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Genotype – Environment Interaction of Segregating and Non Segregating Generation of Four Tomato Crosses for Yield and Yield Attributing Characters

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Abstract

A study was conducted during 2013-2014 to assess the stability of genotypes for yield and yield attributing characters using P_1, P_2, F_1, F_2, B_1 and B_2 generations obtained each of the four tomato crosses viz. Cross-I (H7997 x CLN 1621 E), Cross- II (H7997 x BL 337), Cross - III (H7997 x Nagcarlan) and Cross- IV (H7997 x CLN 2366A) in four test environments. The highly significant environmental variance for almost all the characters suggested considerable difference among environments and their predominant effect on characters. The variance due to genotype was significant for most of the traits under study. Further, the hybrids H7997 x CLN 1621E, H7997 x Nagcarlan and H7997 x CLN2366A with high mean and non significant regression coefficient and deviations mean squares exhibited average stability for fruit yield per plant.

Key words : tomato, yield, yield attributing characters, stability analysis.

Introduction

Gene expression is subject to modification by the environment; therefore, genotypic expression of the phenotype is environmentally dependent (Kang, 7). The development of new cultivars involves breeding of cultivars with desired characteristics and the stability of these traits in target environments. Inconsistent genotypic responses to environmental factors such as temperature, soil moisture, soil type, or fertility level from location to location and year to year are a function of genotype - environment (GE) interactions. The present investigation with six generations obtained from four crosses was undertaken to study the G-E interaction with the objective of obtaining suitable varieties which could perform well over a spectrum of environment and also to identify suitable types suited to particular environment.

Linear regression slope as a measure of stability was considered by Finlay and Wilkinson (3). They suggested that a genotype was maximum stable, when its mean performance was high and regression of its performance over the environmental mean approached zero. Eberhart and Russell (4) observed that the deviation from regression, which is the non linear parameter, should also be taken into consideration along with the linear parameter, i.e. the regression coefficient while examining a variety for phenotypic stability. They observed that an ideal variety should possess regression coefficient equal to unity (b_i=1). This variety would have average response to the changes in environments. Regression value larger than unity indicates the sensitivity of the variety to the changes in environmental condition. Such a variety is termed as ‘below average stable’ and performs much better than its inherent potentially in high yielding environmental conditions, but the performance is poor in stress condition. Regression values less than unity signifies the insensitivity of the variety to changes in the environment and such an ‘above average stable’ variety is suitable specifically for stress environments. They further suggested that, a genotype should exhibit the least deviation from regression (S^2_{di}), to be stable one. The variance due to deviation from regression coefficient is primarily due to the uncontrollable causes and depends on the environment (Bains and Gupta, 1). In most of the studies on regression analysis of genotype x environment interaction, a linear relationship between genotype-environment interaction and environmental index has been reported (Freeman, 3).

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Materials and methods

The experiment was conducted at three different environments during offseason and one in *rabi* season, 2012-2013 at the Experimental Farm, Department of Horticulture, Assam Agricultural University, Jorhat, Assam, India. The farm is situated at 26°44´ N latitude and 94°l0´E longitude with elevation of 9l m above mean sea level. The weekly data obtained from the Department of Agricultural Meteorology, Assam Agricultural University, Jorhat, Assam, Indian on monthly mean maximum and minimum day temperatures during the period of investigation showed that mean maximum ranged from 21.90 – 44.00 ^{o}C and mean minimum temperature ranged from 9.50 – 30.00 ^{o}C. Four heat tolerant tomato genotypes *viz.*, CLN 1621E, BL 337, Nagcarlan and CLN 2366A, and one heat sensitive genotype H 7997 were utilised to generate four crosses. *viz.* Cross-I (H7997 x CLN 1621 E), Cross- II (H7997 x BL 337), Cross - III (H7997 x Nagcarlan) and Cross- IV (H997 x CLN 2366A) by attempting crosses during *rabi,* 2012 and these along with the parental lines H7997, CLN 1621 E, BL 337, Nagcarlan and CLN 2366A comprised the entries for experiment on generation mean analysis. H7997 was used as a recurrent parent in backcross I (B_1) and the heat tolerant genotypes were used as recurrent parent in backcross II (B_2).Two rows of each parent, $F_1$and backcross generations and 8 rows of each F_2 were planted in randomized block design with two replications. Inter and intra row was kept as 50 cm and 30 cm respectively. Observations were recorded on five randomly selected plants in each of P_1, P_2, 10 plants of F_1 and 40 plants in F_2 and 20 plants that of $B_1$and B_2 in each of the replications on days to first flowering, days to fruit maturity, number of primary branches plant, days from flowering to fruit setting, flower shed percentage, number of fruiting clusters per plant, number of fruits per plant and fruit yield per plant (kg/ plant). Six generations of each of the three crosses were screened in four planting dates *viz.,* 5th March (E_1), 10th April (E_2), 5th June (E_3) and 15th October (E_4). In E_3, the experiment was conducted inside polyhouse. The collected data were subjected to statistical analyses using Microsoft Excel 2007. The mean data of each environment was subjected to pooled analysis of variance over environments to study genotype - environment (GE) interaction and phenotypic stability by using the model given by Eberhart and Russell (1966). The three stability parameters were calculated to compare the genotypes: Mean (m_i) = The ideal genotype should have high mean over environments Regression coefficient (b_i) = The ideal genotype should have regression coefficient equal to 1.0. Deviation mean square ($S^2{}_{di}$) = The ideal genotype should have deviation mean square from linear regression equal to zero ($S^2{}_{di}$ = 0). To test the significance of difference of 'b_i' value from unity the procedure given by Gomez (5).

Results and discussion

The pooled analysis of variance for stability revealed that all the generations differed significantly for almost all the characters except for number of primary branches per plant, flower shed percentage and number of fruits per plant. The highly significant environmental variance for almost all the characters suggested considerable difference among environments and their predominant effect on characters.

The linear genotype-environment interactions were significant for all the characters except for number of primary branches per plant and number of fruiting clusters per plant. Non significance of GE linear components for these characters signifies that they do not show genetic difference for their regression on environmental index revealing the absence of divergent genetic response to the linear effect of the environment. It was further observed that the characters differed in respect to the contribution of linear components towards GE variance. In this investigation, for most of the characters the GE interaction is due to the linear and non linear components. However, linearity was more pronounced for most of the characters. This indicated that variation among the genotypes can be largely explained by differences in regression slopes for these characters. Thus response of the genotypes to the changing environments can be portrayed as orderly and predictable with respect to these characters. This obviously indicated that the accurate prediction of the phenotypic performances of the genotypes could be deduced for these characters. Among all the characters, number of primary branches per plant, number of fruits per plant and number of fruiting clusters per plant were the characters for which non linear component was observed to be mainly responsible for the GE interaction. This revealed that phenotypic performance of the genotypes for these characters cannot be accurately predicted. The importance of linear and non linear components of GE interaction in tomato were also reported by Ortiz and Lzquido (8) and Kallo *et al*., (6). Among the off seasons, E_1, E_2 and E_3, E_1 (mean average day temperature 30.86°C) was found to cause decisive improvement in most of the characters including yield.

In the present investigation, the hybrids H7997 x CLN 1621E, H7997 x Nagcarlan and H7997 x CLN2366A exhibited average stability for fruit yield per plant. Further, hybrid, H7997 x CLN 1621E exhibited average stability for number of primary branches per plant and number of fruiting clusters per plant. H7997 x Nagcarlan exhibited average stability for number of primary branches per plant and number of fruiting clusters per plant while hybrid H7997 x CLN 2366A also exhibited average stability for days to flowering, number of primary branches per plant, number of fruiting clusters per plant and number of fruits per plant. It was evident that the parents of the hybrids also exhibited average stability for few or more characters. Parent H7997 exhibited average stability for days to fruit maturity. Parent CLN 1621E exhibited average stability for number of primary branches per plant and number of fruits per plant. Nagcarlan exhibited average stability for number of primary branches per plant and number of fruiting clusters per plant. Thus it can be seen that the average stability exhibited by the hybrids H7997 x CLN 1621E, H7997 x Nagcarlan and H7997 x CLN2366A for various characters including fruit yield per plant could be due to transmission of linear and non linear stability from their respective parents. With respect to F_2 generations, the crosses except H7997 x CLN 2366A did not show average stability for fruit yield per plant. It also exhibited average stability for number of fruiting clusters per plant and number of fruits per plant. When the backcross generations were combined it could be seen that out of the four crosses, average stability for fruit yield per plant was evident in B_2 generation of cross H7997 x BL337 .This cross further exhibited average stability for few or more characters like days to flowering, number of primary branches per plant, flower shed percentage and number of fruiting clusters per plant. The recovery of the genotype of the recurrent parent's average stability for these characters might have induced average stability of the respective backcross. The evidence of stability in segregating generations like F_2 and backcross generations suggest transmission of stability characters and scope of subsequent selection facilitating development of phenotypically stable genotype.

The information generated from the present study shapes a framework for the development of heat tolerant tomato genotypes that could be successfully grown during the off season. The present investigation has provided some useful information regarding the performance of the six generations *viz.* P_1, P_2, F_1, F_2, B_1 and B_2 of four tomato crosses involving normal and heat tolerant parents. Among the parents CLN 1621E, Nagcarlan and CLN2366A showed better performance for a number of yield attributing characters. So these three parents could be used as parents in future breeding programme for heat tolerance. The crosses H7997 x CLN1621E, H7997 x Nagcarlan and H7997 x CLN2366A showed better performance for most of the yield and its component characters. These crosses also exhibited average stability for fruit yield per plant besides yield attributing and physiological characters. Further, these crosses resulted consistent heterosis for fruit yield per plant. Thus, these crosses can be potential combinations for development of heat tolerant hybrids or could be further advanced to develop homozygous heat tolerant tomato varieties.

Table 1. Pooled analysis of variance for generations of tomato crosses over environments for yield and yield attributing characters

Source of variation	D.F.	Mean squares							
		DTF	DFM	PB/P	DFFS	FS (%)	FC/P	FRTS/P	FY/P
Genotypes	20	20.98**	90.06**	0.2	3.86**	13.75	3.23**	12.07	29956.61**
Genotype + (Genotype x Envt.)	63	25.01**	285.46**	0.26	0.42	523.42**	0.84	124.52**	182965.2
Environment (linear)	1	1252.15**	14881.90**	1.04**	0.27	30879.90**	1.67	6898.53**	10267435**
Genotype x environment (linear)	20	5.23*	65.95*	0.24	0.98**	1554.75**	0.74	353.17	524884.70**
Pooled deviation	48	3.42**	22.07**	0.23**	0.11	7.36	0.82*	9.69*	11433.74**
Pooled error	84	2.84	14.09	0.06	0.69	3.97	0.42	5.02	8661.44

**Significant at 1 % level of probability, * Significant at 5 % level of probability; DTF-Days to flowering, DTFM-Days to fruit maturity, PB/P-Number of primary branches per plant, DFFS-Days from flowering to fruit setting, FS%-Flower shed percentage, FC/P-Number of fruiting clusters per plant, FP/P-Number of fruits per plant, FY/P- Fruit yield per plant

Table 2. : Estimates of stability parameters of generations of tomato crosses for yield and yield attributing characters

Genotypes	DTF				DTFM				PB/P				DFFS			
	m	b_i	S^2_{di}	Stability	m	b_i	S^2_{di}	Stability	m	b_i	S^2_{di}	Stability	m	b_i	S^2_{di}	Stability
P_1(H7997)	38.00	1.21	0.42	-	92.13	0.79	2.45	AVS	4.51	0.70**	-0.08	-	13.25	2.46**	-0.05	-
P_2(CLN1621E)	37.63	2.13*	19.29**	-	112.63	0.70	68.56**	-	5.71	1.27*	-0.08	AVS	11.25	1.62**	0.47	BAVS
P_3(BL337)	37.38	1.26	1.66	-	111.38	0.80	13.86	-	4.65	1.16	0.09	-	11.00	3.31**	-0.12	BAVS
P_4(Nagcarlan)	36.13	0.96	1.18	-	108.13	1.11	-1.67	-	5.53	0.79	-0.12	AVS	12.25	2.46**	-0.05	-
P_5 (CLN2366A)	36.63	0.9	2.44	-	101.13	1.71**	-4.89	BAVS	4.88	0.80	-0.05	-	11.50	3.31**	-0.12	-
P_1XP_2(Cross I)	33.88	0.79	7.41	-	100.25	0.67	42.50**	-	5.96	0.96	0.40	AVS	13.63	1.15	0.09	-
P_1XP_3(Cross II)	32.00	0.90	-1.35	AVS	105.13	0.79	93.37	-	5.33	0.98	0.19	-	10.25	3.46**	-0.05	-
P_1XP_4(Cross III)	31.25	1.14	2.53	AVS	103.63	1.28	14.09	-	5.70	0.86	0.38	AVS	10.00	8.31**	-0.12	-
P_1XP_5(Cross IV)	31.63	1.17	-0.32	AVS	99.63	1.49**	-1.03	BAVS	5.79	0.96	-0.10	AVS	11.50	3.62**	0.04	BAVS
F_2 (Cross I)	34.13	0.89	2.99	-	101.88	0.66	10.29	AVS	5.14	0.83	0.01	-	11.25	4.15**	-0.16	BAVS
F_2 (Cross II)	32.38	0.81	-0.63	AVS	106.38	1.09	-0.75	-	5.28	0.85	-0.05	-	10.00	8.31**	-0.12	BAVS
F_2 (Cross III)	32.63	0.88	-0.3	AVS	102.13	1.24	0.54	-	5.74	1.15	0.01	AVS	11.00	0.91	-0.18	AVS
F_2 (Cross IV)	34.38	1.09	0.29	-	106.38	0.75**	10.92	-	4.88	0.88	-0.07	-	11.00	3.31**	-0.12	BAVS
B_1 Cross1	31.50	0.86	-0.78	AVS	103.75	1.03	6.72	-	5.95	1.20	0.11	AVS	11.38	0.09	-0.18	-
B_2 Cross1	31.88	0.9	2.42	AVS	99.50	1.12	3.85	AVS	5.33	0.75	0.08	-	10.50	1.85**	-0.09	BAVS
B_1Cross11	32.00	0.93	1.99	AVS	97.63	1.25	7.21	AVS	5.70	1.19	0.21	AVS	11.00	0.91	-0.18	AVS
B_2Cross II	33.00	0.84	0.22	AVS	104.75	1.35	1.72	-	5.79	1.02	-0.13	AVS	10.25	-2.31**	0.16	BAVS
B_1 Cross III	31.88	0.77	0.71	AVS	96.63	0.86	31.58	AVS	5.57	1.11	-0.13	AVS	11.00	8.31**	-0.12	BAVS
B_2 Cross III	33.38	0.8	0.86	AVS	99.50	0.65	-2.99	AVS	6.06	1.31**	0.09	-	12.13	3.15**	0.05	-
B_1 Cross IV	32.25	0.91	1.07	AVS	93.38	0.98	12.5	AVS	5.86	0.88	-0.08	AVS	12.25	4.15**	-0.16	-
B_2 Cross IV	31.50	0.86	-0.17	AVS	96.00	0.68	6.74	AVS	6.23	1.34**	0.10	BAVS	10.50	0.00	-0.18	AVS

**Significant at 1 % level of probability, *Significant at 5 % level of probability; AV- average stable, BAVS- below average stable, AAVS- above average stable

Genotypes	FS%				FC/P				FRTS/P				FY/P			
	m	b_i	S^2_{di}	Stability	m	b_i	S^2_{di}	Stability	m	b_i	S^2_{di}	Stability	m	b_i	S^2_{di}	Stability
P_1(H7997)	34.38	1.22**	9.92	-	6.91	0.41**	-0.75	-	24.37	1.12	-2.22	-	0.78	1.20	-0.18	-
P_2(CLN1621E)	31.75	1.06	-3.02	-	9.03	1.37	0.90	-	30.75	0.85	8.07	AVS	1.07	1.24	-0.16	-
P_3(BL337)	31.50	1.01	2.72	-	9.20	1.14	0.69	AVS	29.37	1.05	10.43	-	0.85	0.47*	-0.17	-
P_4(Nagcarlan)	31.38	0.97	-2.27	-	9.16	1.10	0.27	AVS	29.62	0.74	3.47	-	1.07	0.76	-0.18	
P_5 (CLN2366A)	31.38	1.04	-1.18	-	8.65	1.26	0.19	-	30.12	0.81	1.53	-	1.09	0.93	-.0.18	AVS
P_1XP_2(Cross I)	27.75	1.02	11.93**	-	9.86	0.84	0.45	AVS	34.62	0.93	8.20**	-	1.32	0.93	-0.18	AVS
P_1XP_3(Cross II)	29.25	1.01	-0.55	AVS	9.26	0.62	-0.12	AVS	32.50	1.06	4.41	AVS	0.96	0.62**	-0.17	-
P_1XP_4(Cross III)	30.75	0.89	8.60	-	10.07	1.08	0.05	AVS	33.12	0.65	29.25**	-	1.38	0.92	-0.17	AVS
P_1XP_5(Cross IV)	29.38	1.00	-2.94	-	10.10	1.03	-0.68	AVS	33.87	1.20	1.15	AVS	1.45	0.98	-0.18	AVS
F_2 (Cross I)	29.00	1.02	11.93*	-	8.59	1.16	1.62	-	29.75	0.77	7.44	-	1.01	0.70*	-0.17	-
F_2 (Cross II)	28.13	1.01	-0.55	AVS	9.95	0.88	0.11	AVS	29.37	0.98	4.39	-	1.01	0.98	-0.17	-
F_2 (Cross III)	28.38	0.89**	8.60	-	8.81	1.08	-0.68	-	29.87	1.08	-2.22	-	1.04	1.13	-0.16	-
F_2 (Cross IV)	27.50	0.91	-2.94	-	8.53	0.89	-0.68	AVS	30.50	1.13	-1.17	AVS	1.10	1.17	-0.18	AVS
B_1 Cross1	29.75	0.83	21.05*	-	9.21	0.79	-0.34	AVS	32.87	1.11	18.61*	-	1.02	1.15	-0.18	-
B_2 Cross1	26.88	0.86	4.68	AVS	8.53	0.81	-0.86	-	29.62	1.09	16.86*	-	1.20	1.27	-0.17	AVS
B_1Cross11	28.50	1.03	0.85	AVS	8.94	1.18	-0.65	-	29.75	0.98	6.50	-	1.00	0.97	-0.17	-
B_2Cross II	27.38	0.93	-1.96	AVS	9.07	1.24	0.11	AVS	30.37	1.07	19.10*	-	1.11	1.04	-0.18	AVS
B_1 Cross III	29.13	0.96	14.01	-	9.45	1.02	-0.84	AVS	30.12	0.94	-2.29	-	1.04	1.10	-0.15	-
B_2 Cross III	29.13	1.05	10.87	AVS	8.94	1.24	3.73	-	29.12	1.12	12.26	-	0.98	1.17	-0.17	-
B_1 Cross IV	30.25	1.06	0.15	-	8.46	0.94	-0.66	-	30.12	1.25	6.77	-	1.02	1.34*	-0.17	-
B_2 Cross IV	30.13	1.05	0.40	-	9.53	0.94	-0.85	AVS	31.75	1.09	0.28	AVS	1.04	0.94	-0.18	-

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