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Evaluation of cucumber (*Cucumis sativus*) germplasm for agronomic traits and disease resistance and estimation of genetic variability

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ABSTRACT

The material used in the present study is of diverse nature and can be used in the breeding programme for development of improved genotypes in cucumber (*Cucumis sativus* L.). The unique accessions identified in this study can be useful as genetic stocks. The superior genotypes for fruit trait variability combined with disease resistance may assist the breeders in identifying populations with desired traits for inclusion in crop improvement programme.

Key words: Agronomic traits, Cucumber germplasm, Disease resistance, Estimation, Evaluation, Genetic variability

India is endowed with enormous variability and genetic divergence for cucumber germplams throughout the country. However, several unique indigenous germplasm that could potentially enhance cucumber productivity and nutritional quality, have not yet been wiely utilized in crop improvement programmes due to lack of relevant information. So, there is a great need of screening cucumber germplasm to identify elite genotypes with improved quality and higher yield so that they may be utilized either directly as a selection or as a parent in hybridization programme.

Cucumber (*Cucumis sativus* L.) is known to be highly preferred host for a number of diseases and pests. Among the diseases, downy mildew and virus diseases cause heavy losses particularly during hot and humid season. Downy mildew is one of the most important foliar diseases of cucurbits, causing significant yield losses not only in India but also in the USA, Europe, China and Israel (Thomas 1996). The downy mildew pathogen has a wide geographical distribution and host range of approximately twenty different cucurbitaceous crops (Lebeda and Urban 2007, Palti and Cohen 1980). Downy mildew management relies mainly on the application of fungicides and the use of resistant host. Fungicide resistance of *Pseudoperonospora cubensis* have been documented throughout the world (Lebeda and Urban 2007, Zhu *et al.* 2008). Use of resistant germplasm as source in resistance breeding program may be the answer for developing resistant variety to control the disease(s).

The assessment of variability present in any crop species is the essential pre-requisite for planning and execution of breeding programme for improvement of yield related traits. The genotypic and phenotypic coefficients of variability are helpful in exploring the nature of variability in the breeding populations, whereas estimates of heritability provides index of transmissibility of characters. The information on heritability alone may not help in identifying characters for enforcing selection and heritability estimates in conjunction with predicted genetic advance is more reliable (Johnson *et al.* 1955). Heritability gives the information on the magnitude of inheritance of characters from parent to off spring, while genetic advance will be helpful in finding the actual gain expected under selection. All these measures are important for the identification of genetically distant parents to get superior hybrids and segregants, to evaluate the degree of genetic erosion, or even to determine the extent of the genetic base of cultivated forms to develop heterotic groups. Hence, on the basis of these parameters, suitable selection strategy can be formulated for higher yield as well as disease resistance in cucumber. Information on genetic diversity is used to identify the promising diverse genotypes, which may be used in further breeding programme. Keeping this in view, the present study is designed to characterize and evaluate 42 indigenous cucumber accessions including two checks and to define the level of diversity present among them with respect to agro-morphological traits and reaction to different biotic stresses.

MATERIALS AND METHODS

The experimental materials comprised forty two indigenous collections of cucumber including two checks,

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conserved in National Gene Bank at National Bureau of Plant Genetic Resources, New Delhi of which seven accessions were from Tripura (IC410617, IC410638, IC410654, IC410657, IC410658A, IC410658B, IC410682), twenty from West Bengal (IC527391, IC527394, IC527395, IC527397, IC527400, IC527402, IC527403, IC527404, IC527405, IC527410, IC527412, IC527413, IC527418, IC527419, IC527420, IC527423, IC527426, IC527427, IC527431, IC527434), nine from Uttar Pradesh (IC538121, IC538126, IC538130, IC538137, IC538145, IC538147, IC538155, IC538173, IC538186), two from Mizoram (IC420405, IC420422), one each from Haryana (IC557170) and Odisha (IC257296) and two checks Pusa Uday and Pahari Harit.

The present investigation was carried out at Research Farm of the National Bureau of Plant Genetic Resources, IARI farm, New Delhi in a Randomized Complete Block Design with 2 replications for phenotypic evaluation during *kharif* season in the year 2011 and 2012. The experimental site was situated at 28° 35' N latitude and 77° 12' E longitudes with an altitude of 228.6 m above mean sea level. The soil is sandy loam in texture. The crop was raised in well prepared hills with a spacing of 60 cm between hills and 4 m between channels. The recommended dose of fertilizer and agronomic practices were followed to raise a successful crop. There were seven hills per replication out of which five plants were selected for taking observation on 14 traits, viz. node number bearing first female flower, vine length, number of primary branches, fruit length, fruit diameter, seed cavity length, seed cavity breadth, fruit weight, number of fruits/plant, shelf-life, total soluble solids (TSS), seed length, 100 seed weight and number of seeds/fruit.

Screening of cucumber accessions against the pathogen causing downy mildew (DM) disease was done following 0 to 9 visual rating scales of Jenkins and Wehner (1983). As per the Jenkins and Wehner's scale 0, no disease, immune (I); 1, few small leaf lesions, highly resistant (HR); 2, few lesions on few leaves with no stem lesions, resistant (R); 3, few lesions on few leaves or with superficial stem lesions, moderately resistant (MR); 4, few well-formed leaf lesions or superficial stem lesions, moderately susceptible (MS); 5, few well-formed leaf lesions or enlarging stem lesions, moderately susceptible (MS); 6, many large leaf lesions or deep stem lesions with abundant sporulation, or plant more than 50% defoliated, susceptible (S); 7, many large coalescing leaf or stem lesions, over 75% of plant area affected or defoliated, susceptible (S); 8, plants largely defoliated, leaves or stems with abundant sporulating lesions, highly susceptible (HS); 9, plants dead, highly susceptible (HS). Screening for virus disease resistance was followed with 0-4 scale (0, no symptoms; 1, 1-25% leaf area with symptoms; 2, 26-50% leaf area with symptoms; 3, 51-75% leaf area with symptoms; 4, 76-100% leaf area with symptoms). After scoring, PDI was calculated for each accession. The accessions were grouped into five categories on the basis of PDI: 0-10, resistant (R); 11-20, moderately resistant (MR); 21-30, moderately susceptible (MS); 31-40, susceptible (S); >40, highly susceptible (HS) (Dhillon *et al*. 2007).

Analysis of variance was performed using the GLM procedure of SAS 9.2 (SAS Institute, 2007). The phenotypic and genotypic coefficient of variation were calculated according to Burton and De Vane (1953), heritability, genetic advance and genetic gain were calculated following Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Analysis of variance (Table 1) revealed significant differences for all the fourteen traits under study. Variance due to genotypes was highly significant for all the traits indicating the presence of sufficient variability in the genotypes selected for this study.

Mean performance of genotypes

Genetic variability is the basic need for a plant breeder to initiate any breeding programme. Among the horticultural traits, comparatively wide range was observed for node number bearing first female flower (4.25-18.95) which determines the earliness of a variety. It has been observed that a number of genotypes are having a varying degree of earliness and lateness (Table 2). The genotypes IC257296, IC410617, IC410654, IC410657, IC410658B were found to be the earliest with first female flower at 5th to 6th node while the genotypes IC420405, IC420422, IC538147 and IC538155 are found to be very late, i.e. first female flower at >15th node. Identification of such genotypes would be useful in extending the availability. Judicious planting of early and late genotypes will help in sustainable marketing of cucumber cultivars for a longer period.

Wide range of variations (166.52-227.04 cm, 3.0-9.0) was observed for vine length and number of primary branches which are important traits reflecting vegetative

Table 1 Analysis of variance (ANOVA) for horticultural traits of cucumber (pooled data)

Source of variance	df	nnff	vl (cm)	pb	fl (cm)	fd (cm)	scl (cm)	scb (cm)	fw (g)	nfp	shl (days)	TSS (^{0}B)	sl (cm)	sw (g)	nsf
Replication	1	15.77*	3.52	0.007	4.39*	0.47	2.44*	2.33	250.36	0.01	0.01	0.01	0.003	0.01	702.03
Genotype	41	24.41**	433.88**	3.42**	11.62**	8.47**	1.36**	0.41	3282**	13.26**	1.31**	0.38**	0.08**	0.64**	13583.63**
Error	41	0.763	159.237	0.31	0.697	0.393	0.25	0.265	496.41	0.107	0.04	0.004	0.02	0.02	167.66

Node number bearing first female flower (nnff), vine length (vl), number of primary branch (pb), fruit length (fl), fruit diameter (fd), seed cavity length (scl), seed cavity breadth (scb), fruit weight (fw), number of fruits/plant (nfp), shelf-life (shl), TSS, seed length (sl), 100 seed weight (sw) and number of seed/fruit (nsf)

Table 2 Mean performance of cucumber genotypes for different horticultural traits (pooled data)

Genotypes	nnff	vl (cm)	pb	fl (cm)	fd (cm)	scl (cm)	scb (cm)	fw (g)	nfp	shl (days)	TSS (^{0}B)	sl (cm)	Sw (g)	nsf
IC257296	4.25	166.52	5.60	7.88	4.44	6.50	3.55	115.80	14.27	3.95	3.20	0.76	1.84	184.04
IC410617	5.15	177.44	6.10	14.50	3.71	12.45	3.05	136.75	11.40	3.37	4.70	1.39	3.14	315.00
IC410638	16.70	183.96	4.97	14.45	4.22	13.06	2.75	199.65	9.95	2.92	4.90	1.10	2.43	196.00
IC410654	4.95	178.27	5.70	16.60	4.76	13.36	3.23	246.81	12.50	3.92	4.65	1.32	2.66	220.40
IC410657	5.20	188.16	8.00	13.55	5.85	13.26	3.50	166.33	11.60	4.53	3.95	1.10	2.27	259.00
IC410658A	7.50	227.04	6.80	15.41	4.63	13.64	2.75	178.00	13.20	4.23	4.50	1.16	2.53	355.00
IC410658B	5.80	182.90	4.40	10.46	3.78	8.90	2.35	108.50	5.80	3.92	5.07	0.90	1.25	254.00
IC410682	7.55	187.67	8.10	13.46	3.43	10.86	2.85	122.50	11.00	3.97	4.60	1.27	2.63	250.48
IC420405	17.60	175.80	4.60	19.49	7.00	14.60	3.70	202.34	4.75	3.84	4.40	0.72	1.47	54.98
IC420422	18.95	185.25	4.35	14.60	6.01	11.10	3.75	200.60	5.11	3.72	4.80	0.75	1.66	64.32
IC527391	6.95	172.54	4.50	12.48	3.70	8.61	2.80	140.30	8.90	3.52	4.20	1.25	2.51	268.00
IC527394	8.55	180.76	5.90	13.22	4.47	11.73	3.13	134.69	14.00	4.15	4.60	1.10	2.36	379.00
IC527395	9.25	189.18	3.70	11.84	4.61	10.36	3.37	130.63	6.30	3.25	3.60	1.00	2.26	245.00
IC527397	7.80	177.76	3.90	10.27	4.15	8.56	2.83	82.75	6.00	5.48	4.40	1.10	2.56	101.00
IC527400	8.55	208.28	9.30	12.66	3.15	11.56	2.40	88.70	10.00	3.70	4.50	1.14	2.32	251.00
IC527402	9.65	178.16	5.08	13.25	3.97	11.85	3.15	121.50	13.40	4.88	3.50	1.24	3.13	305.00
IC527403	9.60	169.37	4.50	13.53	4.68	12.26	3.40	127.73	7.10	2.97	4.00	1.10	2.54	215.00
IC527404	9.60	224.88	5.60	15.71	4.28	13.42	2.93	170.69	10.20	2.87	4.10	1.14	2.59	210.00
IC527405	11.50	183.06	5.60	13.30	4.28	10.61	2.70	126.06	7.40	4.00	3.90	1.30	3.23	196.00
IC527410	9.85	171.50	4.80	13.09	4.79	12.40	3.18	124.94	14.20	3.37	3.90	1.20	2.99	365.00
IC527412	9.90	203.80	6.00	14.93	4.29	12.23	2.85	139.40	9.80	3.95	4.20	1.10	2.19	350.00
IC527413	10.25	178.32	4.40	14.13	3.60	11.66	2.75	137.25	8.90	4.15	4.10	1.30	3.48	367.00
IC527418	10.50	177.62	3.80	10.35	3.80	8.03	2.75	82.55	9.90	5.15	4.10	1.10	2.83	280.00
IC527419	11.00	198.44	6.60	13.73	3.35	10.48	2.45	88.55	8.50	4.00	4.00	1.12	3.32	198.00
IC527420	10.50	179.58	4.00	10.96	3.80	8.26	2.50	117.00	8.50	7.00	4.20	1.00	2.26	190.00
IC527423	11.50	180.10	4.60	17.36	4.90	14.30	2.95	127.50	12.40	3.92	3.80	1.20	2.58	245.00
IC527426	10.90	168.22	3.00	12.57	3.35	10.28	2.55	125.50	11.30	4.00	5.40	1.00	2.39	279.11
IC527427	10.95	171.46	4.00	10.50	3.45	8.16	2.45	97.80	9.50	4.93	4.40	1.10	2.69	307.00
IC527431	11.50	201.27	6.40	13.03	3.45	9.71	2.47	102.50	5.80	2.20	4.10	1.10	2.47	180.00
IC527434	10.55	178.72	5.00	9.97	3.45	8.52	2.65	92.25	10.50	2.10	4.30	1.00	1.53	395.00
IC538121	12.60	202.74	5.60	14.43	4.15	11.56	3.25	157.38	8.80	4.00	3.90	1.10	2.47	210.00
IC538126	13.49	175.77	4.70	14.08	3.53	12.46	2.52	178.38	9.40	3.87	3.70	0.50	1.54	234.00
IC538130	11.95	172.54	4.10	11.48	4.40	9.33	3.32	93.30	12.40	4.00	3.90	1.10	2.31	210.00
IC538137	13.15	180.62	4.70	12.20	3.88	10.16	2.48	112.10	6.10	3.50	5.00	0.54	1.43	363.00
IC538145	13.85	181.93	5.10	15.20	3.80	12.26	3.33	135.90	10.20	3.90	4.10	1.10	2.26	178.00
IC538147	15.16	171.14	4.30	20.40	4.60	15.33	3.70	226.34	10.00	3.92	4.10	1.10	3.17	230.00
IC538155	15.10	184.28	4.70	14.40	4.15	11.60	2.70	201.00	8.10	4.21	4.20	1.10	3.52	250.10
IC538173	14.50	184.88	3.55	11.69	3.40	9.70	2.75	86.30	10.00	4.10	4.90	1.10	2.59	144.00
IC538186	14.40	182.62	5.10	14.22	3.62	11.60	2.62	132.83	8.82	3.82	4.30	1.10	2.36	130.00
IC557170	14.55	204.00	5.90	15.57	3.75	14.43	2.60	167.98	10.20	3.90	4.40	0.68	1.66	189.00
Pusa Uday	7.20	175.72	5.25	13.87	5.28	12.00	3.42	169.67	9.20	4.02	4.20	0.84	2.43	144.00
Pahari Harit	8.55	217.26	7.40	15.03	5.90	13.33	4.42	145.80	10.00	3.62	4.20	1.20	3.13	176.00
CD (P=0.05)	1.77	25.50	1.13	1.69	1.01	1.27	1.04	45.03	0.66	0.42	0.13	0.11	0.29	26.17

Node number bearing first female flower (nnff), vine length (vl), number of primary branch (pb), fruit length (fl), fruit diameter (fd), seed cavity length (scl), seed cavity breadth (scb), fruit weight (fw), number of fruits/plant (nfp), shelf-life (shl), TSS, seed length (sl), 100 seed weight (sw) and number of seed/fruit (nsf)

growth (Table 4). IC410658A was found to bear longest vine (227.04 cm) while IC257296 bear shortest (166.52 cm) vine. Wide variations (7.88- 20.40 cm, 3.15-7.00 cm, 82.55-246.81 g) were observed with respect to fruit length, breadth and weight respectively, which are considered as major yield contributing traits. IC538147 (20.4 cm) recorded the longest fruit and was found at par with IC420405 (19.49 cm) while IC257296 recorded the smallest fruit (7.87 cm). For slicing cucumber, thin and long fruits are desirable; however, small fruit types may be desirable for processing industry. Usually pickling cucumbers are canned as a whole fruit but slicing cucumber is canned after making slices.

The accession showing small fruit may be a good source of genes for developing small cucumber suitable for processing. Nevertheless, the small types may also be suitable for growing in kitchen gardens due to small vine length (166.52 cm).

Quite a good variation was observed with respect to number of fruits/plant (4.75-14.40), shelf-life (2.1-7.0 days), seed length (0.50-1.39 cm), 100 seed weight (1.25-3.52 g) and seed per fruit (54.98-395). IC527426 (14.27), IC527410 (14.2) and IC527394 (14.0) were found to bear significantly largest number of fruits per vine. Wide variations for different horticultural traits were earlier reported by Singh *et al.* (2002), Das *et al.* (2003), Verma (2003), Kumar (2006), Munshi *et al.* (2007), Hanchinamani *et al.* (2008), Yogesh *et al.* (2009) and Kumar *et al.* (2013) in cucumber.

All the genotypes under study showed wide variations for fruit colour (green, light green, dark green and white), flesh colour (white, green, orange) and total soluble solid (3.2-5.4° Brix), which decides the consumer's preference. Majority of the genotypes including both the check cultivars had light green coloured fruits which are in general preferred by consumers. Highest TSS was recorded in IC527426 (5.4°B) followed by IC410658B (5.07°B) and three other genotypes namely IC410638, IC410617, IC538173 performed better over both the checks (4.2°B) for total soluble solids. Similar results have also been reported by Verma (2003) and Kumar (2006) for these characters. Two accessions, viz. IC420405 and IC420422 were found to have orange flesh colour. Previously orange flesh cucumber was reported to be derived from a landrace named Xishuangbanna Gourd (*Cucumis sativus* var. *xishuangbannaenensis*) from the Prefecture Xishuangbanna of the Yunnan Province in Southwest China, which is close to North Eastern part of India and incidentally the above two orange flesh cucumber were also collected from Mizoram located in North Eastern part of India. Recent studies indicated that orange fleshed cucumber of China (Xishuangbanna gourd) is closely related to Indian cucumber germplasm (Lv *et al.* 2012). This suggests that the orange flesh Indian cucumber germplasm might have migrated to China from north eastern parts of India, the primary centre of origin. Hence, there is an urgent need to collect more diversity for this trait from the north eastern states, and identify the promising germplasm and use them in breeding program to develop carotenoid rich cucumber, which might play a significant role in achieving nutritional security.

Screening for disease resistance

The check varieties Pahari Harit and Pusa Uday both exhibited susceptible reaction (Score >6) to downy mildew pathogen indicating presence of high inoculum load in the experimental area. Out of 38 accesssions screened for disease reaction, 12 accessions have shown disease symptom categorised in 0 to 2 score (resistant reaction) and 26 accessions in 4 to 9 score (susceptible reaction) as per 0 to 9 scale during both the year (Table 3). Out of 12 germplasm showing resistant reaction, three accessions, viz. IC410617, IC527419 and IC538130 were highly resistant (score = 1). Wehner and Shetty (1997) evaluated several germplasm in multiple environments following the Jenkins and Wehner's scale (1983) and reported responses of germplasm to downy mildew as highly resistant having ratings of 1.3 to 3 and as resistant from 3.3 to 5.0 after analysis. They also classified some germplasm as resistant if the rating is 1.0 to 5.0, when evaluated in only two environments. Thirteen accessions were observed as resistant against virus (PDI= 0 - 10) and seven accessions were moderately resistant (PDI= 11-20). Remaining was observed as moderately resistant to highly susceptible to viruses causing curling, mosaic and severe stunting diseases. High disease severity of curling and

Table 3 Cucumber germplasm showing disease reaction to downy mildew and virus diseases

Disease reaction	Downy mildew	Virus diseases
Immune	IC410617, IC527419, IC538130	-
Highly Resistant	IC410682, IC527391,IC527394, IC527397, IC527400, IC527413, IC527418, IC527423, IC538137	-
Resistant	IC527403, IC527404, IC527405, IC527410, IC527412, IC527420, IC527431, IC538121, IC538173	IC410617, IC410658A, IC410658B, IC410682, IC527394, IC527400, IC527404, IC527410, IC527431, IC538121, IC538145, IC538155, IC538186
Moderately Resistant	-	IC527391, IC527397, IC527402, IC527403, IC527423, IC538130, IC538173, Pusa Uday (Check)
Moderately Susceptible		IC410654, IC410657, IC527426, IC527427, IC557170, Pahari Harit (Check)
Susceptible	IC410658B, IC527402, IC527426, IC527427, IC527434, IC538126, IC538145, IC538147, Pahari Harit (Check), Pusa Uday (Check)	IC527405, IC527412, IC527434, IC538126, IC538137, IC538147, IC410638
Highly Susceptible	IC410654, IC410657, IC410658A, IC527395, IC538155, IC557170, IC538186, IC410638,	IC420405, IC420422, IC527395, IC527413, IC527418, IC527419, IC527420

Table 4 Estimates of phenotypic and genotypic coefficient of variation, heritability, genetic advance and genetic gain for different horticultural traits (pooled data)

Character	Mean±SE	Range	GCV (%)	PCV (%)	Heritability (bs)	GA	GA as % of mean
Node number bearing first female flower	10.64±0.62	4.25-18.95	32.31	33.34	0.94	6.01	63.89
Vine length (cm)	185.23±8.92	166.52-227.04	6.33	9.30	0.46	16.27	8.78
Number of primary branches	5.23±0.39	3.0-9.0	23.86	26.13	0.83	2.56	44.46
Fruit length (cm)	13.57±0.59	7.88-20.4	17.23	18.30	0.89	3.88	33.10
Seed cavity length (cm)	4.23±0.35	3.15-7.0	17.80	18.64	0.91	3.63	34.66
Fruit diameter (cm)	11.3±0.44	6.50-15.33	17.67	21.26	0.69	1.23	29.97
Seed cavity breadth (cm)	2.97±0.36	2.35-4.42	9.35	19.69	0.23	0.28	9.06
Fruit weight (g)	139.11±15.75	82.55-246.81	26.83	31.25	0.74	66.68	46.99
Number of fruits/plant	9.65±0.23	4.75-14.25	26.45	26.66	0.98	6.55	53.51
Shelf-life (days)	3.92±0.15	2.10-7.0	20.32	21.01	0.94	1.57	40.10
TSS (^{0}B)	4.26±0.04	3.20-5.40	10.29	10.40	0.98	0.79	20.77
Seed length (cm)	1.06±0.04	0.50-1.39	18.48	19.15	0.93	0.26	36.39
100 seed weight (g)	2.45±0.1	1.25-3.52	22.73	23.47	0.94	0.79	44.90
Number of seeds/fruit	236.61±9.15	54.98-395.00	34.62	35.05	0.98	130.10	69.75

stunting caused by ToLCNDV were observed in 5 accessions. Twelve accessions were identified as resistant to downy mildew pathogen, 13 accessions resistant to virus. Incidentally the check Pahari Harit (Score = 6) and Pusa Uday (Score = 6) exhibited susceptible reaction to downy mildew pathogen but both have shown resistant reaction to virus. Three accessions, viz. IC410617, IC527419, and IC538130 were found free from DM symptom but only IC410617 was found resistant to virus disease and remaining two acc. IC527419 and IC538130 were observed as susceptible to ToLCNDV. Another three acc. IC410682, IC527394 and IC527400 were highly resistant to DM but resistant to virus disease, whereas IC527404, IC527410, IC527431 and IC538121 were resistant to both DM and virus disease. The accession IC410617, collected from West Tripura district of Tripura during 2003 had shown immunity against DM but resistant (R) reaction against ToLCNV. Besides the resistance to diseases, this novel accession IC410617 has good agro-morphological characters with average fruit length of 14.7 cm, diameter (3.7 cm) and fruit weight (136.7 g). This accession can be utilized as resistant source to both the diseases.

Coefficients of variability

The estimates of phenotypic and genotypic coefficients of variation gave a clear picture on the magnitude of variations presents in the available germplasm (Table 4). High PCV (>20%) and GCV (>20%) were observed for node number bearing first female flower, primary branches, fruit weight, fruits/plant, shelf-life, 100 seed weight, seeds/fruit. High estimates of PCV and GCV for number of fruits/plant and fruit weight has been reported earlier in cucumber (Kumar *et al*. 2008) and culinary melons (Rakhi and Rajamony 2005). Phenotypic coefficient of variation was higher in magnitude than genotypic coefficient of variation for all the characters under study. The high magnitude of variability in the present study may be due the fact that the genotypes were collected from different agro climatic conditions. Low GCV (<10%) was recorded in vine length and seed cavity breadth. These results are in line with Singh (1997), Yogesh *et al.* (2009), Bisht *et al*. (2010) and Kumar *et al*. (2013). However, the difference between PCV and GCV was not higher in all the characters except vine length, seed cavity breadth and fruit weight which reflects that the variability existing in them was mainly due to their genetic makeup. Thus, selection on the basis of phenotype will be effective.

Heritability and genetic gain

Heritability estimate is an informative parameter to the breeder for selecting the desired genotypes for further use. The estimates of heritability were found high (>90%) for all the characters except primary branch and fruit length with moderate heritability (80-90%); and vine length, fruit diameter, seed cavity breadth and fruit weight with low heritability (<80%) indicating major role of genotypes in expression of these characters. High heritability estimates for number of fruits/plant was also reported by Singh (1997), Munshi *et al.* (2007) and Bisht *et al.* (2010). However, Kumar *et al*. (2008) and Yogesh *et al.* (2009) reported high heritability for fruit length but found moderate heritability for node number bearing first female flower.

Selection can be exercised on the basis of phenotypic performance for highly heritable characters. Heritable variation can be found out with greater degree of accuracy when heritability is studied in conjunction with genetic advance. The genetic gain measured in terms of GA as % of mean, was found high (>50%) for node number bearing first female flower, fruits/plant and seeds/fruit. Moderate genetic gain (40-50%) was observed for primary branch, fruit weight, shelf-life and 100 seed weight. These findings are in line with Singh (1997), Kumar *et al.* (2008) and Yogesh *et al.* (2009).

High heritability estimates coupled with high genetic gain were observed for node number bearing first female flower, number of fruits/plant and number of seeds/fruit which reflects that these characters are predominantly controlled by additive gene effects and more responsive to selection. Similar results were reported by Kanwar *et al.* (2003) for node of first female flower in cucumber; Kumar *et al*.(2008) for days to first female flower anthesis, number of fruits/plant, fruit length and fruit diameter; Devmore *et al.* (2010) for fruit weight, number of seeds/fruit, vine length and fruit number/vine in bitter gourd. High heritability coupled with moderate genetic gain was observed for fruit length, seed cavity length, shelf-life and seed length. This showed that these characters are under non-additive gene effects and selection for these characters will be less effective. Such traits are more under the influence of environment and do not respond to selection. Similar results for fruit length were reported by Joshi *et al.* (1981), Kumar *et al.* (2008) and Yogesh *et al.* (2009) and Kumar *et al.* (2013).

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