Plant Archives Vol. 26, Supplement 1, 2026 pp. 2622-2629 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org

DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2026.v26.supplement-1.352

EVALUATION OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR THE IDENTIFICATION OF SUPERIOR GENOTYPES IN CUCUMBER (*CUCUMIS SATIVUS* L.)

Siddharth Kumar*[1], Keshav Arya[1], Rajendra Kumar Yadav[2], Vivek Kumar Tripathi[3], Som Veer Singh[2], Rajiv[1], Rajat Singh[1] and Mohit Kumar[4]

[1]Department of Vegetable Science, Chandra Shekhar Azad University of Agriculture & Technology, Kanpur (U.P.), India.

[2]Department of Genetics & Plant Breeding, Chandra Shekhar Azad University of Agriculture & Technology, Kanpur (U.P.) India.

[3]Department of Fruit Science, Chandra Shekhar Azad University of Agriculture & Technology, Kanpur (U.P.) India.

[4]Project Associate-I, CSIR- Indian Institute of Integrative Medicine, Jammu (J&K) India.

*Corresponding author E-mail: siddharth9264@gmail.com

(Date of Receiving : 06-09-2025; Date of Acceptance : 08-11-2025)

ABSTRACT

The present investigation was conducted at the Vegetable Research Farm, Department of Vegetable Science, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur, to assess genetic variability, heritability and genetic advance in cucumber (*Cucumis sativus* L.) by using the Line × Tester design. Ten parental lines and three testers were crossed and the resulting F_1 hybrids along with their parents were evaluated in a Randomized Complete Block Design (RCBD) with three replications during two consecutive seasons (2023-2024). Observations were recorded for the yield and quality traits and the data were analyzed for genetic parameters. The significant variability was observed among the genotypes for all the traits studied. Broad-sense heritability estimates ranged from 65.20% (vine length) to 98.34% (days to appearance of first male flower). High heritability coupled with high genetic advance and genotypic coefficient of variation (GCV) was recorded for number of fruits per plant, fruit yield per plant, internodal length, and number of nodes per vine, indicating the predominance of additive gene action and suggesting that direct selection would be effective for improvement. The traits such as total sugar, ascorbic acid content and shelf life exhibited high heritability but low genetic advance, implying non-additive gene effects. Overall, the study revealed considerable genetic variability and high heritable variation among cucumber genotypes, highlighting the potential for effective selection and genetic improvement for higher yield and quality.

Keywords: Cucumber, Genetic variability, Heritability, Genetic advance, Line × Tester and gene action.

Introduction

Cucumber (*Cucumis sativus* L.) is the most important crop of the family Cucurbitaceae grown commercially throughout the country. The fruits are used for preparation of cosmetic items like soap and cream and in many other ways (Dhiman and Parkash, 2005). The crop is of Asian origin and the progenitor may be closely related to its wild relative *Cucumis sativus var. hardwickii,* first found in the Himalayan Mountains (foothills of Nepal) and used by native peoples of Northern India as a laxative (Deakin *et al.*, 1971). 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 (Shah *et al.,* 2016). Cucumber is well known for its pleasant aroma which is due to 2,6-Nonadienal whereas its flavor is due to presence of two compound 2,6-Nonadienal and 2,6-Nonadienol. It may further be mentioned that cucumber juice is commonly used for treating diseases of teeth and gums. Its juice is still useful for rheumatic conditions and healthy growing hair (Khulakpam *et al.*, 2015). It is the fourth most important vegetable crop after tomato, cabbage and onion in Asia.

China is the highest producer country which accounts for nearly half of the total world production. The other main producers are Iran, Turkey and USA. Cucumber is commercially grown throughout India ranging from north western Himalayan region to southern peninsular region including riverbeds and floating gardens in Dal lake of Kashmir valley. In India the area under cucumber cultivation is 138.54 thousand hectares and produces 1989.88 thousand metric tons annually. The major cucumber producing states in India are West Bengal, Madhya Pradesh, Haryana, Gujarat, Karnataka, Punjab and Uttar Pradesh. West Bengal is the leading cucumber producing state with the production of 349.95 thousand metric tons from an area of 24.81 thousand hectares followed by Madhya Pradesh which produced 323.79 thousand metric tons from an area of 19.71 thousand hectares. Uttar Pradesh covers 4.60 thousand hectares area under cucumber cultivation with an annual production of 121.03 thousand metric tons production (Anonymous, 2024-25).

Any crop improvement programme primarily depends on the amount of genetic variability available and the extent to which the economic traits are heritable. The coefficient of variation of phenotypic and genotypic is helpful in detecting the amount of variation present in the available strains. Heritability is the ratio of genotypic variance to phenotypic variance. It is a good index of the transmission of characters from parents to offspring (Falconer, 1981). Heritability indicates the extent to which improvement is possible through selection and relative degree to which a character is transmitted from parent to offspring. Most of the quantitative characters, which are of economic value, are highly influenced by environment. Therefore, some of the highly heritable characters associated with yield, which are influenced to a lesser degree by environment, serve as an indicator of yield in selection programme. Additionally, nature of gene action is also important where progress from selection depends primarily on the additive gene action (Pradhan *et al.*, 2016). Heritability and genetic advance serve as useful tools for the breeders in determining the direction and magnitude of selection. Estimates of heritability have to be considered with conjunction with genetic advance as alone it does not provide idea about expected gain in next generation. For a successful planning of breeding improvement program, the analysis of variability among the traits and their association of a particular character in relation to yield and yield attributing traits it would be great importance. To start an efficient breeding improvement program, it is necessary to evaluate the genetic parameter such as genetic coefficient of variation, heritability and genetic advance.

Materials and Methods

The present investigation was carried out at the Vegetable Research Farm, Department of Vegetable Science, C.S. Azad University of Agriculture and Technology, Kanpur, situated in a subtropical climatic region with sandy loam soil of moderate fertility. The experimental material consisted of ten cucumber (*Cucumis sativus* L.) parental lines collected from reputed agricultural research institutions and three testers. The study was conducted to assess genetic variability, heritability, and combining ability for yield and quality traits using the Line × Tester mating design as described by Kempthorne (1957). The breeding programme was executed over two consecutive growing seasons. In the first season (2023), all parental lines and testers were grown for preliminary evaluation and crossing. Controlled hybridization was carried out to develop F_1 seeds. Cucumber, being a monoecious crop bearing separate male and female flowers on the same plant, was subjected to manual pollination to ensure genetic purity. Male and female flower buds of selected parents were bagged a day before anthesis to prevent unwanted pollination. On the following morning, pollen from freshly opened male flowers of the designated male parent was applied to the stigma of the female flowers, followed by re-bagging to maintain isolation. The mature fruits from these crosses were harvested, and seeds were extracted, cleaned, dried, and stored properly for subsequent sowing. In the second season (2024), the F_1 hybrids along with their respective parents were evaluated in a Randomized Complete Block Design (RCBD) with three replications. Each plant was spaced at 2.0 m × 0.5 m, and standard agronomic practices were followed, including land preparation and fertilization with 100:50:50 kg ha^{-1} NPK and 20 t ha^{-1} of well-decomposed farmyard manure. Regular irrigation, weeding and plant protection measures were undertaken to ensure optimal growth and development. The observations were recorded on randomly selected plants for a comprehensive set of yield and quality traits to assess genetic variability among genotypes. The traits studied included: days to appearance of first male flower, days to appearance of first female flower, node number bearing the first female flower, sex ratio (male/female), days to first fruit harvest, days to last fruit harvest, vine length (m), number of primary branches per plant, number of nodes per vine, and internodal length (cm), fruit length (cm), fruit diameter (cm), number of fruits per plant, average fruit weight (g), and fruit yield per plant (kg). Quality attributes included fruit flesh thickness (mm), total soluble solids (°Brix) measured using a refractometer, ascorbic acid content (mg/100 g fresh fruit) determined as per AOAC (1970), total sugar content (%) estimated by the anthrone method (Dubois *et al.*, 1956), dry matter percentage and shelf life (days).

The recorded data were subjected to analysis of variance (ANOVA) under the RCBD model to test the significance of variation among genotypes. Concurrent meteorological data, including weekly maximum and minimum temperatures, rainfall, relative humidity and evaporation rates, were recorded throughout both cropping seasons to facilitate interpretation of genotype-environment interactions.

Estimation of Genetic Parameters

Heritability, genetic variability and genetic advance were estimated from the mean performance of parental lines, hybrids and segregating generations to assess the magnitude of genetic control over different traits in cucumber. The variance components were obtained from the analysis of variance (ANOVA) as per the experimental design. Heritability in the broad sense (H^2) was computed following the method of Johnson *et al.,* (1955) and Hanson *et al.* (1956) by using the formula:

$$H^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

where σ_g^2 represents the genotypic variance and σ_p^2 denotes the phenotypic variance. The genotypic variance was derived by partitioning the total variance into genetic and environmental components based on mean squares from ANOVA.

To quantify the degree of variability present among the genotypes, the Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) were calculated using the following expressions as suggested by Burton and Devane (1953):

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100 \text{ and } PCV = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

where $\bar{X}$ is the grand mean of the respective trait. These coefficients provide insight into the relative magnitude of genetic and environmental influences on phenotypic expression, with the difference between PCV and GCV indicating the extent of environmental impact.

The Genetic Advance (GA) as a percentage of the mean was determined to assess the expected improvement under selection, using the following formula suggested by Johnson *et al.* (1955) and Allard (1960).

$$GA = k \times \sqrt{\sigma_p^2} \times H^2 \text{ and } GA\% = \frac{GA}{\bar{X}} \times 100$$

where, k is the selection differential, taken as 2.06 for 5% selection intensity, $\sqrt{\sigma_p^2}$ is the phenotypic standard deviation, and H^2 is heritability in the broad sense. The estimation of these genetic parameters provided a comprehensive understanding of the variability, heritable portion of total variance, and the scope for genetic improvement in cucumber breeding populations.

Statistical Analysis

The recorded mean data for all observed traits were subjected to one-way analysis of variance (ANOVA) to assess the significance of variation among genotypes, as per the procedure outlined for the Randomized Complete Block Design (RCBD). The variance components obtained from ANOVA were used to compute the genotypic variance (σ^2g) and phenotypic variance (σ^2p). Based on these values, heritability in broad sense was categorized as suggested by Hanson *et al.* (1956) and the genotypic and phenotypic coefficients of variation (GCV and PCV) were estimated by following the method of Burton and Devane (1953) and classified as suggested by Sivasubramanian and Madhavamenon (1973) to determine the extent of genetic and environmental influence on trait expression. The expected genetic advance (GA) and genetic advance as percentage of mean (GA%) were calculated and categorized to estimate the potential improvement under selection pressure, following the standard formulae described by Johnson *et al.* (1955). All statistical analyses were carried out using standard biometrical procedures and the results were interpreted to evaluate the magnitude of genetic variability, heritability and the scope for selection in the studied cucumber genotypes.

Results and Discussion

Analysis of variance

Analysis of variance revealed that the genotypes differed significantly for all the characters studied, as the mean sum of squares due to genotypes were highly significant for each trait evaluated (Table-1). Highly significant differences were observed for days to appearance of first male and female flowers, node number bearing first female flower, sex ratio, days to first and last fruit harvest, vine length, number of primary branches, number of nodes per vine, internodal length, fruit length, fruit diameter, number of fruits per plant, average fruit weight, fruit yield per plant, flesh thickness, total soluble solids, ascorbic acid content, total sugar, dry matter percentage and shelf life. The existence of such significant variability among genotypes indicates the presence of considerable genetic diversity in the experimental material, thereby providing substantial scope for selection and genetic improvement in cucumber for yield and quality traits. Similar results were also reported by Kumar *et al.* (2019), Rajaguru *et al.* (2019), Sahoo and Singh (2020) and Shukla *et al.* (2025), who observed significant genetic variability among cucumber genotypes for growth, yield and quality attributes, suggesting ample opportunity for effective selection and improvement.

Table 1 : Analysis of variance (ANOVA) for different Yield and Quality traits in Cucumber

S.N.	**Characters**		**Mean Sum of Square**		
		Source of Variation	**Replications**	**Genotypes**	**Error**
		Degree of Freedom	**2**	**43**	**86**
1.	Days to appearance of first male flower		0.48	130.47**	0.81
2.	Days to appearance of first female flower		0.08	128.70**	1.15
3.	Node number bearing first female flower		0.001	1.245**	0.118
4.	Sex ratio (M/F)		0.080	3.137**	0.138
5.	Days to first fruit harvest		0.85	132.63**	1.90
6.	Days to last fruit harvest		0.30	119.05**	4.99
7.	Vine Length (m)		0.003	0.032**	0.009
8.	Number of primary branches per plant		0.004	0.948**	0.038
9.	Number of nodes per vine		0.29	114.55**	2.11
10.	Internodal length (cm)		0.06	7.91**	0.13
11.	Fruit length (cm)		0.01	14.13**	0.83
12.	Fruit diameter (cm)		0.010	0.288**	0.040
13.	Number of fruits per plant		0.002	11.95**	0.25
14.	Average fruit weight (gm)		0.57	977.78**	76.92
15.	Fruit yield per plant (kg)		0.003	0.347**	0.006
16.	Fruit flesh thickness (mm)		0.001	0.052**	0.001
17.	Total Soluble Solids (^{0}Brix)		0.001	0.096**	0.004
18.	Ascorbic Acid (mg/100 gm fresh fruit)		0.001	0.107**	0.009
19.	Total Sugar (%)		0.001	0.027**	0.004
20.	Dry Matter (%)		0.011	0.300**	0.011
21.	Shelf life (days)		0.009	0.312**	0.024

Estimation of Heritability, Coefficient of Variation and Genetic Advance (as % Mean)

The estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h^2) and genetic advance as per cent over mean (GAM) were statistically analyzed for different yield and quality traits has been given in Table-2 and depicted in Figure-2, and the findings have been explained under following heads:

Heritability (h^2)

The estimates of broad-sense heritability ranged from 65.20% for vine length to 98.34% for days to appearance of first male flower. High heritability (>75%) was observed for most of the studied traits including days to appearance of first male (98.34%) and female (98.01%) flowers, fruit yield per plant (97.41%), number of fruits per plant (96.87%), days to first fruit harvest (96.03%), internodal length (95.09%), and number of nodes per vine (94.86%). Such high heritability values suggest that these traits are predominantly under genetic control and less influenced by environmental fluctuations, thereby allowing effective selection (Allard, 1960; Singh & Narayan, 2022). Moderate heritability (50-75%) was recorded for total sugar (74.73%) and vine length (65.20%), implying moderate environmental influence. High heritability coupled with high GCV, as observed for yield-related traits, implies additive gene action and suggests that selection based on phenotype would be reliable for genetic improvement (Panse and Sukhatme, 1985; Burton and DeVane, 1953). Similar findings have been reported in cucumber by Alam *et al.* (2019), Agashi *et al.* (2020), Singh *et al.* (2022), Khedkar *et al.* (2023) and Yadav *et al.* (2022), emphasizing the consistency of genetic expression in such traits.

Coefficient of Variation

The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all traits studied, indicating the influence of environmental factors on trait expression. However, the relatively small differences between PCV and GCV values for most traits suggested that the environment had a limited effect and that the observed variability was largely genetic in nature. Such findings are consistent with those reported by Singh *et al.* (2017) and Kumar *et al.* (2021) in cucumber. The PCV ranged from 4.57% for shelf life to 27.10% for number of fruits per plant. High PCV (>20%) was recorded for number of fruits per plant (27.10%), fruit yield per plant (26.00%), number of nodes per vine (20.10%), and internodal length (20.08%), suggesting that these traits exhibit considerable phenotypic variability and offer good prospects for selection. Moderate PCV (10-20%) was recorded for days to appearance of first male flower (16.30%), number of primary branches per plant (15.49%), sex ratio (13.80%), fruit length (13.08%), days to appearance of first female flower (12.83%), average fruit weight (10.56%), days to first fruit harvest (10.20%), and node number bearing the first female flower (10.07%). The remaining traits exhibited low PCV (<10%), indicating limited variability. The GCV ranged from 3.99% (total sugar) to 26.67% (number of fruits per plant). High GCV (>20%) was observed for number of fruits per plant (26.67%) and fruit yield per plant (25.66%), both key yield attributes. Moderate GCV (10-20%) was recorded for internodal length (19.58%), number of nodes per vine (19.57%), days to appearance of first male flower (16.17%), number of primary branches per plant (14.83%), sex ratio (13.09%), days to appearance of first female flower (12.70%), fruit length (12.28%) and days to first fruit harvest (10.00%).

Table 2: Estimation of different genetic variability parameter for different Yield and Quality traits in Cucumber

S.N.	Characters	Heritability (%)	Coefficient of Variation		GA (% mean)
			GCV (%)	PCV (%)	
1.	Days to appearance of first male flower	98.34	16.17	16.30	33.02
2.	Days to appearance of first female flower	98.01	12.70	12.83	25.90
3.	Node number bearing first female flower	82.87	9.17	10.07	17.19
4.	Sex ratio (M/F)	90.03	13.09	13.80	25.59
5.	Days to first fruit harvest	96.03	10.00	10.20	20.18
6.	Days to last fruit harvest	94.18	6.95	7.16	13.89
7.	Vine Length (m)	65.20	5.78	7.16	9.61
8.	Number of primary branches per plant	91.60	14.83	15.49	29.23
9.	Number of nodes per vine	94.86	19.57	20.10	39.27
10.	Internodal length (cm)	95.09	19.58	20.08	39.33
11.	Fruit length (cm)	88.15	12.28	13.08	23.74
12.	Fruit diameter (cm)	75.07	7.62	8.80	13.60
13.	Number of fruits per plant	96.87	26.67	27.10	54.07
14.	Average fruit weight (gm)	83.89	9.67	10.56	18.25
15.	Fruit yield per plant (kg)	97.41	25.66	26.00	52.16
16.	Fruit flesh thickness (mm)	94.18	8.84	9.11	17.68
17.	Total Soluble Solids (^{0}Brix)	85.84	5.66	6.10	10.79
18.	Ascorbic Acid (mg/100 gm fresh fruit)	83.89	4.82	5.26	9.09
19.	Total Sugar (%)	74.73	3.99	4.62	7.11
20.	Dry Matter (%)	92.99	7.38	7.66	14.67
21.	Shelf life (days)	78.14	4.04	4.57	7.36

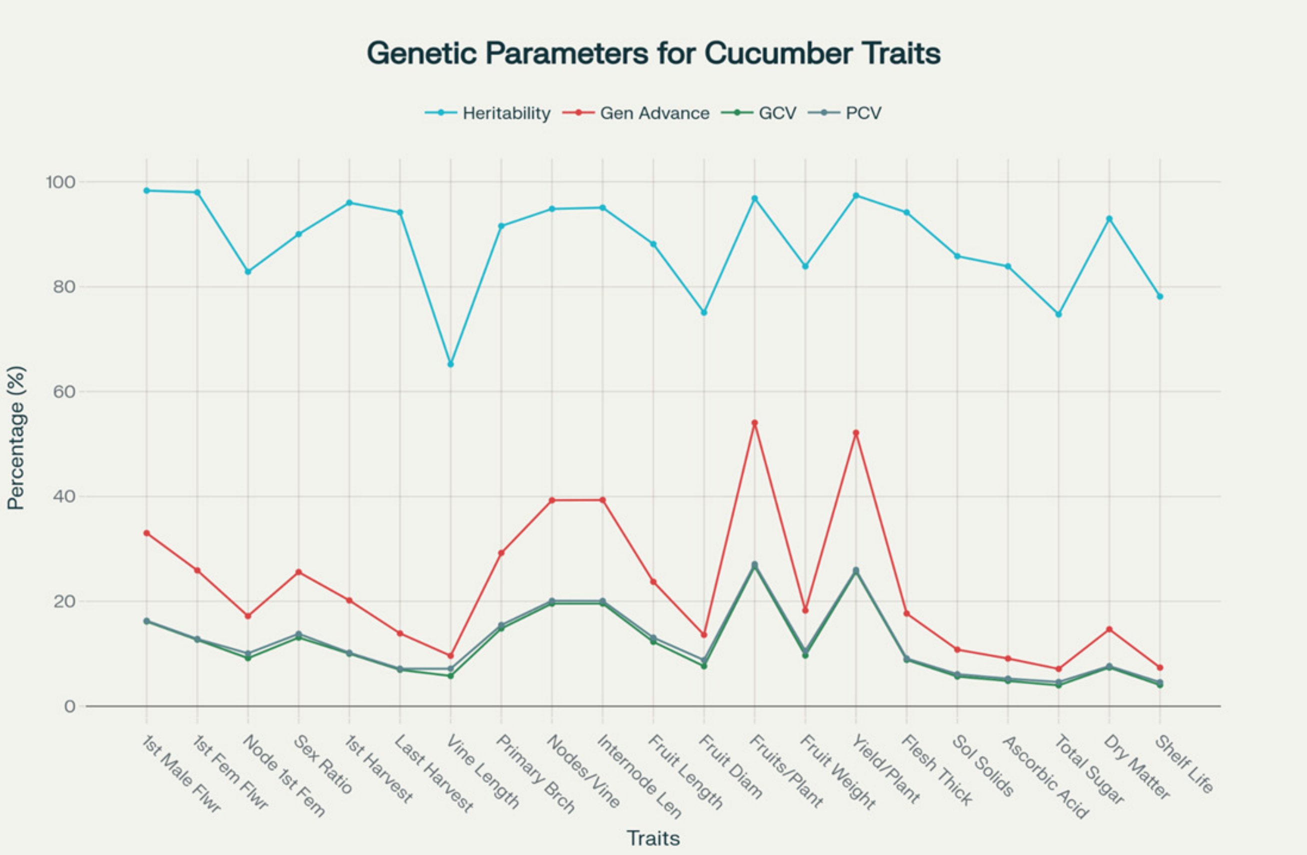

Fig. 2: Estimation of different genetic variability parameter for different Yield and Quality traits in Cucumber

The low GCV (<10%) for traits like total sugar, ascorbic acid, and shelf life indicates limited scope for selection based solely on these traits. The results indicate that traits with high GCV and PCV, such as number of fruits per plant and fruit yield per plant, are governed largely by genetic factors and thus direct selection could be effective. Similar results were reported by Sahoo and Singh (2020), Kumari *et al.* (2020), Devi *et al.* (2020) Yadav *et al.* (2021) and Singh *et al.* (2022) in cucumber, highlighting the potential of yield components for genetic improvement.

Genetic Advance (as % Mean)

The genetic advance as percent of mean ranged from 7.11% for total sugar to 54.07% for number of fruits per plant. High GA (>20%) was observed for number of fruits per plant (54.07%), fruit yield per plant (52.16%), internodal length (39.33%), number of nodes per vine (39.27%), days to appearance of first male flower (33.02%), number of primary branches per plant (29.23%), days to appearance of first female flower (25.90%), sex ratio (25.59%), fruit length (23.74%), and days to first fruit harvest (20.18%). These results suggest a predominance of additive gene action and indicate that these traits can be improved through direct selection. Moderate GA (10-20%) was observed for average fruit weight (18.25%), fruit flesh thickness (17.68%), node number bearing first female flower (17.19%), dry matter (14.67%), days to last fruit harvest (13.89%), fruit diameter (13.60%), and total soluble solids (10.79%), while low GA (<10%) was observed for vine length (9.61%), ascorbic acid (9.09%), shelf life (7.36%), and total sugar (7.11%). Traits with high heritability and high genetic advance, such as number of fruits per plant, fruit yield per plant, and internodal length, are indicative of additive gene effects, suggesting that simple selection methods would be effective for their improvement (Johnson *et al.*, 1955; Panse and Sukhatme, 1985). Conversely, traits with high heritability but low genetic advance, such as total sugar and shelf life, may be governed by non-additive gene action, thus requiring hybridization or recurrent selection strategies.The present findings reveal that yield and its component traits in cucumber possess substantial genetic variability, high heritability, and high genetic advance, indicating the potential for effective selection and genetic improvement in breeding programmes. Similar conclusions were drawn by Rajawat and Collis (2017), Kumar *et al.* (2021), Khedkar *et al.* (2023), Singh *et al.* (2022) and Yadav *et al.* (2022), who also emphasized the importance of these parameters for enhancing cucumber productivity through selection-based breeding.

Conclusion

The present investigation on cucumber revealed substantial genetic variability among the studied parental lines and their hybrids for most of the yield and quality traits. High estimates of heritability coupled with high genetic advance and genotypic coefficient of variation (GCV) for traits such as number of fruits per plant, fruit yield per plant, internodal length and number of nodes per vine indicate that these traits are predominantly governed by additive gene action and can be effectively improved through simple selection methods. The relatively small differences between phenotypic and genotypic coefficients of variation further suggest that environmental influence on the expression of these traits was limited. Conversely, traits exhibiting high heritability but low genetic advance, including total sugar, ascorbic acid content, and shelf life, appear to be controlled largely by non-additive gene effects, suggesting the need for hybridization or recurrent selection strategies for their improvement. The findings also emphasize that yield-related traits, being closely associated with additive genetic variance, provide a strong basis for direct selection in early generations. The results highlight the existence of ample genetic variability and a high degree of heritable variation in cucumber germplasm, offering significant opportunities for genetic enhancement. These insights will be valuable for breeders in developing high-yielding and quality-improved cucumber cultivars through efficient selection and hybridization approaches tailored to subtropical environments.

Acknowledgement: I am grateful to my advisor as well as all of the committee members for their unwavering support and advice throughout the entire experimental research study.

Competing interests: Authors have declared that no competing interests exist.

References

Agashi, A. I., Okporie, E. O., Chukwu, S. C. and Onyishi, G. C. (2020). Studies on genetic variability, heritability and genetic advance in cucumber (*Cucumis sativus* L.) cultivars collected from China and Nigeria. *Hand*, **8**, 10.

Alam, M. S., Rahman, M. M. and Khatun, T. (2019). Genetic variability, heritability, and genetic advance in cucumber (*Cucumis sativus* L.). *Bangladesh Journal of Agricultural Research*, **44**(2), 223-231.

Allard, R. W. (1960). *Principles of Plant Breeding*. John Wiley and Sons.

Anonymous, (2024-25). Department of Agriculture and Farmers Welfare, Government of India. *First Advance Estimates*. https://agriwelfare.gov.in/en/StatHortEst.

AOAC (1970). Official Methods of Analysis of the Association of Official Analytical Chemists. In: *Association of Official Analytical Chemists* (Ed. Horewitz William). Benjamin Franklin Station, Washington, D.C.

Burton, G. W. and DeVane, E. H. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*, **45**(10), 478-481.

Deakin, J. R., G. W. Bohn and T. W. Whitaker (1971). Interspecific hybridization in Cucumis. *Economic Botany,* **25**:195-211.

Devi, L., Singh, M. K. and Singh, S. (2020). Genetic variability and heritability studies in cucumber (*Cucumis sativus* L.). *Journal of Pharmacognosy and Phytochemistry*, **9**(5), 252-255.

Dhiman and Prakash, C. (2005). Correlation and path coefficient analysis in cucumber. *Haryana Journal of Horticultural Sciences*, **34**(1-2):111-112.

Dubois, M., Gilles, K.A., Hamilton, J.K., Robers, P.A. and Smith, F. (1956). A colorimetric method for the determination of sugar. *Analytical Chemistry* **28**: 350-356.

Falconer, D. S. (1981). Introduction to Quantitative Genetics, Ed.2. *Longmans Green*, London/New York.

Hanson, G.H., Robinson, H.F. and Comstock, R.E. (1956). Biometrical studies of yield in segregating population of Korean lespedeza. *Agronomy Journal,* **48**: 268-271.

Johnson, H. W., Robinson, H. F., and Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, **47**(7), 314-318.

Kempthorne, O. (1957). *An Introduction to Genetic Statistics*. John Wiley and Sons, Inc. New York. pp. 468-471.

Khedkar, P. D., Janeja, H. S., Delvadiya, I. R. and Talekar, N. (2023). Interrelationship among elite germplasm of cucumber (*Cucumis sativus* L.) at genotypic and phenotypic level. *Eco. Env. and Cons*. **29**(S511-S516).

Khulakpam, N. S., Singh, V. and Rana, D. K. (2015). Medicinal importance of cucurbitaceous crops. *International Research Journal of Biological Sciences*, **4**(6), 1-3.

Kumar, R., Kumari, R., Sharma, S., Rana, S. and Singh, V. (2019). Genetic assessment for quality, biotic stress and seed traits in cucumber (*Cucumis sativus* L.). *International Journal of Chemical Studies,* **7**(3), 2517-2521.

Kumar, R., Sharma, A. and Singh, J. (2021). Assessment of genetic variability, heritability, and genetic advance in cucumber (*Cucumis sativus* L.). *Indian Journal of Horticulture*, **78**(3), 356-361.

Kumari, M., Ram, C. N., Nath, S., Maurya, N. and Kumar, S. (2020). Studies on genetic variability, heritability and genetic advance in cucumber (*Cucumis sativus* L.), *Journal of Pharmacognosy and Phytochemistry,* **9**(5): 481-484.

Panse, V. G. and Sukhatme, P. V. (1985). *Statistical Methods for Agricultural Workers* (4th ed.). ICAR Publications.

Pradhan, S.R., Dharmatti, P.R., Sahu, G.S. and Sahoo, T.R. (2016). Combining ability studies for yield and yield attributing characters in cucumber (*Cucumis sativus* L.). *The Bioscan*, **11**(4), 3075-3080.

Rajaguru, K., Arumugam, T., Sassi Kumar, D., Jeeva, S. and Baskaran, R. (2019). Assessment of Genetic Variability of Cucumber (*Cucumis Sativus* L.) Gene Pool of Tamil Nadu through Principal Component Analysis. *International Journal of Chemical Studies*, **7**(5), 335-338.

Rajawat, K. S. and Collis, J. P. (2017). Genetic variability, Heritability and Genetic advances analysis for quantitative and qualitative traits in Cucumber (*Cucumis sativus* L.). *Journal of Pharmacognosy and Phytochemistry*, **6**(4), 882-885.

Sahoo, T. R. and Singh, D. K. (2020). Estimation of genetic variability, heritability and genetic advance in Cucumber (*Cucumis sativus* L.) for yield and its components under protected structure. *International Journal of Current Microbiology and Applied Sciences,* **9**(4), 2756-64.

Shah, K.N., Rana, D.K. and Singh, V. (2016). Evaluation of different cucumber strain for various horticultural traits under valley condition of Garhwal Himalaya. *Journal of Plant Development Sciences*, **8**(12): 599-603.

Shukla, H., Upadhyay, D., Jha, A., Paswan, S., Singh, A. P. and Yadav, R. (2025). Genetic Evaluation for Variability, Heritability and Genetic Advance in Cucumber (*Cucumis sativus* L.) Genotypes. *Journal of Advances in Biology & Biotechnology*, **28**(6), 1441-1448.

Singh, D. and Narayan, R. (2022). Genetic variability studies in cucumber (*Cucumis sativus* L.) for yield and yield contributing traits. *Journal of Crop and Weed*, **18**(1), 155-160.

Singh, S. P., Malik, S., Singh, B., Gangwar, L. K., Singh, M. K., Kumar, M. and Chandra, A. (2022). Studies on genetic variability, heritability, and genetic advance for selection of genotypes in Cucumber (*Cucumis sativus* L.). *The Pharma Innovation Journal*, **11**(7): 2535-2537

Sivasubramanian, S. and Madhavamenon, P. (1973). Genotypic and phenotypic variability in rice. *Madras Agricultural Journal*, **60**: 1093 -1096.

Yadav, P., Singh, S. K. and Meena, M. (2022). Genetic parameters and variability studies in cucumber (*Cucumis sativus* L.) for yield and related traits. *Vegetable Science*, **49**(2), 238-243.

Yadav, S., Singh, D. K., Singh, S. S., Bisht, Y. S. and Bhatt, R. (2021). Assessment of genetic variability in cucumber (*Cucumis sativus* L.). *International Journal of Chemical Studies*, **9**(1): 3347-3349.