Bangladesh J. Bot. **48**(3): 481-488, 2019 (September)

GENETIC DIVERSITY AMONG LANDRACES OF CUCUMBER (*CUCUMIS SATIVUS* L.) FROM NORTH EAST INDIA

DHIMAN CHAKRABORTY, MUKUL KUMAR[1]*, LOBSANG WANGCHU[2], SIDDHARTHA SINGH[3] AND AK PANDEY[4]

Department of Vegetable Science, College of Horticulture & Forestry, Central Agricultural University, Pasighat, Arunachal Pradesh, India

Keywords: *Cucumis sativus*, Coefficient of variation, Genetic diversity, Morphological traits

Abstract

Twenty eight diverse landraces collected from various parts of North Eastern Region of India along with two checks were evaluated to study the diversity pattern among the genotypes on 17 morphological traits. High magnitude of genotypic coefficients of variation (GCV) and heritability coupled with high genetic gain were observed for average fruit weight, fruit yield per plant, number of fruits per plant, fruit length, number of branches per plant, number of seeds per fruit and 100 seed weight. However, these parameters were moderate for early fruit harvest and total soluble solids (TSS). Thirty genotypes were grouped into 6 clusters which showed intercluster D^2 values ranging between 115.81 and 670.08. Grouping of genotypes of same location in different clusters indicated that the geographical diversity may not necessarily be related to genetic diversity. The cumulative contribution (82.28%) of fruit weight, 100-seed weight, number of branches per plant and fruit yield per plant to the total divergence indicate the importance of these traits in choice of parents for hybridization programme in cucumber.

Introduction

Cucumber *(Cucumis sativus* L.) is one of the most important cucurbitaceous vegetable crops grown extensively in tropical and sub-tropical parts of Asia. It is a thermophilic and frost susceptible species growing best at a temperature above 20°C and cultivated both in summer and rainy seasons in Asia. It is grown for its tender fruits, which are consumed either raw as salad, making pickles, cooked as vegetable or as pickling cucumber in its immature stage and even brined on commercial scale in almost all parts of the world. It is a rich source of vitamin B and C, carbohydrates, Ca and P (Yawalkar 1985). It is ideal for people suffering from jaundice and also very much useful in preventing constipation. Seeds contain oil, which is helpful for brain development and body smoothness and it is being used in Ayurvedic preparations.

North-eastern India is endowed with micro-climatic conditions, which are quite suitable for commercial cultivation and seed production of cucumber. This region has vast diversity of cucumber based on morphological traits which can be utilized in breeding programme for development high yielding genotypes for commercial cultivation. Therefore, an attempt was made to evaluate the landraces collected from different parts of the north-eastern region of India in order to characterize the potential lines which may be further utilized for genotypic selection suitable under climatic pattern of this region.

*****Author for correspondence: <mukulbreeder@rediffmail.com>. [1]Department of Plant Breeding & Genetics, College of Agriculture, Banda University of Agricultural & Technology, Banda-210001, Uttar Pradesh, India. [2]Department of Fruit Science, College of Horticulture & Forestry, CAU, Pasighat-791102, Arunachal Pradesh, India. [3]Department of Basic science and Humanities, College of Horticulture & Forestry, CAU, Pasighat-791102, Arunachal Pradesh, India. [4]College of Horticulture and Forestry, CAU, Pasighat-791102, Arunachal Pradesh, India.

Materials and Methods

The present investigation was carried out at Vegetable Research Farm, Department of Vegetable Science, College of Horticulture and Forestry, Central Agricultural University, Pasighat, Arunachal Pradesh. The geographical location of the research farm is having an altitude of 153 m above mean sea level, latitude of 28°04`N and longitude of $95^0$22`E. The climate of this area is humid, sub-tropical and maximum rainfall occurs between June-September. The soil is sandy loam with pH 6.7 and 2.1% of organic carbon.

The experimental materials comprised of 28 diverse landraces of cucumber (*Cucumis sativus* L.) collected from different places of North-eastern region along with two checks. The land races with its code and their place of collection are presented in Table 1. The experimental materials were sown in RBD with three replications at spacing of 150 × 80 cm during February, 2016. The standard cultural practices were followed to produce a healthy crop. Observations were recorded on five randomly selected plants from each genotype in each replication for 17 quantitative traits *viz.*, number of branches per plant, days to first pistillate flower anthesis, days to first staminate flower anthesis, node bearing first pistillate flower, node bearing first staminate flower, number of pistillate flowers, number of staminate flowers, days to first fruit set, days to first harvest, number of fruits per plant, length of fruit (cm), fruit diameter (cm), average fruit weight (cm), number of seeds per fruit, 100-seed weight (g), fruit yield per plant (kg) and total soluble solids (^{0}Brix). Severity of economically important diseases *viz.*, powdery mildew, anthracnose and angular leaf spot were recorded periodically in each genotype. The mean plot data were subjected to estimation of phenotypic and genotypic coefficient of variation (PCV and GCV) as per method given by Burton (1952), heritability and expected genetic advance as per Johnson *et al.* (1955). To assess the genetic divergence among the landraces, Mahalanobis D^2 statistics (Singh and Chaudhary 1985) was used. Based on the genetic distance, all the genotypes were grouped into different clusters (Rao 1952). The disease severity of anthracnose and angular leaf spot were recorded on 0 - 5 scale (Bhat 2007) and disease severity for powdery mildew was recorded by adopting the scale given by Ransom *et al.* (1991).

Table 1. Cucumber landraces with code number and their place of collection.

Place of collection	Code with number*
CHES, Ranchi	CHFC-1 (Swarna Sheetal)
CHES, Ranchi	CHFC-30 (Swarna Ageti)
Tripura	CHFC-2, CHFC-3, CHFC-5, CHFC-9, CHFC-11, CHFC-19
Meghalaya	CHFC-4, CHFC-15, CHFC-26
Arunachal Pradesh	CHFC-6, CHFC-7, CHFC-8, CHFC-12, CHFC-24
Manipur	CHFC-10, CHFC-13, CHFC-14, CHFC-18, CHFC-25
Nagaland	CHFC-16, CHFC-28
Sikkim	CHFC-17, CHFC-29
Mizoram	CHFC-20, CHFC-21, CHFC-22, CHFC-23, CHFC-27

*College of Horticulture and Forestry code and collection number.

Results and Discussion

The analysis of variance in the present investigation revealed significant differences among 30 cucumber genotypes for all the traits and indicated the scope for selection of suitable initial breeding material for further crop improvement. The mean performances of 17 quantitative

characters and severity of three economically important diseases (powdery mildew, anthracnose and angular leaf spot) for comparison among thirty genotypes are presented in Table 2. The estimates of phenotypic and genotypic coefficients of variability provided a clear picture of amount of variations presents in the collected germplasm. The highest estimates (>20%) of phenotypic (PCV) and genotypic (GCV) coefficient of variation were observed for average fruit weight, fruit yield per plant, number of seeds per fruit, number of branches per plant, 100-seed weight, fruit length, node bearing first staminate flower, number of staminate flowers and number of fruits per plant (Table 3). This reflects greater genetic variability among the genotypes for these characters for producing further improvement by selection. Similar results for high GCV was also reported by Pal *et al.* (2016) for fruit weight, branches per plant and 100-seed weight, Ullah *et al.* (2012) for fruit weight, fruit yield per plant and number of fruits per plant, Kumar *et al*. (2013) for fruit weight and fruit length. The moderate estimates (10 - 20%) of PCV and GCV were recorded

Table 2. Mean performance of 30 genotypes for 17 traits and severity of powdery mildew, anthracnose and leaf spot diseases.

Genotype	NBP[$]	DFPA	DFSA	NPF	NSF	DFFS	DFH	NBFP	NBFS	NFP
CHFC-1	4.23	46.56	41.05	10.61	21.70	50.37	55.62	7.80	5.01	9.54
CHFC-2	3.20	37.10	33.53	7.35	17.95	40.66	46.92	4.85	2.88	5.32
CHFC-3	6.30	47.69	41.20	6.86	8.24	51.15	56.04	7.98	4.90	4.86
CHFC-4	1.96	44.83	36.95	11.19	24.65	47.96	54.06	8.23	3.74	9.70
CHFC-5	7.10	42.37	35.42	12.47	26.11	46.71	51.66	6.33	3.18	10.33
CHFC-6	7.94	44.01	38.30	10.12	22.44	48.03	53.06	7.76	4.18	8.87
CHFC-7	4.96	43.44	37.11	7.01	15.97	47.54	52.13	7.50	3.34	6.16
CHFC-8	3.58	47.51	40.11	9.83	19.26	51.12	56.58	8.29	4.68	7.76
CHFC-9	7.05	44.13	36.05	13.56	31.61	48.23	53.71	6.48	3.60	11.75
CHFC-10	5.52	39.17	34.27	10.50	23.50	43.16	48.46	5.06	3.06	8.01
CHFC-11	4.05	44.76	38.86	10.77	21.01	48.97	54.20	5.93	3.85	9.16
CHFC-12	5.70	44.16	38.55	9.18	19.81	48.62	54.31	8.02	4.36	7.67
CHFC-13	6.84	48.25	42.19	11.18	27.45	52.45	57.48	8.85	5.30	8.67
CHFC-14	4.53	41.32	35.68	9.51	24.67	44.94	50.45	5.50	3.52	7.39
CHFC-15	8.14	47.86	40.28	12.65	32.88	51.88	57.85	8.65	4.13	10.08
CHFC-16	7.41	52.23	46.18	9.91	28.40	56.50	61.80	10.14	6.03	7.87
CHFC-17	4.50	46.31	41.21	12.18	34.86	50.11	56.11	7.21	4.20	9.05
CHFC-18	8.10	53.58	46.73	6.93	19.04	57.17	61.96	10.91	6.30	6.06
CHFC-19	6.44	43.58	35.68	13.97	30.30	47.97	53.60	7.00	3.51	10.45
CHFC-20	5.11	46.89	41.52	10.30	29.20	50.81	56.80	7.34	4.74	8.90
CHFC-21	3.74	43.08	35.07	12.26	31.02	47.03	52.52	7.52	3.26	9.87
CHFC-22	2.16	53.13	47.14	13.36	27.38	56.78	61.38	10.66	6.72	10.81
CHFC-23	2.74	49.58	40.69	10.25	23.10	53.76	58.87	9.31	4.60	9.63
CHFC-24	5.85	44.31	40.81	8.13	25.36	48.15	54.05	7.50	4.37	6.53
CHFC-25	3.09	45.01	41.45	14.81	36.18	49.00	53.12	7.69	5.10	12.43
CHFC-26	7.03	49.22	46.41	9.08	18.03	53.60	58.65	9.08	6.23	7.27
CHFC-27	3.91	46.42	36.36	11.12	29.36	50.21	55.26	8.41	3.63	9.33
CHFC-28	4.01	48.52	42.43	8.03	26.30	51.96	57.00	8.91	5.40	6.77
CHFC-29	2.96	44.67	39.43	10.95	31.24	48.20	54.31	7.81	4.04	8.06
CHFC-30	3.47	45.16	40.39	11.91	28.06	48.89	54.52	6.58	4.31	8.77
LSD (5%)	0.61	1.77	2.44	1.25	2.51	2.07	2.00	1.01	0.85	0.96

(Contd.)

Right hand side of the table

FL	FD	AFW	NSF	SW	TSS	FYP	SPM	SA	SALS
14.90	4.50	163.00	139.66	2.45	2.45	1.55	17.46	15.24	10.26
17.00	5.50	152.00	180.00	2.56	3.01	0.81	12.23	10.50	9.50
16.00	4.66	139.00	199.00	1.60	3.73	0.67	21.1	18.50	16.64
15.30	4.40	176.00	240.00	3.15	2.75	1.71	18.76	12.25	10.4
10.30	4.96	94.06	98.00	2.49	3.16	0.97	8.15	7.75	7.04
10.00	6.40	80.66	120.00	3.62	2.90	0.72	11.65	10.96	11.10
21.30	4.93	225.00	266.00	2.42	3.15	1.38	23.26	22.30	15.70
10.50	4.86	148.00	135.00	2.14	2.75	1.14	12.78	11.10	8.60
9.86	5.10	111.00	76.00	2.63	2.33	1.30	16.30	15.70	12.15
21.16	6.33	395.00	214.00	2.68	2.74	3.16	9.78	4.44	6.44
7.10	4.80	90.00	83.00	2.34	3.08	0.82	15.80	15.10	13.36
17.73	5.43	249.00	253.66	4.00	2.66	1.90	16.90	11.74	8.10
11.56	3.66	134.00	232.33	1.99	2.03	1.15	23.58	22.80	20.13
18.33	6.10	303.66	270.00	2.10	3.04	2.24	26.25	21.38	14.51
10.40	5.33	118.00	117.00	1.87	2.73	1.18	20.60	19.34	9.11
20.06	6.33	358.00	298.66	2.40	2.26	2.81	25.60	25.03	13.64
19.76	5.73	289.00	259.00	1.73	2.92	2.61	18.03	17.40	13.90
20.00	5.63	350.33	280.00	1.15	2.26	2.12	21.20	20.90	9.28
12.16	4.03	172.33	153.33	2.68	2.71	1.80	22.95	21.80	10.86
22.40	5.96	334.00	167.66	2.60	2.67	2.97	10.86	9.60	7.60
21.40	6.40	313.33	205.00	2.80	2.10	3.09	14.66	13.00	12.50
15.03	4.33	187.00	216.33	1.42	2.52	2.02	13.96	7.20	7.10
13.63	4.23	129.06	271.33	1.56	2.50	1.24	20.58	24.40	17.56
15.10	5.93	225.23	303.00	2.33	2.84	1.47	22.44	20.25	16.96
11.96	7.10	77.13	68.00	2.54	3.72	0.94	24.12	23.20	14.74
16.86	4.86	213.60	188.00	3.87	2.80	1.55	17.81	17.00	14.20
15.83	4.70	186.00	170.00	3.34	2.23	1.73	27.26	26.06	21.50
15.16	5.73	270.66	204.67	2.70	2.21	1.76	25.00	19.04	19.15
17.66	4.36	240.66	318.33	3.80	1.80	1.87	13.02	13.50	6.67
16.66	4.94	264.00	198.00	2.55	2.62	2.31	19.55	16.45	11.30
1.88	0.41	16.12	34.96	0.25	0.49	0.30	--	--	--

[$]NBP = Number of branches per plant, DFPA = Days to first pistillate flower anthesis, DFSA = Days to first staminate flower anthesis, NPF = Number of pistillate flowers, NSF = Number of staminate flowers, DFFS = Days to first fruit set, DFH = Days to first harvest, NBFP = Node bearing first pistillate flower, NBFS = Node bearing first flower staminate flower, NFP = Number of fruits per plant, FL = Fruit length (cm), FD = Fruit diameter (cm), AFW = Average fruit weight (g), NSF = Number of seeds per fruit, SW = 100-seed weight (g), TSS = Total soluble solids (^{0}Brix), FYP = Fruit yield per plant (kg), SPM = Severity of powdery mildew (%), SA = Severity of anthracnose (%), SALS = Severity of angular leaf spot (%),

for total soluble solids and fruit diameter whereas the low estimates (< 10%) of PCV and GCV were recorded in case of days to first staminate flower anthesis, days to first pistillate flower anthesis, days to first fruit set and days to first harvest (Table 3). The similar magnitude of coefficients of genetic variability was also observed by Rajawat and Collis (2017) for fruit diameter, days to first staminate and pistillate flowers anthesis and Kumar *et al.* (2013) for total soluble solids.

High estimates (>60%) of heritability (broad sense) was recorded for all the characters under studied which indicated that large proportion of phenotypic variance has been attributed to genotypic variance and suggested that selection could be made for these traits on the basis of

phenotypic expression. The high heritability values for yield and its component traits are in agreement with the findings of Ullah *et al*. (2012), Kumar *et al.* (2013), Pal *et al*. (2016) and Rajawat and Collis (2017).

Table 3. Estimates of genetic parameters of 17 characters in cucumber.

Characters	Mean ± SE	Range		Coefficient of variation (%)		Herita-bility (%)	Genetic advance	Genetic advance as % of mean (Genetic gain)
				PCV	GCV			
Number of branches per plant	5.05 ± 0.21	1.96	8.14	36.98	36.22	95.89	3.69	73.06
Days to first pistillate flower anthesis	45.83 ± 0.62	37.10	53.58	8.26	7.91	91.77	7.15	15.61
Days to first staminate flower anthesis	39.70 ± 0.86	33.53	47.14	9.88	9.14	85.45	6.91	17.40
Number of pistillate flowers	10.53 ± 0.44	6.86	14.81	21.09	19.78	87.85	4.02	38.23
Number of staminate flowers	25.17 ± 0.88	8.24	36.18	24.95	24.19	94.01	12.16	48.31
Days to first fruit set	49.73 ± 0.73	40.66	57.17	7.69	7.26	89.03	7.01	14.11
Days to first harvest	55.08 ± 0.70	46.92	61.96	6.63	6.25	88.86	6.69	12.15
Node bearing first pistillate flower	7.78 ± 0.35	4.85	10.91	20.04	18.37	84.07	2.70	34.71
Node bearing first staminate flower	4.40 ± 0.30	2.88	6.72	25.04	22.03	77.41	1.76	39.94
Number of fruits per plant	8.57 ± 0.33	4.86	12.43	21.82	20.71	90.25	3.47	40.50
Fruit length (cm)	15.50 ± 0.66	7.10	22.40	27.06	26.02	92.43	7.99	51.53
Fruit diameter (cm)	5.24 ± 0.14	3.66	7.10	16.39	15.67	91.41	1.61	30.87
Average fruit weight (g)	206.29 ± 5.69	77.13	395.00	43.99	43.73	98.81	184.73	89.55
Number of seeds per fruit	197.50 ± 12.34	68.00	318.33	37.13	35.51	91.49	138.22	69.98
100 seed weight (g)	2.51 ± 0.09	1.15	4.00	28.73	28.06	95.35	1.42	56.45
TSS (^{0} Brix)	2.69 ± 0.17	1.80	3.73	18.88	15.19	64.72	0.67	25.17
Fruit yield per plant (kg)	1.70 ± 0.10	0.67	3.16	43.10	41.66	93.46	1.41	82.98

Further, Johnson *et al.* (1955) reported that high heritability estimates along with high genetic gain were useful than heritability alone for effective selection. Similarly, in the present study (Table 3) the characters like average fruit weight, fruit yield per plant, number of branches per plant, number of seeds per fruit, 100-seed weight, fruit length, number of fruits per plant, fruit diameter, number of pistillate flowers, node bearing first pistillate flower and total soluble solids recorded high heritability with high genetic advance which indicated that these characters are under additive gene effects and hence these characters are more reliable for effective selection. Pal *et al*. (2016) and Rajawat and Collins (2017) also reported high heritability coupled with high genetic gain for primary branches per plant, node bearing first pistillate flowers, fruit length and fruit yield per plant. High heritability coupled with moderate genetic gain was observed for days to

first pistillate flower anthesis, days to first fruit set, days to first harvest (Table 3) which indicated that these characters are under non-additive gene effects and selection for these characters will not be much rewarding. However, the breeder should adopt suitable breeding methodology to utilize both additive and non-additive gene effects simultaneously, since varietal and hybrid development will go a long way in the breeding programmes in case of cucumber.

Based on D^2 value, 30 genotypes were grouped in to 6 clusters which indicated a large genetic diversity (Table 4). Out of the 6 clusters, maximum number of genotypes were accommodated in cluster II with 10 genotypes, followed by cluster III with 9 genotypes, cluster I with 5 genotypes, cluster IV with 4 genotypes and cluster V and VI were solitary containing single genotype each namely, CHFC-2 and CHFC-25, respectively. This clearly showed that the genotypes did not cluster according to geographical distributions. These results were in concurrence with Hanchinamani and Patil (2011), Kumar *et al*. (2013) and Hasan *et al*. (2015). The absence of relationship between genetic diversity and geographical distance indicated that forces other than geographical origin, such as exchange of genetic stocks, genetic drift, variation, natural and artificial selection were responsible for genetic diversity.

Table 4. Average intra- (bold) and inter-cluster distances (D^2) and clustering pattern for 30 genotypes in cucumber.

Cluster number	I	II	III	IV	V	VI	Genotypes included in clusters
I(5)	**54.35**	137.62	115.81	334.92	269.08	211.51	CHFC-1, CHFC-8, CHFC-11, CHFC-4, CHFC-27
II (10)		**88.90**	220.64	222.16	279.68	385.25	CHFC-17, CHFC-30, CHFC-20, CHFC-21, CHFC-28, CHFC-24, CHFC-12, CHFC-29, CHFC-14, CHFC-7
III (9)			**109.17**	384.71	425.43	250.37	CHFC-5, CHFC-9, CHFC-19, CHFC-15, CHFC-13, CHFC-6, CHFC-23, CHFC-26, CHFC-22
IV (4)				**221.79**	504.11	670.08	CHFC-16, CHFC-18, CHFC-10, CHFC-3
V (1)					**0.00**	571.21	CHFC-2
VI (1)						**0.00**	CHFC-25

Thirty genotypes were grouped into 6 clusters which showed inter-cluster D^2 values ranging between 115.81 and 670.08 (Table 4). The inter cluster distance between clusters I and III (115.81) indicated that genotypes (CHFC-1, CHFC-8, CHFC-11, CHFC-4 and CHFC-27) and (CHFC-5, CHFC-9, CHFC-19, CHFC-15, CHFC-13, CHFC-6, CHFC-23, CHFC-26 and CHFC-22) were genetically close to each other. Maximum inter cluster distance was observed between cluster IV and VI (670.08) and indicated that genotypes (CHFC-16, CHFC-18, CHFC-10 and CHFC-3) and (CHFC-25) are highly divergent. These two clusters revealed highly divergent parents with desirable traits and may be recommended for future breeding programmes. Intercrossing the genotypes from these two clusters may generate wider variability and is expected to throw high yielding transgressive segregants in a population improvement programme.

The cluster means for various characters (Table 5) revealed that cluster IV recorded the highest mean value for number of primary branches per plant, node bearing first both for pistillate and staminate flowers, fruit length, average fruit eight, number of seeds per fruit and fruit yield per plant. The cluster VI with one genotype had maximum number of both pistillate and staminate

flowers, fruits per plant, maximum fruit diameter and total soluble solids, whereas the earliest days to anthesis of both pistillate and staminate flowers, fruit set and fruit harvest was observed in cluster V with single genotype.

Table 5. Cluster mean values for 17 traits and per cent contribution of each trait towards genetic divergence.

Character	Clusters						Contribution (%)towards divergence
	I	II	III	IV	V	VI	
Number of branches per plant	3.55	4.48	6.16	6.84	3.20	3.09	12.64
Days to first pistillate flower anthesis	46.02	44.79	46.91	48.17	37.11	45.01	0.00
Days to first staminate flower anthesis	38.67	39.22	40.24	42.10	33.54	41.45	0.46
Number of pistillate flowers	10.71	9.95	11.85	8.55	7.35	14.81	0.69
Number of staminate flowers	23.20	26.65	26.59	19.80	17.95	36.19	2.07
Days to first fruit set	49.73	48.63	51.05	52.00	40.67	49.01	0.00
Days to first harvest	55.15	54.22	56.25	57.07	46.93	53.12	4.60
Node bearing first pistillate flower	7.73	7.39	8.24	8.53	4.86	7.69	1.84
Node bearing first staminate flower	4.19	4.16	4.61	5.08	2.88	5.10	0.00
Number of fruits per plant	9.10	7.92	9.76	6.70	5.33	12.43	0.00
Fruit length (cm)	12.73	18.55	12.20	19.31	17.00	11.97	1.61
Fruit diameter (cm)	4.65	5.55	4.77	5.74	5.51	7.10	4.83
Average fruit weight (g)	152.60	271.46	137.75	310.58	152.00	77.13	48.28
Number of seeds per fruit	153.53	244.53	163.59	247.92	180.00	68.00	0.92
100-seed weight (g)	2.69	2.71	2.46	1.96	2.57	2.54	13.56
Total soluble solids (°BRIX)	2.66	2.60	2.63	2.75	3.02	3.72	0.69
Fruit yield per plant (kg)	1.39	2.16	1.33	2.19	0.81	0.95	7.82

Further, the ability of D^2 analysis is also enhanced by its applicability to estimate the relative contribution of the various traits to the total divergence. The average fruit weight contributed most i.e. 48.28% followed by100-seed weight (13.56%), number of branches per plant (12.64%) and fruit yield per plant (7.82%) towards total divergence (Table 5). The appreciable contribution of fruit weight and fruit yield was also reported by Punitha *et al*. (2012) and Hasan *et al*. (2015) in cucumber.

On the basis of inter-cluster distance along with *per se* performance and severity of diseases of powdery mildew, anthracnose and angular leaf spot, the genotypes CHFC-10, CHFC-16 and CHFC-18 of cluster IV, CHFC-2 and CHFC-25 as single genotype from clusters V and VI, respectively may be utilized for hybridization for generating materials suitable for agro-climatic conditions of north-east region of India. Further, traits namely, fruit weight, 100-seed weight, number of branches per plant and fruit yield per plant together accounted 82.28% contribution to the total divergence. Hence, it is suggested to consider these traits as parameter in selecting genetically diverse parents for hybridization programme.

References

Bhat NA, Masood SD, Mushtaq A and Zarga MR 2007. Occurrence and severity of angular leaf spot of cucumber in Kashmir. Ann. Plant Prot. Sci. **15**(2): 51-54.

Burton GW 1952. Quantitative inheritance in grasses. Proc. 6th Int. Grassland Cong. **1**: 277-283.

Hanchinamani CN and Patil MG 2011. Breeding potential of cucumber genotypes using D^2 analysis. Crop Res. **41**:164-167.

Hasan R, Hossain MK, Alam N, Bashar A, Islam S and Tarafder MJA 2015. Genetic divergence in commercial cucumber (*Cucumis sativus* L.) genotypes. Bangladesh J. Bot. **44**(2): 201-207.

Johnson HW, Robinson HF and Comstock RE 1955. Estimate of genetic and environmental variability in soybean. Agro. J. **47**: 314-318.

Kumar S, Kumar D, Kumar R, Thakur KS and Dogra, BS 2013. Estimation of genetic variability and divergence for fruit yield and quality traits in cucumber (*Cucumis sativus* L.) in north-western Himalayas. Universal J. Plant Sci. **1**(2): 27-36.

Pal S, Sharma HM, Rai AK and Bhardwaj RK 2016. Genetic variability, heritability and genetic gain for yield and quality traits in cucumber (*Cucumis sativus* L.). Bioscan. **11**(3): 1985-1990.

Punitha A, Bharathi A and Devi DS 2012. Studies on genetic divergence on cucumber (*Cucumis sativus* L.). Asian J. Bio Sci. **7**(2): 169-173.

Rajawat KS and Collis JP 2017. Genetic variability, Heritability and Genetic advances analysis for quantitative and qualitative traits in Cucumber (*Cucumis sativus* L.). J. Pharmacognosy and Phytochemistry. **6**(4): 882-885.

Ransom LM, Briens RGO and Glass RJ 1991. Chemical control of powdery mildew in green peas. Aus. Plant Pathol. **20**(1): 16-20.

Rao R 1952. Advanced Statistical Methods in Biometrical Research. John Wiley and Sons Inc. New York. 390pp.

Singh RK and Chaudhary BD 1985. Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi 318 pp.

Ullah MZ, Hasan MJ, Chowdhury AZMKA, Saki AI and Rahman AHMA 2012. Genetic variability and correlation in exotic cucumber (*Cucumis sativus* L.) varieties. Bangladesh J. Plant Breed. Genet. **25**(1): 17-23.

Yawalkar KS 1985. Vegetable Crops of India. Agri-Horticultural Publishing House, Nagpur. p. 300.

(Manuscript received on 20 February, 2018; revised on 6 January, 2019)