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Studies on Genetic Divergence for Yield and Quality Traits in Cucumber (*Cucumis sativus* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. Author OPK designed the study, performed the statistical analysis, wrote the protocol and wrote the first draft of the manuscript. Authors UK and SKS managed the analyses of the study. Authors SM and BMS managed the literature searches. All authors read and approved the final manuscript.

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ABSTRACT

Genetic divergence analysis, using Mahalanobis D^2 statistics, was carried out in twenty one cucumber genotypes including one check for fourteen characters. All the characters under study showed considerable divergence and the genotypes were grouped into four clusters. The clustering pattern had no parallelism between genetic diversity and geographical distribution, suggesting that the selection of parental genotypes for hybridization will be more appropriate based on genetic diversity. Cluster III contained the maximum (5) number of genotypes, whereas remaining all clusters I, II and IV contained similar (4) genotypes. The Intra-cluster distance was maximum (306.685) in cluster III whereas, it was minimum (163.11) in cluster II. Maximum average inter-cluster distance (1439.432) was recorded between cluster IV and cluster V, suggesting the greater chances of getting superior hybrids in F_1 or transgressive segregants in subsequent generations. Genotypes in cluster IV were superior in node number of first female flower, days to first flowering, shelf-life, TSS, fruit length, fruit weight and fruit yield per plant. Cluster V had superiority in terms of

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vine length and number of seeds per fruit. Fruit weight, TSS, number of seeds per fruit, node number of first female flower, shelf-life, days to first harvest and days to first flowering contributed towards genetic divergence.

Keywords: Cucumber (Cucumis sativus L.); genotype; divergence; mahalanobis and cluster.

1. INTRODUCTION

Cucumber (*Cucumis sativus* L.) is one of the most important cucurbitaceous vegetables grown throughout the world as well as in India in tropical and sub-tropical climatic conditions. It is an ideal summer vegetable crop chiefly grown for its edible tender fruits, preferred as a salad ingredient, pickles and as a cooked vegetable. Globally, it is regarded as the second most widely cultivated cucurbit after watermelon and is also regarded as the fourth most important vegetable after tomato, cabbage and onion Tatlioglu, [1]. It is one of the potent crops suitable for protected as well as open field conditions to meet the year-round domestic demand as well as for export. It is a rich source of vitamin B and C, carbohydrates, Ca and P. Cucumber is thought to be indigenous to India. India is endowed with the wealth of cucumber germplasm, comprising of both wild and cultivated forms. Due to continuous cultivation of this cross-pollinated crop large variation has occurred for fruit and vegetative characters Sharma et al. [2]. The success of any breeding program depends to a large extent on the amount of genetic variability present in the population Afangideh and Uyoh, [3]. Suitable breeding strategy can be formulated for the improvement of cucumber based on the magnitude of parameters of variability. Therefore, the present study has been undertaken to estimate the extent of variability and genetic divergence in twenty-one genotypes of cucumber. The concept of D^2 as measures of divergence was first introduced by Mahalanobis (1928). Mahalanobis D^2 statistic has been widely used to determine the extent of genetic diversity in the material irrespective of the number of populations. The uses of Mahalanobis D^2 statistic for estimating genetic divergence have been emphasized by Chohata et al. (1994) because it permits precise comparison among all the possible pairs of populations in any group before effecting actual crosses. For the selection of parents for hybridization, genetic divergence among the population is necessary for heterotic effects. Keeping above points in view, twenty one genotypes were evaluated for the study of genetic divergence in cucumber.

2. MATERIALS AND METHODS

The experiment was conducted during 2018-19 (Rainy season) at Vegetable Research Farm, Dr Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar. Pusa is located at a longitude of 85.67^0 E and latitude of 25.98^0 N. This place is situated at an altitude of 52.0 meter above mean sea level. Soil of Pusa (Samastipur) are mainly young alluvium and calcareous. Soil is deep, light to heavy in texture having $CaCo_3$ more than 10 per cent and upto 30 per cent. This region has a subtropical climate with extreme of summer and winter. The experimental materials consisted of twenty-one lines of cucumber genotypes including one check variety *viz.* Swarna Ageti. The genotypes were collected from North Bihar area and few were from research institute. The experiment was laid out in Randomized Complete Block Design with three replications of each genotype. Seeds were directly sown in the field in the month of June, 2018. Three to four seeds per basin were sown at a spacing of 150 x 50 cm in a plot had size of 2.5 x 1.5 m^2, accommodating 10 plants per plot. After the emergence of seedlings, only one healthy plant per hill was retained. The standard cultural practices as recommended in the Package of Practices for Vegetable Crops, were followed to ensure a healthy crop stand. The observations were recorded from five randomly selected plants in each replication for all characters following *viz*.,vine length, node number bearing first female flower, number of primary branches, days to first flowering, days to first harvesting, harvest duration, number of fruits per plant, shelf-life, TSS, seeds per fruit, fruit length, fruit diameter, fruit weight and fruit yield per plant.

The collected data were subjected to Analysis of Variance (ANOVA) using MS-Excel, OP-STAT software available from HAU, Hisar and presented in Table 1 and genetic divergence (D^2) was worked out according to Mahalanobis [4] using SPAR-1 software. A dendrogram was generated using MS Wards method and Euclidan distance as a measure of similarity with the help of SPSS software version 16 and is presented in Fig. 1.

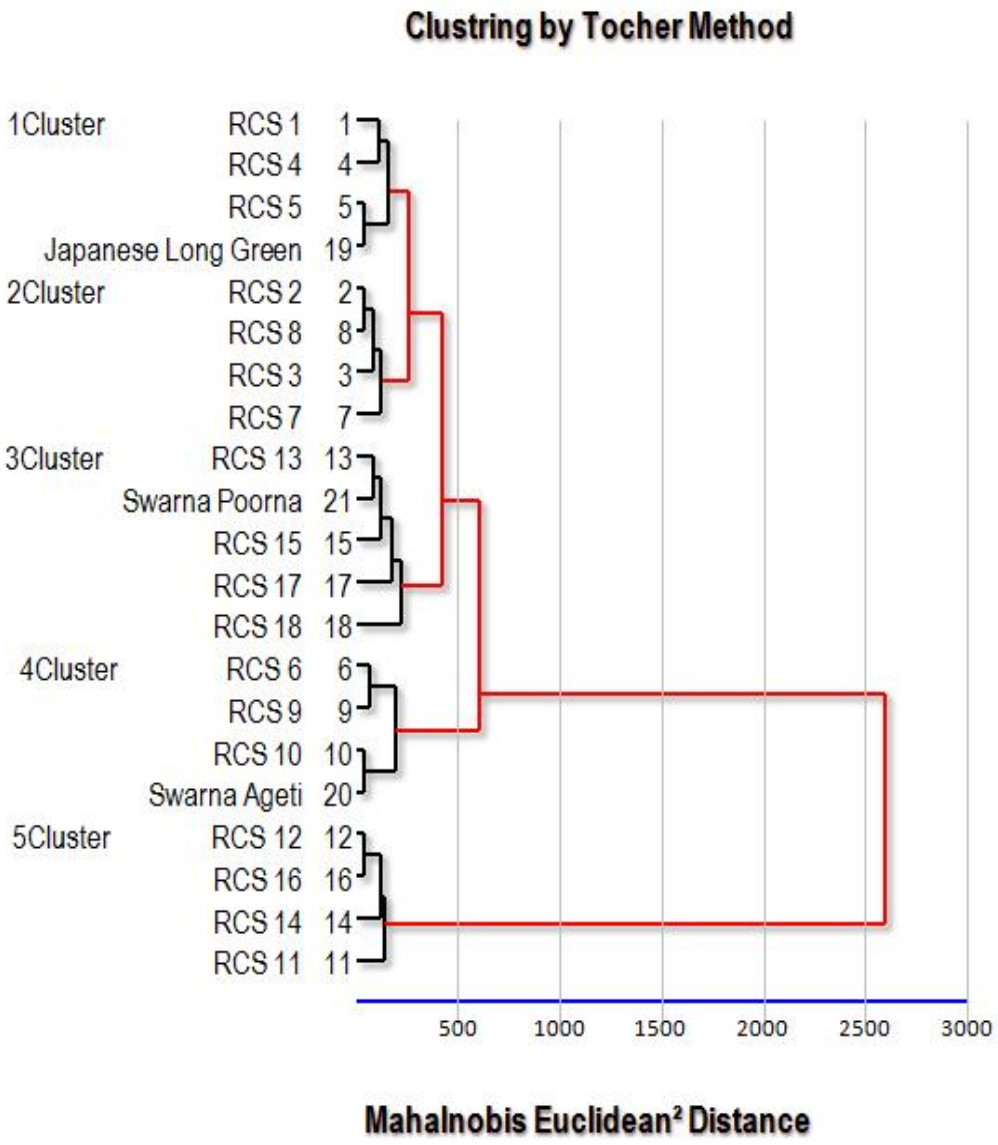

Fig. 1. Clustering pattern of 21 cucumber genotype on the basis of D^2 statistic by Tocher's method

3. RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the genotypes for all the characters studied, indicating the existence of wide genetic divergence among them. Information on genetic diversity was also used to identify promising diverse genotypes, which may further be used in breeding programmes.

On the basis of performance of various traits, the clustering pattern of 21 diverse genotypes of cucumber has been presented in Table 2. All the genotypes were grouped into 5 clusters. Maximum number of genotypes were accommodated in cluster III (5) followed by cluster I, II, IV and V had a similar number of genotypes (4). Average inter and intra cluster divergence (D^2) values are presented in the Table 3. The diagonal figures in the table represent the intra cluster distances. The intra cluster distance was maximum in cluster III (306.685) and minimum in cluster I (163.11). Whereas, the highest (1439.432) inter cluster

distance was recorded between cluster V and IV and lowest (263.468) was observed among cluster I and II suggesting wide diversity between the groups. The crosses made between the genotypes from the above clusters may give transgressive segregants. Similar studied based on D^2 statistics was also performed by Yadav et al. [5], Sharma and Sharma [6], Soleimani et al. [7], Hossain et al. [8], Punithaet al. [9] and Visen et al.[10] and reported similar findings.

The highest contribution in the manifestation of genetic divergence (Table 4) was exhibited by fruit weight (44.76) followed by TSS (20.00), node number of first female flower (11.90), shelf-life (6.67), number of seeds per fruit (5.71), days to first harvest (3.81), fruit length (3.33), days to first flowering (2.38), harvest duration (0.95) and fruit yield per plant (0.48).Similar results were also reported by earlier workers Islam [11], Yadav et al. [5], Manohar and Murthy[12], Punit et al. [9] and Ahirwar et al.[13].

Table 1. Analysis of Variance for fourteen characters in cucumber

Sl No.	Characters	Mean Sum of Square		
		Replication	Treatment	Error
1.	Vine Length (cm)	291.2485	8377.5159**	528.1817
2.	Node Number of First Female Flower	0.1448	15.1762**	0.2641
3.	Number of Primary Branches	0.08826	3.8692**	0.5823
4.	Days to First Flower	0.9035	52.2546**	1.6502
5.	Days to First Harvest	5.5251	1713.9440**	1.6819
6.	Harvest Duration (days)	0.3016	19.7999**	1.8583
7.	Number of Fruit per Plant	1.4331	4.5554**	0.5537
8.	Number of Seeds per Fruit	588.0400	19120.6707**	282.4440
9.	Shelf life(days)	0.0160	3.2395**	0.0550
10.	TSS	0.0206	1.4248**	0.0184
11.	Fruit Length (cm)	3.1328	30.2485**	1.4374
12.	Fruit Diameter (cm)	0.0340	4.0564**	0.3587
13.	Fruit Weight (g)	433.5967	5969.0798**	264.7904
14.	Yield per Plant (kg)	0.0854	0.6432**	0.0503

**Significant at 5% level of significance*

Table 2. Clustering pattern of twenty-one genotypes of cucumber on the basis of D^2 statistic

Cluster No.	No. of Genotypes within cluster	Genotypes in cluster
I	4	RCS 1, RCS 4, RCS 5, Japanese long Green
II	4	RCS 2, RCS 8, RCS 3, RCS 7
III	5	RCS 13, RCS 15, RCS 17, RCS 18, Swarna Poorna
IV	4	RCS 6, RCS 9, RCS 10, Swarna Ageti
V	4	RCS 12, RCS 16, RCS 14, RCS 11

Table 3. Mean intra and inter cluster distance (D^2) among five clusters in cucumber

Cluster	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster
1 Cluster	204.466	263.468	397.649	487.294	1045.781
2 Cluster		163.108	326.139	299.583	816.790
3 Cluster			306.685	447.395	893.469
4 Cluster				199.681	1439.432
5 Cluster					201.773

Table 4. Contribution percentage of fourteen characters towards genetic divergence in cucumber

Sl. No.	Source	Times ranked 1st	Contribution (%)
1	Vine Length (cm)	0	0.00
2	Node No of First Female Flower	25	11.90
3	No. of Primary Branches	0	0.00
4	Days to First Flowering	5	2.38
5	Days to First harvest	8	3.81
6	Harvest Duration (days)	2	0.95
7	Fruits Per Plant	0	0.00
8	No. of Seeds Per Fruit	12	5.71
9	Shelf life (days)	14	6.67
10	TSS	42	20.00
11	Fruit Length (cm)	7	3.33
12	Fruit Diameter (cm)	0	0.00
13	Fruit Weight (g)	94	44.76
14	Yield Per Plant (kg)	1	0.48

Table 5. Cluster mean for fourteen characters in cucumber

Characters / Cluster	VL	NNFFF	NPB	DFF	DFH	HD	NF/P	NS/F	SL	TSS	FL	FD	FW (g)	Y/P(kg)
Cluster I	213.25	6.93	8.93	40.90	63.38	20.51	9.00	335.31	5.25	3.15	17.79	5.20	217.61	1.96
Cluster II	177.25	5.81	8.43	40.60	58.61	20.83	10.21	303.81	5.35	4.00	19.39	5.29	199.51	1.99
Cluster III	249.48	10.20	9.40	43.44	65.38	19.61	9.52	299.98	5.64	4.14	20.93	5.46	233.80	2.22
Cluster IV	234.31	5.73	9.20	39.36	59.23	20.88	9.35	362.03	6.58	4.72	21.46	5.25	251.58	2.35
Cluster V	151.06	8.06	8.20	46.30	68.45	21.83	8.86	168.30	4.03	4.45	15.01	3.59	141.96	1.25

Table 6. Mean performance of twenty-one genotypes of cucumber for fourteen characters

Characters / Genotypes	VL	NNFFF	NPB	DFF	DFH	HD	NF/P	NS/F	SL	TSS	FL	FD	FW	Y/P
RCS 1	236.13	5.87	9.27	41.07	61.53	18.67	9.27	278.40	4.31	3.29	18.44	3.12	183.40	1.71
RCS 2	178.73	7.13	7.73	37.40	58.07	21.73	9.73	297.07	5.64	3.83	15.51	4.40	194.07	1.90
RCS 3	206.73	4.93	8.87	38.47	62.93	19.73	10.53	240.53	4.61	4.29	21.49	6.49	199.60	2.09
RCS 4	266.93	8.13	9.87	45.73	70.13	20.60	7.93	323.07	5.98	2.65	17.24	5.38	213.40	1.70
RCS 5	196.20	7.47	7.33	35.87	60.60	23.33	9.47	375.13	5.18	3.56	16.05	6.45	232.87	2.20
RCS 6	217.07	6.27	8.13	39.73	63.93	20.27	8.40	408.80	6.29	4.67	23.52	3.84	229.87	1.94
RCS 7	130.67	5.07	7.40	46.73	57.13	17.53	12.67	349.73	5.79	3.89	19.69	4.81	168.53	2.13
RCS 8	192.87	6.13	9.73	39.80	56.33	24.33	7.93	327.93	5.38	3.99	20.89	5.49	235.87	1.87
RCS 9	164.53	4.27	8.00	44.67	59.73	18.13	9.53	388.93	7.27	5.21	17.63	4.36	238.40	2.26
RCS 10	277.60	5.13	9.13	34.67	54.53	22.60	9.07	309.93	5.93	4.63	22.71	6.39	288.13	2.61
RCS 11	171.27	5.33	8.33	47.80	70.80	25.47	10.60	249.07	3.91	4.91	16.75	4.36	157.40	1.66
RCS 12	112.13	8.67	7.47	45.27	66.47	21.93	7.53	120.73	4.41	3.83	13.68	2.65	128.20	0.96
RCS 13	213.27	9.47	8.80	42.67	64.87	17.47	9.13	301.93	6.19	4.99	20.67	4.73	224.87	2.05
RCS 14	180.07	11.53	7.53	49.40	72.27	18.40	8.07	162.47	3.91	4.81	17.36	3.70	179.73	1.45
RCS 15	256.13	10.60	9.60	39.60	57.53	18.73	8.47	286.40	4.58	3.65	24.49	5.37	248.07	2.09
RCS 16	140.8	6.73	9.47	42.73	64.27	21.53	9.27	140.93	3.91	4.29	12.28	3.65	102.53	0.95
RCS 17	308.07	8.93	10.80	48.87	72.27	25.40	11.13	258.27	5.63	4.37	19.63	5.56	217.20	2.42
RCS 18	241.07	11.87	9.53	43.20	67.87	19.13	10.20	268.47	7.14	3.17	21.63	6.38	256.37	2.62
Japanese long green	153.73	6.27	9.27	40.93	61.27	19.47	9.33	364.67	5.55	3.13	19.43	5.86	240.80	2.25
Swarna Poorna	228.87	10.13	8.27	43.27	64.40	17.33	8.67	384.87	4.67	4.57	18.24	5.29	222.53	1.93
Swarna Ageti	278.07	7.27	11.53	38.40	58.73	22.53	10.40	340.47	6.83	4.39	21.97	6.43	249.93	2.60
CD (5%)	37.925	0.848	1.260	2.120	2.140	2.250	1.227	27.734	0.387	0.223	1.978	0.988	26.852	0.370

Where, VL= Vine Length, NNFF= Node Number of First Female Flower, NPB= Number of Primary Branches, DFF= Days to First Flowering, DFH= Days to First Harvest, HD= Harvest Duration, NFP= Number of Fruits per Plant , NSF= Number of Seeds per Fruit, SL= Self Life, TSS= Total Soluble Solids, FL= Fruit length, FD= Fruit Diameter, FW= Fruit Weight, YP= Fruit Yield per Plant

Further, for getting the reliable conformity on the basis of cluster means, it was calculated for various horticultural traits and has been presented in the Table 5. Moreover, mean performances of genotypes for different horticultural and yield traits have been presented in Table 6 for getting reliable conformity about selection of parental genotypes to be used in hybridization. Genotypes of cluster IV recorded maximum cluster mean value for fruit weight (251.583), fruit length (21.460), number of seeds per fruit (362.033), shelf-life (6.580), TSS (4.723) and fruit yield per plant (2.352) and minimum cluster mean value for node number of first female flower (5.733) and days to first flowering (39.667). Cluster V had maximum cluster mean value for days to first flowering (46.30), days to first harvest (68.45) and harvest duration (21.833) and minimum cluster mean value for vine length (151.067), number of primary branches (8.20), fruit diameter (3.591), fruit length (15.016), shelf-life (4.037) and number of seeds per plant (168.30).Cluster III had maximum mean value for vine length (249.480), node number of first female flower (10.20), number of primary branches (9.40) and fruit diameter (5.467) and minimum cluster mean value for harvest duration (19.613). Earlier workers like Rao et al. (2003), Hossain et al. [8], Hasan et al. [14], Ahirwar et al. [13], Sharma et al. [15] and Kumar et al. [16] have also indicated significance of genetic divergence in cucumber.

4. CONCLUSION

On the basis of obtained results, it can be concluded that more importance should be given to improve number of nodes per vine, vine length, number of primary branches, early flowering and number of fruits per vine while selection of high yielding genotypes in cucumber. Therefore, the genotypes falling in clusters IV were genetically more divergent. Inter-crossing the genotypes from this cluster may generate wider variability and is expected to throw high yielding transgressive segregants in a population improvement programme.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Tatlioglu T. Cucumber (*Cucumis sativus* L.). Pergamon Press, Ltd; Tarrytown, New York. 1993;197-233.
2. Sharma S, Kumar R, Sharma HR. Studies on variability, heritability and genetic gain in cucumber (*Cucumis sativus* L.). Indian Journal of Ecology. 2017;44(6):829-833.
3. Afangideh U, Uyoh EA. Genetic variability and correlation studies in some varieties of cucumber (*Cucumis sativus* L.) Jordan Journal of Agricultural Sciences. 2007; 3(4):376-384.
4. Mahalanbis PC. On the generalized distance in statics. Proc. Nat. Inst. Sci. (India). 1936;2:49-55.
5. Yadav JR, Gaurav M, Shukla NS, Singh HC, Singh B, Srivastava JP. Genetic divergence in long melon (*Cucumis melo*vari. *utillissimus*). Progressive Agriculture. 2005;5(1&2):50-52.
6. Sharma HR, Sharma D. Genetic divergence for yield and yield-contributing traits in cucumber (*Cucumis sativus* L.). Journal of Horticultural Sciences. 2006; 1(2):141-143.
7. Soleimani A, Ahmadikah A. Performance of different greenhouse cucumber cultivars (*Cucumis sativus* L.) in southern iran. African Journal of Biotechnology. 2009; 8(17):4077-4083.
8. Hossain MD, Rabbani MG, Hakini MA, Amanullah ASM. Study on variability character association and yield performance of cucumber (*Cucumis sativus* L.). Bangladesh Research Publication Journal. 2010;4(3):297-311.
9. Punitha A, Bharathi A, Devi DS. Studies on genetic divergence in cucumber (*Cucumis sativus* L.). Asian Journal of Bio Science. 2012;7(2):169-173.
10. Visen VK, Thakur P, Sharma D, Nair SK. Genetic divergence studies in bottle gourd [*Lagenariasiceraria* (Mol.) Standl.]. Plant Archives. 2015;15(2):1175-1178.
11. Islam MT. Genetic divergence in bottle gourd. Bulletin of the Institute of Tropical Agriculture Kyushu University. 2004;l27: 19-24.
12. Manohar SH, Murthy HN. Estimation of phenotypic divergence and powdery mildew resistance in a collection of cucumber (*Cucumis sativus* L.). African Journal of Biotechnology. 2011;10(11): 1978-1987.
13. Ahirwar CS, Singh DK, Kushwaha ML. Assessment of genetic divergence in cucumber (*Cucumis sativus* L.) germplasm through clustering and principle component analysis. Journal of Pharmacognosy and Phytochemistry. 2017;6(5):804-807.

14. Hasan R, Hossain MK, Alam N, Bashar A, Islam S, Tarafder MJA. Genetic divergence in commercial cucumber (*Cucumis sativus* L.) genotypes. Bangladesh Journal of Botany. 2015;44(2):201-207.
15. Sharma S, Kumar R, Sharma HR, Sharma A, Gautam N. Divergence studies for different Horticulture traits in cucumber (*Cucumis sativus* L.). Int. J. Curr. Microbiol. App. Sci. 2018;7(2):1733-1741.
16. Kumar JS, Pandit MK, Pathy TL. Genetic Variability, Diversity and Character association in Sponge Gourd [*Luffa cylindrica* (Roem.) L.]. Int. J. Curr. Microbiol. Sci. 2019;8(3):278-290.

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