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Assessment of genetic variability for yield and yield related traits in local collections of cucumber

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Abstract

The genetic variability parameters were estimated to elucidate variation available in local collections of Cucumber (*Cucumis sativus* L.). Forty local types with four checks of cucumber were evaluated in Augmented Block Design. Significant variation among the forty local types and the checks was reported for most of the traits. Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the characters studied. High genotypic and phenotypic coefficient (GCV and PCV) was observed for sex ratio (29.07 and 29.52), number of fruits per plant (20.25 and 23.94) and yield per plant (28.59 and 30.86). Difference between GCV and PCV is less suggesting least environmental influence on these characters. High heritability with high genetic advance as per cent mean (GAM) was observed for node number first female flower appearance, sex ratio, number of branches per plant, number of nodes per plant, internodal length, number of fruits per plant, individual fruit weight, yield per plant and fruit diameter representing the presence of predominant additive interactions, henceforth direct selection to be practiced for these traits.

Keywords: Cucumber, GCV, PCV, Heritability, Genetic advance and GAM

Introduction

Among the vegetables Cucumber (*Cucumis sativus* L.) is fourth most important vegetable crop (Tatlioglu *et al.* 1993) [14]. It belongs to the tribe cucumerinae in the family of cucurbitaceous. It closely resembles the wild form *Cucumis hardwicki* which is a native of Himalayas and originated in India. Cucumber is commonly a monoecious annual crop with a vine length of 1 to 3mt. It is a highly cross pollinated crop in nature. Presence of vitamins considerable amounts of proteins, carbohydrates, calcium, iron, phosphorous, vitamin C, crude fibers and minerals made this crop nutritionally rich (Vora *et al.*, 2014) [16]. Cucumber has property of cooling effect because of higher percentage of moisture and in the eastern countries fruits are often used as cooling vegetable. Owing to its high cross pollination nature of Cucumber lot of variability will be expected in growth and yield traits. It represents diverse variability in the existing germplasm and there is no uniformity in yield related traits. To develop uniform and stable genotypes for these traits a good understanding of genetic stock of cucumber is essential for selection of desirable genotypes hybridization programme.

Local cultivars are important as a crop in general that have socio-economic importance. These local cultivars are ideal for low input agricultural production systems since they are adapted to the local environmental and climatic conditions, which make less negative pressure on the environment. Local cultivars are also grown for their particular flavour, characteristics related to their production, disease resistance, and cultural or personal reasons. In cucumber wide diversity is available for fruits traits *viz*, shape, size, colour, maturity, taste and also yield.

Genetic variability plays an important role in selection and heritability of the traits available in the germplasm for crop improvement programmes. Greater the variability in the available germplasm, the chances of selecting superior genotypes (Simmonds. 1962) [13] will be high. Variability is a prerequisite for any breeding programme, further, phenotypic variability being controlled by both genotypic and environmental factors both the factors to be considered to know the total variability and heritable portion of the variability. Genetic advance is important, as it predicts the extent of advancement to next generation through selection. All these variability parameters are estimated in this investigation. Karnataka is the major growing states and diverse local ecotypes of cucumber are abundantly available in Belagavi, Badami and Bagalkot, which are under exploited.

The study focused on exploration and utilisation of the local cucumber ecotypes of Northern Karnataka to assess the genetic variability based on yield and yield related traits.

Materials and Methods

Local ecotypes were evaluated at College of Horticulture, Bagalkot falls under agro-climatic zone-3 (northern dry zone) of region-2 of Karnataka. Total 44 local ecotypes, collected from Karnataka were evaluated in the study. The local ecotypes used are listed in Table 1.

The experiment was laid out in an augmented block design with 40 treatments and 4 checks during *Kharif* 2017-18 at college of Horticulture, Bagalkot. Each treatment was represented by size of 2.0 m² and each line consisting of 15 plants, which are not replicated, but the checks are replicated in each block. Recommended dose of fertilizers and cultivation aspects were considered.

For evaluation from each treatment five plants were selected. Characters *viz.*, plant height (cm), days to first male flower, days to 50 per cent flowering, days to first female flower, node number first female flower appearance, sex ratio, number of branches per plant, number of nodes per plant, internodal length (cm), number of fruits per plant, individual fruit weight (g), fruit length (cm), fruit diameter (cm) and yield per plant. The data was analyzed by INDOSTAT software to estimate the genetic variability parameters. The estimates for variability (Burton *et al.*, 1953) [4], heritability and genetic advance as percent of mean were estimated according to criteria proposed by Johnson *et al.*, 1955 [8].

Results and Discussion

Analysis of variance revealed the existence of significant differences among all the checks for plant height at 30, 45 and 60 DAS, days to first male flower, days to 50 per cent flowering, days to first female flower, node number first female flower, sex ratio, number of branches per plant, number of nodes per plant, internodal length, number of fruits per plant, individual fruit weight, fruit length and fruit diameter. Significant variation was also observed among the 40 local ecotypes for most of the traits (Mean sum of squares) (Table 2). This specifies the magnitude of variability existed among the local ecotypes for the characters studied and also indicates the ample scope for improvement. Estimates of Mean, Genotypic coefficient of variation (GCV) and Phenotypic coefficient of variation (PCV), Heritability, Genetic advance as percent mean are presented Table 3.

In general, for all characters the magnitude of the PCV was higher than the corresponding GCV, indicating the least effect of environment on the expression of traits.

High GCV and PCV were observed for sex ratio (29.07 & 29.52), number of fruits per plant (20.25 & 23.94) and yield per plant (28.59 & 30.86). The PCV were higher than the corresponding genotyping coefficient of variation. Least difference between PCV and GCV indicated least influence of environment on the expression of these traits. This favors effective selection on the basis of phenotype alone. Similar findings were reported by Basavarajeshwari *et al.* 2014 [2], Bhawana *et al.* 2010 [3], Veena *et al.* 2012 [15] and Yadav *et al.* 2012 [17] in cucumber. Moderate GCV and PCV were observed for node at first female flower appears (15.17 & 15.55), number of branches per plant (13.97 & 14.67), number of nodes per plant (14.04 & 15.40), internodal length (18.67 & 19.80), individual fruit weight (18.40 & 18.49), fruit

length (9.76 & 12.41) and fruit diameter (16.66 & 17.32). Results are in line with the findings of Arunkumar *et al.*, 2011 [1], Rajawat *et al.*, 2017 [9] and Ranjan *et al.*, 2015 [11] in cucumber. The low GCV and PCV were reported for plant height (6.13 & 6.44), days to 50 per cent flowering (6.92 & 8.03), days to first male flower (4.99 & 6.06) and days to first female flower (4.90 & 7.41). But the difference between GCV and PCV is less. These findings indicated that less environmental influence with respect to these characters. These findings are in agreement with the results of Arunkumar *et al.*, 2011 [1], Rajawat *et al.*, 2017 [9] and Ranjan *et al.*, 2015 [11].

In this study, all the characters had high heritability in broad sense but genetic advance as per cent of mean (GAM) was varied among the characters suggesting different gene actions. Node number first female flower appearance, sex ratio, number of branches per plant, number of nodes per plant, internodal length, number of fruits per plant, individual fruit weight, yield per plant and fruit diameter showed high heritability coupled with high genetic advance as per cent of mean. Similar observations were reported by Arunkumar *et al.*, 2011 [1], Chandrashekhar *et al.*, 2016 [5], Saheb *et al.*, 2016 [12] and Veena *et al.*, 2012 [15]. This confirms the predominant additive interactions of the components which control the inheritance of these traits. Effective direct selection can be achieved for these. Plant height, days to first male flower appearance, days to 50 percent flowering and fruit length exhibited moderate to low genetic advance as per cent of mean even though they had high heritability. This was in line with observation of by Bhawana *et al.*, 2010 [3], Chikezie *et al.*, 2016 [6] and Yadav *et al.*, 2012 [17]. This suggests non-additive gene interactions that are operating in the inheritance, selection would be ineffective. In such cases heterosis can be exploited through hybridization.

Conclusion

Estimates of variability parameters are important for effective selection in formulating efficient selection and trait-specific breeding. Local ecotypes recorded good fruit yield and desirable fruit parameters can be exploited in further breeding programme. Local varieties have many desirable fruit and yield traits, superior culinary and also the nutritional parameters which are useful in future breeding programme.

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