Original Research Article

Character Association Studies for Various Characters in Local Cucumber (*Cucumis sativus* L.) under Subtropical Regions of Jammu

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A B S T R A C T

The present investigation was carried out at Vegetable Experimental Farm-I, Division of Vegetable Science and Floriculture, FOA, Chatha, SKUAST-J, during the year 2018-2019. The experiment was laid out in Randomized Complete Block Design with three replications. The Analysis of Variance revealed significant differences among the genotypes for all the characters studied. The Phenotypic Coefficient of Variance (PCV) and Genotypic Coefficient of Variation (GCV) were high for number of fruits/vine and fruit yield/vine. High estimates of heritability were recorded for number of seeds/fruit, fruit yield/vine, average fruit weight, vine length, 1000 seed weight, fruit length, number of fruits/vine, fruit diameter, days to first harvest, days to 50 % flowering, node number at which first female flower appears, total soluble solids and days to first female flowering. High genetic gain as percentage of mean was observed for fruit yield/vine, number of fruits/vine, number of seeds/fruit, node number at which first female flower appears, 1000 seed weight, fruit yield/hectare, fruit length, average fruit weight and fruit diameter. The traits viz. number of fruits/vine, fruit yield/vine gave high heritability, genetic advance and GCV indicating that these are controlled by additive gene action and could be improved by direct selection. In general, genotypic correlations were higher in magnitude than phenotypic ones. Fruit yield/hectare showed negatively significant correlation with days to 50 % flowering while positive significant correlation with days to first harvest and number of fruits/vine. Maximum positive direct effect towards fruit yield/hectare was exerted by days to first female flowering followed by fruit yield/vine, total soluble solids, days to 50% flowering, number of seeds/fruit and number of fruits/vine.

Introduction

Cucumber (*Cucumis sativus* L., 2n = 2x = 14) also called "Khira" belonging to family Cucurbitaceae, is a warm season vegetable crop grown under tropical and sub-tropical regions. It is one of the most important summer vegetable crops grown both under open field and protected conditions throughout India and world. Cucumber is considered as second most widely cultivated cucurbit after watermelon. The center of origin of cucumber is India and *Cucumis sativus* L. var. *hardwickii*, a wild relative of

cucumber is its progenitor, which is found in the Himalayan foothills of Nepal. Cucumber has tremendous economic and dietic importance. It is grown for its tender fruits, which are consumed either raw as salad (Arunkumar *et al.,* 2011), cooked as vegetable or as pickling cucumber in its immature stage. It is a low energy and high water content vegetable, and it is also a rich source of vitamin B and C, carbohydrates, calcium and phosphorus (Yawalkar, 1985). Fruits of cucumber are used as an astringent and antipyretic, prevents constipation and also useful in jaundice and indigestion. As deep cooling effect, the demand of cucumber is increasing day by day. Everyone is fond of eating this vegetable as raw for refreshment, especially as salad with fast food (Reshma, 2011). The seed oil also has antipyretic property. Seeds contain oil, which is helpful for brain development and body smoothness. Hence, it is being used in Ayurvedic preparations (Robinson and Decker's Walter, 1999). Besides this, the whole fruit is used in cosmetic and soap industries. Its juice is still useful for rheumatic conditions and healthy growing hair (Khulakpam *et al.,* 2015).

Materials and Methods

The experimental material comprised of 21 diverse genotypes of local cucumber collected from different areas of J&K viz. Cucumber selection-1 [Local Selection (S1)], Cucumber selection-2 [Local Selection (S2)], Cucumber selection-3[Local Selection from Khera, Udhampur], Cucumber selection-4[Barnai, Jammu], Cucumber selection-5[Advance Breeding line (ABL: 2017-7)], Cucumber selection-6 [Advance Breeding line (ABL: 2017-4)], Cucumber selection-7 [Advance Breeding line (ABL: 2017-10)], Cucumber selection-8 [Durga seeds], Cucumber selection-9 [Kisan Kheti], Cucumber selection-10 [Local selection from Udhampur (Chenani)], Cucumber selection-11 [Local

selection from Udhampur (Jallow)], Cucumber selection-12 [Advance Breeding line (ABL: 2017-9)], Cucumber selection-13[Green Express Global Seeds], Cucumber selection-14 [Raunak seeds], Cucumber selection-15 [RangaBalanda, Udhampur], Cucumber selection-16 [Pancheri, Udhampur], Cucumber selection-17[Khirmoo, Udhampur], Cucumber selection-18[Kora, Udhampur], Cucumber selection-19[Rajouri], Cucumber selection-20 [Srinagar (Tral)] and Cucumber selection-21 [Lander, Udhampur] were transplanted in Randomized Complete Block Design with three replications during 2018 - 2019 in a plot size of 1.20×1.20 m with spacing of 1.0 m $\times$ 1.0 m. All the recommended cultural practices were followed during the growth and development period of the crop to raise a healthy crop.

The averaged values of all the 4 plants of various genotypes were subjected to statistical analysis at the computer lab of Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, Chatha, Jammu and were analyzed as per Gomez and Gomez (1976). The genotypic and phenotypic coefficients of variability were calculated as per the method suggested by Burton and De Vane (1953). Heritability (broad sense) was estimated as per Allard, 1960 a. Heritability percentage was categorized as per Robinson (1966). Genetic advance was calculated as per Allard (1960 b). Genetic advance expressed as per cent of population mean was calculated by the formula suggested by Johnson *et al.,* (1955 a).

Results and Discussion

The analysis of variance for various characters in cucumber showed significant differences among the genotypes for all the traits studied and revealed the existence of substantial amount of variability in the

germplasm. The knowledge of genetic coefficient of variation is necessary for improvement of a crop which helps to measure the extent of genetic variability in the characters among genotypes and provides a means to compare the genetic variability present in the various characters.

The phenotypic and genotypic coefficients of variability were found to be high for number of fruits per vine (22.00 % and 20.69 %) and fruit yield per vine (21.13 % and 21.11 %), moderate for node number at which first female flower appears (19.29 % and 17.42 %), number of seeds per fruit (16.02 % and 16.01 %), 1000 seed weight (14.97 % and 14.59 %), fruit length (14.53 % and 13.83 %), fruit diameter (13.49 % and 12.47 %) and average fruit weight (12.02 % and 11.99 %) whereas it was low for vine length (9.78 % and 9.54 %), days to 50% flowering (7.43 % and 6.79 %), days to first harvest (7.32 % and 6.69 %) and days to first female flowering (6.95 % and 6.17 %). Coefficients of variability varied in magnitude from character to character (either low, moderate or high). Therefore, it indicated that there was a great variability in the experimental material used (Table 1). All the characters showed less difference between the GCV and PCV values implying variability due to genetic constitution. This suggested that selection could be effective on the basis of phenotypic characters with chances of success. The results are in line with the findings of Kandasamy (2017), Pal *et al.,* (2017), Ahirwar *et al* (2017), Ranjan *et al.,* (2015) and Choudhary *et al.,* (2015).

The heritable variation can be estimated with accuracy when heritability is studied along with genetic advance (GA). High heritability coupled with high genetic advance offers the most effective criteria for selection (Johnson *et al.,* 1955). Genetic advance as percentage of mean varied from 11.31 % for days to first

female flowering to 43.43 % for fruit yield/vine. It was found high for fruit yield per vine (43.43 %), number of fruits per vine (40.10 %), number of seeds per fruit (32.96 %), node number at which first female flower appears (32.39 %), 1000 seed weight (29.30 %), fruit yield per hectare (28.61 %), fruit length (27.11 %), average fruit weight (24.64 %) and fruit diameter (23.76 %), indicating additive gene action control for the inheritance of these traits and these traits are likely to respond more to selection. The results are in accordance with findings of Pal *et al.,* (2017), Ahirwar *et al.,* (2017), Ranjan *et al.,* (2015), Basavarajeshwari *et al.,* (2014), Kumar *et al.,* (2013), Gaikwad *et al.,* (2011), Shukla *et al.,* (2010), Yogesh *et al.,* (2009).

High heritability was observed for traits viz. number of seeds per fruit (95.90 %), fruit yield per vine (95.80 %), average fruit weight (95.50 %), vine length (95.10 %), 1000 seed weight (93.00 %), fruit length (90.60 %), number of fruits per vine (88.50 %), fruit diameter (85.50 %), days to first harvest (83.60 %), days to 50 % flowering (83.40 %), node number at which first female flower appears (81.50 %), total soluble solids (81.20 %), days to first female flowering (79.00 %) and fruit yield per hectare (66.30 %) was obtained. This realizes that selection can be done quickly for the characters having high heritability. The above results are in accordance with the earlier work of Ahirwar *et al.,* (2017), Pal *et al.,* (2017) Kandasamy (2017), Pal *et al.,* (2016), Ranjan *et al.,* (2015) and Kumar *et al.,* (2013).

In any breeding programme yield (dependent variable) is the end product of interaction of many contributing characters (independent variables) and selection in such programmes is effective only when based on such independent variables. In the present study the genotypic correlation coefficients were higher in magnitude than the corresponding

phenotypic correlation coefficients indicating strong inherent association among these characters (Table 2). The phenotypic and genotypic correlations among different characters showed that days to 50 % flowering was negatively and significantly correlated with fruit yield per hectare and average fruit weight at both phenotypic and genotypic levels, whereas it was positively and significantly correlated with number of fruits per vine and days to first harvest both at phenotypic and genotypic levels, while vine length was positively and significantly correlated at genotypic level only. Days to first female flowering was negatively and significantly correlated with days to first harvest at both phenotypic and genotypic levels, whereas it was positively and significantly associated with node number at which first female flower appears at genotypic level only. Node number at which first female flower appears was positively and significantly correlated with number of seeds per fruit at both phenotypic and genotypic levels. Days to first harvest was negatively and significantly correlated with fruit diameter at both phenotypic and genotypic levels. Fruit length was positively and significantly correlated with fruit diameter at both phenotypic and genotypic levels. Fruit diameter was positively and significantly associated with fruit yield per hectare, fruit yield per vine at both phenotypic and genotypic levels, it was negatively and significantly correlated with total soluble solids, 1000 seed weight and number of seeds per fruit at phenotypic and genotypic levels, while number of fruits per vine at genotypic level only. Average fruit weight was positively and significantly correlated with fruit yield per hectare and fruit yield per vine, whereas it was negatively and significantly correlated with vine length, total soluble solids and number of fruits per vine at phenotypic and genotypic levels. Number of fruits per vine was positively and significantly

correlated with fruit yield per hectare, fruit yield per vine, number of seeds per fruit and total soluble solids at both phenotypic and genotypic levels. Vine length was positively and significantly correlated with 1000 seed weight at phenotypic and genotypic levels. Number of seeds per fruit was positively and significantly associated with fruit yield per hectare, fruit yield per vine and 1000 seed weight at phenotypic level, while it was significantly associated with fruit yield per hectare and 1000 seed weight at genotypic level only. 1000 seed weight was positively and significantly correlated with fruit yield per hectare, fruit yield per vine and total soluble solids at both phenotypic and genotypic levels. Total soluble solid was positively and significantly associated with fruit yield per vine both at phenotypic and genotypic levels, while with fruit yield per hectare at genotypic level only. Fruit yield per vine was positively and significantly correlated with fruit yield per hectare at both phenotypic and genotypic levels. The results corroborate with the findings of earlier work by Pal *et al.,* (2017), Ahirwar *et al* (2017), Khan *et al.,* (2015), Veena *et al.,* (2013), Kumar *et al.,* (2013), Bhardwaj and Kumar (2012), Hasan *et al.,* (2012), Ullah *et al.,* (2012), Kumar *et al.,* (2011), Arunkumar *et al.,* (2011).

The knowledge of correlation coefficients alone is often misleading as it may always be not true. For this the path analysis, which reveals the direct and indirect association is the most reliable method. The results of path analysis (Table 3) revealed that days to first female flowering had maximum positive direct contribution towards fruit yield/hectare, followed by days to first female flowering (0.54), fruit yield per vine (0.44), total soluble solids (0.44), days to 50 % flowering (0.26), number of seeds per fruit (0.24) and number of fruits per vine (0.22).

Table.1 Estimates of variability parameters for different characters in local cucumber (*Cucumis sativus* L.)

Characters	Mean ± SE (m)	Range	Coefficient of variability		Heritability (bs) (%)	Genetic advance	Genetic gain as % age of mean
			PCV	**GCV**			
Days to 50% flowering	30.35 ± 0.53	27.33-35.67	7.43	6.79	83.40	3.88	12.77
Days to first female flowering	31.30 ± 0.57	27.67-36.00	6.95	6.17	79.00	3.54	11.31
Node number at which first female flower appears	7.24 ± 0.35	4.42-10.17	19.29	17.42	81.50	2.35	32.39
Days to first harvest	50.70 ± 0.87	46.33-61.33	7.32	6.69	83.60	6.39	12.61
Fruit length (cm)	13.53 ± 0.35	9.86-18.29	14.53	13.83	90.60	3.67	27.11
Fruit diameter (cm)	4.54 ± 0.13	3.64-6.17	13.49	12.47	85.50	1.08	23.76
Average fruit weight (g)	203.81 ± 0.97	157.31-252.23	12.02	11.99	95.50	50.23	24.64
Number of fruits per vine	8.10 ± 0.35	5.58-12.17	22.00	20.69	88.50	3.25	40.10
Vine length (m)	1.80 ± 0.02	1.44-2.24	9.78	9.54	95.10	0.34	19.16
Number of seeds per fruit	244.84 ± 0.82	176.00-308.67	16.02	16.01	95.90	80.71	32.96
1000 seed weight (g)	24.60 ± 0.48	17.91-29.13	14.97	14.59	93.00	7.21	29.30
Total soluble solids (brix)	3.01 ± 0.08	2.75-4.00	11.03	9.94	81.20	0.56	18.46
Fruit yield per vine (kg)	1.47 ± 0.02	0.99-2.24	21.13	21.11	95.80	0.64	43.43
Fruit yield per hectare (q/ha)	143.74 ± 12.16	99.00-224.33	24.65	18.50	66.30	41.12	28.61

Table.2 Phenotypic (P) and Genotypic (G) correlation coefficients among various characters in local cucumber (*Cucumis sativus* L.)

Traits		DFF	DFFF	NNFFF	DFH	FL	FD	AFW	NFPV	VL	NSPF	1000 SW	TSS	FYPV	FYPH
DFF	P	-	0.148	0.006	0.446**	-0.093	0.090	-0.262*	0.251*	0.238	0.150	0.193	0.067	-0.169	-0.244*
	G	-	0.233	-0.031	0.508**	-0.069	0.128	-0.287*	0.261*	0.259*	0.163	0.217	0.093	-0.186	-0.261*
DFFF	P		-	0.217	-0.601**	-0.081	0.032	0.054	-0.046	0.113	0.129	-0.189	0.016	-0.066	-0.023
	G		-	0.333**	-0.689**	-0.109	0.087	0.070	-0.087	0.107	0.147	-0.213	0.021	-0.078	-0.084
NNFFF	P			-	-0.082	0.070	-0.155	-0.012	-0.076	-0.120	0.311*	-0.031	0.009	-0.207	-0.191
	G			-	-0.053	0.078	-0.217	-0.017	-0.090	-0.103	0.346**	-0.044	-0.003	-0.230	-0.133
DFH	P				-	-0.169	-0.491**	0.072	-0.077	0.226	-0.056	-0.118	-0.049	-0.035	-0.028
	G				-	-0.179	-0.591**	0.081	-0.090	0.240	-0.064	-0.133	-0.023	-0.041	-0.133
FL	P					-	0.259*	-0.074	-0.095	-0.049	0.051	0.013	-0.084	0.209	0.124
	G					-	0.256*	-0.077	-0.096	-0.046	0.054	0.018	-0.114	0.217	0.151
FD	P						-	0.124	-0.237	0.156	-0.548**	-0.249*	-0.194	0.303*	0.301*
	G						-	0.133	-0.263*	0.186	-0.591**	-0.263*	-0.257*	0.327**	0.396**
AFW	P							-	-0.363**	-0.291*	-0.197	-0.211	-0.333**	0.309*	0.249*
	G							-	-0.382**	-0.296*	-0.198	-0.219	-0.376**	0.311*	0.323**
NFPV	P								-	0.074	0.338**	0.192	0.259*	0.661**	0.581**
	G								-	0.080	0.360**	0.229	0.316*	0.707**	0.806**
VL	P									-	-0.037	0.282*	-0.014	0.155	0.162
	G									-	-0.039	0.298*	-0.017	0.158	0.243
NSPF	P										-	0.355*	-0.055	0.301*	0.323**
	G										-	0.365**	-0.060	0.302	0.427**
1000 SW	P											-	0.272*	0.342**	0.275*
	G											-	0.326**	0.351**	0.372**
TSS	P												-	0.512**	0.179
	G												-	0.575**	0.295*
FYPV	P													-	0.761**
	G													-	.0.990**
FYPH	P														-
	G														-

*Significant at 5% level of significance **Significant at 1% level of significance
DFF= Days to 50% flowering, DFFF= Days to first female flowering, NNFFF = Nodes number at first female flower appears, DFH =Days to first harvest, FL = Fruit length (cm), FD = Fruit diameter (cm), AFW = Average fruit weight (g), NFPV= Number of fruits per vines, VL= Vine length (m), NSPF= Number of seeds per fruit, 1000sw = 1000 seed weight (g), TSS= Total soluble solids (∘brix), FYPV = Fruit yield per vine and FYPH = Fruit yield per hectare (q/ha).

Table.3 Estimation of direct and indirect effects of different characters on fruit yield in local cucumber (*Cucumis sativus* L.)

Traits	DFF	DFFF	NNFFF	DFH	FL	FD	AFW	NFPV	VL	NSPF	1000 SW	TSS	FYPV	GCCFYPH
DFF	**0.26**	0.06	-0.01	0.13	-0.02	0.03	-0.07	0.07	0.07	0.04	0.06	0.02	0.05	0.26
DFFF	0.12	**0.54**	0.18	0.37	-0.06	0.05	0.04	-0.05	0.06	0.08	-0.11	0.01	0.04	0.08
NNFFF	0.01	-0.14	**-0.43**	0.02	-0.03	0.09	0.01	0.04	0.04	-0.15	0.02	0.00	-0.10	0.13
DFH	-0.41	-0.56	0.04	**-0.81**	-0.14	-0.48	-0.06	0.07	-0.19	0.05	0.11	0.02	0.03	-0.13
FL	0.01	0.01	-0.01	-0.01	**0.10**	-0.03	0.01	0.01	0.00	-0.00	-0.00	0.01	-0.02	0.15
FD	0.05	0.03	-0.09	0.24	0.10	**-0.41**	0.05	-0.11	0.07	-0.24	-0.11	-0.10	-0.13	-0.40
AFW	0.02	-0.00	0.00	-0.00	0.00	-0.01	**0.06**	0.02	0.02	0.01	0.01	0.02	0.02	-0.32
NFPV	-0.06	0.02	0.02	0.02	0.02	0.06	0.08	**0.22**	-0.02	-0.08	-0.05	-0.07	-0.15	0.80
VL	-0.02	-0.01	0.01	-0.02	0.00	-0.01	0.02	-0.01	**-0.07**	0.00	-0.02	0.01	0.01	-0.24
NSPF	0.04	0.03	0.08	-0.01	0.01	-0.14	-0.05	0.09	-0.01	**0.24**	0.09	-0.01	0.07	0.43
1000 SW	0.00	-0.00	-0.00	-0.00	0.00	-0.00	-0.00	0.00	0.01	0.01	**0.02**	0.01	0.01	0.37
TSS	-0.04	-0.01	0.00	0.01	0.05	0.11	0.17	-0.14	0.01	0.03	-0.14	**0.44**	-0.25	0.29
FYPV	0.27	0.11	0.33	-0.06	0.31	-0.47	-0.45	0.94	-0.23	0.43	0.50	0.83	**0.44**	0.94

Residual value: 0.5352

DFF= Days to 50% flowering, DFFF= Days to first female flowering, NNFFF = Nodes number at first female flower appears, DFH =Days to first harvest, FL = Fruit length (cm), FD = Fruit diameter (cm), AFW = Average fruit weight (g), NFPV= Number of fruits per vines, VL= Vine length (m), NSPF= Number of seeds per fruit, 1000sw = 1000 seed weight (g), TSS= Total soluble solids (◦brix), FYPV = Fruit yield per vine and GCCFYPH = Genotypic correlation coefficient of Fruit yield per hectare (q/ha)

Maximum positive indirect effect towards fruit yield per hectare was shown by number of fruits per vine via fruit yield per vine (0.94) followed by total soluble solids via fruit yield per vine (0.83), 1000 seed weight via fruit yield per vine (0.50), number of seeds per fruit via fruit yield per vine (0.43) and days to first harvest via days to first female flowering (0.37) was observed. The results are in agreement with earlier results of Pal *et al.,* (2017), Ahirwar *et al.,* (2017), Kandasamy (2017), Choudhary *et al.,* (2015), Kumar *et al.,* (2013). The very low residual value depicted that the influence of traits other than those taken into account in the present study had very less effect on yield/ha.

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