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Genotype-environment interaction and stability analysis for yield and yield attributing characters in muskmelon

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ABSTRACT

Stability analysis in muskmelon for seven quantitative traits namely, days to first female flower, node to first female flower, fruit polar diameter, fruit equatorial diameter, fruit flesh thickness, TSS and fruit weight using Eberhart and Russell and Perkins and Jinks models showed significant genotypic mean square for all the characters indicating enough variability among the 24 muskmelon genotypes. Fourteen genotypes for days to first female flower, 23 for node to first female flower, 20 for fruit polar diameter, 16 for fruit equatorial diameter, 15 for TSS and 13 for fruit weight were found stable across the environments. Two genotypes namely, PMM-97-19 and PMM-251 were found stable across the five environments for all the characters under study. On over all basis, the desirable stable genotypes for fruit weight having superior fruit quality traits were Pusa Madhuras, PMM-249, PMM-97-19 and PMM-208. However, the genotype PMM-97-19 was found most superior genotype.

Key words: Muskmelon, genotype-environment interaction, and stability analysis.

INTRODUCTION

The genotype x environment interaction is an important aspect of both plant breeding programmes and the introduction of new crop cultivars (1). To identify stable variety/ genotype over different environments and to breed varieties separately for different regions of predictable environmental condition study of GxE interaction is felt essential as a preliminary step. Stability in performance is one of the most desirable properties of a genotype to be released as a variety for wide cultivation. Though studies have been conducted on genetic variability, combining ability and correlation coefficient on muskmelon (*Cucumis melo*) by various workers (2, 3, 4, 12) but, less efforts have been made to find out stable genotypes for different environmental conditions. The TSS, fruit weight, juiciness, flavour and yield are major attributes which affects consumers' preference and all these characters are highly influenced by environmental condition (5, 13). For evolving better and stable varieties in muskmelon, it is necessary to screen the available genotypes over wide range of agroclimatic condition for their direct commercial exploitation or effective utilization in breeding programmes. Since inadequate information is available in muskmelon regarding the stability of genotypes over different fertility regimes. Therefore, the present investigation was conducted to determine GxE interaction and stability parameters for yield and quality characters to identify the stable genotypes.

MATERIALS AND METHODS

The present experiment on muskmelon was conducted at Vegetable Research Centre (VRC) of the G.B. Pant University of Agriculture and Technology, Pantnagar during spring-summer season, 2002-2003. This included evaluation of 24 genotypes of muskmelon under five planting conditions (environments) i.e. E_1: Recommended dose of N:P:K (100 : 60 : 60 kg/ha), E_2: FYM (4kg/pit) equivalent to recommended dose of N, E_3: Half FYM (2 kg/pit) + half NPK of the recommended dose, E_4: Recommended dose of N:P:K (100 : 60 : 60 kg/ha) + staking and pinching of side shoots and allowing only one vine with two first set fruits, E_5: Control (no fertilizer).The experiment was laid out in a randomized complete block design (RBD) using 3 replications. Each environment represented one independent experiment. The seeds were sown in hills with spacing of 2 m between rows and 1 m between plants. Initially 3 seeds were sown at each hill and finally one plant/hill was maintained. Thus, each genotype was represented by 5 hills, each containing one plant. The full dose of FYM and half of NPK were applied at the time of sowing and the remaining half dose of NPK was applied before flowering. The fertilizers were applied at the individual

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hills. In staking experiment (E_4) plants were staked on slanting support before flowering and all the side branches were removed leaving only one vine (generally main shoot) with two first set fruits during flowering. All the standard cultural practices were maintained to raise the crops. The quantitative data were recorded on 5 randomly selected plants for each genotype in each replication. The stability analysis was done following Eberhart and Russell (6) and Perkins and Jinks (7) models.

RESULTS AND DISCUSSION

Table 1 shows pooled analysis of variance (Eberhart and Russell model) and Table 2 shows joint regression analysis of GxE interaction (Perkins and Jinks model) for 7 characters namely, days to first female flower, node to first female flower, fruit polar diameter, fruit equatorial diameter, fruit flesh thickness, TSS and fruit weight. The mean square due to genotypes was highly significant for all the characters under study. This showed enough variability among the 24 muskmelon genotypes. The environmental mean square was also highly significant for all the traits except node to first female flower and TSS. This indicated that the five environments were variable enough to induce significant changes in the above characters. The G × E interaction was highly significant for days to first female flower, fruit equatorial diameter, TSS and fruit weight in both the models. The G × E (linear) mean squares in case of Eberhart and Russell (Table 1) and heterogeneity between regression mean squares in case of Perkins and Jinks (Table 2) were significant for days to first female flower, node to first female flower, fruit equatorial diameter and TSS. However, the E (linear) was highly significant for days to first female flower, fruit polar diameter, fruit equatorial diameter, fruit flesh thickness and fruit weight. For node to first female flower and TSS, the E (linear) was significant. This indicated that the differences among the regression coefficients of the 24 muskmelon genotypes were present. The pooled deviation (Eberhart and Russell model) and remainder (Perkins and Jinks model) mean square were highly significant for all the characters. This suggested that for all the characters, there were unexplained deviations from the regression on the environmental index.

According to Eberhart and Russell model, a desirable and stable genotype is the one having high mean, b = 1 and s^2d = 0. Depending upon particular character, however, the desirable mean could be towards high level or low level. For example days to first female flower and node to first female flower, low mean could be considered as the desirable one. In case of Perkins and Jinks model, the regression coefficient (b) was used as measure of stability (sensitivity to the environmental variation) where observed mean values were adjusted for location effects before the estimation of regression (b). The 1 + b stability parameter of Perkins and Jinks model is theoretically equal to b of Eberhart and Russell model. Therefore, X, b, s^2d and 1 + b are presented together in Table 3.

With respect to days to first female flower six genotypes namely; Pusa Madhuras, PMM-263, PMM-251, PMM-208, PMM-231 and PMM-236 had b values significantly different from unity. Thus, these genotypes performed differently to different environments and were suitable for high fertility condition. The remaining genotypes could be considered suitable for all the five environments. Fourteen genotypes namely, PMM-249, PMM-255, PMM-263, PMM-97-19, PMM-216, PMM-242, PMM-251, PMM-208, PMM-255, PMM-221, PMM-217, PMM-218, PMM-191 and PMM-266 had s^2d values non significant from zero, indicating there stable performance across the environments for days to first female flower. For days to first female flower, early flowering will be desirable. Therefore, an ideal stable variety would be one which has mean lower than the average mean, b = 1 and s^2d = 0. Based on this, genotypes PMM-242 (mean = 51, b = 1.01 and s^2d = 0.80) and PMM-191 (mean = 52, b = 1.05 and s^2d = 0.91) were found stable and

Table 1. Pooled analysis of variance (Eberhart and Russell, 1966).

Characters	Mean squares							
	Genotype (G)	Environment (E)	G × E	E + (G × E)	E (linear)	G × E (linear)	Pooled deviation	Pooled error
D.F	23	4	92	96	1	23	72	230
Days to first female flower	19.60**	788.07**	2.64**	35.37	3152.21**	4.24*	2.02**	1.84
Node to first female flower	3.97**	0.71	0.65	0.65	2.82*	1.09**	0.48**	1.16
Fruit polar diameter (cm)	14.34**	17.94**	1.30	2.00	71.76**	1.82	1.08**	2.29
Fruit equatorial diameter (cm)	10.05**	29.77**	1.68**	2.85	119.06**	2.61*	1.32**	1.47
Fruit flesh thickness (cm)	0.34**	1.68**	0.07	0.14	6.73**	0.09	0.07**	0.13
TSS (%)	9.69**	1.65	1.74**	1.73	6.58*	2.60*	1.39**	1.46
Fruit weight (G)	385759.40**	1365211.20**	47991.16**	102875.34	5460837.80**	57946.27	42811.53**	36847.70

* Significant at 5%; ** Significant at 1%

Table 2. Joint regression analysis of genotype × environment interaction (Perkins and Jinks, 1968).

Characters	Mean squares					
	Genotype (G)	Environment (E)/ joint regression	G × E	Heterogeneity between regression	Remainder	Pooled error
DF	23	4	92	23	69**	230
Days to first female flower	19.61**	788.05**	2.64**	4.24*	2.11**	1.84
Node to first female flower	3.97**	0.71	0.65	1.09**	0.50**	1.16
Fruit polar diameter (cm)	14.34**	17.94**	1.30	1.82	1.13**	2.29
Fruit equatorial diameter (cm)	10.05**	29.77**	1.68**	2.61*	1.38**	1.47
Fruit flesh thickness (cm)	0.34**	1.68**	0.07	0.09	0.07**	0.13
TSS (%)	9.69**	1.65	1.74**	2.60*	1.45**	1.46
Fruit weight (G)	385759.31**	1365209.40**	47991.17**	57946.27	44672.90**	36847.70

* Significant at 5%; ** Significant at 1%

desirable.

For node to first female flower, the genotype PMM-274 was earliest due to lowest node to first female flower. However, the genotype PMM-214 was late due to highest number of node to first female flower. Three genotypes namely, PMM-216, PMM-208 and PMM-225 were suitable to high fertility condition due to significantly higher regression value. However, the genotype PMM-207 was suitable for low yielding environment due to its regression value significantly lower than unity. The remaining genotypes were suitable for average fertility/ environment. The 1+ stability parameter of Perkins and Jinks model was similar to b of Eberhart and Russell model. On the basis of S^2d value all the twenty three genotypes except PMM-212 were found stable for node to first female flower across the all environments. But, none of the genotypes fulfilled the condition of desirable stable genotype i.e. mean lower than the average mean, b = 1 and $s^2d = 0$. Dhakare and More (11) also did similar studies in muskmelon.

For fruit polar diameter, the genotypes PMM-236 (b=2.41*) and PMM-207 (b=2.52*) were suitable to high fertility environment due to significantly higher regression value. While, PMM-217 (b=-0.41*) and PMM-214 (b=-0.40*) were suitable to low yielding environment due to regression value significantly lower than unity. Four genotypes namely, PMM-255, PMM-218, PMM-214 and PMM-191 were unstable to fruit polar diameter due to significant deviation from regression. The remaining 20 genotypes were stable to this character across the fertility regimes.

For fruit equatorial diameter, the genotype PMM-216 had regression value (-0.14*) significantly lower than unity, indicating better response to poor or low yielding environments. However, PMM-236 (b = 2.09*), PMM-207 (b = 2.16*) and PMM-43 (b = 2.72**) had b/1 + b value significantly higher than unity suggesting that these genotypes were specifically adapted to the favourable environments. Sixteen genotypes had s^2d values close to zero (non-significant deviation from regression) suggesting stable performance over the fertility regimes.

The genotypes namely, PMM-217 (b=-0.16*) and PMM-214 (b=-0.21*) had b/1 + value significantly lower than unity, therefore, these two genotypes were suitable for poor fertility condition for higher fruit flesh thickness. The remaining 22 genotypes were suitable for average environment. On the basis of s^2d value PMM-225, PMM-221, PMM-217, PMM-214 and PMM-236 were unstable for fruit flesh thickness across the environments. As per Eberhart and Russell model mean above average mean, b = 1 and $s^2d = 0$, Pusa Madhuras, PMM-216, PMM-97-19 and PMM-43 were found stable and desirable across the environments.

TSS, one of the most important fruit characters from consumer's viewpoint was highest in staking experiment (E_4). Mangal and Pandita (8) also noticed increase in TSS due to pruning in muskmelon. Only two genotypes namely, PMM-217 (b = 6.05*) and PMM-218 (b = 8.07**) had b/1 + b value significantly higher than unity suggesting that these two genotypes were specifically adapted to favourable environment for higher expression of TSS. The remaining genotypes were found average responsive. Fifteen genotypes except Pusa Madhuras, PMM-263, PMM-265, PMM-225, PMM-274, PMM-217, PMM-218, PMM-214 and PMM-236 had s^2d values non significant, indicating their stability for TSS across the five environments.

For fruit weight all the genotypes except PMM-43 had b/1 + b value close to unity indicating their average response across the five environments. The genotype PMM-43 was specially adapted to high yielding environments due to highly significant b/1 + b value (b=2.27**). The s^2d values were non significant in 13 genotypes. On the basis of b/1+b value close to one and non-significant deviation from regression of s^2d, the genotypes, Pusa Madhuras (772 g), PMM-249 (859 g), PMM-97-19 (886 g), PMM-208 (923 g) and PMM-266 (885 g) were found stable and desirable for fruit weight

Table 3. Mean and stability parameters for different muskmelon genotypes over 5 environments

Sl. No.	Genotype	Days to first female flower				Node to first female flower			
		X_i	Eberhart and Russell b	Eberhart and Russell s^2d	Perkins and Jinks $1+\beta$	X_i	Eberhart and Russell b	Eberhart and Russell s^2d	Perkins and Jinks $1+\beta$
1.	Pusa Madhuras	55	0.64**	14.90**	0.64**	8	1.29	1.05	1.29
2.	PMM-249	53	1.24	3.35	1.24	7	3.15	0.61	3.15
3.	PMM-255	57	0.95	2.77	0.95	8	-0.32	0.43	-0.32
4.	PMM-263	53	1.27*	4.17	1.27*	8	1.84	2.40	1.84
5.	PMM-212	54	1.02	5.11*	1.02	9	-2.68	3.60*	-2.68
6.	PMM-97-19	53	0.88	2.76	0.88	8	0.97	1.98	0.97
7.	PMM-216	53	0.87	4.29	0.87	9	7.89**	0.60	7.89**
8.	PMM-242	51	1.01	0.80	1.01	7	2.17	1.13	2.17
9.	PMM-265	55	0.94	17.51**	0.94	8	-2.06	1.19	-2.06
10.	PMM-269	52	1.08	10.15**	1.08	8	-1.84	2.84	-1.84
11.	PMM-251	55	1.34**	3.03	1.34**	9	0.31	1.46	0.31
12.	PMM-208	56	1.26*	1.19	1.26*	8	5.82*	0.59	5.82*
13.	PMM-225	54	0.78	3.69	0.78	8	6.34*	0.83	6.34*
14.	PMM-274	50	1.02	14.93**	1.02	6	1.46	2.19	1.46
15.	PMM-231	56	0.71*	7.05**	0.71*	8	-2.99	0.42	-2.99
16.	PMM-221	56	1.04	0.74	1.04	9	-1.60	2.68	-1.60
17.	PMM-217	57	0.85	1.35	0.85	9	4.10	0.47	4.10
18.	PMM-218	56	1.02	1.99	1.02	9	-1.33	0.37	-1.33
19.	PMM-214	57	1.09	8.49**	1.09	10	0.74	1.62	0.74
20.	PMM-236	55	0.74*	12.49**	0.74*	9	1.46	2.19	1.46
21.	PMM-191	52	1.05	0.91	1.05	7	-0.55	0.85	-0.55
22.	PMM-207	58	1.01	18.16**	1.01	9	-4.34*	2.81	-4.34*
23.	PMM-266	56	1.05	0.59	1.05	8	0.80	0.68	0.80
24.	PMM-43	55	1.14	4.79*	1.14	9	3.36	1.70	3.36
	Population mean	55	1.00		1.00	8	1.00		1.00

Table 3 : *Cont...*

Sl. No.	Genotype	Fruit polar diameter (cm)				Fruit equatorial diameter (cm)			
		X_i	Eberhart and Russell b	Eberhart and Russell s^2d	Perkins and Jinks $1+\beta$	X_i	Eberhart and Russell b	Eberhart and Russell s^2d	Perkins and Jinks $1+\beta$
1.	Pusa Madhuras	9.3	1.04	2.34	1.04	11.7	1.25	2.52	1.25
2.	PMM-249	10.7	0.77	2.82	0.77	12.3	1.25	2.52	1.25
3.	PMM-255	11.6	1.58	9.99**	1.58	12.2	1.22	2.21	1.22
4.	PMM-263	10.4	1.68	2.74	1.68	10.5	1.15	2.61	1.15
5.	PMM-212	11.9	2.04	0.12	2.04	12.6	1.43	5.31*	1.43
6.	PMM-97-19	10.7	1.59	1.30	1.59	12.3	0.68	0.71	0.68
7.	PMM-216	13.1	0.66	0.81	0.66	11.6	-0.14*	0.88	-0.14*
8.	PMM-242	8.3	0.51	1.14	0.51	10.2	0.48	3.38	0.48
9.	PMM-265	9.6	0.97	2.45	0.97	10.3	0.41	1.32	0.41
10.	PMM-269	8.8	1.05	4.39	1.05	10.2	0.61	2.82	0.61
11.	PMM-251	10.6	0.28	1.65	0.28	12.2	0.66	2.14	0.66
12.	PMM-208	10.9	1.15	1.72	1.15	12.4	1.64	7.60**	1.64
13.	PMM-225	12.9	0.60	4.65	0.60	14.8	1.16	5.58**	1.16
14.	PMM-274	9.4	0.82	1.41	0.82	10.7	0.41	0.46	0.41
15.	PMM-231	10.9	0.32	3.41	0.32	11.7	0.72	0.02	0.72
16.	PMM-221	12.1	1.51	1.20	1.51	14.2	1.77	3.37	1.77
17.	PMM-217	11.4	-0.41*	3.62	-0.41*	13.1	0.21	5.58**	0.21
18.	PMM-218	12.8	1.13	6.34*	1.13	14.6	1.26	10.77**	1.26
19.	PMM-214	12.7	-0.40*	9.59**	-0.40*	12.7	0.17	7.09**	0.17
20.	PMM-236	11.1	2.41*	3.47	2.41*	12.1	2.09*	9.39**	2.09*
21.	PMM-191	12.9	-0.10	6.55*	-0.10	11.2	0.01	2.32	0.01
22.	PMM-207	12.8	2.52*	2.62	2.52*	13.7	2.16*	11.97**	2.16*
23.	PMM-266	11.3	0.72	1.13	0.72	11.8	0.68	2.02	0.68
24.	PMM-43	16.0	1.56	2.46	1.56	15.0	2.72**	2.33	2.72**
	Population mean	11.3	1.00		1.00	12.3	1.00		1.00

Table 3. *Cont...*

Sl.	Genotype	Fruit flesh thickness (cm) X_i	Eberhart and Russell b	Eberhart and Russell s^2d	Perkins and Jinks $1+\beta$	TSS (%) X_i	Eberhart and Russell b	Eberhart and Russell s^2d	Perkins and Jinks $1+\beta$	Fruit weight (g) X_i	Eberhart and Russell b	Eberhart and Russell s^2d	Perkins and Jinks $1+\beta$
1.	Pusa Madhuras	2.5	1.01	0.07	1.01	10.2	0.30	8.39**	0.30	772	0.87	8132.17	0.87
2.	PMM-249	2.6	1.33	0.05	1.33	8.7	2.51	2.69	2.51	859	1.09	52306.02	1.09
3.	PMM-255	2.5	1.33	0.06	1.33	8.2	1.87	1.09	1.87	1033	1.45	225097.25**	1.45
4.	PMM-263	2.3	1.27	0.06	1.27	7.8	-3.33	11.58**	-3.33	724	1.18	21615.63	1.18
5.	PMM-212	2.7	0.43	0.21	0.43	7.5	3.19	1.48	3.19	1034	1.24	132469.23*	1.24
6.	PMM-97-19	2.8	0.72	0.03	0.72	10.5	3.67	0.24	3.67	886	0.84	17666.24	0.84
7.	PMM-216	2.6	1.03	0.04	1.03	8.1	4.14	1.64	4.14	1009	0.65	63872.94	0.65
8.	PMM-242	2.0	1.95	0.16	1.95	8.5	5.39	3.51	5.39	557	0.42	3568.72	0.42
9.	PMM-265	2.1	1.23	0.01	1.23	6.8	0.96	6.49**	0.96	596	0.47	23848.10	0.47
10.	PMM-269	2.3	1.04	0.04	1.04	9.7	-1.83	2.15	-1.83	550	0.53	33369.02	0.53
11.	PMM-251	2.5	0.91	0.22	0.91	7.6	1.18	3.06	1.18	901	0.51	54271.66	0.51
12.	PMM-208	2.8	1.13	0.18	1.13	8.7	-3.50	2.46	-3.50	923	0.78	67815.76	0.78
13.	PMM-225	3.0	1.14	0.54*	1.14	7.4	-0.90	7.54**	-0.90	1456	1.30	274040.75**	1.30
14.	PMM-274	2.2	0.79	0.03	0.79	9.7	1.51	12.84**	1.51	681	0.55	20157.28	0.55
15.	PMM-231	2.4	1.30	0.12	1.30	5.9	1.06	2.31	1.06	978	0.79	127180.70*	0.79
16.	PMM-221	3.0	1.83	0.47*	1.83	7.2	-1.04	2.96	-1.04	1308	1.69	235034.53**	1.69
17.	PMM-217	2.7	-0.16*	0.46*	-0.16*	6.9	6.05*	4.27*	6.05*	1064	0.75	93430.54*	0.75
18.	PMM-218	2.9	0.99	0.24	0.99	8.4	8.07**	6.48**	8.07**	1343	1.44	411476.00**	1.44
19.	PMM-214	2.7	-0.21*	0.82**	-0.21*	6.3	-3.48	4.72*	-3.48	1181	0.59	239368.50**	0.59
20.	PMM-236	2.4	1.75	0.44*	1.75	6.3	1.07	5.58**	1.07	976	1.72	203401.28**	1.72
21.	PMM-191	2.5	0.19	0.15	0.19	5.5	-2.30	0.71	-2.30	922	0.36	19684.17	0.36
22.	PMM-207	2.7	1.66	0.13	1.66	8.1	2.07	3.36	2.07	1292	1.65	206708.16**	1.65
23.	PMM-266	2.4	0.54	0.19	0.54	5.6	-1.31	3.09	-1.31	885	0.79	19070.37	0.79
24.	PMM-43	2.8	0.78	0.06	0.78	7.0	-1.35	1.19	-1.35	1615	2.27**	528845.31**	2.27**
	Population mean	2.5	1.00		1.00	7.8	1.00		1.00	981	1.00		1.00

across the five environments. In muskmelon, consumer's generally prefers the medium size fruits rather than the larger fruits. Timothy et al., (9) also did similar studies in muskmelon. High yielding genotypes namely, PMM-225 (1456 g), PMM-221 (1308 g), PMM-214 (1181g), PMM-218 (1343 g), PMM-207 (1292 g) and PMM-43 (1615 g) showed low yield stability. This was probably due to relatively late maturity of these genotypes. Gill and Kumar (10) also found that late maturing varieties of watermelon viz., Sugar Baby (64 days to first female flower), Charleston Gray (63 days to first female flower) and Dixie Queen (63 days to first female flower) were high yielding (mean fruit weight 3.20 kg, 3.54 kg and 4.00 kg respectively) but showed low yield stability.

Two genotypes namely, PMM-97-19 and PMM-251 were found stable across the five environments for all the characters under study. On overall basis the desirable stable genotypes for fruit yield having superior fruit quality were Pusa Madhuras (flat round, TSS 10.2%, very sweet with 772 g fruit weight), PMM-249 (flat round, TSS 8.7%, sweet with 859 g fruit weight), PMM-97-19 (round, TSS 10.5%, very sweet with 886 g fruit weight) and PMM-208 (round, TSS 8.7%, sweet with 923 g fruit weight). The genotype PMM-97-19 had desirable fruit shape (round fruited), high TSS (10.5%), medium size (886 g) and stability for all the characters under study across the environments. Therefore, the genotype PMM-97-19 was found most superior genotype. Thus, these models were found effective in identifying the genotypes that have specific adaptation (interacting) and those which were widely adaptable (non-interacting). It was also useful for characterizing the environments, which were suitable for growing a specific or group of genotypes.

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