

Estimation of Genetic Variability and Divergence for Fruit Yield and Quality Traits in Cucumber (*Cucumis Sativus* L.) in North-Western Himalays

Sandeep Kumar¹, Dharminder Kumar^{1,*}, Ramesh Kumar¹, KS Thakur¹, Balbir Singh Dogra²

¹Department of Vegetable Science, Dr. YS Parmar University of Horticulture and Forestry, Nauni, Solan-173 230, HP, India

²Regional Horticulture and Forestry Research Station, Bhoti, Hamirpur (HP), Dr. YS Parmar University of Horticulture and Forestry, Nauni, Solan-173 230, HP, India

* Corresponding Author: dharmruder@gmail.com

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Abstract Thirty diverse genotypes of cucumber collected from different indigenous sources were planted in randomized complete block design, during rainy season of 2009 and were assessed to know the nature and magnitude of variability and genetic divergence for different horticultural traits. The genotype LC-1 gave maximum mean value for fruit weight and yield per plot. High phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV) and heritability estimates coupled with high genetic gain were observed for seed vigour index-I and yield per plot, indicated the existence of wide range of variations and offers better scope for improvement through selection. The genotypes were grouped into 4 clusters and the highest (6.168) inter cluster distance was recorded between cluster-II and III. The diverse genotypes characterized by maximum inter cluster distance will differ in phenotypic performance and therefore, selection of divergent parents should be based on these cluster distances to obtain favourable hybrids and transgressive segregants in cucumber.

Keywords Cucumber, Genetic Variability, Divergence, Heritability and Mahalanobis D^2 statistics

(Yawalkar, 1985).

In spite of being native of Indian sub-continent and endowed with enormous variability and genetic divergence, cucumber remains underutilized in terms of its economic potential and unexploited from breeding point of view. So, there is a great need of screening cucumber germplasm to select elite genotypes with improved quality and higher yield for direct selection or using as a parent in hybridization programme.

Planning and execution of breeding programme for improvement of quantitative attributes depends, to a great extent, upon magnitude of genetic variability. 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. Hence, on the basis of these parameters, suitable selection strategy can be formulated for higher yield in cucumber. Information on genetic diversity is used to identify the promising diverse genotypes, which may be used in further breeding programme.

Therefore, keeping in view the importance of above facts in mind, the present study has been undertaken to estimate the extent of variability, heritability, coefficients of variation, genetic advance and genetic divergence in thirty diverse genotypes of cucumber.

1. Introduction

Cucumber (*Cucumis sativus* L.) is one of the most important cucurbitaceous vegetable crops grown extensively in tropical and sub-tropical parts of the country. It is considered as 4th most important vegetable crop after tomato, cabbage and onion (Tatlioglu, 1993). Cucumber is a thermophilic and frost susceptible crop species, growing best at a temperature above 20°C. It is grown for its tender fruits, which are consumed either raw as salad, cooked as vegetable or as pickling cucumber in its immature stage. It is a rich source of vitamin B and C, carbohydrates, Ca and P

2. Materials and Methods

2.1. Experimental Site and Environment

The present investigations were carried out at Research Farm of the Department of Vegetable Science, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan in the state of Himachal Pradesh, India during rainy season of 2009. This location is at 30°50' N latitude and 77°11'30" E longitude and is 1260 m above mean sea level and represents the mid-hill zone of Himachal Pradesh. The

total rainfall during growing season was 381.90 mm, most of which was received in July month *viz.* 187.30 mm. Maximum mean temperature varied from 27.2⁰ C to 33.3⁰ C and minimum from 15.9⁰ C to 19.5⁰ C. Maximum relative humidity recorded was 76.0 per cent and minimum was 44.6 per cent during the growing season.

Table 1. List of cucumber genotypes studied along with their sources

Genotype	Source
LC-1, LC-2, LC-3, LC-4, LC-5, LC-6	Hamirpur, Himachal Pradesh, India
LC-7, LC-8	Bilaspur, Himachal Pradesh, India
LC-9, LC-10, LC-11, LC-12	Kangra, Himachal Pradesh, India
LC-13, LC-14, LC-15	Mandi, Himachal Pradesh, India
LC-16, LC-17	Shimla, Himachal Pradesh, India
LC-18, LC-19, LC-20	Kullu, Himachal Pradesh, India
LC-21, LC-22	Chamba, Himachal Pradesh, India
LC-23, LC-24, LC-25	Solan, Himachal Pradesh, India
LC-26, LC-27	Una, Himachal Pradesh, India
LC-28	Jammu, Jammu & Kashmir, India
K-75*, K-90*	UHF, Nauni, Solan, Himachal Pradesh, India

*Control

2.2. Experimental Material, Layout and Observations

The experimental material consisted of diverse group of 30 genotypes of cucumber, including check cultivars *i.e.*, K-75 and K-90 (Table 1) collected from different regions of North-Western Himalays having tremendous genetic diversity of cucumber. The experiment was laid out in randomized block design with three replications of each genotype. The experimental field was disked and levelled. About 10 Mt ha⁻¹ of well decomposed farm yard manure was mixed in the soil at the time of field preparation. The recommended fertilizer dose of N:P₂O₅:K₂O was applied at the time of sowing at the rate of 400, 315 and 100 Kg ha⁻¹ as calcium ammonium nitrate, single- superphosphate, and muriate of potash, respectively. Seeds were directly sown in the field in the month of May, 2009. Three to four seeds per basin were sown at a spacing of 100 x 75 cm in a plot having size of 3.0 x 2.25 m², accommodating 9 plants per plot. After the emergence of seedlings, only one healthy seedling per hill was retained. Standard cultural practices recommended

in the Package of Practices for Vegetable Crops, were followed to ensure a healthy crop stand (Anonymous, 2009). The observations were recorded on node number bearing first female flower, days to marketable maturity, number of marketable fruits per plant, harvest duration, fruit length, fruit breadth, average fruit weight, total soluble solids, yield per plot, seed germination, seed vigour index-I and II and severity of powdery mildew, anthracnose and angular leaf spot from five randomly selected plants in each replication for all characters except for fruit characters for which observations were recorded on ten randomly selected fruits per replication. Colour of fruits was observed visually after harvesting with the help of colour chart of Royal Horticultural Society, London. Seed germination of each genotype was tested in accordance with ISTA (Anonymous, 1985) and seed vigour index-I and II were calculated as per the formula given by Abdul-Baki and Anderson (1973). The disease severity of anthracnose and angular leaf spot was recorded on 0-5 scale as suggested by Bhat (2007) and disease severity for powdery mildew was recorded by adopting the scale given by Ransom *et al.* (1991).

2.3. Statistical Analysis

The data were subjected to analysis of variance as per procedure described by Gomez and Gomez (1983). The genotypic and phenotypic coefficients of variation were calculated as per formulae given by Burton and De-Vane (1953). Heritability and genetic advance were calculated according to Allard (1960) and genetic gain was estimated as per the method given by Johanson *et al.* (1955). Multivariate analysis was done utilizing Mahalanobis D² statistics and genotypes were grouped into four different clusters following Tochers method as described by Rao (1952).

3. Results and Discussion

3.1. Variability studies

3.1.1. Analysis of Variance

Genetic variability is the basic need for a plant breeder to initiate any breeding programme. Genetic improvement can be brought about by manipulating the genetic makeup of the plant for desirable characters or to remove the undesirable genes which retard, or inhibit, certain pathways. Analysis of variance (Table 2) indicated significant differences among the genotypes for all the characters under study. These differences indicated the presence of variability in the available germplasm and offers opportunity for improvement in yield and quality traits of cucumber.

Table 2. Analysis of variance for different horticultural traits in cucumber

Character	Source of variation			
	Genotype (29) ^a	Replication (2)	Error (58)	Total (89)
Node number bearing first female flower	23.61*	114.00	5.29	142.90
Days to marketable maturity	119.11*	289.43	15.36	423.90
Number of marketable fruits / plant	3.70*	3.52	0.29	7.51
Harvest duration (days)	63.14*	249.87	10.75	323.76
Fruit length (cm)	26.07*	17.90	0.97	44.94
Fruit breadth (cm)	1.68*	0.31	0.08	2.07
Average fruit weight (g)	12518.49*	11884.63	649.26	25052.38
TSS (⁰ B)	0.95*	2.24	0.11	3.30
Seed germination (%)	203.06*	161.47	12.46	376.99
Seed vigor index-I	664805.62*	2229599.67	96125.43	2990530.70
Seed vigor index-II	684473.69*	2007898.64	96649.04	2789021.40
Severity of powdery mildew (%)	95.20*	424.36	19.13	538.69
Severity of anthracnose (%)	62.95*	422.92	18.61	504.48
Severity of angular leaf spot (%)	33.43*	231.96	10.17	275.56
Yield/plot (kg)	86.71*	5.94	1.51	94.16
Yield/hectare (q) [converted]	9325.70*	639.59	162.57	10127.86

*Significant at 5% level of significance

^a Values in the parenthesis are degree of freedom

3.1.2. 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 (3.53-13.53) and days to marketable maturity (55.67-78.33), which determine the earliness of a variety (Table 3). Fruit length, breadth and weight are the major yield contributing traits, wide variations were observed with respect to these traits (8.11-22.76 cm, 3.08-7.18 cm, 95.00-430.00 g, respectively). Tremendous variations with respect to number of marketable fruits per plant (5.01 - 8.57), harvest duration (14.00 - 28.67 days) and yield per plot (4.37 – 27.31 kg) were obtained. The genotype LC-1 was found highest in yield (27.31 kg/ha) among all and four other genotypes namely LC-2, LC-3, LC-15 and LC-28 gave higher yield than both the checks. Wide variations with respect to various horticultural characters were also reported by Singh *et al.* (2002), Das *et al.* (2003), Verma (2003), Kumar (2006), Munshi *et al.* (2007), Kumar *et al.* (2008), Hanchinamani *et al.* (2008) and Yogesh *et al.* (2009) in cucumber.

All the genotypes under study also showed wide variations for fruit colour (green, light green, dark green and white) and total soluble solids (2.03 – 4.07 0B), 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. Higher TSS was recorded in LC-28 (4.07 0B) and six other genotypes namely LC-2, LC-3, LC-15, LC-19, LC-25 and LC-26 performed better over both the checks for total soluble solids. Similar results have also been reported by Verma (2003) and Kumar (2006) for these characters.

For seed characters viz. seed germination (61.00-87.67 %), seed vigor index-I (438.33-1930.00) and seed vigor index-II (1642.28-3167.28), a wide variation was observed. Maximum seed germination was recorded in LC-6 and LC-20 (87.67), respectively, while LC-3 performed better for seed vigor index-I and II (1930.00 and 3167.28, respectively). Similar results were also reported by Hamid *et al.* (2002) for seed germination and by Nerson (2007) for seedling vigour.

All the genotypes studied, respond differently to the attack of different diseases viz. powdery mildew (8.50-29.40 %), anthracnose (7.70-26.20 %) and angular leaf spot (6.50-18.30 %). Minimum severity of powdery mildew, anthracnose and angular leaf spot was recorded in LC-21 (8.50 %), LC-15 (7.70 %) and LC-22 (6.50 %), respectively. Hence, these genotypes can be used as resistant sources in further breeding programmes. These findings are in agreement with Webner and Shetty (2000) and Cohen *et al.* (1995). These wide variations in the genotypes for different characters would help in selecting the best genotypes from existing collections.

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Table 3. Mean performance of cucumber genotypes for different horticultural traits

Genotyp e	NNBFF	DMM	NMF	HD	FL	FB	AFW	FC	TSS	SG*	SVI-I	SVI-II	SPM**	SA**	SALS**	YPP
LC-1	7.47	75.67	7.08	25.33	21.71	6.58	430.00	LG (G 141C)	2.57	72.33 (58.25)	1345.00	2438.67	16.50 (3.99)	10.30 (3.02)	7.35 (2.59)	27.31
LC-2	6.23	66.33	8.06	26.33	15.76	5.73	331.67	LG (G 134D)	3.77	76.33 (60.89)	1729.00	2968.97	19.70 (4.41)	8.40 (2.78)	8.55 (2.88)	23.91
LC-3	6.00	65.33	8.07	24.00	16.56	5.37	303.33	LG (G 130C)	3.53	79.33 (63.06)	1930.00	3167.28	14.70 (3.77)	10.50 (3.09)	11.60 (3.35)	21.96
LC-4	11.00	73.67	6.04	17.67	11.15	4.48	143.33	LG (G 136C)	2.07	62.67 (52.35)	765.33	1665.67	21.30 (4.59)	15.30 (3.87)	12.70 (3.54)	7.67
LC-5	10.87	74.67	6.57	19.33	12.43	5.27	248.33	LG (G 141C)	2.77	70.67 (57.20)	666.33	1918.67	18.00 (4.22)	18.80 (4.31)	8.20 (2.82)	14.68
LC-6	9.50	74.33	6.79	20.67	12.53	5.18	246.67	G (G 141B)	2.77	87.67 (69.67)	1570.00	2873.67	21.10 (4.55)	9.40 (2.91)	13.30 (3.60)	14.81
LC-7	10.47	77.67	5.60	14.33	12.48	5.00	236.67	LG (G 143B)	2.10	61.67(51 .75)	484.33	1790.02	22.30 (4.69)	16.45 (4.00)	13.60 (3.66)	11.68
LC-8	13.07	78.33	5.68	16.00	15.47	7.18	343.33	W (W 155A)	2.17	62.00 (51.95)	438.33	1652.00	24.50 (4.93)	11.80 (3.38)	15.40 (3.91)	17.54
LC-9	11.27	75.33	6.40	17.33	15.59	5.46	290.00	LG (G 141C)	2.43	70.00 (56.86)	1438.00	2801.67	29.40 (5.40)	12.50 (3.44)	8.30 (2.80)	16.63
LC-10	11.50	76.67	5.40	14.33	14.27	5.18	251.67	G (G 135C)	2.07	61.33 (51.54)	608.00	1880.48	23.30 (4.79)	13.80 (3.64)	15.50 (3.91)	12.18
LC-11	8.67	74.33	5.09	14.00	13.31	3.08	146.67	G (G 135C)	2.43	62.33 (52.13)	463.00	1642.28	25.50 (5.02)	14.60 (3.76)	15.30 (3.88)	6.66
LC-12	9.68	67.33	7.15	19.33	16.64	3.88	241.67	G (G 141B)	2.83	64.00 (53.13)	1166.67	2157.90	17.70 (4.16)	25.30 (5.01)	7.10 (2.57)	15.43
LC-13	11.20	75.33	5.17	14.67	8.11	4.81	95.00	G (G 132C)	2.03	76.67 (61.17)	721.67	1967.93	19.80 (4.41)	17.10 (4.08)	18.30 (4.26)	4.37
LC-14	4.87	61.33	7.12	21.33	13.12	4.98	243.33	LG (G 141C)	2.73	66.33 (54.53)	601.00	1926.73	14.40 (3.76)	21.50 (4.62)	7.20 (2.63)	15.61
LC-15	4.67	58.67	8.57	28.67	14.70	5.46	285.00	G (G 141B)	3.20	78.33 (62.25)	1736.67	2367.00	12.30 (3.44)	7.70 (2.60)	13.60 (3.67)	21.91
LC-16	9.10	76.67	5.40	15.00	10.11	4.01	130.00	LG (G 140B)	2.33	62.67 (52.35)	486.33	1932.89	25.50 (5.03)	20.80 (4.54)	9.50 (3.04)	6.25
LC-17	13.53	78.33	5.01	14.67	11.59	5.05	235.00	LG (G 142B)	2.23	62.33 (52.13)	624.67	1836.00	24.60 (4.93)	19.50 (4.37)	10.50 (3.19)	10.52
LC-18	6.73	67.67	6.27	16.33	14.73	5.23	258.33	LG (G 136C)	2.70	61.00 (51.35)	458.67	1889.48	28.80 (5.34)	14.40 (3.73)	13.50 (3.64)	14.50

LC-19	5.20	65.67	7.01	17.33	14.08	4.73	241.67	G (G 141B)	3.37	74.67 (59.88)	1166.67	2671.00	20.50 (4.49)	12.70 (3.49)	9.50 (3.03)	15.17
LC-20	11.93	76.33	6.04	17.00	13.17	4.78	223.33	LG (G 135D)	2.33	87.67 (69.67)	1360.00	2997.00	21.60 (4.61)	15.20 (3.84)	13.90 (3.70)	12.05
LC-21	8.33	74.67	8.02	26.67	13.14	5.23	266.67	LG (G130D)	3.07	75.67 (60.51)	1400.00	2431.67	8.50 (2.68)	12.50 (3.43)	13.60 (3.65)	19.11
LC-22	3.53	55.67	6.02	15.33	13.02	5.08	251.67	G (G 134B)	2.43	66.00 (54.32)	714.67	1976.33	26.50 (5.14)	21.10 (4.59)	6.50 (2.48)	13.55
LC-23	12.47	75.67	5.11	14.67	11.68	4.98	228.33	G (G 135C)	2.47	61.67 (51.73)	494.33	1655.39	25.70 (5.06)	16.80 (4.08)	15.20 (3.88)	10.39
LC-24	10.70	74.67	5.97	16.33	13.65	5.00	265.00	G (G 137A)	2.07	65.67 (54.13)	612.33	1876.80	21.60 (4.64)	11.80 (3.41)	12.30 (3.48)	14.14
LC-25	8.37	74.33	6.54	18.00	22.76	4.29	251.67	G (G 135C)	3.17	69.33 (56.37)	586.33	1846.93	13.50 (3.65)	26.20 (5.11)	11.20 (3.31)	14.67
LC-26	8.10	73.67	6.56	17.33	12.19	4.53	225.00	LG (G 130C)	3.77	84.00 (66.44)	1733.67	2766.33	9.50 (3.01)	15.90 (3.96)	17.80 (4.20)	13.14
LC-27	4.23	60.33	8.38	21.67	14.28	4.35	236.33	DG (G 136A)	2.80	81.67 (64.65)	1340.00	2913.00	11.50 (3.37)	12.50 (3.52)	12.40 (3.50)	17.77
LC-28	7.40	67.33	8.15	26.33	16.58	5.40	308.33	G (G 141B)	4.07	73.67 (59.12)	1216.67	2562.00	12.40 (3.47)	13.60 (3.65)	7.10 (2.55)	22.58
K-75	6.16	66.67	7.91	24.67	13.23	4.91	261.67	LG (G 141C)	3.07	72.67 (58.53)	1072.67	2433.33	18.50 (4.28)	14.20 (3.74)	11.40 (3.33)	18.56
K-90	6.60	73.33	8.02	26.00	15.85	5.25	269.33	LG (G 141C)	3.10	76.33 (60.96)	1133.33	2493.67	19.50 (4.40)	15.30 (3.88)	8.20 (2.77)	19.33
Mean	8.63	71.20	6.64	19.36	14.13	5.01	249.63	-	2.75	70.89 (57.63)	1002.12	2250.03	19.62 (4.34)	15.20 (3.79)	11.62 (3.33)	15.14
S.E. (d) ±	1.88	3.20	0.44	2.68	0.81	0.24	20.80	-	0.28	2.88	253.15	253.84	3.57	3.52	2.60	1.00
C.D.(0.05)	3.76	6.40	0.88	5.36	1.61	0.48	41.65	-	0.55	3.83	506.80	508.18	0.88	1.04	0.83	2.01

Where,

NNBFFF = Node number bearing first female flower, NMF = Number of marketable fruits per plant, FL = Fruit length (cm), FB = Fruit breadth (cm), AFW = Average fruit weight (g), DMM = Days to marketable maturity, HD = Harvest duration, FC = Fruit colour, LG = Light green, G = Green, DG = Dark green, W = White, TSS = Total soluble solids (^oB), SG = Seed germination (%), SVI-I = Seed vigor index-I, SVI-II = Seed vigor index-II, SPM = Severity of powdery mildew (%), SA = Severity of anthracnose (%), SALS = Severity of angular leaf spot (%), YPP = Yield per plot (kg) and YPH = Yield per hectare (q)

*Figures in the parenthesis are Arc sine transformed

** Figures in the parenthesis are Square root transformed

Table 4. Estimates of phenotypic and genotypic coefficients of variability, heritability, genetic advance and genetic gain for different horticultural traits

Characters	Variance (σ^2)		Coefficients of variability (%)		Heritability (%)	Genetic advance	Genetic gain (%)
	Phenotypic	Genotypic	Phenotypic	Genotypic			
Node number bearing first	11.39	6.10	39.12	28.63	53.60	3.73	43.22
Days to marketable	49.94	34.58	9.93	8.26	69.20	10.07	14.14
Number of marketable	1.42	1.13	18.00	16.06	79.60	1.96	29.52
Harvest duration (days)	28.21	17.46	27.44	21.59	61.90	6.77	43.97
Fruit length (cm)	9.34	8.36	21.63	20.47	89.60	5.64	39.92
Fruit breadth (cm)	0.61	0.53	15.71	14.57	86.00	1.39	27.74
Average fruit weight (g)	4605.67	3956.40	27.19	25.20	85.90	120.09	48.11
TSS ($^{\circ}$ B)	0.39	0.27	22.85	19.21	70.70	0.92	33.45
Seed germination	75.99	63.53	12.30	11.24	83.60	15.01	21.17
Seed vigor index-I	285685.49	189560.06	53.34	43.45	66.40	731.10	72.96
Seed vigor index-II	292590.59	195941.54	24.04	19.67	67.00	746.57	33.18
Severity of powdery	44.49	25.35	34.00	25.66	57.00	7.83	39.91
Severity of anthracnose	33.39	14.77	38.02	25.29	44.00	5.24	34.47
Severity of angular leaf	17.93	7.75	36.44	23.96	43.00	3.75	32.27
Yield per plot (kg)	29.91	28.40	36.12	35.20	94.90	10.69	70.61

3.1.3. Parameters of Variability

3.1.3.1. Coefficients of Variability

The estimates of phenotypic and genotypic coefficients of variability gave a clear picture of amount of variations presents in the available Germplasm (Table 4). For all the characters studied, phenotypic coefficients of variability were higher in magnitude than genotypic coefficients of variability, though difference was not much in all the cases. Thus, showing that these traits are not much influenced by environmental factors. Hence, selection based on phenotypic performance will be more reliable. Coefficients of variability varied in magnitude from character to character, indicating that there was a great diversity in the experimental material used. The genotypic coefficients of variability (GCV) were high for seed vigor index-I and yield per plot. This reflects greater genetic variability among the genotypes for these characters for making further improvement by selection. Whereas, moderate GCV were recorded for node number bearing first female flower, severity of powdery mildew, anthracnose and angular leaf spot, average fruit weight, harvest duration, fruit length, seed vigor index-II, total

soluble solids, number of marketable fruits per plant and for fruit breadth. For, seed germination and days to marketable maturity, GCV were low. Similar results had also been reported by Singh (1997) and Yogesh *et al.* (2009).

3.1.3.2. Heritability and Genetic gain

The estimates of heritability were found high for the characters *viz.* yield per plot, fruit length and breadth, average fruit weight and seed germination and it was moderate for number of marketable fruits per plant, total soluble solids, days to marketable maturity, seed vigor index, harvest duration, severity of powdery mildew and node number bearing first female flower, while it was low for severity of anthracnose and angular leaf spot (Table 2). Kumar *et al.* (2008) reported high heritability estimates for fruit diameter, fruit length and fruit yield per plant and moderate heritability for node number bearing first female flower and days to fruit harvest. Similarly, high heritability was reported by Yogesh *et al.* (2009) for fruit diameter, fruit length, fruit weight at edible maturity and fruit yield per plant and moderate heritability was found for node number bearing first female flower. High heritability estimates for

fruit length, fruit breadth, fruit weight and fruit yield per plant were also reported by Singh (1997) and Munshi *et al.* (2007). In the light of results obtained in the present studies, it is concluded that selection can be performed at phenotypic performance for highly heritable characters *viz.* fruit length, fruit breadth and average fruit weight and yield per plot.

Genetic gain (expressed as per cent of population mean) was low to high in nature for different characters. It was found high for seed vigour index-I and yield per plot. Moderate genetic gain was observed for average fruit weight, harvest duration, node number bearing first female flower, fruit length, severity of powdery mildew, anthracnose and angular leaf spot, total soluble solids, seed vigor index-II, number of marketable fruits per plant and fruit breadth, whereas it was recorded low for seed germination and days to marketable maturity. 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 seed vigour index-I and yield per plot, indicated that these characters are under additive gene effects and these characters are more reliable for effective selection (Panse, 1957). Similar results for fruit yield per plant have been reported by Solanki and Seth (1980), Joshi *et al.* (1981), Rastogi and Rathore (1990) and Singh (1997). High heritability coupled with moderate genetic gain was observed for fruit length, fruit breadth and average fruit weight, indicated 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 were also reported by Joshi *et al.* (1981), Kumar *et al.* (2008) and Yogesh *et al.* (2009).

3.2. Genetic Divergence Studies

3.2.1. Cluster composition

After computing D^2 values for all the possible pairs, 30 genotypes were grouped into 4 clusters, which indicated a large genetic diversity (Table 5). Maximum number of genotypes were accommodated in clusters-II (11) followed by cluster-III with 9 and cluster-I and cluster-IV with 5 genotypes, respectively. The resultant four clusters showed considerable genetic diversity. Genotypes from different geographical regions were grouped in the same cluster indicating no relationship between geographic distribution and genetic divergence, while genotypes collected from same location were grouped into different clusters, showing great genetic diversity. Similar results were also obtained by Rao *et al.* (2003), Khan (2006) and Kabir *et al.* (2009). Intra-cluster distance revealed that, cluster IV showed maximum intra-cluster distance (2.494) followed by cluster I (2.443), cluster II (2.410) and cluster III with minimum intra-cluster distance (2.383), respectively. Based on distance between clusters, *i.e.*, inter-cluster distance, the maximum divergence was observed between cluster II and III (6.168) and lowest (3.432) was recorded between cluster I and III (Figure 1).

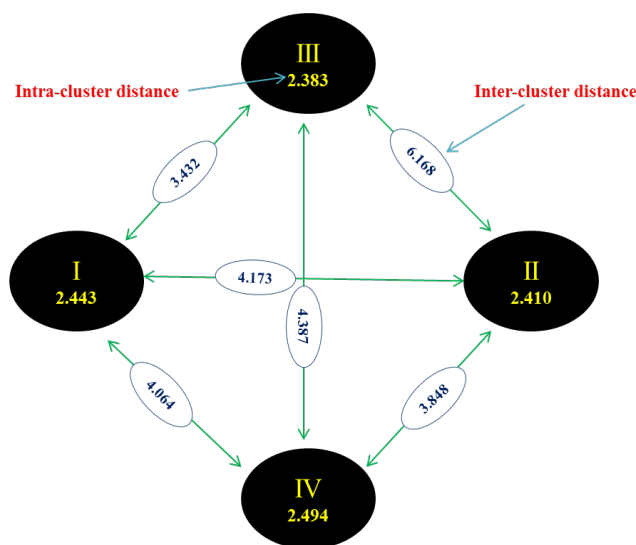


Figure 1. Diagram showing average intra and inter-cluster distances (D^2) of 30 genotypes of cucumber **Table 5.** Clustering pattern and average intra and inter cluster distance (D^2) of 30 genotypes of cucumber

Table 5. Clustering pattern and average intra and inter cluster distance (D^2) of 30 genotypes of cucumber

Cluster	Number of genotypes	Genotypes	Cluster	I	II	III	IV
I	5	LC-6, LC-9, LC-19, LC-20, LC-26	I	<u>2.443*</u>			
II	11	LC-4, LC-7, LC-8, LC-10, LC-11, LC-13, LC-16, LC-17, LC-18, LC-23, LC-24	II	4.173	<u>2.410</u>		
III	9	LC-1, LC-2, LC-3, LC-15, LC-21, LC-27, LC-28, K-75, K-90	III	3.432	6.168	<u>2.383</u>	
IV	5	LC-5, LC-12, LC-14, LC-22, LC-25	IV	4.064	3.848	4.387	<u>2.494</u>

* Diagonal bold figures represent the intra-cluster distance

Table 6. Cluster means for different characters among 30 genotypes of cucumber

Characters	Clusters			
	I	II	III	IV
Node number bearing first female flower	9.20	10.77	6.34*	7.46
Number of marketable fruits per plant	6.56	5.52	8.03	6.68
Fruit length (cm)	13.51	12.41	15.76	15.60
Fruit breadth (cm)	4.94	4.91	5.36	4.70
Average fruit weight (g)	245.33	212.12	299.15	247.33
Days to marketable maturity	73.07	75.36	67.59	66.67
Harvest duration (days)	17.93	15.27	25.52	18.67
TSS (0B)	2.93	2.24	3.24	2.79
Seed germination (%)	80.80	63.64	76.26	67.27
Seed vigor index-I	1453.67	559.73	1433.70	747.00
Seed vigor index-II	2821.93	1799.00	2641.73	1965.31
Severity of powdery mildew (%)	20.42	23.90	14.84	18.02
Severity of anthracnose (%)	13.14	15.67	11.67	22.58
Severity of angular leaf spot (%)	12.56	13.80	10.42	8.04
Yield per plot (kg)	14.36	10.54	21.38	14.79

*Bold figures represent better performance of a character in the respective cluster

3.2.2. Cluster means

For crop improvement, inter-crossing among genotypes with outstanding mean performance was suggested by Roy and Sharma (1996). The cluster means of the various horticultural traits are presented in Table 6. Moreover, for getting the reliable conformity on the basis of cluster means, cluster-III exhibited higher means for number of marketable fruits per plant (8.03), fruit length (15.76), fruit breadth (5.36), average fruit weight (299.15), harvest duration (25.52), total soluble solids (3.24) and yield per plot (21.38) and lowest mean values for node number bearing first female flower (6.34) and severity of powdery mildew (14.84) and anthracnose (11.67). Cluster-I gave maximum mean values for seed germination (80.80) and seed vigour index-I (1453.67) and II (2821.93). Cluster-IV recorded minimum mean value for severity of angular leaf spot (8.04), while cluster-II did not possess superiority for any character. The genotypes having wide genetic base and desirable

characteristics can be involved in intra-specific crosses which would lead to transmission of good genetic gain for various putative traits including yield for practical utility. Hence, Crossing between the genotypes of maximum two clusters (II and III) appeared to be most promising to combine the desirable characters. Earlier workers like Ram (2001), Kushwah *et al.* (2005) and Khan (2006) have also indicated the significance of genetic divergence. But, Mian and Bhal (1989) reported that parental clusters separated by medium D^2 values had significant positive heterosis. Thus, heterosis could also be exploited by crossing between genotypes belonging to clusters with moderate diversity like genotypes of cluster I and II, cluster I & IV and III & IV. They are likely to produce new recombinant with desired traits.

Considering the magnitude of genetic distance and cluster means for different characters performance, the genotypes LC-22 and LC-25 of cluster IV could be selected for earliness and severity of angular leaf spot, and fruit

length, respectively. In the cluster III the genotypes LC-1 for fruit breadth, fruit weight and total yield, LC-15 for number of fruits per plant and harvest duration, LC-28 for total soluble solids, LC-3 for seed vigor index-I and II, LC-15 for severity of anthracnose and LC-21 for severity of powdery mildew could be selected. The genotypes LC-6 and LC-20 of cluster I could be selected for better seed germination, if used in hybridization programme.

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