The Pharma Innovation Journal 2022; 11(2): 1978-1982

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; 11(2): 1978-1982

www.thepharmajournal.com
Received: 13-12-2021
Accepted: 23-01-2022

Sheetal Tak
Department of Horticulture, Rajasthan College of Agriculture, MPUAT, Udaipur, Rajasthan, India

RA Kaushik
Department of Horticulture, Rajasthan College of Agriculture, MPUAT, Udaipur, Rajasthan, India

KD Ameta
Department of Horticulture, Rajasthan College of Agriculture, MPUAT, Udaipur, Rajasthan, India

RB Dubey
Department of Plant Breeding and Genetics, Rajasthan College of Agriculture, MPUAT, Udaipur, Rajasthan, India

RS Rathore
Department of Horticulture, Rajasthan College of Agriculture, MPUAT, Udaipur, Rajasthan, India

Corresponding Author:
Sheetal Tak
Department of Horticulture, Rajasthan College of Agriculture, MPUAT, Udaipur, Rajasthan, India

Effect of GXE interaction on yield analysis of selected cucumber and Snapmelon breeding lines in Rajasthan

Sheetal Tak, RA Kaushik, KD Ameta, RB Dubey and RS Rathore

Abstract
This study was carried out to assess the nature and magnitude of genotype-environment interaction (GEI) and the correlation among some stability parameters. 15 parents along with 36 hybrids and three standard checks were evaluated in randomized block design with three replications at three locations *viz*. Udaipur, Banswara and Chittorhgarh region during *kharif* 2014 at Rajasthan. Combined analysis of variance indicated that the main effect due to location, genotype and genotype by environment interaction were highly significant. Interspecific hybridization is used to improve crops by transferring specific traits, such as yield, improve quality, pest and stress resistance to crops from their wild relatives. When applicable, this approach is a very effective method of gene transfer. Genotype x environment interaction and yield stability was evaluated for total yield per vine for 36 cucumber and snapmelon breeding lines in Rajasthan using the Additive Main Effects and Multiplicative Interaction stability parameter. Genotype x environment interactions showed the inconsistency of the performance of the breeding lines over environments and seasons. The analysis of variance showed that the genotype x environment interaction were significant for total yield.

Keywords: Cucumber, Snapmelon, genotype plus genotype by environment, genotype- environment interaction, principal component, stability parameters, interspecific

Introduction
Genera *Cucumis* includes many species like *Cucumis sativus* (cucumber), *Cucumis melo* (muskmelon), *Cucumis melo* var. *utilissimus* (kakri), *Cucumis melo* var. *momordica* (snap melon), *Cucumis melo* var. *agrestis* (weed melon) etc. All these species are monoecious and highly cross pollinated in nature. Cucumber is warm season vegetable. It is said to be the native of northern India (Pursglove, 1969) [12]. Cucurbits are composed of 118 genera and 825 species. Members of this family are distributed primarily in tropical and subtropical regions of the world (Wang *et al*. 2007) [20]. The cultivated species *Cucumis sativus* L. originated from the wild progenitor *Cucumis* hardwickii in the Himalayan belt of Indo Chinese region. Now, it is extensively cultivated in diverse agroclimatic conditions ranging from tropical to subtropical regions of the world. India being the primary centre of origin has accumulated a wide range of variability which can be exploited for crop improvement. Cucumber has been cultivated in India since last three thousand years. It is grown throughout the year in southern states of India. In plains of northern India it is grown in summer and rainy season. Muskmelon is originated from Tropical Africa (Sahara dessert). It has a good inter-state trade in India. Being a warm season crop require warm weather and cool nights for sugar accumulation. Edible portion of melons contains water (90%) and CHO (10%). The fruits of cucumber is said to have cooling effect, prevent constipation, checks jaundice and indigestion (Nandkarni, 1927) [10]. Besides this, the seed of cucumber is also used in Ayurvedic preparations and raw fruits are being used for cosmetic purpose. Snap melon (*Cucumis melo var. momordica*) belongs to the family cucurbitaceae is used as a vegetable in variety of ways. Snap melon is rich in quality and now snapmelon juice is gaining popularity as squash. Knowledge of the nature and magnitude of variation promotes a rational choice of the characters in which selection can be exercised. Chromosomal, genetic, cytoplasmic or mechanical isolation barriers can handicap successful hybridization and utilization. Significant benefits and difficulties make interspecific hybridization an important objective for geneticists and plant breeders. Interspecific hybrids in the Cucurbitaceae have been produced in several genera, including *Cucumis* (Deakin *et al*. 1971, Tak *et al*. 2017) [2, 16], *Citrullus* (Valvilov, 1925) [19], *Luffa* (Singh, 1991) [15], and *Cucurbita* (Weeden and Robinson, 1986) [21]. Crop improvement to a large extent depends on the existing genetic variability.

Considering the importance of a wide genetic base in plant breeding, identification and characterization of available germplasm is a pre-requisite for estimation of diversity, determination of genetic relatedness, documentation and management of germplasm. Evaluation of various genotypes is the basic step for breeding programmes, which will help us to find out the growth and yield difference among various genotypes in field itself.

The main objectives of the crop improvement include the development of high yielding varieties, free from bitterness, possessing earliness and other quality attributes along with tolerance to major diseases and insect pest. The consorted efforts are going on to make an effective improvement in characters of economic importance. The open pollinated cultivar of cucumber possess regional adoptability and have attain a plateau in yield. To overcome this, heterosis breeding or exploitation of hybrid vigour approach may be an ideal tool to boost the cucumber production in different parts of the world.

Material and Methods

The present investigation entitled "Heterosis, Combining Ability and Stability in Interspecific Hybrids of *Cucumis*", was conducted during *Kharif*, 2014 at three different locations (Horticulture Farm, Department of Horticulture, Rajasthan College of Agriculture, Udaipur, Agricultural Research Station, Banswara and KVK Chittorgarh).

Twelve inbred lines (female) of *cucumis melo* were crossed with three testers of *cucumis sativus* in line x tester mating design to develop a total 36 hybrids at Hi-Tech Horticulture unit, Department of Horticulture, Rajasthan College of Agriculture, Udaipur. These 15 parents along with 36 hybrids and three standard checks (Mamta-5002, Sedona, Kakri surya prabha) were evaluated in randomized block design with three replications at three locations *viz*. Udaipur, Banswara and Chittorhgarh during *kharif* 2014 (metrological data of selected enviornment is mention in Table 1). The row length was 27 meter with row to row and plant to plant spacing 1.0 m and 40 cm respectively with 2 meter spacing for vine spreading. Recommened POP of Zone IV A and IV B of Rajasthan was used to raise a healthy crop. Lines and testers accessions were collected from NBPGR, New Delhi (Table 2).

Table 1: Description of the selected environment

Experimental site	Date of sowing	Geographical location	Elevation (M.S.L)	Metrological Data				
				Temperature (C^0)		RH (%)		Rainfall (mm)
				Max.	Min.	Max.	Min.	
Udaipur	June 2, 2014	$24^0$35‟ N,$73^0$42‟ E	582.17	31^0	24^0	80	63	95
Banswara	June 10, 2014	23^0 33' N, 74^0 27' E	220	33	22	86	74	92.7
Chittorgarh	June 17, 2014	$23^0$32‟ to $25^0$13‟ N $74^0$12’ to,$75^0$49’E	394	31	24	79	54	50

The mean rainfall data, temperature and sunshine hour shown above is only the average of the growing months from June through September

Table 2: Description of Parents and Checks

S. No.	Symbol	Species Name	IC Number	Source
A. Lines (Female Parents)				
1.	L1	*C.melo var. momoradica*	IC-415539	NBPGR, New, Delhi.
2.	L2	*C.melo var. momoradica*	IC-415521	NBPGR, New, Delhi.
3.	L3	*C.melo var. momoradica*	IC-433621	NBPGR, New, Delhi.
4.	L4	*C.melo var. utilissimus*	IC-315294	NBPGR, New, Delhi.
5.	L5	*C.melo var. utilissimus*	IC-258163	NBPGR, New, Delhi.
6.	L6	*C.melo var. utilissimus*	IC-313031	NBPGR, New, Delhi.
7.	L7	*C.melo var. momoradica*	VRSM-44	NBPGR, New, Delhi.
8.	L8	*C.melo var. agrertris*	IC-258165	NBPGR, New, Delhi.
9.	L9	*C.melo var. momoradica*	VRSM-32	NBPGR, New, Delhi.
10.	L10	*C.melo var. momoradica*	DR/KPS/26	NBPGR, New, Delhi.
11.	L11	*C.melo*	BS-41	NBPGR, New, Delhi.
12.	L12	*C.melo var. momoradica*	VRSM-58	NBPGR, New, Delhi.
B. Tester (Male Parent) Source				
1.	T1	*C.sativus*	SKY/DR/RS	NBPGR, New, Delhi.
2.	T2	*C.sativus*	SPP-58	NBPGR, New, Delhi.
3.	T3	*C.sativus*	SPP-56	NBPGR, New, Delhi.
C. Check Variety Hybrids				
1.	C Check-1	*C.sativus* (NBH-Mamta-5002)	_	Hi- Tech Horticulture Unit, RCA, Udaipur
2.	Check-2	*C.sativus* (Mahyco-Sedona)	_	Hi- Tech Horticulture Unit, RCA, Udaipur
3.	Check-3	*C.melo var. utilissimus* (Kakri Surya Prabha)	_	Hi- Tech Horticulture Unit, RCA, Udaipur

Stability analysis

The data analysis was conducted using appropriate statistical software’s. The phenotypic stability of genotype for characters had homogenity of error mean square was estimated by regression analysis according to Eberhart and Russell (1966) [5]. The linear model of the analysis was as follows:

$$Yij = \mu i + \beta iIj + \Sigma ij$$

Where

Yij = Mean of the ith genotype in jth environment, (i = 1,2,...g, j = 1,2,...s)

i = Mean of ith genotype over all environments,

Bi = Regression coefficient that measure the response of the ith genotype to varying environments,

Σij = Deviation from regression of the ith genotype in jth environment

Ij = Environmental index of jth environment

Result and Discussion

Analysis of variance (Table 3) for experimental design revealed significant difference among genotypes for all characters in all the three environments Among the parents difference was also significant for all the characters in all the environments. Difference between means of parents Vs crosses was significant for all the characters in all the three environments

The expression of quantitative traits is highly influenced by the environment. The magnitude of this influence of environment on genotype expression is reflected through G x E interactions. This interaction if not separated or minimized remains confounded with genetic variance and leads to biased estimates of genetic parameters. This bias can be minimized by growing the genotypes in different favourable and unfavourable environments. The present investigation was under taken to examine the genotype x environment interactions in relation to various quantitative traits and for screening and identification of stable and superior genotypes for yield and its component traits in *Cucumis* sp. using Eberhart and Russell (1966) [5] statistical model.

The mean square due to stability with regards to different traits on the basis of pooled data are presented in Table 4. Analysis of variance revealed significant difference among genotypes, environment linear, G x E linear and pooled deviation for all the characters. The mean square due to genotypes (lines, testers, hybrids, and check varieties) was significant for all the characters. The mean square due to G x E interaction were partitioned into linear and non linear components. The environment (linear) component of variance was significant for all the traits, indicating that macro environmental differences were present under all the three environments studied.

In the present investigation, model proposed by Eberhart and Russell (1966) [5] was used for analysis of G x E interactions. It considered both linear (bi) and non-linear (S2di) components of G x E interactions for the prediction of performance of the individual genotypes (parental line/tester/hybrid/check variety). The stability parameters, such as regression coefficient (bi) and deviation from regression (S2di) along with mean performance of genotypes for various characters were computed to parameters are presented in Table 5. The linear regression coefficient (bi) was considered as a measure of responsiveness and deviation from regression (S2di) as a measure of stability. The high mean performance of parents was decided on the basis of average performance of all the parents (i.e. parental mean) as well as population mean. The high mean performance of hybrids was seen in relation to the best check along with population mean and the high mean performance of check varieties was seen in relation to the overall mean performance of checks. The character wise results are as under (Table 6).On the basis of yield per vine five best highest yielding identified hybrids are *viz.*, L3× T3, L3× T2, L2× T2, L12× T1, L3× T1.

Out of total 54 genotypes, only 14 genotypes showed non-significant deviation from regression (S2di), indicating their predictable behavior (Table 5).Hybrids L3 x T2 and exhibited non-significant deviation from regression (S2di) and regression coefficient more than unity (bi>1) along with higher mean value than population mean, thereby indicating their stability under favourable environments and suitability for higher yield.

Lewis (1954) [9] measured the phenotypic stability based on mean performance in the highest yielding environment with that in the lowest yielding environment. Finlay and Wilkinson (1963) [6] used linear regression as a quantitative measure of phenotypic stability to describe varietal adaptability on a range of environments. Eberhart and Russell (1966) [5] suggested that both linear (bi) and non-linear (S2di) components of the genotypes environment interactions should be considered while judging the phenotypic stability of a particular genotype.

The significant G x E interaction for yield and fruit quality traits were reported by Das *et al.* (2005) [1] and Dijkhuizen and Staub (2002) in cucumber and in watermelon by Dia (2012) [3]. Similar findings for identification of genotypes for their stability under varying environmental conditions were also reported by Krishnaprasad and Singh (1992) [8], Rajput *et al*. (1994) [13] and Prasad *et al.* (1999) [11] in bittergourd, Tak *et al*. (2017) [16]. in cucumber for yield and its component and in watermelon by Dia(2012) [3]. In cucumber for quantitative characters by Hanchinamani *et al.* (2008) [7] and yield and its component by Singh and Ram (2012) [14].

Table 3: Analysis of variance for total yield per vine in individual environments**.**

S.N.	Character	Env	Rep	Genotype	Checks	Chk Vs P	Parents	Tester	Lines
1.	Total yield/ vine	1	0.09	13.69**	3.71**	32.53**	13.10**	3.97**	15.92**
		2	0.02	15.42**	4.20**	18.63**	16.23**	3.96**	18.56**
		3	0.11	3.61**	1.73**	1.11**	2.27**	0.49**	2.76**

Table 3: Continued.....

Character	Env	L Vs L	P Vs C	Crosses	Tester	Lines	L X T	Error
Total yield/ vine	1	0.39	1.10*	14.06**	3.45**	34.52**	4.79**	0.18
	2	15.15**	45.54**	13.90**	5.64**	32.02**	5.59**	0.15
	3	0.37**	6.40**	4.16**	2.02**	8.54**	2.17**	0.05

Table 4: Analysis of variance for phenotypic stability (Eberhart and Russel, 1966)

SN	Characters	Genotype	E+(G x E)	E (L)	G x E (L)	Pool dev.	Pool Err
		[53]	[108]	[1]	[53]	[54]	[318]
1.	Total yield/ vine	8.437**	2.574**	0.0504**	3.788**	1.429**	0.042

Table 5: Stability parameters for Total yield/ vine.

S.N.	Genotype		Total yield/ vine (kg)	
		μ_i	b_i	S^2d_i
1	T1	2.59	0.80	0.810**
2	T2	3.12	1.12	0.023
3	T3	4.23	1.48	0.393**
4	L1	2.25	0.48	2.566**
5	L2	3.40	1.31	1.247**
6	L3	6.98	2.31	2.862**
7	L4	0.46	0.16	-0.005
8	L5	2.12	0.76	0.262**
9	L6	1.23	0.26	0.235*
10	L7	2.59	0.38	3.849**
11	L8	2.75	0.95	0.255**
12	L9	2.38	0.79	0.705**
13	L10	2.31	0.72*	-0.036
14	L11	1.91	0.53	-0.032
15	L12	5.65	2.04	9.003**
16	L1 x T1	2.52	1.02	0.880**
17	L2 x T1	5.12	2.02	0.083
18	L3 x T1	5.41	0.75	7.651**
19	L4 x T1	1.47	0.18	0.190*
20	L5 x T1	4.36	1.26	2.949**
21	L6 x T1	2.77	0.76	0.800**
22	L7 x T1	2.80	0.67	-0.003
23	L8 x T1	4.67	1.24	0.796**
24	L9 x T1	3.99	0.67	-0.032
25	L10 x T1	4.12	1.60	1.606**
26	L11 x T1	1.62	0.18	0.304**
27	L12 x T1	5.72	1.80	0.646**
28	L1 x T2	2.52	0.89	2.098**
29	L2 x T2	6.19	0.63	10.178**
30	L3 x T2	6.81	2.05*	-0.023
31	L4 x T2	1.36	0.49*+	-0.040
32	L5 x T2	3.72	1.37	0.219*
33	L6 x T2	3.23	1.40	0.355**
34	L7 x T2	3.07	0.51	0.009
35	L8 x T2	2.81	1.30	3.104**
36	L9 x T2	3.10	1.16	0.092
37	L10 x T2	1.04	0.42+	-0.039
38	L11 x T2	0.82	0.02	0.120*
39	L12 x T2	4.45	2.13	2.638**
40	L1 x T3	2.49	1.02	2.395**
41	L2 x T3	3.45	1.49	1.851**
42	L3 x T3	7.73	1.88	1.425**
43	L4 x T3	1.63	0.45	0.485**
44	L5 x T3	4.59	1.21	0.809**
45	L6 x T3	2.63	1.19	1.086**
46	L7 x T3	2.34	0.64	0.689**
47	L8 x T3	3.95	1.64	3.410**
48	L9 x T3	3.59	1.49	1.075**
49	L10 x T3	4.93	1.49	4.676**
50	L11 x T3	1.53	0.23	0.132*
51	L12 x T3	4.94	1.95	0.272**
52	Mamta-5002	2.60	0.42*+	-0.041
53	Sedona	1.59	0.27+	-0.041
54	Surya Prabha	0.56	0.03+	-0.035

Table 6: Five best hybrids identified on the basis of *per se* performance on pooled basis for total yield per vine.

S. No.	Hybrids	*Per se* performance for yield per vine (Kg)	rank
1	L3× T3	7.73	1
2	L3× T2	6.81	2
3	L2× T2	6.19	3
4	L12× T1	5.72	4
5	L3× T1	5.41	5
Best check 'Mamta-5002' - 2.60			

References

1. Das S, Choudhary DN, Maurya KR. Genotype x environment interaction in cucumber (*Cucumis sativus* L.). Vegetable Science. 2005;32(2):182-183.
2. Deakin JR, Bohn GW, Whitaker TW. Interspecific hybridization in *Cucumis.* Economic Botany. 1971;25(2):195-211.
3. Dia M. Genotype x Environment interaction and stability analysis of performance and mega-environment identification of fruit yield and yield components in watermelon [*Citrullus lanatus* (Thumb.) Matsum, Nakai]. 2012.
4. Dijkhuizen A, Staub JE. QTL conditioning yield and fruit quality traits in cucumber (*Cucumis sativus* L.). Journal of New Seeds. 2002;4(4):1-30.
5. Eberhart SA, Russell WA. Stability parameters for comparing varieties. Crop Science.1966;6(1):36-40.
6. Finlay KW, Wilkinson GN. The analysis of adaption in plant breeding programme. Australian Journal of Agriculture Research. 1963;14(1):742-754.
7. Hanchinamani CN, Patil MG. Stability analysis for some quantitative characters in cucumber (*Cucumis sativus* L.). Crop Research. 2008;36(1/3):265-269.
8. Krishnaprasad VSR, Singh DP. Phenotypic stability in bitter gourd. Indian Journal of Horticulture. 1992;49(2):179-182.
9. Lewis D. Gene interaction, environment and hybrid vigour. In: Proceedings of the Royal Society of London B: Biological Sciences. 1954;144(915):178-185.
10. Nandkarni KM. Indian materia medica. Nandkarni & Co. Bombay. 1927.
11. Prasad VSRK, Singh DP, Pal AB, Rai M, Yadav IS. Assessment of adoptability in bitter gourd. Indian Journal of Horticulture. 1999;56(1):52-61.
12. Pursglove JW. Tropical crops dicotyledons I. longamans. Green & co. Ltd. London & Harlow. 1969.
13. Rajput JC, Patil SL, Jamdagni BM, Patil VH. Stability of yield and its component in bitter gourd. Vegetable Science. 1994;21(2):137-139.
14. Singh A, Ram HH. Estimates of stability parameters for yield and its components in cucumber (*Cucumis sativus* L.). Vegetable Science. 2012;39(1):31-34.

15. Singh BP. Interspecific hybridization in between new and old-world species of *Luffa* and its phylogenetic implication. Cytologia. 1991;56(3):359-365.
16. Tak S, Kaushik RA, Ameta KD, Dubey RB, Rathore RS, Nath A. Combining Ability Studies on Cucumber and Snapmelon Hybrids. Int. J Curr. Microbiol. App. Sci. 2017;6(6):942-949.
17. Tak S, Kaushik RA, Nath A. Studies on heterosis in interspecific hybrids of Cucumis. The bioscan tested in multiple US location. Ph.D. dissertation of North Carolina State University, Raleigh, North Carolina. 2016;11(4):3155-3159.
18. Valvilov N. Inter-genetic hybrids of melons, water melons and squashes. Bulletin of Applied Botany and Genetics. 1925;14:3-35.
19. Wang YH, Joobeur T, Dean RA, Staub JE. Cucurbits. Genome Mapping and Molecular Breeding in plants 5: Vegetables Whitehouse. 2007.
20. Weeden NF, Robinson RW. Allozyme segregation ratios in the interspecific cross *Cucurbita maxima* x *C. ecuadorensis*. Genetics. 1986;114(2):593-609.