

Genetic Variation and Character Association Study in Local Cucumber (*Cucumis sativus* L.) Genotypes of Sikkim

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Authors' contributions

This work was carried out in collaboration between all authors. All authors read and approved the final manuscript.

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ABSTRACT

Cucumber is one of the most cultivated cucurbitaceous crop throughout the world known for its unique texture. Sikkim is one of the important states of India located in northeast Himalayas known for its richest diversity in the crop like cucumber with unique bigger sized fruit. Knowledge of genetic variability and inheritance patterns paved the way open for selection and further crop improvement. Total ten genotypes of cucumber were collected from different agro-climatic zones of Sikkim grown locally and evaluated under randomised block design (RBD) for measuring the magnitude of variability and genetic association of traits for cucumber improvement. The genotype SC-401 gave maximum mean value of 2.78 kg for fruit weight and SC-40 gave 28.36 kg for fruit yield per plant. All the genotypes performed differently in biochemical parameters. High phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV) and heritability estimates coupled with high genetic gain was observed for the fruit weight, fruit length, fruit girth, and fruit yield per plant. Fruit weight and vine length are highly correlated with fruit yield per plant. It indicated the existence of a wide range of variation and offers wide scope for selection of the traits found in this study will be rewarding for further cucumber improvement.

Keywords: Diversity; cucumber; genetic advance; heritability.

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1. INTRODUCTION

Cucumber (*Cucumis sativus* L.) is one of the most important cucurbitaceous vegetable crops grown extensively in tropical and sub-tropical parts of the world. It is originated in India but is now grown in most of the continents around the world. Genetic diversity in the primary centre of origin (India) and secondary centre for diversity (China) has been described. Cucumber is an economic major crop throughout the country due to its varied use as food and medicine. It is known for its edible fruits because it is more delicious, crispy, high in nutrients, low in energy and an excellent source of dietary fibre needed for a healthy digestive system. Cucumber is cultivated because it has soothing, cleansing and softening properties which are important criteria for the cosmetics industry [1].

Sikkim is a fully organic State in the lap of Eastern Himalaya bordered by Nepal, Tibet and Bhutan blessed with great diversity among vegetables. Cucumbers found in Sikkim are bigger in size as compared to other parts of the country and unique in texture. A lot of diversity in this crop exists in the state but most of the farmers grow their own landraces to fulfil their domestic or local market demands. A huge portion of the diversity is, thus, still restricted to kitchen gardens or individual farms. Hence, efforts were made to collect this diversity from farmers' fields or kitchen gardens from all over Sikkim and to use it in active crop improvement programme. Therefore, the study of phenotypic variation exhibited among cucumber genotypes could be suitable for genetic improvement of cucumber crop.

2. MATERIALS AND METHODS

The investigation was carried out during the year 2016. The location was located at 27°14'20" N, latitude and 88°18'15" E longitude with an altitude of 400 m above mean sea level. The total rainfall during the growing season was 1625 mm with a temperature ranging from 27-30°C. All the necessary facilities were provided by department of Horticulture, Sikkim University for conducting the study. Ten genotypes were collected from various locations of Sikkim, details of genotypes collected are shown in (Table 1). The experiment was laid out in randomized block design which is replicated thrice. Seeds are sown in the plug tray nursery that consisted of FYM and soil in the ratio 1:1 and transplanting was done after one month. All the essential care was taken during

early age of seedlings in the nursery. The plants were carefully observed after transplanting. The sign of permanent wilting and the advent of new growth was considered as indications of mortality and survival respectively. Gap filling was done by transplanting uniform, a healthy and well-developed seedling of same age in each plot with same line and proper care was taken for their proper establishment. The organic control measures for insects, pests and diseases incidence were also taken from time to time as required. The observations were recorded like germination percentage, Fruit length (cm), node number to first staminate flower appearance, fruit girth (cm), node number to first pistillate flower appearance, fruit length –breadth ratio, inter nodal length(cm), flesh thickness, number of fruits per vine, fruit weight(kg), fruit yield per vine (kg), vine length (m), number of seed per fruit, number of primary branches for all the characters from five randomly selected plants in each treatment an average value was calculated. Total soluble solid (TSS) was determined by using a handheld refractometer. TSS content was determined in the extracted juice samples of respective treatments and their corresponding replications. Ascorbic acid content (mg/100g) was determined by using the method as described [2]. Reducing sugar, non reducing sugar and total sugar was determined by Lane and Eynon method [3].

The experimental data were subjected to statistical difference exhibited various genotypes was tested for significance using analysis of variance for Randomized Block Design [4]. Genotypic and phenotypic coefficients of variations were analyzed following Burton and De vane [5]. Heritability broad sense and expected genetic advance were calculated as per formulae suggested by Lush, [6] Character association of the morphological traits were analysed following Dewey and Lu [7]. Correlation helps to measure and analysis the degree of relationship between two variables by Al-Jibouri et al. [8].

3. RESULTS AND DISCUSSION

The mean sum of squares due to genotypes for all the characters differed. This result indicated that there was significant ($P= 0.05$) variation between the genotypes for all characters under the experiment. Mean performance of all genotypes for different traits is given in (Tables 2 and 3). Germination percentage varied from 68.33-91.66%. The grand mean value of node

no. to first female flower appearance was recorded in 16.95, the trait ranged 14.11-19.33. Mean value of node number to first staminate flower appearance was 4.43, trait ranged 2.89-6.22. The grand mean value of Internodal length was 15.52 cm, character ranged 12.4-18.37. SC-301 was found to be earliest genotype, the grand mean for days taken to 50% flowering (days) was 72.96 days, and character ranged 62.00-82.00 days. Vine length (m) ranged 5.53-7.05 m. A number of seed per fruit ranged 229.00-540.33 with a grand mean of 393.13. A number of primary branches was ranged from 12.66-19.33 with the grand mean of 15.83. Fruit length (cm) ranged 13.87 -34.08 cm with the grand mean of this character was 23.88 cm. The fruit girth (cm) of different genotypes was recorded which ranged from 13.78 -31.98 cm with grand mean of this character was 21.30 cm. Fruit length and breadth ratio (LB ratio) was ranged from 2.66-4.76 with grand mean of this character was 3.87. The average fruit weight ranged from 1.26-2.78 kg with grand mean 2.15 kg. Number of fruits per vine ranged from 8.45 - 13.04 with grand mean of this character was 10.13. SC-40 genotype was found to be the highest yielder (28.36 kg/plant) among all genotypes studied because of its unique bigger sized fruits with a grand mean of 19.79 kg/plant. TSS °Brix ranged from 2.33-3.73 with grand mean of this character was 3.33. Ascorbic acid observed 4.28-6.45 mg/100 g with grand mean was 5.55 mg/100 g. Reducing sugar in cucumber was recorded 0.37-0.49 % with grand mean was 0.41 %. Non-reducing sugar ranged from 1.86-2.64% with grand mean of 2.17. Total sugar of cucumber observed from 2.32-3.02 % with grand mean of this character was 2.59 %. The data in the present study revealed significant ($p=0.05$) differences among genotypes for all the traits studied, indicated genetic variability among the genotypes might be due to the natural crossing, environmental condition, soil type etc. The highest heritability was observed for the fruit yield per plant was 100 %, fruit length (99 %) followed by internodal length (99 %), fruit weight (98 %), fruit girth (98 %), seed per fruit (98%), non reducing sugar (98 %),vine length (95 %), days taken to 50 % flowering (95 %). While fruit yield per plant (58.42 %) followed by average fruit weight (56.38 %) exhibited highest genetic advance express as percent of mean, while the lowest genetic advance as percentage of the mean was found in vine length 14.66%. Heritability estimates together with genetic advance provide better response during selection then either of the

parameters alone [9] in the present study. High genetic advances couple with the high heritability was obtained for fruit yield per plant, seed per fruit, fruit girth and fruit length indicating the individual plant selection could be effectively utilized for development of superior genotypes for these traits. The finding was found to be in close conformity with the results of Das *et al.* [10] in cucumber. The highest genotypic coefficient variation found in fruit yield per plant (28.39%) followed by average fruit weight (27.84%). which indicated the possibility of obtaining high selection response for these traits (Table 2). The phenotypic coefficients of variation (PCV) are higher than the corresponding genotypic coefficients Of variation (GCV) for all the traits. However narrow genetic differences between them indicated less influence of environment in the expression of these traits. In this condition effective selection can be made on the basis of phenotypic coefficient of variation. Liu and Stub [11] reported high heritability with a range of 60% to 80% for most of the characters under study. All the genotypes under study also showed wide variations for fruit colour (green, light green, dark green and white) and total soluble solids (2.33-3.73), which decides the consumer's preference. Majority of the genotypes had light green coloured fruits. Same results were revealed in the report by Verma [12] and Kumar [13] for these characters. Huge variations with regards to various horticultural traits were also reported by Singh *et al.* [14], Das *et al.* [10], Verma [12], Kumar [13], Munshi *et al.* [15], Kumar *et al.* [16] and Yogesh *et al.* [17] in cucumber. The phenotypic correlation coefficient between for fruit yield and its component in cucumber are presented in Table 5. It was evident from table that fruit yield per plant showed highest significant positive correlation with vine length ($r_p = 0.758$) followed by fruit weight ($r_p = 0.744$) this is in agreement with the result obtained by Prasad and Singh [18] in cucumber and Reddy [19] in snap melon. Fruit weight showed the highest positive correlation with yield. Increase in fruit length and diameter resulted in an increase in fruit weight which ultimately increases the yield per plant. Similar findings were also reported by Thangamani and Jansirani [20]. So direct selection for traits like fruit weight and number of fruit per plant could be effectively utilized for improving the yield in cucumber. Significant positive correlation of fruit yield was found with days to the opening of first female flower. This is in agreement with results reported by Bhavne *et al.* [21] in musk melon.

Table 1. List of cucumber genotypes collected from Sikkim

| S. No. | Treatment | Name of genotype | Place/Location of collection |
|--------|-----------------|------------------|-------------------------------|
| 1 | T ₁ | SC-101 | Gangtok (East Sikkim) |
| 2 | T ₂ | SC-201 | Tumin Dhan Bari (East Sikkim) |
| 3 | T ₃ | SC-301 | Daramden(west Sikkim) |
| 4 | T ₄ | SC-401 | Khamdong(East Sikkim) |
| 5 | T ₅ | SC-501 | Yangyang (South Sikkim) |
| 6 | T ₆ | SC-601 | Pakyong (East Sikkim) |
| 7 | T ₇ | SC-701 | BermiokTokal(South Sikkim) |
| 8 | T ₈ | SC-801 | Mangan (North Sikkim) |
| 9 | T ₉ | SC-901 | Sang (East Sikkim) |
| 10 | T ₁₀ | SC-40 | Ranipool (East Sikkim) |

Table 2. Mean performance of twenty characters of cucumber

| GENOTYPE | G% | NNFSFA | NNFPFA | INL (cm) | DTTF 50% | VL (m) | NOPB | FL (cm) | FG(cm) | FLB ratio | FT(cm) | FWT(kg) | NOS/F | NOF/V | FY/P(kg) |
|-----------------------|-------|--------|--------|----------|----------|--------|-------|---------|--------|-----------|--------|---------|--------|-------|----------|
| T ₁ Sc-101 | 91.66 | 3.89 | 19.33 | 16.70 | 76.66 | 6.43 | 12.66 | 27.11 | 25.36 | 3.63 | 2.71 | 2.38 | 384.00 | 8.45 | 16.66 |
| T ₂ Sc-201 | 81.66 | 2.89 | 16.66 | 12.47 | 76.00 | 5.85 | 15.00 | 21.95 | 20.67 | 3.90 | 2.29 | 1.52 | 410.33 | 9.53 | 14.43 |
| T ₃ Sc-301 | 73.33 | 6.22 | 18.99 | 16.45 | 67.66 | 6.22 | 13.00 | 19.49 | 18.02 | 4.76 | 2.79 | 1.74 | 465.66 | 9.20 | 16.03 |
| T ₄ Sc-401 | 86.66 | 3.77 | 16.66 | 12.86 | 77.66 | 6.36 | 16.33 | 23.85 | 22.98 | 4.40 | 2.28 | 2.78 | 336.33 | 8.31 | 19.47 |
| T ₅ Sc-501 | 81.66 | 4.33 | 17.77 | 17.64 | 79.66 | 6.52 | 15.33 | 30.98 | 15.09 | 2.66 | 1.64 | 1.44 | 229.00 | 10.83 | 15.04 |
| T ₆ Sc-601 | 73.33 | 4.77 | 18.88 | 18.37 | 76.33 | 6.21 | 16.66 | 18.17 | 18.26 | 4.03 | 1.47 | 2.76 | 540.33 | 9.19 | 21.58 |
| T ₇ Sc-701 | 88.33 | 5.33 | 16.44 | 13.60 | 82.00 | 7.05 | 15.66 | 34.08 | 31.98 | 3.43 | 2.99 | 2.50 | 366.00 | 10.63 | 26.16 |
| T ₈ Sc-801 | 85.00 | 4.44 | 14.11 | 14.23 | 62.00 | 5.53 | 15.00 | 13.87 | 13.78 | 3.90 | 2.71 | 1.26 | 266.00 | 11.75 | 13.35 |
| T ₉ Sc-901 | 83.33 | 5.33 | 15.77 | 15.19 | 67.66 | 7.04 | 19.33 | 24.75 | 23.83 | 3.86 | 2.24 | 2.75 | 524.66 | 10.38 | 26.88 |
| T ₁₀ Sc-40 | 68.33 | 3.33 | 14.88 | 15.19 | 64.00 | 6.52 | 19.33 | 24.50 | 22.95 | 4.10 | 2.38 | 2.36 | 409.00 | 13.04 | 28.36 |
| GM | 81.33 | 4.43 | 16.95 | 15.52 | 72.96 | 6.37 | 15.83 | 23.87 | 21.29 | 3.87 | 2.35 | 2.15 | 393.13 | 10.13 | 19.79 |
| SE(m) | 1.86 | 0.18 | 0.35 | 0.10 | 0.90 | 0.46 | 0.65 | 0.30 | 0.45 | 0.15 | 0.49 | 0.45 | 4.60 | 0.14 | 0.10 |
| C.D AT 5% | 5.54 | 0.54 | 1.04 | 0.30 | 2.67 | 0.13 | 1.95 | 0.90 | 1.33 | 0.46 | 0.14 | 0.13 | 13.67 | 0.43 | 0.10 |
| Range Lowest | 68.33 | 2.89 | 14.11 | 12.4 | 62.00 | 5.53 | 12.66 | 13.87 | 13.78 | 2.66 | 1.47 | 1.26 | 229.00 | 8.31 | 13.35 |
| Range highest | 91.66 | 6.22 | 19.33 | 18.37 | 82.00 | 7.05 | 19.33 | 34.08 | 31.98 | 4.76 | 2.99 | 2.78 | 540.33 | 13.04 | 28.36 |

G%=Germination percentage NOPB= Number of primary branches
 NNFSFA= Node number to first staminate flower appearance
 NNFPFA=Node number to first pistillate flower appearance
 FT=Flesh thickness (cm)
 DTTF50%= Days taken to 50% flowering (days)
 FWT= Average fruit weight (g)
 VL=Vine length (m)
 NOS/F= Number of seed per fruit
 FY/P= Fruit yield per plant (kg).

FL= Fruit length (cm)
 FG=Fruit girth (cm)
 FLB= Fruit length and breadth ratio (LB ratio)
 NOF/V= Number of fruits per vine

Table 3. Mean performance of biochemical observation for different characters of cucumber

| Genotype | TSS° Brix | Ascorbic acid (mg/100 g) | Reducing sugar% | Non-reducing sugar% | Total sugar% |
|-----------------------|------------------|---------------------------------|------------------------|----------------------------|---------------------|
| T ₁ Sc-101 | 3.23 | 6.22 | 0.39 | 2.14 | 2.54 |
| T ₂ Sc-201 | 2.33 | 6.45 | 0.49 | 2.15 | 2.65 |
| T ₃ Sc-301 | 3.23 | 4.84 | 0.40 | 1.98 | 2.38 |
| T ₄ Sc-401 | 3.63 | 4.45 | 0.42 | 1.91 | 2.34 |
| T ₅ Sc-501 | 3.53 | 5.36 | 0.44 | 2.27 | 2.72 |
| T ₆ Sc-601 | 3.46 | 4.28 | 0.39 | 2.47 | 2.89 |
| T ₇ Sc-701 | 3.40 | 6.21 | 0.38 | 2.64 | 3.02 |
| T ₈ Sc-801 | 3.23 | 6.45 | 0.39 | 2.20 | 2.60 |
| T ₉ Sc-901 | 3.73 | 4.83 | 0.46 | 1.86 | 2.32 |
| T ₁₀ Sc-40 | 3.56 | 6.45 | 0.37 | 2.09 | 2.46 |
| GM | 3.33 | 5.55 | 0.41 | 2.17 | 2.59 |
| CV. | 4.29 | 4.87 | 4.78 | 1.71 | 2.37 |
| SE(m) | 0.57 | 0.15 | 0.85 | 0.13 | 0.03 |
| C.D AT 5% | 0.17 | 0.46 | 0.25 | 0.40 | 0.10 |
| Range Lowest | 2.33 | 4.28 | 0.37 | 1.86 | 2.32 |
| Range highest | 3.73 | 6.45 | 0.49 | 2.64 | 3.02 |

Table 4. Mean, range, co-efficient of variation, heritability, genetic advance and genetic advance as % of mean

| Characters | General mean | Range | Co-efficient of variation | | | Heritability% (broad sense) | Genetic advancement | Gen.adv as of % mean |
|------------|--------------|---------------|---------------------------|-------|-------|-----------------------------|---------------------|----------------------|
| | | | GCV | PCV | ECV | | | |
| G% | 81.33 | 68.33-91.66 | 8.86 | 9.71 | 3.98 | 83 | 13.55 | 16.65 |
| FL(cm) | 23.88 | 13.87-34.08 | 25.01 | 25.10 | 2.22 | 99 | 12.25 | 51.31 |
| NNTFSFA | 4.43 | 2.89-6.22 | 22.25 | 24.13 | 9.34 | 85 | 1.87 | 42.26 |
| FG(cm) | 21.30 | 13.78-31.98 | 25.05 | 25.32 | 3.66 | 98 | 10.88 | 51.07 |
| NNTFPFA | 16.95 | 14.11-19.33 | 10.27 | 10.88 | 3.59 | 89 | 3.33 | 19.98 |
| FLB(ratio) | 3.87 | 2.66-4.76 | 12.46 | 18.06 | 13.07 | 48 | 0.69 | 17.72 |
| INL (cm) | 15.52 | 12.4-18.37 | 13.82 | 13.88 | 1.34 | 99 | 4.40 | 28.33 |
| FT | 2.35 | 1.47-2.99 | 20.72 | 21.04 | 3.67 | 96 | 0.99 | 42.02 |
| F/V | 10.13 | 8.31-13.04 | 14.68 | 14.89 | 2.50 | 97 | 3.02 | 29.81 |
| DTT 50% | 72.97 | 62-82.0 | 9.50 | 9.74 | 2.14 | 95 | 13.93 | 19.09 |
| FWT. (kg) | 2.15 | 1.26-2.78 | 27.60 | 27.84 | 3.63 | 98 | 1.21 | 56.38 |
| FY/P | 19.80 | 13.35-28.36 | 28.37 | 28.39 | 3.63 | 100 | 11.57 | 58.42 |
| VL(m) | 6.38 | 5.53-7.05 | 7.30 | 7.49 | 1.67 | 95 | 0.93 | 14.66 |
| S/F | 393.13 | 229.00-540.33 | 25.63 | 25.85 | 3.38 | 98 | 205.8 | 52.35 |
| PB/P | 15.83 | 12.66-19.33 | 13.52 | 15.32 | 7.20 | 78 | 3.89 | 24.59 |
| (TSS) | 3.33 | 2.33-3.73 | 11.54 | 12.32 | 4.29 | 88 | 0.74 | 22.29 |
| Vitamin-C | 5.56 | 4.28-6.45 | 15.84 | 16.57 | 4.87 | 91 | 1.73 | 31.18 |
| RS | 0.42 | 0.37-0.49 | 8.89 | 10.10 | 4.78 | 78 | 0.07 | 16.13 |
| NRS | 2.17 | 1.86-2.64 | 11.11 | 11.24 | 1.71 | 98 | 0.49 | 22.61 |
| TS% | 2.60 | 2.32-3.02 | 8.92 | 9.23 | 2.37 | 93 | 17.76 | 17.76 |

G%= Germination percentage, F/V= Fruit per vine

FL= Fruit length (cm), DTT50%= Days taken to 50% flowering (days)

NNTFSFA=Node number to first staminate flower appearance,

PB/P= Primary branches per plant

FG=Fruit girth (cm)

NNTFPFA= Node number to first pistillate flower appearance

INL= Inter nodal length (cm),

FY/V= fruit yield per vine,

FT=Flesh thickness

TS=Total sugar

VL= Vine length (m)

S/F=number of seed per fruit

FWT = Average fruit weight (kg),

RS= Reducing sugar

TSS= Total soluble solid

NRS= Non reducing sugar

Table 5. Estimates of phenotypic correlation co-efficient between different characters in Cucumber

| | G% | FL | NNTOFSFA | TSS | FG | VIT. C | NNTOFPFA | RS | FLB (LB) | NRS | DTT50%F | NOF/V | FT | TS | INL | FWT | FY/V | VL | NOS/F | PB/P |
|-------------------|----|--------------|---------------|---------------|--------------|--------------|---------------|--------------|---------------|---------------|---------------|---------------|---------------|---------------|--------------|--------------|----------------|----------------|--------------|---------------|
| G% | - | 0.360 | -0.063 | -0.080 | 0.362 | 0.198 | 0.016 | 0.178 | -0.382 | 0.083 | 0.451* | -0.398 | -0.382* | 0.098 | -0.555 | 0.036 | -0.260 | 0.127 | -0.414 | -0.381* |
| FL | | - | -0.002 | 0.230 | 0.657** | 0.148 | 0.157 | 0.061 | -0.622** | 0.302* | 0.663** | 0.014 | -0.622 | 0.304* | -0.010 | 0.261 | 0.376* | 0.786** | -0.233 | 0.061 |
| NNTOFSFA | | | - | 0.392* | 0.028 | -0.459 | 0.265 | -0.206 | 0.168 | 0.084 | -0.089 | -0.112 | 0.168 | 0.054 | 0.194 | 0.112 | 0.140 | 0.345* | 0.312* | -0.142 |
| TSS ^{°B} | | | | - | 0.120 | -0.492 | -0.083 | -0.400 | -0.068 | -0.110 | -0.088 | 0.185 | -0.068 | -0.179 | 0.424* | 0.557* | 0.559* | 0.582* | 0.038 | 0.489* |
| FG | | | | | - | 0.177 | 0.014 | -0.160 | -0.021 | 0.207 | 0.408* | -0.130 | -0.021 | 0.171 | -0.296 | 0.647** | 0.647** | 0.751** | 0.249 | 0.162 |
| AAC | | | | | | - | -0.441 | -0.441 | -0.304 | 0.249 | -0.175 | 0.522* | -0.304 | 0.213 | -0.227 | -0.472 | -0.094 | -0.206 | -0.428 | -0.145 |
| NNTOFPFA | | | | | | | - | 0.019 | 0.011 | 0.121 | 0.529* | -0.736 | 0.011 | 0.144 | 0.410* | 0.160 | -0.277 | 0.096 | 0.294 | -0.584 |
| RS | | | | | | | | - | -0.177 | -0.391 | 0.192 | -0.275 | -0.177 | -0.244 | -0.387 | -0.216 | -0.273 | -0.023 | 0.061 | 0.065 |
| FLB (LB) | | | | | | | | | - | 0.485* | -0.476 | -0.253 | 1.000 | -0.528 | -0.158 | 0.234 | 0.071 | -0.280 | 0.727** | 0.002 |
| NRS | | | | | | | | | | - | 0.497* | 0.146 | -0.485 | 0.987** | 0.119 | -0.029 | 0.075 | 0.077 | -0.144 | -0.155 |
| DTT50%F | | | | | | | | | | | - | -0.540 | -0.476 | 0.552* | -0.146 | 0.246 | -0.061 | 0.348* | -0.146 | -0.282 |
| NOF/V | | | | | | | | | | | | - | -0.253 | 0.097 | 0.205 | -0.293 | 0.356* | 0.037 | -0.260 | 0.531* |
| FT | | | | | | | | | | | | | - | -0.528 | -0.158 | 0.234 | 0.071 | -0.280 | 0.527* | 0.002 |
| TS | | | | | | | | | | | | | | - | 0.080 | -0.056 | 0.031 | 0.064 | -0.119 | -0.145 |
| INL | | | | | | | | | | | | | | | - | 0.096 | 0.162 | 0.143 | 0.223 | 0.094 |
| FWT | | | | | | | | | | | | | | | | - | 0.744** | 0.641** | 0.578* | 0.468* |
| FY/V | | | | | | | | | | | | | | | | | - | 0.758** | 0.477* | 0.775** |
| VL | | | | | | | | | | | | | | | | | | - | 0.259 | 0.414* |
| NOS/F | | | | | | | | | | | | | | | | | | | - | 0.300* |

*significant at 5% level; **significant at 1% level

G% = Germination percentage

FL= Fruit length (cm)

NNTOFSFA= Node number to first staminate flower appearance

TSS = total soluble solid ([°]B)

FG = Fruit girth (cm)

AAC = Ascorbic acid content (mg/100 g)

NNTOFPFA = Node number to first pistillate flower appearance

RS = Reducing sugar (%)

FLB = Fruit length and breadth ratio (LB ratio)

NRS = Non reducing sugar (%)

DTT50% = Days taken to 50% flowering (days)

FY/V= Fruit yield per vine

TS = Total sugar (%)

INL= Inter nodal length (cm)

FWT. = Fruit weight (kg)

FY/V= Fruit yield per vine

VL= Vine length (m)

NOS/F = Number of seed per fruit

4. CONCLUSION

On the basis of above experiment, it can be concluded that the present set of material have wide range of genetic variability for all the traits which can be utilised for hybridization programme aimed for heterotic combination yield improvement. In case of variability studies highest genotypic coefficient of variation was seen in characters number of fruits per plant, fruit weight, fruit length, vine length, number of primary branches per plant, and node at which first female flower appeared. These traits can be exploited during selection. The characters showed high heritability and high genetic advance can be further improved through a selection procedure. The highest genetic advance as percentage of mean was obtained for fruit yield per plant. The genotypes of highly diverse may also be utilised in a breeding programme for the development of high yielding varieties and F_1 hybrids with desirable quantitative traits.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Akshay J, Singh SP, Pandey VP. Character association among the yield and yield attributes in bottle gourd [*Lagenaria siceraria* (Molina) Standl] genotypes. Plant Archives. 2017;17(1):711-714.
2. Ranganna. Handbook of Analysis and Quality Control for Fruit and Vegetable Product. Tata Mc Graw Hill Pub. Co. Ltd., New Delhi, India; 2012.
3. AOAC, Official Methods of Analysis, 17th ed, Association of Official 28 Agricultural Chemists, (Washington D.C., 1995).
4. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. ICAR, 2nd edn, New Delhi, India. 1967;2381.
5. Burton and Devane. Genetic relationship of growth and development traits with fruit yield in F_2 population of BGD L x Hot season of cucumber (*Cucumis sativus* L.). Karnataka J. Agril. Sci. 1953;24(4):497-500.
6. Lush. Genetic variability for quantitative and qualitative characters in Brinjal (*Solanum melongena* L). African J. Agril. Res. 1949;8(39):4956-4959.
7. Dewey DR, Lu KH. A correlation and path coefficient analysis of components of crested wheat grass and seed production. Agron. J. 1959;51:515-7.
8. Al-Jibouri HA, Miller PA, Robinson HF. Genotypic and environmental variance in an upland cotton cross of interspecific origin. Agron. J. 1958;50:633-637.
9. Johnson HW, Robinson HF, Comstock RE. Estimation of genetic and environmental variability in soyabean. Agron. J. 1955;41: 314-318.
10. Das S, Maurya KR, Chaudhary DN. Heritability study in cucumber. J. Applied Biol. 2003;13(1-2):54-57.
11. Lui JS, Staub JE. Analysis of genetic correlation for several major characters of botanical varieties and cultivars in cucumber. China Vegetable. 1999;5:16-19.
12. Verma S. Genetic variability and correlation studies in cucumber (*Cucumis sativus* L.). M. Sc. Thesis, Department of Vegetable Science, Dr. Y. S. Parmar University of Horticulture and Forestry, Nauni, Solan, H.P; 2003.
13. Kumar A, Prasad B, Saha BC. Genetic variability in garlic (*Allium sativum* L.). J. Inter-academica. 2006;10(4):467-472.
14. Singh RV, Verma TS, Thakur PC. Characters association in cucumber. Haryana J. Hort. Sci. 2002;31(12):91-93.
15. Munshi AD, Panda B, Behera TK, Kumar R, Bisht IS, Behera TK. Genetic variability in *Cucumis sativus* var. *hardwickii* R. germplasm. Cucurbit Genet. Coop. 2007;30:5-10.
16. Kumar A, Kumar S, Kumar P. Genetic variability and characters association for fruit yield and yield traits in cucumber. Indian J. Horticulture. 2008;65(4):423-428.
17. Yogesh C, Yadav SK, Brijpal B, Dixit SK. Genetic variability, heritability and genetic advance for some traits in cucumber. Indian J. Hort. 2009;66(4):488-491.
18. Prasad VRS, Singh DP, Singh RP. Biological divergence in the land races of Indian cucumber (*Cucumis sativus* L.). Indian. Journal of Horticulture. 1992;50(1): 57-63.
19. Reddy. Studies on genetic variability in snap melon (*Cucumis melo* L. var. *momordica*). M.Sc. Thesis submitted to (P.G.) School. Indian agricultural Research Institute New Delhi-12; 2004.

20. Thangamani C, Jansirani P. Correlation and path coefficient analysis studies on yield and attributing characters in brinjal (*Solanum melongena* L.). Electro. J. Plant Breed. 2012;3(3):939-944.
21. Bhave SG, Mehta JL, Bendale VW, Mhatre PP, Pethe. Character association and path co-efficient analysis of bitter gourd (*Momordica charantia* L.). Orissa J. Horticulture. 2003;31(1):44-46.

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