Quantification of Diverse Local Germplasm of Pumpkin Through Genetic Variability Components in Garhwal Region of Uttarakhand

Chandni Negi, D. K. Rana, V. Singh, Himani Rana, K. N. Shah

ABSTRACT

An experiment was conducted at Horticultural Research Center, Department of Horticulture, H.N.B Garhwal University, Srinagar (Garhwal), Uttarakhand, India, during summer season 2019, to study "Quantification of diverse local germplasm of Pumpkin through genetic variability components in Garhwal regions of Uttarakhand". Experimental material for the study consisted of 25 genotypes. The experiment was conducted using a Randomized Block Design with three replications. The genotypes have been collected from different regions of Uttarakhand and other parts of India. Observations were recorded on 23 economic traits. Each of the traits under study, genetic variability analysis revealed that the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were nearly identical. Highest coefficient of variability both at phenotypic and genotypic level was observed for yield per vine (50.48% and 50.33%) and lowest for days to 1st fruit harvest (5.49% and 5.49%). Maximum heritability was found in number of seeds per fruit (100%) and moderate was found for number of ridges per fruit (40.10%). Highest genetic advance was observed for number of seeds per fruit (79.26) and lowest for rind thickness (0.15mm). In terms of percentages above the mean, vine length, number of primary branches/ vine, number of nodes upto first male flower and female flower, number of fruits / vine, percent of fruits setting, average fruit weight and yield/vine all demonstrated high genetic advance. In order to continue crop development programs for pumpkin in the Garhwal Region of Uttarakhand, factors like vine length, percent of fruit setting, average fruit weight, and yield per vine could be taken into consideration through selection.

Keywords Co-efficient, Genotypic, Phenotypic, Heritability, Pumpkin.

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INTRODUCTION

Pumpkin (*Cucurbita moschata* Duch Ex Poir) is locally known in hindi as "Kasiphal", "Sitaphal" and "lalkaddu". The genus *Cucurbita* is comparatively a closed group or system of about 27 species deter-

mined in the tropical regions of Central and South Africa and comprising both wild and cultivated species having the chromosome number of 2n=40. Around the world, pumpkin is grown under a variety of agro climatic conditions. The crop is widely grown in China, India, Mexico and United States of America. Assam, West Bengal, Tamil Nadu, Karnataka, Madhya Pradesh, Uttar Pradesh, Orissa, Kerala, and Bihar. Pumpkin is a good source of vitamins, especially those with strong carotenoid and minerals. In the form of provitamin A, pumpkin offers an excellent source of carotenoids, which play a significant role in nutrition (Roy 1973). It is also quite high in energy and carbohydrates (Bose and Som 1998). It is used as a vegetable as well as processed product in both its mature and immature stages.

A successful breeding effort for any crop species requires genetic diversity. Direct selection for yield in plant breeding programs on the basis of phenotypical traits as such may be deceptive. Environmental factors have a significant impact on most economically significant traits and characters that are related to them; this makes it challenging to exercise selection since heritable (genotypic) variation is frequently masked by non-heritable (environmental) variation. The amount of diversity contained in the available strains can be determined using the coefficient of phenotypic and genotypic variation. The ratio of genotypic variance to phenotypic variance is known as heritability. It is a reliable indicator of how traits are passed on from parents to offspring (Falconer 1981). Heritability describes the precision with which a genotype may be identified based on its phenotypic behavior. In broad sense heritability, both additive and non-additive effects exist. The plant breeder can predict the behavior of the next generation and make desirable selections for improvements with the use of heritability and genetic advancement information. In view of the above-mentioned facts and their economic significance, there is a need to enhance and assess the quantitative and qualitative characteristics of pumpkin. So, the present investigation was design to quantify various components of genetic variability and to identify the most suitable genotypes for yield and its related traits in Garhwal region of Uttarakhand.

MATERIALS AND METHODS

The current study was carried out in the summer of 2019 at the Horticultural Research Center, HNB. Garhwal University, Srinagar (Garhwal), Uttarakhand, India. During the experiment, 24 different genotypes of pumpkin were employed collected from different geographical regions of Uttarakhand, with one check variety "Baramasi". The climate of experimental site comes under subtropical, which is marked by temperature extremes in both the summer and winter. For sowing seeds, furrows of 15m length were made at a distance of 2.0 m from each other.

Each furrow was marked at 1.50 m distance to indicate the location of a hole that was dug for sowing of seeds. Throughout the investigation period, the entire recommended package of practices for successful crop growth for pumpkin was followed Thamburaj (2001). Three replications were used in the Randomized Block Design during the experiment. From each replication of each treatment, five plants were randomly chosen and tagged in order to record the parameters. 23 various growths, yield, and quality related parameters were examined during the experiment. The methodology outlined by Ranganna (2015) was used to conduct the quality analysis. The data recorded for various characters was subjected to statistical analysis to draw the suitable interferences. Analysis of variance (ANOVA) was done by the method given by Panse and Sukhatme (1961). The genotypic and phenotypic coefficient of variation were calculated as per formula given by Burton and De vane (1953), heritability (in broad sense) and genetic advance was estimated as per Allard *et al.* (1960).

RESULTS AND DISCUSSION

Twenty-five pumpkin genotypes were studied to assess genetic variability, heritability, and genetic advance (as a percentage of mean). The mean sum of squares attributable to treatment for growth, yield and quality traits evaluated in the current experiment demonstrated significant differences at the 5% level, according to the analysis of variance as shown in Table 1. This demonstrated that the genotypes under study showed substantial diversity. Both Pandey *et al.* (2002) and Srikanth *et al.* (2017) showed similar results in pumpkin.

Table 1. Analysis of variance for growth and yield characters of pumpkin.

| Source of variation | Mean sum of square | | | |
| Degree of freedom | Replication | Treatment | Error | Total |
	2	24	46	74
Vine length (m)	0.25	2.22*	0.04	0.75
No. of primary branches/vine	0.05	0.75*	0.02	0.26
Internodal length (cm)	0.05	3.29*	0.05	1.10
Number of nodes upto 1st male flower	0.05	17.37*	0.03	5.66
Number of nodes upto 1st female flower	0.00	45.36*	0.04	14.74
Days taken to appearance of 1st male flower	0.10	132.74*	0.03	43.07
Days taken to appearance of 1st female flower	0.02	151.30*	0.01	49.08
Total number of male flowers	0.00	124.70*	0.00	40.44
Total number of female flowers	0.04	17.35*	0.02	5.64
Number of fruits/vine	0.01	7.35*	0.00	2.39
Percent of fruits setting	0.92	798.51*	0.72	259.47
Average fruit weight (kg)	0.00	2.29*	0.01	0.75
Yield/vine (kg)	0.14	84.86*	0.16	27.63
Day to first fruit harvest	0.31	171.29*	0.18	55.66
Rind thickness (mm)	0.00	0.02*	0.00	0.01
Fruit length (cm)	0.02	272.15*	0.01	88.27
Fruit diameter (cm)	0.01	245.07*	0.01	79.49
Flesh thickness (cm)	0.01	0.32*	0.01	0.11
Sex ratio (F: M)	0.13	1.04*	0.04	0.37
Number of seed/fruit	0.44	4440.98*	0.03	1440.33
Beta carotene (mg/100g)	0.00	1.30*	0.00	0.42
Number of ridges/fruit	0.01	11.87*	3.95	6.41
TSS (^{0}Brix)	0.01	1.07*	0.10	0.41

*Significant at 5 %.

All the 23 traits related to various growth, yield and quality presented in Table 2, the mean, range, genotypic coefficient of variance (GCV), phenotypic coefficient of variance(PCV), heritability, genetic

Table 2. Variability parameters for different characters in pumpkin.

Characters	Range	Mean	GCV (%)	PCV (%)	Heritability (%)	Genetic advance (GA)	Genetic advance over mean GAM (%)
Vine length (m)	2.27 - 6.73	5.56	15.32	15.78	94.25	1.70	30.63
No. of primary branches/vine	2.00- 3.48	2.74	18.01	18.86	91.18	0.97	35.42
Internodal length (cm)	14.03- 18.43	16.66	6.24	6.38	95.82	2.10	12.59
Number of nodes upto 1st male flower	2.07- 11.37	5.93	40.52	40.64	99.42	4.94	83.23
Number of nodes upto 1st female flower	12.68 -28.30	19.34	20.10	20.13	99.74	8.00	41.35
Days taken to appearance of 1st male flower	44.37- 77.69	64.02	10.39	10.39	99.95	13.70	21.40
Days taken to appearance of 1st female flower	67.36- 98.27	81.64	8.70	8.70	99.98	14.63	17.92
Total number of male flowers	10.39- 34.21	22.21	29.03	29.03	100.00	13.28	59.79
Total number of female flowers	5.17- 13.16	8.96	26.82	26.86	99.71	4.94	55.17
Number of fruits/vine	1.18 -7.58	3.66	42.70	42.74	99.82	3.22	87.89
Percent of fruits setting	18.88- 100.00	41.08	39.70	39.75	99.73	33.55	81.66
Average fruit weight (kg)	1.64 -4.50	2.88	30.25	30.37	99.18	1.79	62.05
Yield/vine (kg)	2.53 - 21.06	10.56	50.33	50.48	99.42	10.91	103.39
Day to first fruit harvest	120.45 -153.39	137.71	5.49	5.49	99.72	15.54	11.28
Rind thickness (mm)	0.15 -0.41	0.29	25.72	25.76	99.67	0.15	52.89
Fruit length (cm)	11.80 -43.33	31.79	29.96	29.96	99.99	19.62	61.72
Fruit diameter (cm)	23.26 -74.15	39.78	22.72	22.72	99.99	18.62	46.80

Table 2. Continued.

Characters	Range	Mean	GCV (%)	PCV (%)	Heritability (%)	Genetic advance (A)	Genetic advance over mean GMA (%)
Flesh thickness (cm)	3.50 -4.77	4.02	8.08	8.36	93.56	0.65	16.11
Sex ratio (F:M)	1.62 -4.52	2.61	22.15	23.47	89.05	1.12	43.06
Number of seed/fruit	120.45 -274.55	183.65	20.95	20.95	100.00	79.26	43.16
Beta carotene (mg/100g)	2.25 -4.38	3.52	18.70	18.72	99.82	1.36	38.49
Number of ridges/fruit	13.08 -20.12	14.59	11.14	17.59	40.10	2.12	14.53
TSS (^{0}Brix)	2.96 -5.15	4.06	14.01	16.02	76.49	1.03	25.25

advance (GA) and genetic advance as per cent over mean (GAM) were calculated in order to determine to which extent the observed variation is caused by genetic factors. The analysis of the current experiment showed that, for all the traits under examination, the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were practically identical. Suggesting that, these attributes were only slightly influenced by their environment, which is why it would be feasible to select these based on phenotypic values. Nearly all of the characteristics had high heritability.

Analysis of variance (Table 1) revealed that the genotypes exhibited significant differences for all the traits under study. One of the ways to appreciate the extent of variability is to examine the range, which reflects the extent of phenotypic variability in respect of the trait under consideration, encompassing genotypic, environmental and interaction components. In the present study, the pumpkin genotypes exhibited wide range values for all characters viz., vine length, number of primary branches per vine, internodal length, number of nodes upto first male flower, number of nodes upto first female flower, days taken to appearance of 1st male, days taken to appearance of 1st female flower, total number of male flowers, total number of female flowers, number of fruits per vine, percent of fruits setting, average fruit weight and yield per vine. High range values indicated good scope for selection for any trait of interest for the breeder to exercise his selection.

Coefficient of variation

In the current study, high coefficients of variation at both phenotypic and genotypic levels were found for yield per vine (50.48% and 50.33%), number of fruits per vine (42.74% and 42.70%), number of nodes upto first male flower (40.64% and 40.52%), percent of fruits setting (39.75% and 39.70%) and average fruit weight (30.37% and 30.25%) which was also agreed with the conclusions made by Kumar *et al*. (2018).

Genotypic coefficient of variation and Phenotypic coefficient of variation were quite high for yield per vine, number of fruits per vine, number of nodes upto first male flower, average fruit weight and percent of fruist setting indicating that there is greater scope for selection for improvement of these characters (Table 2). These findings are in confirmation with Uddin (2008) Pathak *et al*. (2014) and Kumar *et al*. (2018) in pumpkin. Contrary to the above, the traits namely total number of male flowers, total number of female flowers, number of nodes upto first female flower, number of primary branches and vine length showed moderate values of PCV and GCV while for the remaining characters viz., days taken to appearance 1st female flower and internodal length, PCV and GCV values were low. Similar results have been reported by Chaudhari *et al*. (2017) in pumpkin.

Heritability

High heritability coupled with high genetic advance reveals the presence of lesser environmental influence and prevalence of additive gene actions in their expression (Panse 1957). But lower values of genetic advance indicate the prevalence of narrow range of variability, high G x E interaction or non-additive gene action. For moderate values of genetic advance, both additive and non-additive gene actions might be

responsible for the expression of traits. Heritability estimate provides information on relative magnitude of genetic and environmental variation in germplasm pool. Higher heritability was found in total number of male flowers (100%), days taken to appearance of 1st female flower (99.98%), days taken to appearance 1st male flower (99.95%), number of fruits per vine (99.82%), number of nodes upto 1st female flower (99.74%), percent of fruit setting (99.73%), total number of female flowers (99.71%), yield per vine (99.42%), number of nodes upto 1st male flower (99.42%), average fruit weight (99.18%), internodal length (95.82%), vine length (94.25%), and number of primary branches (91.18%). Similar results have also been reported by Rana (1982).

Genetic advance

Higher GAM was found in yield per vine (103.9%), number of fruits per vine (87.89%), number of nodes upto 1st male flower (83.23), percent of fruit setting (81.66%), total number of male flowers (59.79%), total number of female flowers (55.17%), days to 1st fruit harvest (11.28%), number of nodes upto 1st female flower (41.35%), number of primary branches(35.42%), vine length (30.63), days taken to appearance 1st male flower (21.40%) and days taken to appearance 1st female flower (17.92%). These observed high to moderate estimates of GAM are indicative of the fact that improvement could be quickly achieved in these characters through selection.

High heritability coupled with high genetic advance over percent mean was observed for the characters yield per vine (103.39%), number of fruits per vine (87.89%) and percent of fruit setting (81.66%) these characters are under the control of additive genes and phenotypic selection for these characters may be effective. These results are in agreement with the results obtained in pumpkin by Muralidhara *et al.* (2014) and Ahmed *et al.* (2018).

CONCLUSION

Based on the obtained results from the present investigations, it can be concluded that, the genotypes studies showed a fair amount of genetic variability. The difference between the PCV and GCV is less which indicates less influence of environment on the expression of these traits, which favors direct selection based on phenotypic performance for further improvement of the genotypes. Most of the traits observed high heritability coupled with high genetic advance. Hence, these traits can be considered ideal for improvement through selection.

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