# Genetic Variability and Divergence Studies in Cucumber (*Cucumis sativus* L.)

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**ABSTRACT: Genetic variability in a crop population is important for successful plant breeding. An experiment was conducted to study Genetic variability, heritability, genetic advance and genetic divergence for some traits in Cucumber (*Cucumis sativus* L.). The experiment was carried out at the Rajendrapuara Farm, Hill Millet Research Station, Navsari Agricultural University, Waghai (The Dangs), Gujarat during the summer 2019 using twenty-five cucumber genotypes including the checks, Shubhangi and Himangi, in Randomized Block Design with three replications. The analysis of variance revealed significant differences among genotypes indicating presence of sufficient amount of variability in all the characters studied except days to last fruit harvest and moisture content. Magnitudes of GCV and PCV were found high for primary branches per plant, Node number of first male flower and seeds per fruit. Whereas, moderate GCV and PCV were recorded for fruit length, yield per vine, fruit girth, node number of first female flower, fruit weight, total sugar content and vine length. High heritability coupled with high genetic advance was observed for the traits *viz*., node number of first female flower, node number of first male flower, primary branches per plant, vine length, fruit length, fruit weight, fruit girth, seeds per fruit, yield per vine and total sugar content. The magnitude of genotypic correlations was recorded higher as compared to corresponding phenotypic correlations for majority of the traits under study indicating that there was an inherent association between these characters at genotypic level. Path coefficient analysis revealed the highest positive direct effect on yield per vine by primary branches per plant, followed by fruit girth, total sugar content, days to first fruit harvest, ascorbic acid content, seeds per fruit, days to first male flower, moisture content, node number of first female flower, internodal length and node number of first male flower.**

**The D[2] analysis indicated presence of ample genetic diversity among the genotypes studied, which were grouped into seven clusters through Mahalanobis D[2] statistics. Cluster V contained the maximum (6) number of genotypes, whereas cluster VI and cluster VII contained minimum (1) genotype only. The intra cluster D[2] value ranged from 0.00 (Cluster VI and Cluster VII) to 29.07 (Cluster VI). The inter cluster D[2] values of the seven clusters revealed that highest inter cluster distance (512.39) was between cluster II and cluster VI.**

**Keywords:** Variability, heritability, Correlation, Path analysis and D[2].

## INTRODUCTION

Cucumber (*Cucumis sativus* L.) with diploid chromosome (2n=14) is one of the most important cucurbitaceous vegetable crops grown extensively in tropical and subtropical parts of the country. It belongs to the family *Cucurbitaceae* consisting of 118 genera and 825 species (Jeffrey, 1990). It is an annual monoecious vine with trailing or climbing habit. It is highly cross pollinated crop. Cucumber is a warm season crop which is grown extensively throughout the year in southern states of India. In plains of northern India, it is grown in summer and rainy season, but it does not tolerate cold injury (Rastogi, 1998). It grows best at a temperature range of 18-30 ºC. It is one of the

most important crops grown under greenhouse conditions for its year round demand and supply for domestic consumption as well as for export.

Today cucumber is grown throughout the world in small or large commercial farms, glasshouses and small gardens (Hossain *et al.,* 2010). It has tremendous economic and dietic importance. It is cultivated for its tender fruits, which are consumed either raw as salad (Arunkumar *et al.*, 2011), cooked as vegetable or as pickle in its immature stage. It is a low energy and high water content vegetable, and it is also a rich source of vitamin B and C, carbohydrates, calcium and phosphorus. The fruit has about 95% water content (Anonymous, 2012) which makes it diuretic, possessing a deep cooling effect. The fruits are also used as an

astringent and antipyretic. In addition, cucumber extract has smoothing, cleansing and softening properties which are important for the cosmetics industry and soap industries (Wang *et al.,* 2007). Most skin infections had been successfully treated with a cucumber extract, alpha hydroxyl acid (Uzodike and Onuoha 2009).

At present, India is the second largest producer of vegetable in the world. In India, the area under cucumber is about 78.16 thousand ha with production 1142.03 thousand MT (2016-2017). Highest production recorded by Haryana followed by Karnataka and Madhya Pradesh. Cucumber covered 107.0 thousand hectare area and 1658 thousand metric tonnes production of total vegetable production in India (Anonymous, 2019).

Genetic variability is a prerequisite for any improvement in a crop. The success of any crop improvement programme depends on the quantum of genetic variability and extent to which the desirable characters are heritable. The ultimate goal of breeding programme aims to improve the characteristic of plants so that they become more desirable. Heritability is estimated either performing analysis of variance or regressing the value of the offspring on the mean value of the parents. An important aspect of heritability estimates is that it applies to a particular environment at a particular time. Heritability has been used as an index of transmissibility of a character from the parent to its offspring and thus an aid to predict the improvement that can be made in a crop by selection for various characters.

The knowledge of correlation between fruit yield and its attributing characters is important for simultaneous improvement of several characters in selection breeding programs. Genotypic correlation refers to the heritable association between any two characters. It is either due to pleiotropic gene action or due to linkage. The phenotypic correlation refers to the observable association between two characters. The environmental correlation is entirely due to environmental effects. However, only correlation studies do not provide an exact value of direct and indirect effects towards the yield. So, there is utilization of path coefficient analysis, it is standardized regression coefficient which splits the correlation coefficient into the estimate of direct and indirect effects. It helps in determining the casual factors of seed yield.

Genetic divergence can be judged by multivariate analysis, a procedure that is widely used in different crops for parent selection. Multivariate analysis by means of Mahalanobis (1936) $D^2$ cluster analysis has been proved to be useful in selecting accessions for hybridization in several crops. It is powerful tool in identifying the degree of genetic divergence among parents.

## MATERIALS AND METHODS

The twenty-five different genotypes of cucumber were grown in randomized block design in three replications. In experiment, each plot consisted of ten plants in a row at 2 m × 0.7 m inter and intra row spacing. All the recommended agronomical and plant protection package of practices were adopted for raising a successful and healthy crop under prevailing environmental condition.

Five randomly selected plants, excluding the border ones, from each plot of all the three replications were tagged and used for recording the observations. The average value of data from these plants was computed and used for statical analysis. The observations were recorded on eighteen characters *viz.,* days to first female flower, days to first male flower, node number of first female flower, node number of first male flower, internodal length (cm), primary branches per plant, vine length (cm), days to first fruit harvest, fruits per vine, fruit length (cm), fruit weight (g), fruit girth (cm), seeds per fruit, yield per vine (g), days to last fruit harvest, moisture content (%), total sugar content (g/100g) and ascorbic acid content (%). The data recorded for all the characters were subjected to analysis of variance with the formula suggested by Panse and Sukhatme (1978).

Genotypic and phenotypic co-efficient of variation were calculated by using the following formula suggested by Cockerham (1963). Heritability has been estimated as per the formula stated by Allard (1960) and genetic advance as percentage over mean was also worked out using formula. The genetic divergence in 25 genotypes for 18 characters was analysed through Mahalanobis's $D^2$ statistic technique.

## RESULTS AND DISCUSSION

The analysis of variance indicated highly significant differences among the genotypes for all the traits studied (Table1). The results revealed that the values of PCV were higher than the GCV values but the difference between PCV and GCV were very low indicating these characters are less influenced by environment.

**Variability Parameters.** The genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) were high for primary branches per plant (28.62 %, 29.90%), Node number of first male flower (27.10 %, 28.15%) and seeds per fruit (24.84 %, 25.22%). Similar results were attained by Veena *et al.* (2012); Shah *et al.* (2018); Tamang *et al.* (2018); Karthick *et al.* (2019) for node number of first male flower; Basava *et al.* (2014); Ranjan *et al.* (2015); Kumar *et al.* (2018), for primary branches per plant; Veena *et al.* (2012); Ranjan *et al.* (2015); Kumar *et al.* (2018); Tamang *et al.* (2018) for seeds per fruit.

**Table 1: Analysis of variance for yield attributing traits in cucumber.**

| Sr. No. | Character | Mean sum of squares | | |
|---|---|---|---|---|
| | | Replications | Genotypes/ treatments | Error |
| **Degree of freedom** | | **2** | **24** | **48** |
| 1. | Days to first female flower | 65.54* | 69.25** | 14.81 |
| 2. | Days to first male flower | 7.59 | 20.49** | 6.31 |
| 3. | Node number of first female flower | 0.20 | 8.70** | 1.33 |
| 4. | Node number of first male flower | 0.05 | 0.95** | 0.02 |
| 5. | Internodal length (cm) | 0.35 | 1.63** | 0.45 |
| 6. | Primary branchesper plant | 0.02 | 5.66** | 0.17 |
| 7. | Vine length (cm) | 283.37 | 1245.87** | 143.83 |
| 8. | Days to first fruit harvest | 2.55 | 51.01** | 18.46 |
| 9. | Fruits per vine | 0.35 | 3.85** | 0.70 |
| 10. | Fruit length (cm) | 0.20 | 34.14** | 1.35 |
| 11. | Fruit weight (g) | 908.38 | 2415.84** | 434.23 |
| 12. | Fruit girth (cm) | 1.28* | 6.03** | 0.39 |
| 13. | Seeds per fruit | 140.83 | 8999.89** | 91.11 |
| 14. | Yield per vine (g) | 120607.70 | 718784.83** | 74053.18 |
| 15. | Days to last fruit harvest | 3.64 | 39.87 | 46.98 |
| 16. | Moisture content (%) | 86.89 | 33.49 | 52.37 |
| 17. | Total sugar content (g/100g) | 0.01 | 0.31** | 0.05 |
| 18. | Ascorbic acid content (%) | 0.05 | 0.24** | 0.08 |

**Table 2: Mean, range and coefficient of variation for different characters in Cucumber.**

| Sr. No. | Character | Mean | Range | | C.V. (%) |
|---|---|---|---|---|---|
| | | | Minimum | Maximum | |
| 1. | Days to first female flower | 44.19 | 36.00 | 51.83 | 8.71 |
| 2. | Days to first male flower | 38.40 | 32.43 | 42.50 | 6.54 |
| 3. | Node number of first female flower | 11.62 | 8.33 | 14.80 | 9.91 |
| 4. | Node number of first male flower | 2.05 | 1.00 | 2.90 | 7.60 |
| 5. | Internodal length (cm) | 8.35 | 6.97 | 9.60 | 8.02 |
| 6. | Primary branches per plant | 4.73 | 2.30 | 6.40 | 8.64 |
| 7. | Vine length (cm) | 161.94 | 127.40 | 206.53 | 7.41 |
| 8. | Days to first fruit harvest | 61.77 | 55.60 | 68.90 | 6.96 |
| 9. | Fruits per vine | 14.04 | 12.13 | 15.93 | 5.95 |
| 10. | Fruit length (cm) | 17.64 | 12.40 | 22.70 | 6.58 |
| 11. | Fruit weight (g) | 197.69 | 142.63 | 248.33 | 10.54 |
| 12. | Fruit girth (cm) | 8.67 | 6.06 | 10.60 | 7.16 |
| 13. | Seeds per fruit | 219.38 | 120.63 | 301.43 | 4.35 |
| 14. | Yield per vine( g) | 2898.63 | 2180.83 | 3735.60 | 9.39 |
| 15. | Days to last fruit harvest | 75.33 | 70.13 | 80.80 | 9.09 |
| 16. | Moisture content (%) | 88.09 | 82.10 | 94.20 | 8.21 |
| 17. | Total sugar content (g/100g) | 2.38 | 2.00 | 2.93 | 8.95 |
| 18. | Ascorbic acid content (%) | 3.45 | 3.00 | 3.90 | 8.04 |

Moderate genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) were recorded for fruit length (18.75 %, 19.87%) yield per vine (15.99 %, 18.55%), fruit girth (15.81 %, 17.36%), node number of first female flower (13.49 %, 16.74%), fruit weight (13.00 %, 16.74%), total sugar content (12.54 %, 15.41%) and vine length (11.84 %, 13.96%). High PCV and GCV values indicate large amount of variation and consequently more scope for their improvement through selection. The higher the GCV, the more will be the chance for exploitation of that particular character in a selection programme. PCV values were greater than GCV values of all the traits but these two magnitudes, GCV and PCV differed slightly for most of the traits which suggests influence of environment on these traits but to some extents only for expression of these traits.

**Heritability and Genetic Advance.** Broad sense heritability is the ratio of genetic variance to total variance or phenotypic variance. It includes all three types of genotypic variances *i.e.*, additive, dominance and epistatic, confirmation of any one gene effect is not possible to find out as it includes both fixable and non-fixable variances unless couples with genetic advance. High heritability in broad sense was recorded for number of seeds per fruit (97.02 %) followed by node number of first male flower (92.70 %), primary branches per plant (91.64 %), fruit length (89.01 %), fruit girth (82.96 %), yield per vine (74.37 %), vine length (71.86 %), total sugar content (66.28 %), node

number of first female flower (64.94 %), fruit weight (60.34 %) and fruit per vine (60.06 %).

Moderate heritability in broad sense was recorded for days to first female flower (55.07 %), internodal length (46.75 %), and days to first male flower (42.83 %), ascorbic acid content (40.90 %) and days to first fruit harvest (37.02 %). For moisture content (13.66 %) and days to last fruit harvest (5.31 %), heritability in broad sense were low in magnitude. Equivalent results were attained by Kandasamy *et al.* (2017); Rajawat and Collis (2017); Karthick *et al.* (2019) for node number of first female flower; Pal *et al.* (2017); Kandasamy *et al.* (2017); Shah *et al.* (2018); Gangadhara *et al.* (2019) for vine length; Salam *et al.* (2010); Ranjan *et al.* (2015); Kandasamy *et al.* (2017).

Hence, Heritability alone is not plentiful for sufficient improvement through selection usually in advance generation. If it is complemented with genetic advance, it can be used for comprehending improvement in mean genotypic value of selected plants over parental population and also to know which gene effects are dominant and whether selection would be effective or not. Genetic advance describe improvement in mean genotypic value of selected plants over parental population. High magnitude of genetic advance shows the effect of additive genes and low magnitude describe that trait is governed by non-additive genes. As a result, as per the magnitude, whether selection will be helpful or heterosis breeding that can be confirmed.

Heritability and genetic advance collectively, giving more detailed idea of gene action, extent of environmental influence and improvement strategy. So in accordance to that, high heritability coupled with high genetic advance was perceived for node number of first female flower, node number of first male flower, primary branches per plant, vine length, fruit length, fruit weight, fruit girth, seeds per fruit, yield per vine and total sugar content showing role of additive gene effects and less influence of environment. Thus, for improvement of these traits can be achieved by selection.

**Table 3: Genetic variability parameters of different characters in Cucumber.**

| Sr. No. | Characters | Genotypic variance ($\sigma^2_g$) | Phenotypic variance ($\sigma^2_p$) | Genotypic coefficient of variation GCV (%) | Phenotypic coefficient of variation PCV (%) | Broad sense heritability $h^2_{(b.s)}$ (%) | Genetic advance (GA) | Genetic advance per cent mean (GAM) |
|---|---|---|---|---|---|---|---|---|
| 1. | Days to first female flower | 18.15 | 32.96 | 9.64 | 12.99 | 55.07 | 6.51 | 14.74 |
| 2. | Days to first male flower | 4.73 | 11.04 | 5.66 | 8.65 | 42.83 | 2.93 | 7.64 |
| 3. | Node number of first female flower | 2.46 | 3.79 | 13.49 | 16.74 | 64.94 | 2.60 | 22.40 |
| 4. | Node number of first male flower | 0.31 | 0.33 | 27.10 | 28.15 | 92.70 | 1.10 | 53.75 |
| 5. | Internodal length (cm) | 0.39 | 0.84 | 7.52 | 10.99 | 46.75 | 0.88 | 10.59 |
| 6. | Primary branches per plant | 1.83 | 1.99 | 28.62 | 29.90 | 91.64 | 2.67 | 56.44 |
| 7. | Vine length (cm) | 367.35 | 511.18 | 11.84 | 13.96 | 71.86 | 33.47 | 20.67 |
| 8. | Days to first fruit harvest | 10.85 | 29.31 | 5.33 | 8.76 | 37.02 | 4.13 | 6.68 |
| 9. | Fruits per vine | 1.05 | 1.75 | 7.30 | 9.42 | 60.06 | 1.64 | 11.65 |
| 10. | Fruit length (cm) | 10.93 | 12.28 | 18.75 | 19.87 | 89.01 | 6.43 | 36.44 |
| 11. | Fruit weight (g) | 660.53 | 1094.77 | 13.00 | 16.74 | 60.34 | 41.12 | 20.80 |
| 12. | Fruit girth (cm) | 1.88 | 2.27 | 15.81 | 17.36 | 82.96 | 2.57 | 29.66 |
| 13. | Seeds per fruit | 2969.60 | 3060.70 | 24.84 | 25.22 | 97.02 | 110.57 | 50.40 |
| 14. | Yield per vine (g) | 214910.55 | 288963.73 | 15.99 | 18.55 | 74.37 | 823.58 | 28.41 |
| 15. | Days to last fruit harvest | -2.37 | 44.61 | 2.04 | 8.86 | 5.31 | -0.73 | -0.97 |
| 16. | Moisture content (%) | -6.29 | 46.07 | 2.85 | 7.70 | 13.66 | -1.90 | -2.17 |
| 17. | Total sugar content (g/100g) | 0.09 | 0.13 | 12.54 | 15.41 | 66.28 | 0.50 | 21.03 |
| 18. | Ascorbic acid content (%) | 0.05 | 0.13 | 6.69 | 10.46 | 40.90 | 0.30 | 8.81 |

**Genotypic Correlation.** Yield per vine showed highly significant and positive correlation with node number of first female flower (1.00), node number of first male flower (0.96), internodal length (1.05), primary branches per plant (0.98), vine length (0.98), fruits per vine(1.06), fruit length (0.96), fruit weight (1.07), fruit girth (0.97), seeds per fruit(0.36), days to last fruit harvest (2.23), total sugar content(0.94) and ascorbic acid content (1.08) at genotypic level. It suggested that the strong association between those characters with yield per vine and correlation is positive, it means that increase in one-character leads to increase in second and vice versa. Selection for these traits will reward in terms of yield per vine. Such associations were commonly reported in Cucumber by Hanchinamani and Patil (2009) for vine length, internodal length, fruit length and fruit weight, Pal *et al.* (2017) for primary branches per plant; Arunkumar *et al.* (2011), for vine length; Gangadhara *et al.* (2019) for fruits per vine; Veena *et al.* (2013); Ullah *et al.* (2012); Sharma *et al.* (2018) for fruit weight and fruit girth. So direct selection in this trait indirectly lead to improvement of yield as shown in Table 4.

**Table 4: Genotypic correlation coefficient for different characters in Cucumber.**

| Character | DFFF | DFMF | NNFFF | NNFMF | IL | PBPP | VL | DFFH | FPV | FL | FW | FG | SPF | DLFH | MC | TSC | AAC |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DFFF | 1 | | | | | | | | | | | | | | | | |
| DFMF | 1.36** | 1 | | | | | | | | | | | | | | | |
| NNFFF | -1.19** | -1.18** | 1 | | | | | | | | | | | | | | |
| NNFMF | -1.08** | -1.15** | 1.04** | 1 | | | | | | | | | | | | | |
| IL | -1.26** | -1.27** | 1.13** | 1.15** | 1 | | | | | | | | | | | | |
| PBPP | -1.09** | -1.17** | 1.05** | 1.01** | 1.16** | 1 | | | | | | | | | | | |
| VL | -1.17** | -1.27** | 1.08** | 1.04** | 1.21** | 1.01** | 1 | | | | | | | | | | |
| DFFH | 1.33** | 1.40** | -1.34** | -1.23** | -1.36** | -1.24** | -1.25** | 1 | | | | | | | | | |
| FPV | -1.18** | -1.30** | 1.14** | 1.08** | 1.30** | 1.10** | 1.12** | -1.40** | 1 | | | | | | | | |
| FL | -1.14** | -1.17** | 1.06** | 0.98** | 1.14** | 0.99** | 1.03** | -1.18** | 1.11** | 1 | | | | | | | |
| FW | -1.24** | -1.29** | 1.24** | 1.06** | 1.27** | 1.08** | 1.17** | -1.36** | 1.17** | 1.09** | 1 | | | | | | |
| FG | -1.09** | -1.08** | 1.08** | 0.98** | 1.11** | 1.01** | 1.06** | -1.27** | 1.09** | 1.02** | 1.10** | 1 | | | | | |
| SPF | -0.47** | -0.48** | 0.46** | 0.30** | 0.33** | 0.28* | 0.44** | -0.46** | 0.39** | 0.38** | 0.47** | 0.40** | 1 | | | | |
| DLFH | -2.28** | -3.02** | 2.36** | 2.25** | 2.73** | 2.29** | 2.46** | -2.94** | 2.41** | 2.35** | 2.95** | 2.32** | 0.76** | 1 | | | |
| MC | 1.55** | 1.58** | -1.48** | -1.31** | -1.44** | -1.28** | -1.48** | 1.83** | -1.64** | -1.31** | -1.40** | -1.29** | -0.55** | -3.40** | 1 | | |
| TSC | -1.15** | -1.29** | 1.11** | 1.01** | 1.21** | 1.00** | 1.10** | -1.28** | 1.02** | 1.05** | 1.10** | 0.98** | 0.35** | 2.59** | -1.09** | 1 | |
| AAC | -1.31** | -1.28** | 1.22** | 1.17** | 1.33** | 1.21** | 1.26** | -1.52** | 1.31** | 1.23** | 1.31** | 1.15** | 0.45** | 2.55** | -1.60** | 1.32** | 1 |
| YPV | -1.09** | -1.06** | 1.00** | 0.96** | 1.05** | 0.98** | 0.99** | -1.12** | 1.06** | 0.96** | 1.07** | 0.97** | 0.36** | 2.23** | -1.13** | 0.94** | 1.08** |

\* and** = significant at 5% and 1% levels, respectively.

| | | |
|---|---|---|
| DFFF: Days to first female flower | VL: Vine length (cm) | SPF: seeds per fruit |
| DFMF: Days to first male flower | DFFH: Days to first fruit harvest | DLFH: Days to last fruit harvest |
| NNFFF: Node number of 1st female flower | FPV: Fruits per vine | MC: Moisture content (%) |
| NNFMF: Node number of 1st female flower | FL: Fruit length (cm) | TSC: Total sugar content (g/100g) |
| IL: Internodal length (cm) | FW: Fruit weight (g) | AAC: Ascorbic acid content (%) |
| PBPP: Primary branches per plant | FG: Fruit girth (cm) | YPV: Yield per vine (g) |

**Path coefficient Analysis.** Path coefficient has greater significance and could be effectively utilized in formulating an effective selection scheme. Hence, knowledge of association between the traits can greatly help in avoiding inversely related compensation effects during selection. Yield is a complex character and it is the sum total of the several component characters which directly or indirectly contributed to it. The direct and indirect effect of different characters on yield per vine presented in Table 5.

Direct and indirect effects of various characters on yield per vine indicated that there is an agreement between direction and magnitude of direct effect of various character and correlation with yield per vine. Yield per vine considered as dependent variable and all other characters were considered as causal variable. Path coefficient analysis revealed the highest positive direct effect on yield per vine by primary branches per plant, followed by fruit girth, total sugar content, ascorbic acid content, seeds per fruit, days to first male flower, moisture content, node number of first female flower, internodal length and node number of first male flower. It revealed that there was true relationship between these characters and fruit yield per plant. Hence, direct selection of these characters could be carried out for improvement of fruit yield per vine. Such positive direct effects were also perceived by Cramer and Wehner (2000) for primary branches per plant; Arunkumar *et al.* (2011) for days to first male flower; Veena *et al.* (2013) for node number of first female flower, node number of first male flower and seeds per fruit; Pal *et al.* (2017) for primary branches per plant.

The negative direct effect of days to last fruit harvest was high, followed by fruit per vine, days to first fruit harvest, fruit length, fruit weight and vine length. Such negative direct effects were also reported by Arunkumar *et al.* (2011) for days to first fruit harvest and fruits per vine; Kumar *et al.* (2013) for fruit length; Veena *et al.* (2013) for days to first fruit harvest; Pal *et al.* (2017) for days to first fruit harvest. Murtadha and Sanni (2018) for vine length and fruit length.

Indirect effects via the characters *viz.,* node number of first female flower, node number of first male flower, internodal length, primary branches per plant, vine length, fruits per vine, fruit length, fruit weight, fruit girth, seeds per fruit, days to last fruit harvest, total sugar content and ascorbic acid content were high. Therefore, indirect selection practiced on these characters will results in the improvement of respective characters and ultimately increase fruit yield.

**Table 5: Genotypic path coefficient analysis of seventeen characters for fruit yield in cucumber.**

| Character | DFFF | DFMF | NNFFF | NNFMF | IL | PBPP | VL | DFFH | FPV | FL | FW | FG | SPF | DLFH | MC | TSC | AAC | Correlation with yield per vine |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **DFFF** | **0.34** | 0.27 | -0.11 | -0.05 | -0.08 | -1.63 | 0.68 | -0.29 | 0.25 | 0.26 | 0.44 | -0.56 | -0.12 | 0.11 | 0.23 | -0.44 | -0.39 | **-1.09\*\*** |
| **DFMF** | 0.47 | **0.19** | -0.11 | -0.05 | -0.08 | -1.75 | 0.74 | -0.30 | 0.28 | 0.27 | 0.45 | -0.55 | -0.12 | 0.15 | 0.23 | -0.49 | -0.38 | **-1.06\*\*** |
| **NNFFF** | -0.41 | -0.23 | **0.10** | 0.05 | 0.07 | 1.56 | -0.63 | 0.29 | -0.25 | -0.24 | -0.44 | 0.55 | 0.11 | -0.12 | -0.22 | 0.43 | 0.36 | **1.00\*\*** |
| **NNFMF** | -0.37 | -0.22 | 0.10 | **0.04** | 0.07 | 1.50 | -0.61 | 0.27 | -0.23 | -0.23 | -0.37 | 0.50 | 0.08 | -0.11 | -0.19 | 0.39 | 0.35 | **0.96\*\*** |
| **IL** | -0.43 | -0.25 | 0.11 | 0.05 | **0.06** | 1.74 | -0.70 | 0.29 | -0.28 | -0.26 | -0.45 | 0.57 | 0.08 | -0.13 | -0.21 | 0.46 | 0.40 | **1.05\*\*** |
| **PBPP** | -0.37 | -0.23 | 0.10 | 0.04 | 0.07 | **1.50** | -0.59 | 0.27 | -0.24 | -0.23 | -0.38 | 0.51 | 0.07 | -0.11 | -0.19 | 0.38 | 0.36 | **0.98\*\*** |
| **VL** | -0.40 | -0.25 | 0.10 | 0.05 | 0.08 | 1.50 | **-0.58** | 0.27 | -0.24 | -0.24 | -0.41 | 0.54 | 0.11 | -0.12 | -0.22 | 0.42 | 0.38 | **0.99\*\*** |
| **DFFH** | 0.45 | 0.27 | -0.13 | -0.05 | -0.08 | -1.85 | 0.73 | **-0.22** | 0.30 | 0.27 | 0.48 | -0.65 | -0.11 | 0.14 | 0.27 | -0.49 | -0.46 | **-1.12\*\*** |
| **FPV** | -0.40 | -0.25 | 0.11 | 0.05 | 0.08 | 1.64 | -0.66 | 0.30 | **0.22** | 0.25 | 0.41 | 0.56 | 0.10 | -0.12 | -0.24 | 0.39 | 0.39 | **1.06\*\*** |
| **FL** | -0.39 | -0.23 | 0.10 | 0.04 | 0.07 | 1.49 | -0.60 | 0.25 | -0.24 | **0.23** | -0.38 | 0.52 | 0.09 | -0.11 | -0.19 | 0.40 | 0.37 | **0.96\*\*** |
| **FW** | -0.43 | -0.25 | 0.12 | 0.05 | 0.08 | 1.61 | -0.69 | 0.29 | -0.25 | 0.25 | **0.35** | 0.56 | 0.12 | -0.14 | -0.21 | 0.42 | 0.39 | **1.07\*\*** |
| **FG** | -0.38 | -0.21 | 0.10 | 0.04 | 0.07 | 1.51 | -0.62 | 0.27 | -0.24 | -0.24 | -0.39 | **0.51** | 0.10 | -0.11 | -0.19 | 0.37 | 0.34 | **0.97\*\*** |
| **SPF** | -0.16 | -0.09 | 0.04 | 0.01 | 0.02 | 0.43 | -0.26 | 0.10 | 0.08 | 0.09 | 0.16 | 0.21 | **0.25** | -0.04 | -0.08 | 0.14 | 0.13 | **0.36\*\*** |
| **DLFH** | -0.78 | -0.59 | 0.23 | 0.10 | 0.17 | 3.43 | -1.44 | 0.63 | 0.52 | 0.54 | 1.03 | 1.18 | 0.19 | **-0.05** | -0.50 | 0.99 | 0.76 | **2.23\*\*** |
| **MC** | 0.53 | 0.31 | -0.14 | -0.06 | -0.09 | -1.92 | 0.86 | -0.39 | 0.35 | 0.30 | 0.49 | -0.66 | -0.14 | 0.17 | **0.15** | -0.42 | -0.48 | **-1.13\*\*** |
| **TSC** | -0.39 | -0.25 | 0.11 | 0.04 | 0.08 | 1.49 | -0.64 | 0.28 | -0.22 | -0.24 | -0.38 | 0.50 | 0.09 | -0.13 | -0.16 | **0.38** | 0.40 | **0.94\*\*** |
| **AAC** | -0.45 | -0.25 | 0.12 | 0.05 | 0.08 | 1.81 | -0.74 | 0.33 | -0.28 | -0.28 | -0.46 | 0.59 | 0.11 | -0.12 | -0.24 | 0.51 | **0.30** | **1.08\*\*** |

\*\* - Significant at 1.0 per cent level of probability, Residual =0.288 , bold diagonal figures are the direct effect

DFFF: days to 1st female flower
DFMF: days to 1st male flower
NNFFF: Node no. of 1st female flower

NNFMF: Node no. of 1st male flower
IL: Internodal length (cm)
PBPP: primary branches per plant

VL: Vine length (cm)
DFFH: Days to 1st fruit harvest
FPV: Fruit per vine

FL: Fruit length(cm)
FW: Fruit weight (g)
FG: Fruit girth (cm)

SPF: Seeds per fruit
DLFH: Days to last fruit harvest
MC: Moisture content (%)

TSC: Total sugar content(g/100g)
AAC: Ascorbic acid content (%)

### Diversity Analysis

**Grouping of genotypes into clusters.** Plant breeders are always interested to assess and utilize the genetic diversity among the germplasm in direct breeding programme because genetically diverse parents are likely to produce high heterotic effects and the distantly related parents within the same species when utilized in cross breeding programme are likely to produce wider spectrum of variability. Twenty five genotypes of cucumber were grouped into seven clusters by Tocher's method and the distribution of genotypes into seven clusters shown in (Table 6) as well as presented in Fig. 1. The results indicated that a maximum number of diverse genotypes (6 genotypes) appeared in cluster V followed by cluster I and cluster II (5 genotypes), cluster IV (4 genotypes), cluster III (3 genotypes) and remaining cluster like VI and VII had only 1 genotype.

**Cluster distances among seven clusters.** The intra and inter cluster distances (D) between all possible pair of seven cluster were computed and presented in Table 5 as well as shown in Fig. 1. Inter cluster distance ranged from 27.22 to 512.39 and intra cluster distance ranged from 0.00 to 29.07. The maximum inter cluster distance was observed between cluster II and VI ($D^2$= 512.39). Whereas, the minimum inter cluster distance was observed between cluster I and cluster IV ($D^2$= 27.22). The maximum intra-cluster distance was observed within cluster V (D = 29.07) which included 6 genotypes followed by cluster IV (D = 20.89) which included 4 genotypes. The minimum intra-cluster distance was observed within cluster III (D = 6.40) which include 3 genotypes followed by cluster I (D = 10.42) which include 5 genotypes. The cluster VI and cluster VII contained single genotype therefore; its intra-cluster distance was zero.

**Table 6: Cluster composition of twenty-five genotypes of cucumber.**

| Cluster No. | No. of genotypes within cluster | Genotypes in cluster |
|---|---|---|
| I | 5 | Punjab navin, NCUC-38, NCUC-64, NCUC- 22, CSJ-88 |
| II | 5 | NCUC-41, NCUC-99, NCUC- 47, NCUC- 44, NCUC -13 |
| III | 3 | Phuleshubhangi, CSJ- 118, NCUC-3 |
| IV | 4 | Swarnasheetal, CSJ-84, NCUC-7, GC-1 |
| V | 6 | Himangi, NCUC-65, NCUC-12, CSJ-61, NCUC-18, NCUC-67 |
| VI | 1 | CSJ-61 |
| VII | 1 | NCUC-9 |

| Cluster | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V | Cluster VI | Cluster VII |
|---|---|---|---|---|---|---|---|
| Cluster I | **10.42** | 81.74 | 76.64 | 27.22 | 97.43 | 208.84 | 44.33 |
| Cluster II | | **10.49** | 288.73 | 49.27 | 277.50 | 512.39 | 63.35 |
| Cluster III | | | **6.40** | 139.24 | 71.95 | 56.11 | 176.90 |
| Cluster IV | | | | **20.89** | 182.45 | 324.27 | 70.95 |
| Cluster V | | | | | **29.07** | 74.10 | 107.85 |
| Cluster VI | | | | | | **0.00** | 295.50 |
| Cluster VII | | | | | | | **0.00** |

Numbers in bold indicate intra cluster distance.
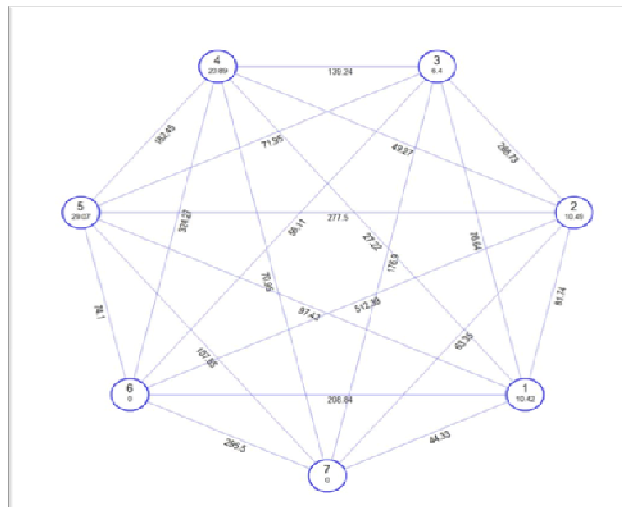


**Fig. 1.** Cluster diagram of twenty-five genotypes of cucumber.

## CONCLUSIONS

To conclude, the analysis of variance for all the traits revealed differences among the genotypes studied, indicating sufficient amount of variability present among twenty-five genotypes under study. High heritability was also coupled with high genetic advance as per cent of mean for these traits, which indicated the predominance of additive gene effects, thus more emphasis should be given to mass selection and progeny selection for further improvement of these characters.

Yield per vine showed highly significant and positive correlation with node number of first female flower, node number of first male flower, internodal length, primary branches per plant, vine length, fruits per vine, fruit length, fruit weight, fruit girth, seeds per fruit, total sugar content and ascorbic acid content at both genotypic and phenotypic levels while days to last fruit harvest at genotypic level only. These revealed that due weightage should be given to these traits during selection to improve the yield in cucumber whereas, yield per vine showed highly significant and negative correlation with days to first female flower, days to first male flower and days to first fruit harvest. There is no need of direct selection in trait which showed negative correlation with yield because it decrease the yield.

Path coefficient analysis showed the positive direct effect on yield per vine was recorded by primary branches per plant, fruit girth, total sugar content, days to first fruit harvest, ascorbic acid content, seeds per fruit, days to first male flower, moisture content, node number of first female flower, internodal length and node number of first male flower. Hence, these traits were considered as the most important yield contributors and due emphasis should be given while attempting yield improvement in cucumber.

D$^2$ analysis indicated wider genetic diversity among the twenty five genotypes, which were grouped in seven different clusters. Cluster V comprised of 6 genotypes, Cluster I and cluster II comprised of 5 genotypes, cluster IV comprised of 4 genotypes, cluster III comprised of 3 genotypes and remaining cluster (VI and VII) comprised of single genotype. (monogenotypic). The maximum inter cluster distance was observed between cluster II and cluster VI. From the results, it will be stated that inter-crossing from cluster II and cluster VI genotypes might result in wide array of variability for exercising effective selection.

## FUTURE SCOPE

The future scope of study on variability in cucumber could include exploring genetic diversity to develop new cultivars with improved traits such as disease resistance, yield, flavor, and nutritional content. Additionally, studying environmental factors and their impact on cucumber variability could lead to more resilient varieties adapted to changing climate conditions. Furthermore, investigating the potential health benefits of specific cucumber varieties could provide insights into their medicinal properties and nutritional value.

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