.78	79.56	92.11	1.13	4.25
40	G41	114.23	84.60	86.23	95.02	1.01	70.44
41	G42	107.34	92.45	87.11	95.63	0.69	-26.35
42	G43	105.22	82.15	73.03	86.80	1.10	-23.30
43	G30	106.64	92.34	89.75	96.24	0.59	-20.23
Range		**86.34 - 133.88**	**81.90 - 124.29**	**70.56 - 120.78**	**82.88 - 125.91**		
Mean		**113.74**	**95.60**	**84.26**	**97.86**		
LSD ($P \leq 0.05$)		19.56	12.95	13.49	9.70		
LSD ($P \leq 0.01$)		25.92	17.17	17.88	12.78		
SE of b_i		-	-	-	-	0.26	

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

Table 4b. Mean ($\bar{X}$), regression coefficient (b_i) and deviation from regression (S^2d_i) for plant spread (cm)

S. No.	Codes	E1	E2	E3	Overall mean ($\bar{X}$)	b_i	S^2d_i
1	G1	62.05	58.45	55.17	58.56	0.27	-10.04
2	G2	85.79	63.29	50.55	66.54	1.37	1.86
3	G3	76.18	64.00	46.12	62.10	1.16	-2.31
4	G4	76.46	63.71	50.00	63.39	1.03	-9.43
5	G5	62.33	56.63	49.75	56.23	0.49	-9.60
6	G6	82.98	77.25	55.95	72.06	1.04	35.64*
7	G7	77.59	60.17	53.13	63.63	0.95	4.95
8	G8	77.89	68.43	48.28	64.87	1.14	13.09
9	G9	85.67	72.33	50.52	69.51	1.36	5.83
10	G10	86.20	65.13	48.38	66.57	1.47	-8.62
11	G11	80.88	72.90	49.97	67.92	1.19	33.05*
12	G12	83.15	66.82	53.48	67.82	1.15	-9.44
13	G13	88.07	73.75	56.56	72.79	1.22	-7.36
14	G14	69.21	59.27	48.71	59.06	0.79	-9.73
15	G15	69.65	57.12	49.73	58.83	0.78	-6.79
16	G16	71.32	58.95	49.85	60.04	0.83	-9.01
17	G17	68.03	57.47	45.88	57.13	0.86	-9.49
18	G18	69.63	56.94	48.39	58.32	0.83	-8.16
19	G19	74.36	64.10	46.01	61.49	1.10	3.06
20	G20	67.30	52.02	44.11	54.48	0.90	-2.97
21	G21	67.54	59.26	46.21	57.67	0.82	-4.91
22	G22	65.59	53.43	46.61	55.21	0.74	-6.46
23	G23	81.64	58.82	49.37	63.27	1.26	14.70
24	G24	87.78	66.38	50.95	68.37	1.43	-6.49
25	G25	78.49	63.91	49.06	63.82	1.14	-9.74
26	G26	75.80	61.86	50.28	62.65	0.99	-9.71
27	G27	89.24	72.66	58.52	73.47	1.19	-9.76
28	G28	76.51	64.46	51.94	64.30	0.95	-9.73
29	G29	62.96	56.13	49.83	56.31	0.51	-10.05
30	G31	87.09	72.45	54.56	71.36	1.26	-6.76
31	G32	79.98	68.15	57.43	68.52	0.87	-10.03
32	G33	78.73	61.77	47.28	62.59	1.22	-9.76
33	G34	76.90	65.98	53.26	65.38	0.92	-8.86
34	G35	83.25	70.41	56.83	70.17	1.02	-9.56
35	G36	76.17	63.39	55.00	64.85	0.82	-7.88
36	G37	72.67	57.14	51.95	60.58	0.81	5.25
37	G38	79.56	69.72	52.23	67.17	1.06	2.45
38	G39	77.61	64.37	53.22	65.07	0.95	-9.81
39	G40	77.45	56.99	49.28	61.24	1.10	12.78
40	G41	75.90	55.18	47.99	59.69	1.09	15.99
41	G42	75.78	63.23	52.00	63.67	0.92	-10.01
42	G43	73.16	56.39	46.60	58.72	1.03	-4.05
43	G30	75.04	64.00	49.83	62.96	0.98	-7.31
Range		**62.05 - 89.24**	**52.02 - 77.25**	**44.11 - 58.52**	**54.48 - 73.47**		
Mean		**76.50**	**63.14**	**50.72**	**63.45**		
LSD ($P \leq 0.05$)		9.32	10.33	6.99	5.36		
LSD ($P \leq 0.01$)		12.35	13.69	9.27	7.06		
SE of b_i		-	-	-		0.15	

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

The stability of genotypes based on regression coefficient and deviation from regression for plant height was given in Table 4a. The genotype S 343 (G32) had maximum plant height followed by IS 262 (G10), PAU 114 (G2), IS 261 (G13) and PL 412 (G27) across the environments. The genotype namely S 343 (G32) had non significant deviation and regression coefficient less than one (0.27) indicating that genotype was performed best under unfavorable environments, while the genotypes IS 262 (G10) and PAU 114 (G2) were suitable for favorable environments. The genotype PAU 212 (G3) had significantly higher plant height in E_1; similarly the genotypes S 343 (G32) and IS 261 (G13) had significantly higher plant heights in E_2, while the genotypes S 343 (G32), PL 412 (G27) and SL 473 (G36) had higher plant height in E_3. A similar study was also conducted by CABRAL *et al.* (2017) finds the differences in plant height over the two distinct environments.

The genotypes AC 102 (G6), IS 261 (G13), PL 412 (G27), AC 101 (G31), SL 475 (G35) and FL 201 (G9) had significantly higher mean values for plant spread across the environments (Table 4b). The genotype FL 201 (G9) had regression coefficient >1.0 and non-significant deviation from regression showing the suitability of this genotype for favorable environments. In E_1, the genotypes IS 262 (G10), IS 261 (G13) and AC 101 (G31) had significant higher plant spread. However, AC 102 (G6) and IS 261 (G13) had significant higher plant spread in E_2 and PL 412 (G27) had significant higher plant spread in E_3. Similar studies were conducted by GURUNG *et al.* (2012) and DATTA and DEY (2009), they found significant G×E interaction for plant spread.

The genotypes AC 101 (G31), SL 466 (G33) and YL 581 (G42) had significantly higher number of primary branches plant^{-1} in all the three environments (Table 5a). The genotypes AC 101 (G31) and YL 581 (G42) had regression coefficient >1.0 and non-significant deviation from regression indicating suitability of these genotypes for favorable environments. The genotype PP 414 (G28) had significantly higher number of primary branches in E_1, similarly in E_3 the genotypes IS 263 (G12), AC 101 (G31) and YL 581 (G41) had significantly higher number of primary branches. The genotype PC 408 (G26) had regression coefficient close to one (1.02) and non-significant deviation from regression, thus showed general adaptability to all the three environments. The present results were confirmed by the study of SENAPATI and SARKAR (2002) they found non-significant interactions for number of primary branches plant^{-1}. As far as days to first picking is concerned, the genotypes FL 201 (G9), KC 302 (G14), KC 303 (G15), KC 304 (G16), KC 305 (G17), KC 310 (G22) and PL 412 (G27) had significantly lower values than grand mean indicated that these genotypes were preferred for earliness while, S 343 (G32), SL 466 (G33), SL 468 (G34), SU 478 (G37) and VR 521 (G41) had significantly higher mean values exhibited that these genotypes were not suitable for earliness (Table 5b). All the former genotypes coped with regression value <1.0 represented better performance of genotypes under unfavorable environments. In E_1, the genotype KC 308 (G20) had significantly lower value than mean showed its suitability for earliness in this environment. Similarly, genotype KC 303 (G15) in E_2 and KC 309 (G21) in E_3 had significantly lower values than mean. Similar findings on variability among genotypes related to days to first picking observed by MUNSHI *et al.* (2000) and SAMNOTRA *et al.* (2011).

The eleven genotypes had significant higher values than grand mean, among them genotypes PG 417 (G29) and SU 478 (G37) had highest number of fruits plant^{-1} (Table 6a). The genotypes DL161 (G8) and S 343 (G32) had significantly higher mean value and regression

Table 5a. Mean ($\bar{X}$), regression coefficient (b_i) and deviation from regression (S^2d_i) for number of primary branches

S. No.	Codes	E1	E2	E3	Overall mean ($\bar{X}$)	b_i	S^2d_i
1	G1	3.00	2.33	4.33	3.22	1.59	0.40*
2	G2	3.00	4.33	5.00	4.11	1.59	0.43*
3	G3	3.00	3.33	3.33	3.22	0.23	-0.05
4	G4	3.67	2.00	5.00	3.56	1.94	2.09**
5	G5	2.67	2.33	3.67	2.89	1.12	0.06
6	G6	2.67	2.00	3.67	2.78	1.25	0.34*
7	G7	3.00	2.67	6.00	3.89	3.18	0.40*
8	G8	2.33	2.67	4.33	3.11	1.93	-0.09
9	G9	2.67	2.33	4.33	3.11	1.82	0.15
10	G10	3.67	2.67	4.00	3.44	0.69	0.57*
11	G11	2.00	4.00	3.00	3.00	0.33	1.83**
12	G12	2.00	2.67	5.33	3.33	3.18	-0.10
13	G13	3.00	3.00	4.33	3.44	1.36	-0.06
14	G14	2.67	2.67	3.33	2.89	0.68	-0.09
15	G15	2.67	4.33	3.33	3.44	0.10	1.30**
16	G16	2.67	3.00	2.67	2.78	-0.17	-0.04
17	G17	4.00	2.67	3.33	3.33	-0.22	0.76**
18	G18	3.00	2.33	2.67	2.67	-0.11	0.11
19	G19	2.67	3.00	3.67	3.11	0.91	-0.09
20	G20	2.67	3.67	3.00	3.11	-0.01	0.42*
21	G21	2.00	4.67	4.67	3.78	1.79	2.64**
22	G22	3.00	2.67	3.00	2.89	0.17	-0.04
23	G23	3.00	3.67	4.67	3.78	1.47	-0.03
24	G24	2.33	3.67	4.33	3.44	1.59	0.43*
25	G25	2.67	2.00	4.00	2.89	1.60	0.40*
26	G26	2.67	3.67	4.00	3.44	1.02	0.23
27	G27	3.00	3.33	4.67	3.67	1.59	-0.10
28	G28	4.33	3.67	3.00	3.67	-1.13	-0.00
29	G29	3.00	3.67	3.33	3.33	0.11	0.11
30	G31	3.67	3.67	6.33	4.56	2.73	0.06
31	G32	2.67	4.67	4.00	3.78	0.67	1.69**
32	G33	3.00	4.67	5.67	4.44	2.15	0.69**
33	G34	3.33	2.67	4.00	3.33	0.91	0.27
34	G35	2.67	3.67	3.33	3.22	0.33	0.35*
35	G36	3.00	2.33	4.67	3.33	1.94	0.48*
36	G37	3.33	2.67	2.67	2.89	-0.45	0.07
37	G38	3.00	2.67	3.33	3.00	0.46	-0.01
38	G39	3.67	2.67	3.33	3.22	0.01	0.42*
39	G40	2.33	2.00	2.67	2.33	0.46	-0.01
40	G41	3.00	3.00	4.33	3.44	1.37	-0.06
41	G42	3.33	3.67	5.67	4.22	2.27	-0.09
42	G43	3.00	2.33	3.00	2.78	0.23	0.16
43	G30	3.33	5.33	4.33	4.33	0.33	1.83**
Range		**2.00 - 4.33**	**2.00 - 5.33**	**2.67 - 6.33**	**2.33 - 4.56**		
Mean		**2.94**	**3.14**	**3.98**	**3.35**		
LSD ($P \leq 0.05$)		0.94	0.76	0.95	0.74		
LSD ($P \leq 0.01$)		1.24	1.00	1.26	0.98		
SE of b_i		-	-	-	-	0.91	

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

Table 5b. Mean ($\bar{X}$), regression coefficient (b_i) and deviation from regression (S^2d_i) for days to first picking

S. No.	Codes	E1	E2	E3	Overall mean ($\bar{X}$)	b_i	S^2d_i
1	G1	138.67	90.00	69.00	99.22	1.30	-14.31
2	G2	135.00	104.00	74.67	104.56	1.09	-10.49
3	G3	127.00	104.33	72.33	101.22	0.98	44.15
4	G4	128.33	90.33	69.33	96.00	1.09	-33.94
5	G5	135.00	84.67	68.67	96.11	1.25	22.60
6	G6	118.33	89.33	64.33	90.67	0.98	-23.58
7	G7	123.33	100.33	61.33	95.00	1.10	116.19*
8	G8	122.67	96.33	73.33	97.44	0.90	-24.74
9	G9	108.00	81.00	65.67	84.89	0.78	-35.14
10	G10	131.33	96.33	73.67	100.44	1.06	-35.46
11	G11	114.00	87.33	72.00	91.11	0.78	-35.28
12	G12	109.33	100.00	79.33	96.22	0.53	19.33
13	G13	122.00	79.33	71.33	90.89	0.97	49.82
14	G14	104.67	78.00	67.33	83.33	0.70	-26.96
15	G15	96.33	69.67	68.00	78.00	0.55	19.72
16	G16	95.00	74.67	66.33	78.67	0.54	-31.04
17	G17	117.67	70.33	66.00	84.67	1.00	121.17*
18	G18	113.33	90.00	68.33	90.56	0.82	-22.91
19	G19	103.00	95.67	64.67	87.78	0.66	138.37*
20	G20	94.00	96.33	66.00	85.44	0.46	215.83**
21	G21	111.33	85.67	58.67	85.22	0.95	-5.32
22	G22	95.33	89.33	66.67	83.78	0.50	53.60
23	G23	117.67	89.33	68.00	91.67	0.91	-32.23
24	G24	129.33	98.00	66.00	97.78	1.15	3.34
25	G25	136.00	102.67	73.33	104.00	1.14	-17.23
26	G26	125.67	95.67	65.67	95.67	1.09	-3.62
27	G27	100.33	84.00	72.00	85.44	0.52	-34.82
28	G28	147.33	96.00	76.33	106.56	1.33	1.71
29	G29	151.33	113.33	86.33	117.00	1.19	-32.84
30	G31	132.67	98.67	73.33	101.56	1.09	-31.29
31	G32	162.33	99.33	98.33	120.00	1.25	327.12**
32	G33	154.33	110.33	81.00	115.22	1.35	-34.70
33	G34	156.00	104.00	91.67	117.22	1.22	63.93
34	G35	135.67	93.00	70.67	99.78	1.21	-31.28
35	G36	127.33	100.33	68.00	98.56	1.07	24.49
36	G37	154.00	113.33	90.33	119.22	1.18	-34.36
37	G38	151.00	84.00	71.00	102.00	1.52	168.84*
38	G39	138.67	83.33	69.00	97.00	1.32	64.65
39	G40	110.00	81.67	74.00	88.56	0.68	-11.01
40	G41	155.00	113.00	76.67	114.89	1.43	-9.68
41	G42	121.33	83.00	69.00	91.11	0.98	-11.58
42	G43	142.33	94.33	67.67	101.44	1.38	-33.15
43	G30	128.00	90.33	70.33	96.22	1.07	-32.75
Range		**94.00 - 162.33**	**69.67 - 113.33**	**58.67 - 98.33**	**78.00 - 120.00**		
Mean		**126.05**	**92.57**	**71.76**	**96.79**		
LSD ($P \leq 0.05$)		23.29	14.07	10.22	11.16		
LSD ($P \leq 0.01$)		30.87	18.65	13.54	14.70		
SE of b_i		-	-	-		0.19	

coefficient <1 indicating their suitability for unfavorable environments. The genotypes PG 417 (G29), AC 101 (G31), SL 466 (G33), SL 468 (G34), SL 473 (G36), SU 478 (G37) and VR 521 (G41) had significantly higher mean values across the three environments. In E_1 highest number of fruits plant^{-1} observed in PG 417 (G29), followed by SL 468 (G34) and VR 521 (G41). Similarly in E_2 the genotypes PG 417 (G29) followed by VR 521 (G41) and SL 473 (G36) had significantly higher number of fruits plant^{-1}. The genotypes PG 417 (G29) had highest number of fruits plant^{-1} followed by VR 521 (G41) and SU 478 (G37). Significant interactions of genotypes with environments for fruits plant^{-1} were observed by NSABIYERA *et al.* (2012) and CABRAL *et al.* (2017). For the fruit yield plant^{-1} ten genotypes had significantly higher mean values than grand mean (Table 6b). The genotypes PAU 114 (G2), IS 267 (G11), Punjab Sindhuri (G30) and S 343 (G32) had significantly higher fruit yield across the three environments. Among these, genotype PAU 114 (G2) had regression coefficient more than one (1.08) but had significant deviation, hence had more vulnerability to unpredictable response arising from G×E interactions under poor environments. The other genotypes had non-significant deviation and >1 regression coefficient, indicating their performance was better under favorable environments. In E_1 only the genotypes S 343 (G32) and PL 412 (G27) had significantly higher yield than the check Punjab Sindhuri. Similarly in E_2 the genotypes S 343 (G32) followed by PAU 114 (G2) and IS 267 (G11) had highest yield than check Punjab Sindhuri. In E_3, the genotype S 343 (G32) followed by PAU 114 (G2) and FL 201 (G9) had highest yield plant^{-1}. These results are in accordance with the findings of the KAUR (2014), who reported that S 343 had highest fruit yield plant^{-1}.

Based on mean at LSD 5%, eleven genotypes had higher mean values for fruit weight over the grand mean. The maximum fruit weight was given by the genotypes FL 201 (G9) and KC 309 (G21). On the contrary, the genotypes PG 417 (G29) and VR 521 (G41) had least mean fruit weight. The genotype KC 309 (G21) had regression coefficient >1.0 and non-significant deviation from regression, indicating suitability of this genotype for favorable environments (Table 7a). In E_1, highest fruit weight was observed in the genotypes FL 201 (G9) followed by KC 309 (G21) and YL 582 (G43) whereas in E_2, the genotypes FL 201 (G9) had highest fruit weight followed by AC 102 (G6) and YL 581 (G42). Similarly, in E_3 the genotype FL 201(G9) had highest fruit weight followed by YL 582 (G43) and KC 309 (G21). The genotypes PAU 115 (G1) and IS 262 (G10) indicated the stable performance and general adaptability for fruit weight in all the three environments as their regression coefficient close to one (1.04). The findings by KUMAR *et al.* (2003) and DHALIWAL *et al.* (2014) revealed that environment had significant impact on the fruit weight.

Nine genotypes had significantly greater mean value than grand mean for fruit length. Among these, genotypes AC 102 (G6) and FL 201 (G9) had highest fruit length. The genotypes US 501 (G38) and YL 582 (G43) had significantly higher mean value and regression coefficient <1.0 indicating their suitability for unfavorable environments. The performance of genotype PAU 212 (G3) can’t be predicted under poor environments due to significant deviation from regression (Table 7b). In E_1 the genotype FL 201 (G9) had significantly highest fruit length followed by PAU 212 (G3) and AC 102 (G6). The genotype FL 201 (G9) had significantly highest fruit length in E_2 and E_3 followed by AC 102 (G6). CABRAL *et al.* (2017) observed significant variation regarding the fruit length among two distinct environments revealed significant G×E interactions. It was exhibited that thirteen genotypes had significantly higher

Table 6a. Mean ($\bar{X}$), regression coefficient (b_i) and deviation from regression (S^2d_i) for number of fruits plant^{-1}

S. No.	Codes	E1	E2	E3	Overall mean ($\bar{X}$)	b_i	S^2d_i
1	G1	169.45	169.71	163.32	167.49	0.09	-99.86
2	G2	217.74	218.85	118.96	185.18	1.48	1803.75**
3	G3	159.84	138.15	102.56	133.52	0.88	-57.20
4	G4	158.65	139.87	99.33	132.62	0.90	-0.25
5	G5	118.29	108.27	107.12	111.23	0.17	-96.93
6	G6	134.76	128.89	95.27	119.64	0.60	43.78
7	G7	187.40	166.38	148.23	167.34	0.60	-108.05
8	G8	314.27	302.17	260.00	292.15	0.82	78.18
9	G9	67.50	64.90	62.37	64.92	0.08	-108.07
10	G10	221.27	178.34	125.36	174.99	1.47	-65.26
11	G11	341.59	306.85	234.40	294.28	1.63	219.81
12	G12	158.72	132.30	124.62	138.54	0.53	-62.10
13	G13	173.08	163.68	134.36	157.04	0.59	-25.04
14	G14	111.19	91.86	86.39	96.48	0.39	-82.87
15	G15	129.66	114.76	110.94	118.45	0.29	-91.75
16	G16	216.80	213.82	210.77	213.79	0.09	-108.05
17	G17	149.31	144.76	134.54	142.87	0.23	-100.84
18	G18	209.07	144.17	142.34	165.19	1.05	469.41*
19	G19	234.55	165.50	159.10	186.39	1.18	450.64*
20	G20	107.23	102.56	89.28	99.69	0.27	-92.36
21	G21	88.75	80.21	72.03	80.33	0.26	-108.00
22	G22	120.01	113.95	106.00	113.32	0.21	-106.81
23	G23	139.01	125.11	150.68	138.27	-0.17	160.90
24	G24	235.89	221.20	103.55	186.88	1.99	1950.33**
25	G25	159.82	132.94	109.59	134.12	0.77	-108.05
26	G26	281.48	209.04	143.79	211.44	2.17	-107.75
27	G27	202.97	163.86	194.13	186.98	0.16	680.54**
28	G28	385.27	307.24	221.58	304.70	2.51	-55.12
29	G29	598.08	524.68	503.36	542.04	1.47	246.71
30	G31	339.39	267.28	213.07	273.25	1.95	-91.41
31	G32	232.15	223.34	218.06	224.51	0.22	-106.90
32	G33	345.58	269.53	192.23	269.11	2.35	-88.59
33	G34	449.78	340.84	280.09	356.90	2.62	127.31
34	G35	207.36	171.90	149.02	176.09	0.90	-94.77
35	G36	378.66	349.99	225.61	318.09	2.32	1735.60**
36	G37	419.03	316.44	315.44	350.30	1.62	1398.13**
37	G38	159.14	75.16	67.20	100.50	1.44	714.23**
38	G39	205.09	156.41	150.83	170.77	0.85	154.48
39	G40	209.20	171.64	123.50	168.11	1.31	-65.92
40	G41	428.27	386.26	316.77	377.10	1.70	89.32
41	G42	130.82	109.36	96.89	112.36	0.52	-100.25
42	G43	142.06	101.78	78.28	107.38	0.99	-80.80
43	G30	239.12	177.63	139.33	185.36	1.54	-60.17
Range		**67.5 - 598.08**	**64.90 - 524.68**	**62.37 - 503.36**	**64.92 - 524.04**		
Mean		**225.05**	**190.50**	**160**	**191.85**		
LSD ($P \leq 0.05$)		33.32	26.47	27.16	26.47		
LSD ($P \leq 0.01$)		44.16	35.08	36.00			
SE of b_i		-	-	-		0.4	

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

Table 6b. Mean ($\bar{X}$), regression coefficient (b_i) and deviation from regression (S^2d_i) for fruit yield g plant^{-1}

S. No.	Codes	E1	E2	E3	Overall mean ($\bar{X}$)	b_i	S^2d_i
1	G1	487.53	426.89	364.87	426.43	0.51	-506.54
2	G2	841.81	822.82	586.16	750.26	1.08	5682.16**
3	G3	485.36	438.62	287.15	403.71	0.83	699.57
4	G4	735.89	502.50	373.50	537.30	1.48	2685.12*
5	G5	542.69	447.54	353.56	447.93	0.78	-462.88
6	G6	642.10	547.95	345.95	512.00	1.23	528.41
7	G7	461.06	411.28	376.29	416.21	0.35	-437.23
8	G8	781.30	560.43	448.17	596.63	1.36	2751.09*
9	G9	575.77	541.95	491.86	536.52	0.35	-512.92
10	G10	792.64	554.61	323.26	556.84	1.93	-83.99
11	G11	757.15	647.04	426.37	610.19	1.38	512.66
12	G12	554.82	445.43	381.26	460.50	0.71	110.00
13	G13	616.94	538.28	375.22	510.15	1.01	100.64
14	G14	440.29	416.81	349.55	402.22	0.38	-319.42
15	G15	420.15	408.21	315.24	381.20	0.44	313.56
16	G16	420.31	429.68	378.64	409.55	0.18	4.99
17	G17	510.98	542.24	468.32	507.18	0.19	1174.29
18	G18	665.70	448.69	396.91	503.77	1.09	5530.40**
19	G19	469.69	443.15	383.86	432.23	0.36	-424.15
20	G20	441.93	403.69	349.51	398.38	0.38	-515.84
21	G21	553.61	453.43	359.39	455.48	0.79	-423.15
22	G22	463.77	415.84	393.77	424.46	0.29	-348.35
23	G23	492.99	394.92	427.49	438.47	0.25	2589.80*
24	G24	586.56	561.67	239.36	462.53	1.47	11081.68**
25	G25	740.33	566.33	377.50	561.39	1.50	-459.13
26	G26	572.77	473.08	273.58	439.81	1.25	319.28
27	G27	874.53	545.00	435.26	618.26	1.78	10856.03**
28	G28	619.92	556.88	355.24	510.68	1.11	1610.04*
29	G29	643.97	556.67	466.31	555.65	0.73	-492.23
30	G31	601.90	477.87	336.21	471.99	1.10	-514.34
31	G32	1019.86	844.35	668.96	844.39	1.45	-336.54
32	G33	693.50	555.95	270.70	506.72	1.76	1390.99
33	G34	544.63	427.80	286.93	419.79	1.07	-524.21
34	G35	759.33	552.77	424.06	578.72	1.37	1480.78
35	G36	584.25	529.69	271.09	461.68	1.32	4515.02**
36	G37	580.81	363.01	298.30	414.04	1.14	4861.63**
37	G38	616.78	350.82	260.37	409.32	1.45	6770.21**
38	G39	502.72	462.21	357.47	440.80	0.61	-102.60
39	G40	557.09	477.20	261.70	431.99	1.24	1393.22
40	G41	454.22	387.66	272.98	371.62	0.75	-366.39
41	G42	588.03	556.39	367.05	503.82	0.93	2576.74*
42	G43	825.85	534.77	329.51	563.38	2.03	2423.26*
43	G30	842.55	635.58	449.38	642.50	1.62	40.09
Range		**420.15 - 1019.86**	**350.82 - 844.35**	**239.36 - 668.96**	**371.62 - 844.39**		
Mean		**613.12**	**503.67**	**371.12**	**495.97**		
LSD ($P \leq 0.05$)		77.81	62.50	51.34	64.34		
LSD ($P \leq 0.01$)		103.13	82.84	68.04	84.74		
SE of b_i		-	-	-		0.3	

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

Table 7a. Mean ($\bar{X}$), regression coefficient (b_i) and deviation from regression (S^2d_i) for fruit weight (g)

S. No.	Codes	E1	E2	E3	Overall mean ($\bar{X}$)	b_i	S^2d_i
1	G1	4.10	3.22	2.65	3.33	1.04	-0.01
2	G2	4.83	4.26	3.35	4.15	1.06	-0.01
3	G3	4.25	3.68	3.30	3.74	0.68	-0.02
4	G4	5.78	5.20	3.17	4.72	1.88	0.30**
5	G5	6.24	5.14	3.77	5.05	1.77	-0.02
6	G6	6.27	4.57	4.13	4.99	1.53	0.26**
7	G7	3.50	3.29	3.04	3.28	0.33	-0.02
8	G8	3.31	2.36	2.23	2.63	0.77	0.09*
9	G9	10.51	8.85	8.39	9.25	1.52	0.23**
10	G10	4.53	3.61	3.08	3.74	1.04	0.01
11	G11	3.01	2.61	2.32	2.65	0.49	-0.02
12	G12	4.63	4.07	3.38	4.03	0.90	-0.02
13	G13	4.65	3.94	3.30	3.96	0.97	-0.02
14	G14	5.36	6.10	4.31	5.25	0.77	1.03**
15	G15	5.03	4.42	2.93	4.13	1.51	0.09*
16	G16	2.90	2.51	2.30	2.57	0.43	-0.02
17	G17	4.59	4.25	3.98	4.27	0.44	-0.02
18	G18	4.16	3.62	3.29	3.69	0.63	-0.02
19	G19	3.95	3.41	2.15	3.17	1.30	0.05
20	G20	6.57	4.58	3.91	5.02	1.90	0.29**
21	G21	8.65	6.80	4.55	6.67	2.95	-0.01
22	G22	5.82	4.70	3.78	4.77	1.47	-0.02
23	G23	4.53	4.18	3.34	4.02	0.85	0.01
24	G24	3.27	3.04	2.82	3.04	0.33	-0.03
25	G25	5.76	4.76	3.95	4.82	1.30	-0.02
26	G26	2.89	2.65	2.41	2.65	0.35	-0.03
27	G27	5.30	3.83	2.74	3.96	1.84	0.01
28	G28	2.59	2.32	1.43	2.11	0.84	0.03
29	G29	1.75	1.56	1.43	1.59	0.23	-0.02
30	G31	3.28	2.97	2.61	2.95	0.48	-0.03
31	G32	5.81	4.14	3.57	4.51	1.61	0.20**
32	G33	2.81	2.56	1.91	2.43	0.64	0.00
33	G34	1.89	1.76	1.52	1.72	0.26	-0.02
34	G35	5.50	4.21	2.55	4.09	2.12	-0.01
35	G36	2.60	2.00	1.70	2.10	0.64	-0.01
36	G37	2.10	1.63	1.45	1.73	0.47	-0.01
37	G38	5.55	5.17	4.37	5.03	0.85	0.00
38	G39	3.75	3.35	2.87	3.32	0.63	-0.02
39	G40	3.72	3.28	2.62	3.21	0.79	-0.02
40	G41	1.79	1.45	1.36	1.54	0.31	-0.01
41	G42	5.77	5.44	4.29	5.16	1.07	0.08*
42	G43	7.02	5.76	4.71	5.83	1.66	-0.01
43	G30	3.44	3.19	2.91	3.18	0.38	-0.03
Range		**1.75 - 10.51**	**1.45 - 8.85**	**1.36 - 8.39**	**1.54 - 9.25**		
Mean		**4.50**	**3.82**	**3.11**	**3.81**		
LSD ($P \leq 0.05$)		0.44	0.50	0.39	0.44		
LSD ($P \leq 0.01$)		0.59	0.67	0.51	0.57		
SE of b_i		-	-	-	-	0.28	

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

Table 7b. Mean ($\bar{X}$), regression coefficient (b_i) and deviation from regression (S^2d_i) for fruit length (cm)

S. No.	Codes	E1	E2	E3	Overall mean ($\bar{X}$)	b_i	S^2d_i
1	G1	7.16	6.41	6.05	6.54	1.24	-0.12
2	G2	6.81	6.46	6.35	6.54	0.53	-0.11
3	G3	9.86	6.76	6.52	7.71	3.91	0.48*
4	G4	8.08	6.68	6.36	7.04	1.97	-0.06
5	G5	8.17	6.68	5.98	6.94	2.44	-0.11
6	G6	9.81	8.31	7.73	8.62	2.35	-0.10
7	G7	7.04	6.49	6.43	6.65	0.72	-0.10
8	G8	6.71	5.42	4.97	5.70	1.97	-0.10
9	G9	12.68	11.81	11.00	11.83	1.82	-0.09
10	G10	6.61	6.29	5.49	6.13	1.17	-0.01
11	G11	5.21	5.14	4.94	5.10	0.29	-0.11
12	G12	6.26	6.14	5.55	5.98	0.72	-0.04
13	G13	6.66	6.50	6.30	6.49	0.38	-0.11
14	G14	5.42	5.21	4.79	5.14	0.66	-0.09
15	G15	6.89	6.43	6.18	6.50	0.78	-0.17
16	G16	5.94	5.55	5.29	5.59	0.72	-0.17
17	G17	6.78	6.28	6.16	6.41	0.70	-0.11
18	G18	6.41	6.00	5.43	5.95	1.04	-0.09
19	G19	6.84	5.53	5.16	5.84	1.91	-0.08
20	G20	7.18	6.98	6.41	6.86	0.79	-0.06
21	G21	6.89	6.28	6.27	6.48	0.73	-0.09
22	G22	6.31	6.11	5.33	5.92	1.00	0.00
23	G23	6.79	6.65	6.32	6.59	0.49	-0.10
24	G24	7.01	6.59	6.40	6.66	0.68	-0.17
25	G25	4.96	4.46	4.28	4.57	0.77	-0.11
26	G26	6.85	6.36	6.05	6.42	0.89	-0.17
27	G27	6.96	6.52	6.29	6.59	0.74	-0.17
28	G28	6.35	6.25	5.56	6.05	0.79	-0.01
29	G29	5.21	4.49	4.43	4.71	0.91	-0.09
30	G31	5.35	5.27	5.07	5.23	0.28	-0.11
31	G32	7.09	5.83	5.16	6.03	2.15	-0.17
32	G33	5.81	5.43	5.33	5.52	0.55	-0.11
33	G34	5.23	4.91	4.56	4.90	0.73	-0.11
34	G35	8.32	7.68	7.16	7.72	1.26	-0.11
35	G36	5.41	5.28	5.04	5.24	0.40	-0.11
36	G37	4.13	3.81	3.67	3.87	0.52	-0.17
37	G38	8.00	7.54	7.26	7.60	0.82	-0.17
38	G39	7.00	6.46	6.40	6.62	0.69	-0.10
39	G40	7.04	6.51	6.51	6.69	0.62	-0.09
40	G41	5.26	5.03	5.37	5.22	-0.06	-0.06
41	G42	8.36	7.83	7.24	7.81	1.20	-0.09
42	G43	7.63	7.41	7.19	7.41	0.48	-0.11
43	G30	6.41	6.28	6.16	6.28	0.28	-0.17
Range		**4.13 - 12.68**	**3.81 - 11.81**	**3.67 - 11.00**	**3.87 - 11.83**		
Mean		**6.86**	**6.28**	**5.96**	**6.37**		
LSD ($P \leq 0.05$)		1.26	0.86	0.65	0.55		
LSD ($P \leq 0.01$)		1.66	1.13	0.86	0.73		
SE of b_i		-	-	-		0.29	

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

Table 8a. Mean ($\bar{X}$), regression coefficient (b_i) and deviation from regression (S^2d_i) for fruit width (mm)

S. No.	Codes	E1	E2	E3	Overall mean ($\bar{X}$)	b_i	S^2d_i
1	G1	12.57	10.32	8.93	10.61	1.20	-0.09
2	G2	12.08	11.40	9.96	11.14	0.71	-0.19
3	G3	12.57	11.56	7.98	10.70	1.53	0.69
4	G4	13.87	12.01	10.17	12.02	1.22	-0.26
5	G5	13.97	12.73	11.71	12.80	0.75	-0.25
6	G6	14.82	12.86	10.45	12.71	1.45	-0.25
7	G7	9.92	9.43	8.57	9.30	0.45	-0.25
8	G8	10.52	8.80	6.71	8.67	1.26	-0.25
9	G9	16.13	14.95	12.54	14.54	1.19	-0.06
10	G10	11.77	9.33	8.59	9.90	1.05	0.29
11	G11	9.26	8.40	8.28	8.65	0.32	-0.16
12	G12	13.44	10.61	7.36	10.47	2.02	-0.26
13	G13	10.52	9.58	7.03	9.04	1.16	0.10
14	G14	14.82	13.22	11.68	13.24	1.04	-0.26
15	G15	13.72	12.28	8.91	11.64	1.60	0.24
16	G16	13.41	11.97	10.38	11.92	1.01	-0.26
17	G17	12.48	10.70	9.43	10.87	1.01	-0.19
18	G18	13.48	11.68	8.47	11.21	1.67	-0.02
19	G19	12.76	12.39	9.96	11.70	0.94	0.37
20	G20	13.70	12.69	11.19	12.53	0.84	-0.24
21	G21	15.46	14.34	11.19	13.66	1.43	0.31
22	G22	14.71	12.19	10.63	12.51	1.35	-0.05
23	G23	14.49	13.06	11.45	13.00	1.01	-0.26
24	G24	9.03	8.21	7.52	8.25	0.50	-0.26
25	G25	12.14	11.17	9.11	10.81	1.01	-0.10
26	G26	9.41	8.58	7.21	8.40	0.73	-0.23
27	G27	11.44	10.27	7.66	9.79	1.26	0.01
28	G28	10.46	9.42	8.32	9.40	0.71	-0.26
29	G29	6.62	6.35	7.17	6.71	-0.19	-0.08
30	G31	9.47	7.99	6.94	8.14	0.84	-0.22
31	G32	14.30	12.74	10.63	12.56	1.22	-0.23
32	G33	10.28	8.65	7.27	8.73	1.00	-0.24
33	G34	8.35	7.75	6.52	7.54	0.61	-0.21
34	G35	13.55	10.33	9.62	11.17	1.29	0.93*
35	G36	10.58	8.25	6.64	8.49	1.30	-0.13
36	G37	7.54	6.56	5.65	6.58	0.63	-0.26
37	G38	14.61	11.42	10.86	12.30	1.23	1.02*
38	G39	10.69	8.65	8.05	9.13	0.87	0.14
39	G40	11.18	9.09	7.42	9.23	1.24	-0.21
40	G41	7.31	6.77	6.01	6.70	0.43	-0.26
41	G42	13.61	12.36	11.53	12.50	0.69	-0.22
42	G43	11.94	10.82	10.37	11.05	0.52	-0.17
43	G30	10.69	9.54	7.86	9.36	0.94	-0.23
Range		**6.62 - 16.13**	**6.35 - 14.95**	**5.65 - 12.54**	**6.58 - 14.54**		
Mean		**11.95**	**10.50**	**8.93**	**10.46**		
LSD ($P \leq 0.05$)		1.29	1.57	1.46	0.91		
LSD ($P \leq 0.01$)		1.71	2.09	1.93	1.19		
SE of b_i		-	-	-		0.21	

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

Table 8b. Mean ($\bar{X}$), regression coefficient (b_i) and deviation from regression (S^2d_i) for pericarp thickness (mm)

S. No.	Codes	E1	E2	E3	Overall mean ($\bar{X}$)	b_i	S^2d_i
1	G1	1.37	1.13	0.76	1.09	1.49	0.00
2	G2	1.56	1.38	1.02	1.32	1.33	0.00
3	G3	1.16	1.13	1.05	1.11	0.29	0.00
4	G4	1.42	1.59	0.95	1.32	1.20	0.09**
5	G5	1.55	1.34	1.17	1.35	0.92	0.00
6	G6	1.45	1.30	1.18	1.31	0.66	0.00
7	G7	1.87	1.08	0.94	1.30	2.22	0.09**
8	G8	1.51	1.24	0.75	1.17	1.88	0.00
9	G9	1.92	1.70	1.48	1.70	1.06	0.00
10	G10	0.99	0.94	0.92	0.95	0.18	0.00
11	G11	1.03	1.01	0.89	0.98	0.35	0.00
12	G12	0.99	0.97	0.81	0.92	0.46	0.00
13	G13	1.22	0.96	0.80	0.99	1.02	0.00
14	G14	1.72	1.61	0.94	1.43	1.94	0.04**
15	G15	1.26	1.66	0.93	1.28	0.90	0.20**
16	G16	1.45	1.38	0.95	1.26	1.23	0.02**
17	G17	1.37	1.25	1.07	1.23	0.73	0.00
18	G18	1.52	1.21	0.82	1.18	1.72	0.00
19	G19	1.53	1.12	1.68	1.44	-0.43	0.15**
20	G20	1.67	1.34	1.10	1.37	1.38	0.00
21	G21	1.93	1.55	1.05	1.51	2.15	0.00
22	G22	1.64	1.39	1.15	1.40	1.19	0.00
23	G23	1.78	1.55	1.28	1.54	1.22	0.00
24	G24	1.43	1.12	0.85	1.13	1.41	0.00
25	G25	1.37	1.28	1.13	1.26	0.60	0.00
26	G26	0.93	0.73	0.86	0.84	0.13	0.02**
27	G27	1.42	1.00	0.87	1.10	1.33	0.02**
28	G28	0.81	0.65	0.53	0.66	0.68	0.00
29	G29	0.83	0.74	0.70	0.76	0.31	0.00
30	G31	0.84	0.80	0.74	0.79	0.23	0.00
31	G32	1.32	1.13	1.04	1.16	0.68	0.00
32	G33	1.18	0.81	0.64	0.88	1.30	0.01*
33	G34	0.83	0.80	0.73	0.78	0.24	0.00
34	G35	1.55	1.03	0.87	1.15	1.64	0.03**
35	G36	1.13	0.83	0.58	0.85	1.35	0.00
36	G37	1.07	0.83	0.44	0.78	1.55	0.00
37	G38	1.39	1.25	1.16	1.26	0.55	0.00
38	G39	1.31	1.07	0.99	1.12	0.77	0.00
39	G40	1.35	1.29	1.09	1.24	0.66	0.00
40	G41	0.92	0.71	0.62	0.75	0.74	0.00
41	G42	1.75	1.58	1.31	1.54	1.08	0.00
42	G43	1.75	1.62	0.79	1.38	2.37	0.06**
43	G30	1.27	1.19	1.13	1.20	0.34	0.00
Range		**0.81 - 1.93**	**0.65 - 1.70**	**0.44 - 1.68**	**0.66 - 1.70**		
Mean		**1.36**	**1.17**	**0.95**	**1.16**		
LSD ($P \leq 0.05$)		0.14	0.14	0.12	0.14		
LSD ($P \leq 0.01$)		0.18	0.18	0.15	0.19		
SE of b_i		-	-	-		0.46	

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

mean values across the environments for fruit width (Table 8a). Among these genotypes, FL 201 (G9) and KC 309 (G21) had highest mean values with non-significant deviation from regression and >1.0 regression coefficient indicated that these genotypes perform better under favorable environments. The genotypes KC 302 (G14), KC 304 (G16) and KC 311 (G 23) had high mean value and regression coefficient near to one (1.04, 1.01 and 1.01 respectively) thus showed moderate response to environmental changes. In E_1 the genotype FL 201 (G9) had significantly highest fruit width followed by KC 309 (G21) and KC 311 (G23). However, in E_2 FL 201 (G9) had highest fruit width followed by KC 309 (G21) and KC 302 (G14). In case of E_3 the highest fruit width was found in the genotype FL 201 (G9) followed by PAU 213 (G5) and KC 302 (G14). Similar findings were observed by KAUR (2014), reported that genotype FL 201 had higher fruit width followed by AC 102.

Twelve genotypes had significantly higher mean values of pericarp thickness above the grand mean. Among these genotypes, FL 201 (G9) and YL 581 (G41) had highest mean values with non-significant deviation from regression and close to one regression coefficient indicated that these genotypes were highly stable and adapted to all the three environments (Table 8b). In E_1, the genotype KC 309 (G21) had highest pericarp thickness followed by FL 201 (G9) and C 142 (G7). In case of E_2 highest pericarp thickness was found in the genotype FL 201 (G9) followed by KC 303 (G15) and YL 582 (G43). However in E_3 the genotype KC 307 (G19) had highest pericarp thickness followed by FL 201 (G9) and YL 581 (G41). Similar study was conducted by NGOZI *et al*. (2013) for genotypic stability and found that genotype × year effects were highly significant for pericarp thickness and also concluded its significant role for increasing fruit weight. This findings exhibits that parameters of interest in chilli that vary with environment may be improved by using suitable cropping season and management practices and therefore for commercial cultivation these genotypes would found useful as elite gene pool in future breeding programs or stable over a wide range of environments.

CONCLUSION

This study revealed that, the genotype S 343 was stable for fruit yield plant^{-1} in all the environments followed by PG 417 (except in E_1) and PL 412. The genotypes S 343 followed by check Punjab Sindhuri and PL 412 were better adapted for E_1 while for E_2, S 343 followed by PG 417 and Punjab Sindhuri showed better adaptability whereas S 343, PG 417 and PL 412 were stable and adapted in E_3. It was also observed that E_1 (November planted crop) was the best environment to evaluate yield and yield related attributes followed by E_2 and E_3, whereas E_2 (February planted crop) was the best environment when quality traits one of higher importance followed by E_3 and E_1. The promising genotypes found in the study could have the potential of being commercially exploited at the farmer's field especially for early and late season.

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MULTI-EKOLOŠKA EVALUACIJA GENOTIPOVA ČILI PAPRIKE ZA PRINOS I KOMPONENTE PRINOSA

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Izvod

Četrdeset tri genotipa čili paprike uključujući jednu kontrolu Punjab Sindhuri su ispitani za prinos i vezana svojstva u cilju određivanja stabilnosti i adaptabilnosti u tri različite sredine (Novembar prenete 2016, Februar prenete 2017 i April prenete 2017) na Punjab Poljoprivrednom Unirvezitetu, Ludhiana. Prosek (MS) u odnosu na genotip je bio značajan za sve ispitane osobine osim primarni broj grana. MS u odnosu na genotip x sredina je bio takođe značajan za sve ispitivane osobine. Genotip S 343 je identifikovan kao obečavajući za prinos ploda po biljci i visinu biljke u sve tri sredine, sledi PG 417 i PL 412 dok na bazi regresije genotip PAU 114 je bio adaptabilan kroz sredine za prinos ploda i težinu ploda. Utvrđeno je da genotip FL 201 ima najduži plod, veću širinu ploda i tanji pericarp u svim sredinama. Ovi genotipovi imaju potencijal da se komercijalno koriste naročito u ranoj i kasnoj sezoni.

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