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Interrelationship among elite germplasm of cucumber (*Cucumis sativus* L.) at genotypic and phenotypic level

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ABSTRACT

The experiment was conducted to work out variability, heritability, genetic advance and interrelationship using twelve genotypes of cucumber (*Cucumis sativus* L.). GCV and PCV were highest for number of fruits per vine; whereas lowest estimate was recorded for days to first harvesting and days to last harvesting. The high heritability showed by vine length and number of fruit per vine and as compare to other characters, whereas days to last harvesting, showed lower value of heritability. Genetic advance in percentage of mean was found highest for number of fruits per vine show that these characters are under the control of additive gene action and that environmental factors have a lesser influence on the expression of these traits, thus further development of these traits through direct selection. The path coefficient analysis revealed high and positive direct is possible effect on fruit weight and days to last harvesting. As a result, these traits turned out to be important components of fruit yield thus direct selection effective *via* these two traits.

Key words: Cucumber, GCV, PCV, Correlation, Heritability, Path, Genetic advance.

Introduction

Cucumber (*Cucumis sativus* L.) an important crop of cucurbitaceous family cultivated widely in the tropical and sub-tropical regions. After tomatoes, cabbage and onions, it is the fourth most valuable vegetable (Sandeep Kumar, *et al.*, 2013). Cucumber fruit is versatile and is used in salads, pickles, and desserts. Cucumber is useful in lowering high and low blood pressure because of its high potassium content 50-80 mg/100g (Kashif *et al.*, 2008). Cucumber pulp has 2.16 g carbohydrate dietary fibre (0.7g), total sugars (1.38g), glucose (0.63g), fructose (0.75g) and starch (0.08g) thereby considered an ideal digestive fruit with higher water content. (Department of

agriculture, U.S. 2010). In addition, consumption of cucumber has additional health benefits, *i.e.* anticancer activity, skin diseases, high and low blood pressure treatment; bone health etc (Jony *et al.*, 2013).

The understanding of genetic architecture and direct and indirect selection parameters of agronomically important traits helps in deciding the type of variety to be developed and the breeding methodology to be followed in a particular growing situation. In this context to develop high yielding inbred line varieties, it is essential to screen germplasm lines for gene action, combining ability and nature and magnitude of heterosis for different characters (Shrivastav *et al.*, 2020).

The farmers are facing many problems while cul-

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tivating cucumber. Farmer is not getting the improved varieties of cucumber cultivation. Therefore there is immense need to development of wider adaptive multiple resistance/tolerance as well as high yielding with quality are important (Shrivastav *et al.*, 2022).

Materials and Methods

The present investigation was conducted during summer season of 2021 and 2022, at experimental farm, Department of Genetics and Plant Breeding, Lovely Professional University, Phagwara, Punjab (31°13' 26.4720" N and 75°46' 14.8728" E.) A diverse group of 12 genotypes of cucumber (*Cucumis sativus* L.) were used as experimental material. The selected genotypes exhibiting sufficient amount of variation was grown with respect to morphological and important economical traits. The experiments conducted three replications and in a randomised block design. The Five plant from each plot were randomly selected for recording the observations on the following traits days to first female flower (DFFF), days to first male flower (DFMF), node number at first female flower (NFFF), first fruit bearing node (FFBN), days to first harvest (DFH), fruit weight (g) (FW), fruit length (cm) (FL), fruit diameter (cm) (FD), internodal length (IL), vine length (VL), number of fruits per vine (NFPV), fruit yield per vine (FYPV) and days to last harvest (DLH). The recorded data were analyzed as suggested by Panse and Sukhatme (1985) for analysis of variance. The genotypic and phenotypic coefficient of variance

was calculated as per the formula suggested by Burton and De Vane and Johnson *et al.*, (1953) for heritability and genetic advance. The direct and indirect path were obtained according to the method given by Dewey and Lu *et al.*, (1959). The statistical analysis of the data was carried out using R Studio software and Variability statistical package. The replicated mean values of data were subjected to analysis of variance.

Results and Discussion

Analysis of variance revealed significant variation for most of the traits except Internodal length (0.88), Node number of first female flowers (0.56) and Fruit diameter (0.52) traits under study (Table 1). The estimation of variability parameter *i.e.*, Phenotypic (PCV) and Genotypic (GCV) coefficient of variation for yield and other characters are presented in (Table 2). Genotypic coefficient of variation and phenotypic coefficient of variation were highest for number of fruit per vine (34.73 and 34.79, respectively) whereas lowest estimate of GCV and PCV was recorded for Days to first harvesting (0.89 and 1.17, respectively) and Days to last harvesting. For several features in cucumber, the coefficients of genotypic and phenotypic variability were moderate to high, according to Rastogi and Arya (1990), Kumar *et al.*, (2008), and Mehdi and Khan (2009).

Variation at the phenotypic level involves a mix of genetic and environmental diversity, which makes selection difficult. As a result, the most important characteristics are genetic variability, specifi-

Table 1. Pooled analysis of variance for yield and its contributing traits in cucumber for 2021 and 2022

Sr. No.	Character	Source of Variance		
		Replications	Genotypes	Error
	Degree of freedom	2	11	22
1.	Days to first female flower	6.65**	163.64**	0.91
2.	Days to first male flower	0.814	98.95**	0.57
3.	Node number at first female flower	0.005	0.56	0.15
4.	First fruit bearing node	0.017	2.34*	0.15
5.	Days to first harvest	0.097	4.61**	1.95
6.	Fruit weight (g)	16.15**	2299.01**	110.18
7.	Fruit length (cm)	0.015	6.15**	0.45
8.	Fruit diameter (cm)	0.014	0.52	0.02
9.	Internodal length	0.04	0.88	0.06
10.	Vine length	0.07	329.95**	0.81
11.	Number of fruits per vine	0.07	55.89**	0.17
12.	Fruit yield per vain	129.61**	3189.99**	94.35
13.	Days to last harvest	19.43**	12.37**	4.41

cally additive genetic variability, which a breeder is most interested in range, mean, coefficient of variation, and heritability analysis for selection of elite genotypes. This also indicates the role of the environment in causing the variance. Phenotypic variation is composed of genotypic and environmental variability, there by not to be considered as a tool for effective selection result, since it has been influenced by environmental factors. For a plant breeder, genetic diversity, (additive genetic), is important because it indicates positive genetic gain through selection.

The estimation of heritability and genetic advance as a percentage of mean is given in (Table 2). The range of heritability for all characters varied from 99.75% to 57.66%. vine length (99.75%) showed highest percentage of heritability as compare to other characters followed by number of fruit per vine (99.69%), days to first female flower(99.44%) and characters, mainly, days to first male flower (99.42%), fruit yield per vine (97.04%), fruit diameter (95.57%), fruit weigh t(95.21%), first fruit bearing node (93.36%), fruit length (92.68%) and internodal length(92.42%), showed moderate value of heritability. characters, namely, node number at first female flower (72.22%), days to last harvesting (64.34%) and days to first harvesting (57.66%), showed lower value of heritability.

Genetic progress refers to the improvement in a population’s genetic makeup that can be achieved through character selection. It is determined by the heritability of phenotypic variation and the selection differential of the breeder. Genetic progress is influenced by the amount of genetic variability, the size of the masking effect of genetic expression (environ-

mental influence) and the strength of selection.

Genetic advance as percentage of mean was found highest for number of fruits per vine (71.45%) followed by fruit length (15.77%). Characters namely, vine length (22.47), days to first female flower (20.84), internodal length(20.19), fruit yield per vine (19.99), first fruit bearing node (17.34), fruit weight (16.82), fruit diameter (15.83) and days to first male flower (15.62) showed moderate value of genetic advance and node number of first female flower (7.47), days to last harvesting (2.21) and days to first harvesting (1.39) were recorded for low value of genetic advance as percentage of mean. The phenotypic coefficient of variation (PCV) was higher

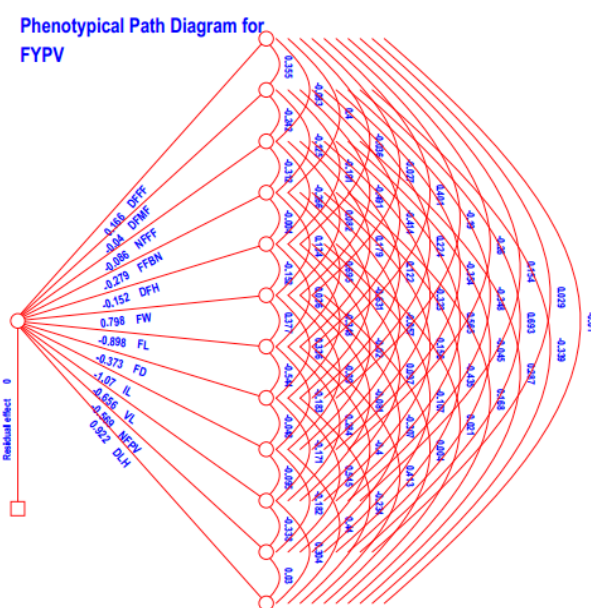


Fig. 1. Diagram for Phenotypic Path coefficient analysis

Table 2. Estimation of coefficient of variation and genetic parameters in cucumber 2021-2022

Sr.No.	Character	\bar{x}^2g	\bar{x}^2p	GCV (%)	PCV (%)	$h^2_{(bs)}$ (%)	GA	GA (%)
1	Days to first female flower	27.12	27.27	10.14	10.17	99.44	10.69	20.84
2	Days to first male flower	16.39	16.49	7.60	7.62	99.42	8.31	15.62
3	Node number at first female flower	0.06	0.09	4.27	5.02	72.22	0.45	7.47
4	First fruit bearing node	0.36	0.39	8.71	9.01	93.36	1.20	17.34
5	Days to first harvest	0.44	0.77	0.89	1.17	57.66	1.04	1.39
6	Fruit weight (g)	364.80	383.16	8.37	8.57	95.21	38.39	16.82
7	Fruit length (cm)	0.95	1.02	7.95	8.26	92.68	1.93	15.77
8	Fruit diameter (cm)	0.08	0.08	7.85	8.03	95.67	58.39	15.83
9	Internodal length	0.13	0.14	10.19	10.60	92.42	0.73	20.19
10	Vine length	54.85	54.99	10.92	10.93	99.75	15.23	22.47
11	Number of fruits per vine	9.28	9.31	34.73	34.79	99.69	6.26	71.45
12	Fruit yield per vain	515.93	531.66	9.85	10.00	97.04	46.09	19.99
13	Days to last harvest	1.32	2.06	1.34	1.67	64.34	1.90	2.21

ber varieties.

Path Coefficient Analysis

The path coefficient analysis indicated high and positive direct effect on fruit weight (0.7978) and days to last harvesting (0.9219). Thus these characters turned out to be major components of fruit yield thus direct selection effective via these two traits. The trait number of fruit per vine exhibited positive and high indirect effect *via* Fruit length (0.3594) so indirect selection reversed via above mention traits. According to Hasan *et al.*, (2015) there was positive and significant association of Fruit weight and days to last harvesting. Ahirwar *et al.*, (2017) observed high positive direct effect of fruit weight and days to last harvesting of cucumber which showed the im-

portance of fruit weight for figuring the yield in cucumber.

Conclusion

From the results, it can be concluded that substantial amount of genetic variations for yield and its components traits studied material. The genotypes had a high genotypic and phenotypic coefficient of variation, heritability and a high value of genetic advance for the number of fruit per vine, vine length, days to first female flower, and days to last harvesting. It indicating that these traits are under the control of additive gene action and that environmental factors have a less influence on the expression of these traits, with the possibility of further



Plate 1. Phenotypic expression of cucumber fruits in two different seasons

Table 4. Phenotypic path coefficient analysis showing direct (diagonal and bold) and indirect effects of various characters in cucumber.

Character	1. DFFF	2. DFMF	3. NFFF	4. FFBN	5. DFH	6. FW	7. FL	8. FD	9. IL	10. VL	11.NFPV	13. DLH
1. DFFF	0.1656	0.0589	-0.0138	0.0663	-0.0060	-0.0044	0.0664	-0.0315	-0.0430	0.0255	0.0049	-0.0017
2. DFMF	-0.0142	-0.0401	0.0097	0.0050	0.0077	0.0197	0.0166	-0.0090	0.0142	0.0139	-0.0278	0.0136
3. NFFF	0.0071	0.0207	-0.0855	0.0267	0.0227	-0.0070	-0.0153	-0.0104	0.0276	-0.0483	0.0038	-0.0245
4. FFBN	-0.1115	0.0349	0.0870	-0.2787	0.0011	-0.0372	-0.1938	0.1759	0.0160	-0.0435	0.1213	-0.0468
5. DFH	0.0055	0.0291	0.0404	0.0006	-0.1521	0.0231	-0.0055	0.0530	0.0031	-0.0147	0.0163	-0.0032
6. FW	-0.0214	-0.3914	0.0657	0.1066	-0.1211	0.7978	0.3011	0.2684	-0.0717	-0.0644	-0.2449	0.0035
7. FL	-0.3600	0.3719	-0.1605	-0.6247	-0.0324	-0.3390	-0.8983	0.4884	0.1643	-0.2554	0.3594	-0.3713
8. FD	0.0709	-0.0837	-0.0454	0.2354	0.1299	-0.1254	0.2027	-0.3729	0.0178	0.0636	-0.2034	-0.0872
9. IL	0.2780	0.3793	0.3459	0.0614	0.0216	0.0962	0.1957	0.0510	-1.0701	0.1017	0.1948	-0.4707
10. VL	-0.1009	0.2282	-0.3705	-0.1024	-0.0635	0.0530	-0.1865	0.1119	0.0624	-0.6560	0.2216	-0.1994
11. NFPV	-0.0167	-0.3942	0.0255	0.2477	0.0611	0.1747	0.2277	-0.3103	0.1036	0.1922	-0.5690	-0.0172
13. DLH	-0.0096	-0.3130	0.2645	0.1547	0.0192	0.0041	0.3810	-0.2157	0.4055	0.2803	0.0279	0.9219
12. FYPV	-0.1071	-0.0993	0.1629	-0.1014	-0.1116	0.6553	0.0918	0.1988	-0.3705	-0.4052	-0.0950	-0.1086
Partial R ²	-0.0177	0.0040	-0.0139	0.0283	0.0170	0.5228	-0.0825	-0.0741	0.3965	0.2658	0.0541	-0.1001

development of these traits through direct selection.

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Authors' Contributions

Prasad D. Khedkar and Harmeet Singh Janeja had conceptualized the idea, worked and prepared the data, and results along with the draft manuscript and have edited final draft manuscript. All authored have written, reviewed, and edited the manuscript.

Conflicts of Interest

The authors report no financial or any other conflicts of interest in this work

References

Ahirwar, C.S. and Singh D.K. 2018. Assessment of genetic variability in cucumber (*Cucumis sativus* L.). *Int. J. Curr. Microbiol. App. Sci.* 7 (03) : 813-822.

Burton, G.W. and Devane, 1953. Quantitative inheritance in grass. Pro. 6th 11411. Grassland Congress J. I. 277-283.

Department of agriculture, U. S. 2010. USDA national nutrient database for standard reference. Nutrient data laboratory home page releases 23 U.S. Department of Agriculture, Agricultural Research Service.

Dewey, J.R. and Lu, K.H. 1959. Correlation and path analysis of components of crested wheat grass seed production. *Agron. J.* 51: 515-518.

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

Jony M. Priyanka, D. and Sourav, D. 2013. Pharmacological activity of *Cucumis Sativus* .A complete review. *Asian J. Pharm. Res. Dev.* 1(1)1-16.

Kashif, W., Kamran, Q.M. and Jilani, M S. 2008. Effect of nitrogen levels on growth and yield of cucumber (*Cucumis sativus* L.). *J. Agril. Res.* 46(3): 259-266.

Kumar, S., Kumar, D., Kumar, R. and Dogra, T.B. S. 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): 27-28.

Kumar, A. Kumar, S. and Pal K. A. 2008. Genetic variability and character association for yield and yield traits in cucumber. *Indian J. Hort.* 65.4: 423-42.

Mehdi, M. and Khan, F. A. S. 2009. Variability and character association analysis in cucumber germplasm. *J. Agri. & Biological Res.* 25.2 : 87-91.

Panse, V.G. and Sukhatme, P.V. 1985 Statistical methods for agricultural workers, IC A.R., New Delhi.

Rastogis, K.B. and Arya, D. 1990. Variability studies in cucumber (*Cucumis sativus* L.). *Veg. Sci.* 17.2: 224-226.

Saikumar, P.M. Shanthi Priya, P. Shanthi and Latha, P. 2020. Genetic variability studies for quantitative traits in a pool of maintainer (B) and restorer (R) lines in pearl millet (*Pennisetum glaucum* L.). *Int. J. Curr. Microbiol. App. Sci.* 9(12): 3234-3241.

Shrivastav S.P., Verma, O.P., Singh V. and Lal, K. 2020. Interrelationship among yield and its contributing triads in rice (*Oryza sativa* L.) under sodic soil. *Electron. J. Plant Breed.* 11(4) : 1044-1052.

Shrivastav, S.P., Verma, O.P., Lal, K. Singh V. Srivastava, K. 2022. Genetic divergence analysis in rice (*Oryza sativa* L.) germplasms under sodic soil. *Indian J. Agric. Res.* 10.18805/IJAR.A-5976.