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Variability and character association studies for yield and yield contributing characters in cucumber (*Cucumis sativus*) under low hills of Himachal Pradesh

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Cucumis sativus L. popularly known as Cucumber (Khira) belongs to family Cucurbitaceae. Cucumber is thermophilic, day neutral and frost sensitive crop which requires tropical and subtropical conditions for its proper development and growth. It is primarily grown for its tender immature fruits and excellent source of vitamin C, thiamine, niacin, iron and minerals like calcium and phosphorus (Kumar *et al.* 2013). Cucurbitacins compound is responsible for slightly bitter taste in cucumber. In India, there is lots of variation in cucumber, but there has been relatively little work done for the improvement of local types. So, analysing locally adopted genotypes is priority research objective for enhancing productivity, uniformity and consumer preference. Therefore, the present investigation was conducted to examine best genotypes by identifying characters which contribute in higher economic yield in cucumber.

Twenty distinct cucumber genotypes (Supplementary Table 1) were sown in randomized complete block design with 3 replications at the field unit of Department of Vegetable Science, College of Horticulture and Forestry (Dr Yashwant Singh Parmar University of Horticulture and Forestry), Neri, Hamirpur, Himachal Pradesh, from June–September 2021. Direct sowing of seeds was done in the mid of June at the spacing of 1.25 m × 0.5 m in a plot having size 2.5 $m^2 \times 2.5$ m^2. To ensure healthy crop, cultural operations were performed in accordance with package of practices. The data was taken for 14 traits by randomly selected five plants from each plot (Table 1). The coefficient of variability was evaluated by using methodology instructed by Burton and De Vane (1953). Heritability and genetic advance under selection were calculated according to Allard (1960) and Johnson *et al.* (1955). Correlation coefficients and path-coefficient calculated were computed as per Al-Jibouri *et al.* (1958) and by Dewey and Lu (1959), respectively.

Significant differences existing among genotypes for all characters were studied. Variations among the genotypes for fruit colour, shape and wart colours was also observed. Majority of the genotypes had dark green coloured fruits, cylindrical shape with black warts, which are generally preferred by consumer. Variation for these traits was also been reported by Kumar *et al.* (2013), Pal *et al.* (2016) and Sharma *et al.* (2017). The broad range of variation was recorded for fruit weight (133.42–307.17 g) with a mean value of 213.07 g. There was great variation among the genotypes for yield which ranged from 2.97–19.00 kg/plot (Table 1). LC-C-9-21 and Solan Srijan were found to be best in disease performance, as they showed minimum present disease index (PDI) for both downy mildew and powdery mildew diseases. In general, phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV), demonstrating their sensitivity to environmental fluctuations.

Coefficient of variation: The high GCV was observed for PDI of downy mildew, number of fruits/plant, total yield/plot and PDI of powdery mildew, moderate for flesh to seed cavity ratio, harvest duration, ascorbic acid, total soluble acid and fruit weight. Low GCV was observed for days to first female flower, internodal length and fruit breadth. A similar trend was observed for these traits for PCV, indicating more variability present in these traits. Veena *et al.* (2012) and Kumar *et al.* (2008) also reported similar findings. Fruit length was recorded moderate PCV with low GCV, which showed the influence of environmental condition on their development.

Heritability and genetic advance: Heritability gives basic information about beneficial parameters which help breeders in effective selection. The heritability values for all

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traits ranged from 63.99–99.31%. Flesh to seed cavity ratio, total yield per plot, ascorbic acid, PDI of downy mildew, number of fruits/plant, fruit length, PDI of powdery mildew, total soluble solids and days to first female flower; less influenced by prevailing environment, showed high value for heritability (Table 1). The genetic advance values for all traits ranged from 10.26–90.64%. High genetic advance for PDI of downy mildew and PDI of powdery mildew, flesh to seed cavity ratio, number of fruits/plant and total yield per plot has been reported. Afroz *et al.* (2012), Veena *et al.* (2012), Pal *et al.* (2016), Bhagwat *et al.* (2018) and Mishra *et al.* (2021) also obtained similar results for these characters.

The traits, viz. PDI of downy mildew, number of fruits/plant, total yield per plot, PDI of powdery mildew and flesh to seed cavity ratio, show additive gene action, which is effective in improvement through selection. This helps in knowing the gene action governed by particular character which contributes in improvement through selection. Ascorbic acid, total soluble solids, fruit length and days to first female flower showed non-additive gene action, thus heterosis breeding may be useful. Afroz *et al.* (2012) reported high heritability with high genetic gain for number of fruits per plant and total yield per plot, whereas Pal *et al.* (2016) also reported predominance of additive gene action for number of fruits per plant, PDI of downy mildew, PDI of powdery mildew and total yield per plot and non-additive gene action for trait, viz. total soluble solids.

Character association: It is defined as the mutual relationship between two or more traits. Association between traits, i.e. positive means changes between two variables in same direction and negative means opposite direction. This study revealed that correlation was genotypically found to be higher than phenotypically, which shows that genetic factor is more involved in causing variation (Table 2). Total yield per plot exhibited highly positive and significant association with number of fruits/plants followed by fruit length, fruit breadth, harvest duration, internodal length and fruit weight. These results showed that yield in cucumber improved by selection based on the traits which showed their positive relation, as these are helpful in production improvement. Similar finding was also reported by Kumar *et al.* (2008), Afroz *et al.* (2012), Pal *et al.* (2017) and Manisha *et al.* (2021).

Fruit weight revealed highest positive and significant correlation with fruit length, followed by fruit breadth, total soluble solids, total yield per plot and internodal length. Ascorbic acid was not found significantly associated with any of traits in this study. These correlations were found in same trends both at genotypic and phenotypic levels. Path coefficient analysis (Table 3) revealed that days to first female flower had highest positive direct effect on total yield per plot which was followed by fruit length, fruit breadth, internodal length, number of fruits/plant, harvest duration, ascorbic acid and PDI of downy mildew. Whereas node number of first female flower, fruit weight, flesh to seed cavity ratio, total soluble solids and PDI of powdery mildew showed negative direct effect, and hence, these traits are not useful in production improvement. These results are in accordance with the findings of Pal *et al.* (2017) and Bhaiya *et al.* (2020).

Internodal length exhibited maximum positive direct effect and had positive significant correlation with yield, whereas fruit breadth had minimum positive direct effect. Maximum negative direct effects toward yield was showed by flesh to seed cavity ratio but correlation was non-significant. Thus, these findings showed that this trait was neglected during selection, as it did not contributed in production.

Knowledge of germplasm about their genetic parameters, viz. transmission from parents to offspring,

Table 1 Genetic parameters of variation for various horticultural traits including total yield per plot in cucumber

Character	Mean	Range	GCV	PCV	Heritability % (H)	Genetic advance (% mean)
Days to first female flower	59.08	47.66–76.66	11.88	13.07	82.72	22.27
Node number of first female flower	17.54	9.50–29.00	28.32	33.59	71.09	49.19
Fruit length (cm)	16.59	11.00–19.16	14.51	15.59	86.58	27.80
Fruit breadth (cm)	4.37	3.74–4.80	5.91	7.02	70.91	10.26
Fruit weight (g)	213.07	133.42–307.17	15.95	19.94	63.99	26.29
Flesh to seed cavity ratio	0.75	0.36–1.37	29.30	29.40	99.31	60.15
Internodal length (cm)	7.79	6.23–9.50	11.55	13.58	72.39	20.25
Number of fruits/plant	6.96	1.67–11.92	42.16	44.08	91.50	83.08
Harvest duration (days)	26.03	16.17–33.17	22.44	26.17	73.57	39.66
Ascorbic acid (mg/100 g)	3.57	2.03–4.46	21.53	21.89	96.74	43.63
TSS (^{o}B)	3.08	2.12–4.02	16.46	18.05	83.18	30.92
PDI of downy mildew	24.72	9.53–52.77	45.92	47.92	91.82	90.64
PDI of Powdery mildew	23.05	6.78–36.66	33.18	36.22	83.91	62.61
Total yield per plot (kg)	11.50	2.97–19.00	39.87	40.29	97.94	81.29

GCV, Genotypic coefficient of variation; PCV, Phenotypic coefficient of variation.

Table 2 Genotypic and phenotypic correlation coefficient between total yield and its component characters in cucumber

		Y1	Y2	Y3	Y4	Y5	Y6	Y7	Y8	Y9	Y10	Y11	Y12	Y13	Y14
Y1	G	1													
	P	1													
Y2	G	0.921**	1												
	P	0.807**	1												
Y3	G	-0.171	-0.282*	1											
	P	-0.196	-0.198	1											
Y4	G	-0.493**	-0.650**	0.434**	1										
	P	-0.444**	-0.526**	0.397**	1										
Y5	G	0.237	-0.007	0.465**	0.423**	1									
	P	0.101	-0.025	0.458**	0.444**	1									
Y6	G	0.141	0.429**	0.052	-0.407**	-0.480**	1								
	P	0.132	0.362**	0.049	-0.347**	-0.378**	1								
Y7	G	0.116	0.021	0.594**	0.522**	0.937**	-0.278*	1							
	P	0.029	-0.109	0.485**	0.406**	0.637**	-0.237	1							
Y8	G	-0.624**	-0.694**	0.513**	0.552**	-0.023	-0.122	0.097	1						
	P	-0.563**	-0.549**	0.489**	0.521**	0.022	-0.115	0.077	1						
Y9	G	-0.927**	-0.966**	0.241	0.489**	-0.127	-0.256*	-0.037	0.693**	1					
	P	-0.834**	-0.735**	0.274*	0.427**	0.035	-0.218	0.001	0.617**	1					
Y10	G	-0.045	0.072	0.041	0.003	0.089	0.239	0.193	-0.101	-0.073	1				
	P	-0.012	0.082	0.043	-0.005	0.079	0.234	0.155	-0.109	-0.083	1				
Y11	G	0.476**	0.361**	0.024	-0.053	0.413**	-0.295*	0.449**	-0.155	-0.197	0.223	1			
	P	0.357**	0.223	0.037	-0.032	0.312*	-0.263*	0.374**	-0.159	-0.180	0.203	1			
Y12	G	0.604**	0.659**	-0.783**	-0.583**	-0.322*	0.195	-0.390**	-0.688**	-0.683**	-0.130	0.097	1		
	P	0.516**	0.483**	-0.682**	-0.430**	-0.226	0.184	-0.295*	-0.632**	-0.560**	-0.132	0.095	1		
Y13	G	0.422**	0.353**	-0.342**	-0.233	0.020	0.065	0.179	-0.481**	-0.483**	0.007	0.357**	0.536**	1	
	P	0.333**	0.258*	-0.277*	-0.230	0.023	0.056	0.173	-0.435**	-0.338**	0.012	0.332**	0.462**	1	
Y14	G	-0.584**	-0.675**	0.715**	0.738**	0.321*	-0.189	0.403**	0.938**	0.653**	-0.036	-0.082	-0.788**	-0.411**	1
	P	-0.515**	-0.567**	0.654**	0.622**	0.272*	-0.183	0.332**	0.902**	0.572**	-0.033	-0.081	-0.747**	-0.369**	1

*5% Level of significance, **1% Level of significance. Y1, Days to first female flower; Y2, Node number of first female flower; Y3, Fruit length; Y4, Fruit breadth; Y5, Fruit weight; Y6, Flesh to seed cavity ratio; Y7, Internodal length; Y8, Number of fruits/plant; Y9, Harvest duration; Y10, Ascorbic acid; Y11, TSS (^{o}B); Y12, PDI of downy mildew; Y13, PDI of powdery mildew; Y14, Total yield/plot.

Table 3 Genotypic path-coefficient analysis among different component characters on yield in cucumber

	Y1	Y2	Y3	Y4	Y5	Y6	Y7	Y8	Y9	Y10	Y11	Y12	Y13	GCCTYP
Y1	0.6215	-0.2181	-0.0169	-0.0186	-0.0933	-0.0129	0.0851	-0.4592	-0.3729	-0.0049	-0.1392	0.0906	-0.0453	-0.584**
Y2	0.5725	-0.2368	-0.0279	-0.0246	0.0028	-0.0394	0.0151	-0.5108	-0.3886	0.0078	-0.1057	0.0989	-0.0380	-0.675**
Y3	-0.1065	0.0667	0.0989	0.0164	-0.1834	-0.0048	0.4355	0.3779	0.0970	0.0045	-0.0069	-0.1175	0.0368	0.715**
Y4	-0.3061	0.1539	0.0429	0.0378	-0.1669	0.0374	0.3827	0.4060	0.1965	0.0003	0.0154	-0.0874	0.0251	0.738**
Y5	0.1471	0.0017	0.0460	0.0160	-0.3945	0.0441	0.6863	-0.0173	-0.0512	0.0097	-0.1210	-0.0483	0.0022	0.321*
Y6	0.0875	-0.1016	0.0052	-0.0154	0.1892	-0.0919	-0.2038	-0.0896	-0.1029	0.0261	0.0863	0.0293	-0.0070	-0.189
Y7	0.0722	-0.0049	0.0588	0.0198	-0.3695	0.0256	0.7326	0.0716	-0.0149	0.0211	-0.1316	-0.0585	-0.0192	0.403**
Y8	-0.3877	0.1643	0.0508	0.0209	0.0093	0.0112	0.0713	0.7361	0.2787	-0.0110	0.0453	-0.1033	0.0517	0.938**
Y9	-0.5763	0.2288	0.0239	0.0185	0.0502	0.0235	-0.0271	0.5101	0.4022	-0.0079	0.0576	-0.1025	0.0519	0.653**
Y10	-0.0280	-0.0169	0.0041	0.0001	-0.0351	-0.0220	0.1417	-0.0740	-0.0292	0.1093	-0.0652	-0.0195	-0.0007	-0.036
Y11	0.2956	-0.0855	0.0023	-0.0020	-0.1630	0.0271	0.3291	-0.1140	-0.0791	0.0243	-0.2928	0.0145	-0.0384	-0.082
Y12	0.3754	-0.1561	-0.0775	-0.0221	0.1271	-0.0180	-0.2857	-0.5065	-0.2747	-0.0142	-0.0284	0.1501	-0.0576	-0.788**
Y13	0.2622	-0.0837	-0.0339	-0.0088	0.0080	-0.0060	0.1308	-0.3540	-0.1944	0.0007	-0.1046	0.0805	-0.1074	-0.411**

Y1, Days to first female flower; Y2, Node number of first female flower; Y3, Fruit length; Y4, Fruit breadth; Y5, Fruit weight; Y6, Flesh to seed cavity ratio; Y7, Internodal length; Y8, Number of fruits/plant; Y9, Harvest duration; Y10, Ascorbic acid; Y11, TSS (ºB); Y12, PDI of downy mildew; Y13, PDI of powdery mildew; Y14, Total yield/plot; GCCTYP, Genotypic correlation coefficient with total yield/plot.

variability, association and more over improvement after one selection cycle is helpful in selection of best genotypes and also for their further improvement. Thus, LC-C-4-21, LC-C-14-21, and LC-C-1-21 were found superior for total yield per plot and other important horticultural traits, viz. fruit length, fruit breadth, fruit weight, internodal length, number of fruits per plant and are recommended as the best genotypes for low hill region of Himachal Pradesh. These genotypes can be recommended to farmers for cultivation or for use in further breeding programmes.

SUMMARY

Cucumber is an important member of family Cucurbitaceae having potential applications across many sectors. Twenty genotypes were evaluated at the Department of Vegetable Science, College of Horticulture and Forestry (Dr Yashwant Singh Parmar University of Horticulture and Forestry), Neri, Hamirpur, Himachal Pradesh during June–September 2021 for studying variability in morphology, yield and its contributing traits. In studying genetic parameters, PDI of downy mildew, number of fruits/plant, total yield per plot and PDI of powdery mildew, traits showed high estimates of PCV and GCV, indicating the considerable amount of variation was present in germplasm. Most of the traits under study showed high heritability with high to moderate genetic advance as a per cent of mean, which showed the influence of additive gene action for controlling traits. Thus, selection is effective for improvement in these cucumber genotypes. Correlation association and path analysis showed fruit length, fruit breadth, internodal length, number of fruits per plant, harvest duration and ascorbic acid. These traits were considered during the selection of superior genotypes among the twenty genotypes. Thus, in this study, LC-C-4-21 and LC-C-14-21 were higher yielders and can be used for further breeding programmes.

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