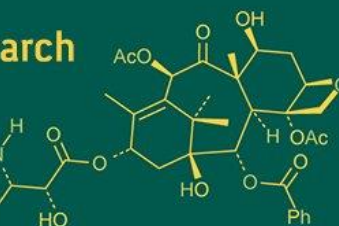
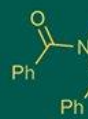


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Krishan Kumar
Department of Vegetable Science,
Chandra Shekhar Azad University
of Agriculture & Technology,
Kanpur, Uttar Pradesh, India

Rajiv
Department of Vegetable Science,
Chandra Shekhar Azad University
of Agriculture & Technology,
Kanpur, Uttar Pradesh, India

Keshav Arya
Department of Vegetable Science,
Chandra Shekhar Azad University
of Agriculture & Technology,
Kanpur, Uttar Pradesh, India

Shweta
Department of Genetics and Plant
Breeding, Chandra Shekhar Azad
University of Agriculture &
Technology, Kanpur, Uttar
Pradesh, India

Somveer Singh
Department of Genetics and Plant
Breeding, Chandra Shekhar Azad
University of Agriculture &
Technology, Kanpur, Uttar
Pradesh, India

Prem Kumar
Department of Genetics and Plant
Breeding, Chandra Shekhar Azad
University of Agriculture &
Technology, Kanpur, Uttar
Pradesh, India

Vishal Yadav
Department of Vegetable Science,
Chandra Shekhar Azad University
of Agriculture & Technology,
Kanpur, Uttar Pradesh, India

Dharmendra Bahadur Singh
Department of Vegetable Science,
Chandra Shekhar Azad University
of Agriculture & Technology,
Kanpur, Uttar Pradesh, India

Ramdatt
Department of Vegetable Science,
Chandra Shekhar Azad University
of Agriculture & Technology,
Kanpur, Uttar Pradesh, India

Corresponding Author:
Krishan Kumar
Department of Vegetable Science,
Chandra Shekhar Azad University
of Agriculture & Technology,
Kanpur, Uttar Pradesh, India

Assessment of genetic variability, heritability and genetic advance for yield and quality traits in cucumber (*Cucumis sativus* L.)

Krishan Kumar, Rajiv, Keshav Arya, Shweta, Somveer Singh, Prem Kumar, Vishal Yadav, Dharmendra Bahadur Singh and Ramdatt

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Abstract

The presents study involved 73 treatments (13 parents 30 F₁s and 30 F₂s) arranged in a Randomized Block Design with three replications during the Summer (*Zaid*) Season 2023 to 2025 at at the Vegetable Research Farm, Department of Vegetable Science, Kalyanpur, C.S. Azad University of Agriculture and Technology, Kanpur. The experimental material consisted of 10 parental lines (VRCU-2304, VRCU-2310, VRCU-2317, VRCU-2318, VRCU-2360, VRCU-2361, VRCU-2365, VRCU-2366, VRCU-2371, VRCU-2383) and three testers (Pusa Uday, Pant Kheera-1, Kalyanpur (Green)). All the thirteen genotypes were crossed in a Line x tester mating design in all possible combinations to produce sufficient F₁ seeds of 30 cross combinations during 2023-2024. The high percent of phenotypic coefficient of variation (>20%) was recorded for fruit flesh thickness. The moderate phenotypic and genotypic coefficient of variation (10-20%) was recorded for number of primary branches followed by node number of first male flower, node number of first female flower and fruit yield per plant. High heritability coupled with high genetic advance was recorded for total soluble solid, ascorbic acid, node number of first male flower, fruit flesh thickness, number of primary branches per plant and node number of first female flower.

Keywords: *Cucumis sativus* L., phenotypic coefficient of variation, genotypic coefficient of variation, line × tester mating design, heritability, genetic improvement

Introduction

Cucumber (*Cucumis sativus* L., 2n = 2x = 14), which belongs to the family Cucurbitaceae. Its primary Centre of origin is India and secondary Centre of diversification is China. Cucumber is a warm season vegetable crop grown throughout the world under tropical, sub-tropical and temperate conditions. Cucurbits are characterized by the bitter principles called cucurbitacin. Cucumber is a rich source of iron (1.5 mg), calcium and phosphorus and rich minerals like K (50 mg), P (25 mg), S (17 mg), Cl (15 mg), Mg (11 mg), Na (10.2 mg) Ca (10 mg) and Vitamin C (7 mg) (Yawalkar and Ram, 2004) [22]. The major cucumber producing states in India are West Bengal, Madhya Pradesh, Haryana, Karnataka, Bihar and Uttar Pradesh. West Bengal is the leading cucumber producing state with the production of 344.64 thousand metric tons from an area of 25.30 thousand hectares followed by Madhya Pradesh which produced 272.60 thousand metric tons from an area of 16.59 thousand hectares. Uttar Pradesh covers 4.09 thousand hectares area under cucumber cultivation with an annual production of 103.74 thousand metric tons production. (Department of Agriculture, Cooperation and Farmer Welfare, final Estimate, 2022) [7]. Enhancement of productivity has been important goal for cucumber breeders in India. However, most of the important features of cultivated crops are not governed by discrete Mendelian traits, but may be of a continuous or quantitative nature. Yielding ability is a prime example of such a trait and is of obvious importance (Kumar *et al.*, 2014) [13]. Parameters like genotypic and phenotypic coefficients of variation, heritability estimates and genetic progress provide useful information for selecting superior genotypes. They also emphasised that genetic gain, in addition to heritability, should be addressed when developing a cohesive selected breeding scheme. Heritability is defined as the proportion of phenotypic variance that is due to genetic variables and it offers an estimate of trait transmissibility from one generation to the next.

In contrast, genetic progress forecasts the predicted improvement in a characteristic under selection and aids in evaluating the success of selection procedures (Johnson *et al.*, 1955) ^[11].

Materials and Methods

The presents study involved 73 treatments (13 parents, 30F₁s, and 30 F₂s) arranged in a Randomized Block Design with three replications during the Summer (*Zaid*) Season 2023 to 2025 at the Vegetable Research Farm, Department of Vegetable Science, Kalyanpur, C.S. Azad University of Agriculture and Technology, Kanpur. The experimental material consisted of 10 parental lines (VRCU-2304, VRCU-2310, VRCU-2317, VRCU-2318, VRCU-2360, VRCU-2361, VRCU-2365, VRCU-2366, VRCU-2371, VRCU-2383) and three testers (Pusa Uday, Pant Kheera-1, Kalyanpur (Green)). All the thirteen genotypes were crossed in a Line x tester mating design in all possible combinations to produce sufficient F₁ seeds of 30 cross combinations during 2023-2024. Each parent and F₁s were planted in single row and F₂s were planted double row plot bases, Spacing: 2.5 m x 0.5 m and Plot Size: 5.0 m x 2.5 m. Recommended cultural practices will be followed to raise a good crop. Observations were recorded on plot basis for Number of primary branches, days to first male flowers, days to first female flowers, node number of first male flower, node number of first female flowers, days to first fruit set, days to last fruit harvest, number of fruits per plant, fruit shape, days to marketable maturity, fruit length (cm), fruit diameter (cm), average fruit weight (g), fruit yield per plant (kg), yield per plot (kg), fruit flesh thickness (mm), total soluble solid (⁰Brix), ascorbic acid (mg/100g fresh fruits) and shelf life of the fresh fruits (days) were recorded on 5 randomly selected plants for 30 F₁ and 30 F₂'s plants. Data were recorded on seventeen characters to estimate heritability in broad sense (h²bs), genetic advance and variance components were calculated using the methods as per Burton and Devane (1953) ^[6], Panse and Sukhatme (2000) ^[14] and Falconer (1981) ^[8] were work out following INDOSTAT software 8.1, Hyderabad.

Result and Discussion

The heritable portion of phenotypic or total variation is known as genotypic variance. It displays the differences between genotypes. The overall variety within a population is referred to as phenotypic variance. It is the total of environmental and genetic variance. Table 1 and Figure 1. shows the results of the computation of the genotypic and phenotypic coefficients of variation (GCV & PCV) for yield and yield-attributing characteristics aggregated over environments. The findings showed that for every feature in the pooled data across the contexts, the phenotypic coefficient of variance was greater than the genotypic coefficient of variation.

Phenotypic and genotypic coefficient of variation

The range of Phenotypic coefficient of variation (PCV) varied from 7.31% (Days to marketable maturity) to 20.44% (Fruit flesh thickness). The high percent of phenotypic coefficient of variation (>20%) was recorded for fruit flesh thickness (20.44%). The moderate phenotypic coefficient of variation (10-20%) was recorded for number of primary branches (19.69%) followed by node number of first male flower (19.69%), node number of first female flower

(16.64%), fruit yield per plant (15.91%), shelf life of the fresh fruit (14.68%), total soluble solid (13.59%), average fruit weight (12.87%), ascorbic acid (11.87%), days to first male flower (11.44%), fruit length (11.43%), fruit diameter (11.01%) and days to first female flower (10.91%), indicating significant genetic diversity and higher potential for improvement through selection. The lowest value of the phenotypic coefficient of variation (< 10%) was observed for days to first fruit set (9.96%), number of fruits per plant (9.36%), days to last fruit harvest (9.01%) and days to marketable maturity (7.31%).

The range of genotypic coefficient of variation (GCV) varied from 4.60% (Number of fruits per plant) to 19.13% (Fruit flesh thickness). The moderate genotypic coefficient of variation (10-20%) was recorded for fruit flesh thickness (19.13%) followed by node number of first male flower (18.47%), number of primary branches per plant (18.33%), node number of first female flower (15.20%), total soluble solids (13.28%), fruit yield per plant (12.92%), shelf life of the fresh fruit (12.12%), ascorbic acid (11.57%) and average fruit weight (10.55%). The lowest value of genotypic coefficient of variation (< 10%) was observed for days to first male flower (9.93%), days to first female flower (9.34%), fruit length (9.56%), days to first fruit set (7.70%), fruit diameter (7.15%), days to last fruit harvest (6.52%), days to marketable maturity (6.05%) and number of fruits per plant (4.60%), showed substantially restricted genetic variation and reduced potential for quick genetic improvement by direct selection. Similar results were also reported by Pushpalatha *et al.*, (2014) ^[15], Bartaula *et al.*, (2019) ^[3], Ahmed *et al.*, (2022) ^[2], Jagesh *et al.*, (2007) ^[10], Bhimappa *et al.*, (2017) ^[5].

Heritability in broad sense

The estimation heritability (broad sense) for all the characters has been presented in Table 1 and Figure 1. Heritability (broad-sense) ranged from 24.17% for number of fruits per plant to 95.51% for total soluble solid. Heritability estimated was categorized as high (> 75%), moderate (50-75%) and low (< 50%). High heritability (>75%) was recorded for total soluble solid (95.51%), ascorbic acid (95.06%), node number of first male flower (88.02%), fruit flesh thickness (87.59%), number of primary branches per plant (86.70%), node number of first female flower (83.46%) and days to first male flower (75.44%), indicating that these traits were primarily determined by genetic factors with little environmental influence. Modest heritability (50-75%) was recorded for days to first female flower (73.31%), fruit length (69.93%), days to marketable maturity (68.64%), shelf life of the fresh fruit (68.10%), average fruit weight (67.26%), fruit yield per plant (65.95%), days to first fruit set (59.81%) and days to last fruit harvest (52.40%). Whereas, the remaining characters namely fruit diameter (42.22%) and number of fruits per plant (24.17%) exhibited lowest heritability (< 50%). These findings are conformed with the results of Uddin *et al.*, (2006) ^[18], Gaikwad *et al.*, (2011) ^[9], Veena *et al.*, (2012) ^[19], Ranjan *et al.*, (2015) ^[16].

Genetic advance (%)

Genetic advance or genetic gain is still a more useful estimate. It is a measure of an improvement in the genotypic value in the new population as compared to the base population presented in Table 1 and Figure 1. Genetic

advance expressed as percentage of mean ranged from 4.66% (Number of fruits per plant) to 36.88% (fruit flesh thickness). Genetic advance as the percentage of mean can be categorized into three groups viz., high (>20%), moderate (10-20%) and low (< 10%). Accordingly, High genetic advance as percentage of mean was recorded for fruit flesh thickness (36.88%), node number of first male flower (35.70%), number of primary branches per plant (35.17%), node number of first female flower (28.61%), total soluble solid (26.74%), ascorbic acid (23.25%), fruit yield per plant (21.62%) and shelf life of the fresh fruit (20.60%). The high GA values coupled with high heritability, suggested that additive gene action is predominant and that selection would be highly effective for

improvement in these traits. Moderate genetic advance as percentage of mean was exhibited by average fruit weight (17.83%), days to first male flower (17.77%), days to first female flower (16.47%), fruit length (16.46%), days to first fruit set (12.27%) and days to marketable maturity (10.33%), suggesting fair improvement possibilities. All the remaining traits namely days to last fruit harvest (9.73%), fruit diameter (9.57%) and number of fruits per plant (4.66%) recorded low genetic advance as percentage of mean, indicated a higher environmental effect and limited possibility for improvement by simple phenotypic selection. Similar results were also reported by Agashi *et al.*, (2020)^[1], Bhaiya *et al.*, (2020)^[4], Singh *et al.*, (2013)^[17].

Table 1; Mean, range, variance, genotypic and phenotypic coefficient of variation, heritability and genetic advance for different traits

Characters	Grand Mean	Range	G.C.V. (%)	P.C.V. (%)	Heritability (%)	Genetic advance as% of mean
NPB	6.07	2.75-8.54	18.33	19.69	86.70	35.17
DFM	35.63	28.32-45.04	9.93	11.44	75.44	17.77
DFFF	37.21	30.21-46.16	9.34	10.91	73.31	16.47
NFM	3.29	2.05-4.69	18.47	19.69	88.02	35.70
NFFF	4.34	2.38-5.68	15.20	16.64	83.46	28.61
DFF	44.38	35.27-50.79	7.70	9.96	59.81	12.27
DMM	57.38	50.21-66.13	6.05	7.31	68.64	10.33
DLFH	75.71	65.15-85.36	6.52	9.01	52.40	9.73
NFP	17.80	15.53-20.15	4.60	9.36	24.17	4.66
FL	20.24	14.84-25.34	9.56	11.43	69.93	16.46
FD	4.11	3.30-4.88	7.15	11.01	42.22	9.57
AFW	136.14	114.32-162.35	10.55	12.87	67.26	17.83
TSS	3.94	3.12-4.98	13.28	13.59	95.51	26.74
ASC	5.58	4.24-6.85	11.57	11.87	95.06	23.25
FLT	11.51	5.90-17.50	19.13	20.44	87.59	36.88
SFF	9.67	6.35-13.12	12.12	14.68	68.10	20.60
FY	2.43	1.79-3.27	12.92	15.91	65.95	21.62

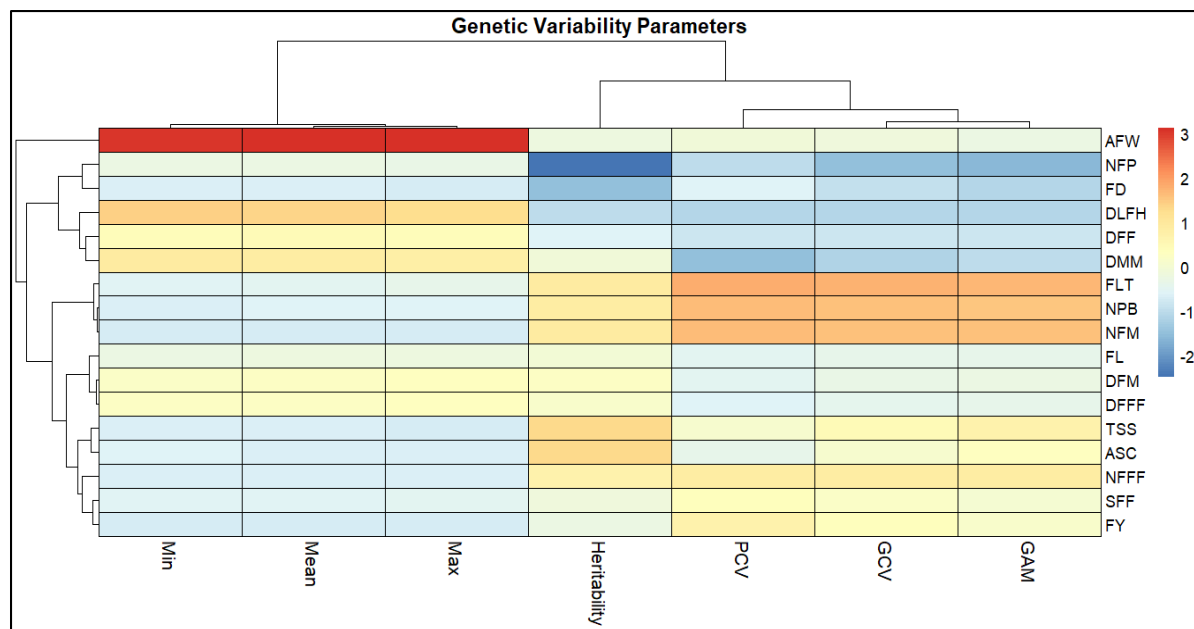


Fig 1: Mean, range, variance, genotypic and phenotypic coefficient of variation, heritability and genetic advance for different traits

Conclusions

The study found significant genetic heterogeneity in cucumber genotypes for yield and quality parameters. Moderate to high PCV and GCV estimates for fruit flesh thickness, node number of first male and female flowers, number of primary branches, total soluble solids, ascorbic acid, shelf life and fruit yield per plant all revealed

significant genetic variation. substantial heritability combined with substantial genetic advance for these qualities indicated the dominance of additive gene action and the efficacy of direct selection. As a result, these characteristics can be used as trustworthy selection criteria in future breeding programs to generate high-yielding and superior-quality cucumber cultivars.

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Disclaimer (Artificial intelligence)

Author(s) hereby declares that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

Competing Interests

Authors have declared that no competing interests exist.

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