Indian Journal of Agricultural Sciences **87** (11): 1519–23, November 2017/Article
https://doi.org/10.56093/ijas.v87i11.75740

Heritability, correlation and genetic divergence for different seed traits in pumpkin (*Cucurbita moschata*)

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Received: 12 January 2017; Accepted: 27 July 2017

ABSTRACT

Seed is the very important input factor in any crop production programme as the success or failure of any crop mainly depends on the quality of seed. The present investigation was carried out to estimate the extent genetic variability, character association and divergence for seed yield and related traits in 76 genotypes of pumpkin (*Cucurbita moschata* Duchesne ex Poir). The experimental results revealed significant differences among the genotypes for all the traits under study. On the basis of mean performance for different seed traits, the genotypes DPU-6, DPU-51-3, DPU-57 and DPU-24 were found most promising. Further, high heritability estimates coupled with high genetic gain were observed for all the seed traits under study, which indicated that these traits are under additive gene effects and are more reliable for effective selection. The maximum PCV and GCV were observed for seed yield/plant (g) followed by 100 seed weight (g), seed area (mm^2) reflecting presence of high genetic variability among all the genotypes for studied characters. Further, the experimental results revealed that seed area followed by seed yield per plant and 100 seed weight had maximum positive direct effect on fruit yield per plant. The maximum positive indirect effect of seed breadth, seed length, 100 seed weight and seed yield/plant via seed area was observed on fruit yield per plant. The genetic divergence observed among seventy six diverse genotypes of pumpkin revealed considerable diversity for seed traits. In the present investigation, the cluster I and cluster IV were found more divergent (9.864) and have chances of getting transgressive segregants in F_2 from crossing of genotypes from cluster I and cluster IV. Therefore, hybridization between these groups can be very effective for improvement of seed yield in pumpkin.

Key words: Correlation, Clusters, *Cucurbita moschata*, D^2 analysis, Genetic diversity, Path analysis, Seed traits.

Pumpkin (*Cucurbita moschata* Duchesne ex Poir.) is one of the important cucurbitaceous vegetable crops native to Northern and Southern America. Out of 27 species under the genus *Cucurbita*, five are in cultivation. Pumpkin is eaten either as immature or mature form. In India, the flowers, leaves, and vine tips of *Cucurbita* are also consumed. Pumpkin is relatively high in energy, carbohydrates and a good source of carotenoid pigments and minerals (Pandey *et al*. 2003). Seeds of pumpkin are consumed throughout the world as snacks but the commercial market for pumpkin seeds is still relatively small (Cascio 2007). Seeds can be eaten whole, roasted, or toasted, and are a good source of pharmacological activities such as anti-diabetics (Li *et al*. 2003), antifungal (Wang and Ng 2003), antibacterial and anti-inflammation activities (Fu *et al*. 2006) and antioxidant effects (Nkosi *et al*. 2006) and also used for the treatment of benign prostatic hyperplasia (Dvorkin and Song 2002). Pumpkin seeds contain omega-3 and -6 essential fatty acids, essential nutrients for normal mental health. The seed oil is edible and be used for cooking. So, there is an immense need to screen out the available pumpkin germplasm to select the superior genotypes having high seed quality attributes. Therefore, the present investigation was carried out to analyze genotypic variation among seeds of 76 pumpkin genotypes.

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MATERIALS AND METHODS

The present investigation was carried out at the Research Farm and Laboratories of Division of Vegetable Science, ICAR-Indian Agricultural Research Institute, New Delhi during the spring-summer season of the year 2014. The experimental material for the present study consisted of 76 promising and diverse genotypes of pumpkin including four check varieties viz., DPU-1, DPU-2, DPU-3, DPU-4, DPU-4-2, DPU-5, DPU-5-2, DPU-5-3, DPU-6, DPU-8, DPU-8-2, DPU-9, DPU-10, DPU-15, DPU-16, DPU-17,

DPU-18, DPU-19, DPU-20-2, DPU-21, DPU-21-3, DPU-22, DPU-22-3, DPU-23, DPU-24, DPU-25, DPU-26, DPU-27, DPU-28, DPU-29, DPU-30, DPU-31, DPU-32, DPU-33, DPU-35, DPU-36, DPU-41, DPU-42, DPU-43, DPU-44, DPU-45, DPU-46, DPU-51, DPU-51-3, DPU-52, DPU-53, DPU-54, DPU-56, DPU-57, DPU-58, DPU-59, DPU-60, DPU-61, DPU-62, DPU-63, DPU-64, DPU-64-2, DPU-65, DPU-66, DPU-67, DPU-68, DPU-69, DPU-70, DPU-71, DPU-72, DPU-73, DPU-74, DPU-75, DPU-76, DPU-77, DPU-79, DPU-80, CM-350 (check), Kashi Harit (check), Pusa Vishwas (check) and Punjab Samrat (check) collected from different parts of the country and maintained at Division of Vegetable Science, Indian Agricultural Research Institute (IARI), New Delhi. The seeds of 76 genotypes of pumpkin were sown in plug-trays and seedlings transplanted in the field during spring-summer season of 2014 for comparative evaluation on various seed traits.The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications of each genotype. Two to three seeds of each genotype were sown in the hills on the ridges at a spacing of 3.5 m × 60 cm. The standard cultural practices as mentioned in Package of Practices for Vegetable Crops (Thamburaj and Singh 2004) were followed to raise the healthy crop stand. Seed length (mm), seed breadth (mm) and seed area (mm^2) were measured by flat bed scanner software "Grain Analyser" developed by Dr. Nachiket Kotwaliwale, ICAR-CIAE, Bhopal, Madhya Pradesh. 100 seed weight (g) measured by 100 randomly selected mature seeds at 8-10 per cent (air dry) seed moisture content was recorded with the help of electronic balance. Seed yield/plant (g) was recorded as mean weight of seeds on five randomly selected plants.

The observations on various seed traits were recorded from five randomly selected plants per replication for each genotype after seed extraction and air drying of seeds up to 8-10 per cent moisture. The mean values of data recorded for different traits were subjected to analysis of variance (Gomez and Gomez 1983) for RCBD using MS Excel-2007 worksheet. The Genotypic and Phenotypic Coefficients of variability (GCV and PCV) were calculated as per formulae (Burton and De-Vane 1953). Heritability in broad sense and genetic advance were calculated by using the formulae (Allard 1960). Genetic gain expressed as per cent ratio of genetic advance and population mean was calculated by the method given by Johnson *et al*. (1955). The genotypic and phenotypic correlations were calculated as per Al-Jibouri *et al*. (1958) by using SPAR 3.0 software (Anonymous 2012). The direct and indirect paths were obtained by following Dewey and Lu (1959). The genetic divergence was estimated by using (Mahalanobis 1936) D^2 statistics as per the Tocher's method described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance indicated significant differences among the genotypes for all the studied traits. The genetic parameter of variability, heritability and expected genetic advance over mean for seed yield and related traits is shown in Table 1.

Highly significant differences were observed among all the genotypes for seed length. It ranged from 14.29 to 18.99 mm with a population mean of 16.20 mm (Table 1). The perusal of data pertaining to seed breadth revealed highly significant variations and ranged from 6.94 to 10.03 mm with general population mean of 8.46 mm. Seed area ranged from 72.22 to 133.77 mm^2 and general mean recorded for this trait was 98.73 mm^2 (Table 1). Lebeda *et al*. (2010) and Mladenovic *et al*. (2012) had also reported significant variations for the above traits. The observations pertaining to 100-seed weight revealed significant variations (6.88-24.61g). The general populations mean recorded for trait was 13.46 g. Analysis of variance indicated the highly significant difference among all the genotypes for the traits under study (Table 1). Similarly high variations were recorded for seed yield per plant in all the genotypes under study (13.55-106.35 g) with general population mean of 51.86 g (Table 1). Earlier workers like Selvi *et al*. (2012) and Cyril *et al*. (2014) had reported the similar variations for 100-seed weight and seed yield per plant in pumpkin.

The differences among PCV and GCV for most of the traits are small indicating the greater role of genetic factors in their expression with less influence of environmental factors offering great scope for improvement.The phenotypic (PCV) and genotypic coefficient of variation (GCV) ranged from 6.78 to 41.46 and 6.02 to 39.86 per cent, respectively (Table 1). The maximum PCV and GCV were observed for seed yield/ plant (g) (41.46 and 39.86) followed by 100

Table 1 Estimates of phenotypic and genotypic coefficients of variability, heritability and genetic gain for seed yield and related traits in pumpkin

Trait	Range	Mean ± SE(d)	Coefficients of variability (%)		Heritability (%)	Genetic gain (%)
			Phenotypic	Genotypic		
Seed length (mm)	14.29-18.99	16.20 ± 0.41	6.78	6.02	79.00**	11.05**
Seed breadth (mm)	6.94-10.03	8.46 ± 0.25	8.73	7.94	82.70**	14.89**
Seed Area (mm^2)	72.22-133.37	98.73 ± 4.87	14.34	13.01	82.30**	24.31**
100 seed weight (g)	6.88-24.61	13.46 ± 0.97	19.09	16.94	78.70**	30.98**
Seed yield/plant (g)	13.55-106.35	51.86 ± 4.83	41.46	39.86	92.40**	78.90**

**Significant at 1% level of significance; df, degrees of freedom seed weight (g) (19.09 and 16.94), seed area (mm^2) (14.34 and 13.01) reflecting presence of high genetic variability among all the genotypes for studied characters, respectively. The present findings pertaining to different estimates of phenotypic and genotypic coefficient of variation are in line with the results of earlier workers like Pandey *et al*. (2008) and Akter *et al*. (2013). Heritability estimates were found higher for the characters viz. seed yield/ plant (g), seed breadth (mm), seed area (mm^2) while it was observed to be moderate for seed length (mm) and 100 seed weight (g). High to moderate heritability coupled with high to low genetic gain were observed for seed yield/ plant (g), 100 seed weight (g), seed area (mm^2), seed breadth (mm) and seed length (mm) indicating the prevalence of additive gene effect which in turn offers good scope for effective selection. Similar results were also reported by Akter *et al*. (2013) for traits under study.

The present investigation on correlation studies was carried out for yield and its component traits, to find out those traits on the basis of which selection will be more effective. Generally, genotypic correlation coefficients were higher in magnitude than phenotypic correlation coefficients (Table 2). The correlation coefficient studies showed that fruit yield per plant (kg) had significantly positive correlation with seed yield per plant (g), 100 seed weight (g), seed area (mm^2), seed breadth (mm) and seed length (mm). Seed length had highly significant and positive correlation with seed area (mm^2) followed by seed breadth (mm), 100 seed weight (g) and seed yield per plant (g). Seed breadth showed positive correlation with seed area (mm^2), 100 seed weight (g) and seed yield per plant (g). Likewise, 100 seed weight (g) had a positive correlation with seed yield per plant (g). Significant positive correlation of 100 seed weight with yield per vine or plant was also reported by Maheswari and Babu (2006) and Shivananda *et al*. (2013). Further, Yadav *et al*. (2006) had also reported significant positive correlation of 100 seed weight, seed length and seed width with fruit weight in pumpkin.

Table 2 Phenotypic and genotypic coefficients of correlation among different seed traits on fruit yield per plant in pumpkin

Trait		1	2	3	4	5	6
1	P	1.00	0.760**	0.909**	0.299**	0.216**	0.146*
	G	1.00	0.782**	0.917**	0.288**	0.244**	0.161*
2	P		1.00	0.948**	0.314**	0.237**	0.282**
	G		1.00	0.955**	0.362**	0.285**	0.335**
3	P			1.00	0.318**	0.195**	0.228**
	G			1.00	0.336**	0.228**	0.262**
4	P				1.00	0.420**	0.363**
	G				1.00	0.412**	0.370**
5	P					1.00	0.485**
	G					1.00	0.482**
6	P						1.00
	G						1.00

*Significant at 5% level of significance; P, phenotypic coefficients of correlation; **Significant at 1% level of significance; G, genotypic coefficients of correlation; 1, seed length (mm); 2, seed breadth (mm); 3, seed area (mm^2); 4, 100 seed weight (g); 5, seed yield/plant (g); 6, fruit yield/plant (kg)

The data on path coefficient analysis at genotypic level showing the direct and indirect effects of significant traits over fruit yield/plant have been presented in Table 3. The experimental results revealed that seed area, followed by seed yield/plant and 100 seed weight had maximum positive direct effect on fruit yield/plant, while significant negative direct effect of seed length and seed breadth was noted on fruit yield/plant. Further, maximum positive indirect effect of seed breadth, seed length, 100 seed weight and seed yield/ plant via seed area, and maximum negative indirect effect of seed area, seed breadth, 100 seed weight and seed yield/ plant via seed length was observed on fruit yield/plant. The present study confirms the findings of Maheswari and Babu (2006), who had reported the high positive direct effect of 100 seed weight on fruit yield.

On the basis of D^2 analysis, seventy six diverse genotypes of pumpkin were clustered into 4 different clusters as presented in Table 4. Maximum number of genotypes were accommodated in the cluster III (34), followed by cluster I (18), cluster II (12) and cluster IV (2).

Average inter- and intra-cluster divergence (D^2) values have been presented in the Table 5. The diagonal figures in the table represent the intra-cluster distances. Maximum intra cluster distance was observed in cluster IV (4.165) while minimum was in cluster III (3.239). Highest inter-cluster distance (9.864) was recorded between cluster I and cluster IV while lowest (3.222) was observed between cluster I and cluster III.

The cluster means for various seed traits have been presented in the Table 6. Highest seed length was observed in cluster II, followed by cluster III, cluster I and cluster IV whereas seed breadth was found to be superior in cluster II (8.77), followed by cluster III, cluster I and cluster IV. Seed yield/plant was recorded maximum in cluster IV (60.97), followed by cluster II, cluster III and cluster I. Fruit yield per

Table 3 Estimates of direct and indirect effects of different seed traits on fruit yield per plant in pumpkin

Trait	1	2	3	4	5	6
1	-0.635	-0.084	0.734	0.043	0.103	0.161
2	-0.497	-0.108	0.765	0.054	0.121	0.335
3	-0.582	-0.103	0.801	0.050	0.096	0.262
4	-0.183	-0.039	0.269	0.149	0.175	0.370
5	-0.155	-0.031	0.182	0.061	0.424	0.482

Residual effect: 0.66888. Diagonal figures represent the direct effect. 1, seed length (mm); 2, seed breadth (mm); 3, seed area (mm^2); 4, 100 seed weight (g); 5, seed yield per plant (g); 6, Genotypic correlation coefficient for fruit yield/plant (kg)

Table 4 Clustering pattern of seventy six genotypes of pumpkin on the basis of genetic divergence for seed traits

Cluster	Number of genotypes	Genotypes
I	18	DPU-2, DPU-3, DPU-4-2, DPU-5, DPU-19, DPU-21-3, DPU-31, DPU-32, DPU-45, DPU-65, DPU-66, DPU-67, DPU-70, DPU-77, CM-350, Kashi Harit, Pusa Vishwas, Punjab Samrat
II	12	DPU-15, DPU-22-3, DPU-23, DPU-24, DPU-26, DPU-28, DPU-42, DPU-44, DPU-45, DPU-51-3, DPU-52, DPU-53, DPU-56, DPU-57, DPU-58, DPU-62, DPU-64, DPU-68, DPU-71, DPU-73, DPU-79, DPU-80
III	34	DPU-1, DPU-4, DPU-5-2, DPU-5-3, DPU-8, DPU-8-2, DPU-9, DPU-10, DPU-16, DPU-17, DPU-18, DPU-20-2, DPU-21, DPU-22, DPU-25, DPU-27, DPU-29, DPU-30, DPU-33, DPU-35, DPU-36, DPU-41, DPU-43, DPU-46, DPU-54, DPU-59, DPU-60, DPU-61, DPU-63, DPU-64-2, DPU-69, DPU-72, DPU-74, DPU-76
IV	2	DPU-6, DPU-75

Table 5 Average intra-cluster and inter-cluster distance (D^2) among seventy six pumpkin genotypes based on seed traits

Cluster	I	II	III	IV
I	3.637			
II	5.607	3.951		
III	3.222	3.267	3.239	
IV	9.864	6.360	7.705	4.165

Table 6 Cluster means for different seed traits in seventy six genotypes of pumpkin

Trait	Clusters			
	I	II	III	IV
100 seed weight (g)	12.58	14.53	13.18	14.46
Seed length (mm)	15.83	16.54	16.24	15.06
Seed breadth (mm)	8.08	8.77	8.49	8.03
Seed yield/plant (g)	37.99	57.36	55.10	60.97
Fruit yield/plant (kg)	3.05	5.95	4.82	8.68

plant was highest in cluster IV (8.68), followed by cluster II, cluster III and cluster I. Earlier workers like Balkaya *et al*. (2010), Borges *et al*. (2011), Shivananda *et al*. (2013), Muralidhara *et al*. (2014) and Yu *et al*. (2014) had also indicated the significance of genetic divergence in pumpkin.

From the present investigation, it can be concluded that four genotypes, viz. DPU 6, followed by DPU 51-3, DPU 57 and DPU 24 recorded higher fruit yield and also performed better for various seed traits. High heritability estimates coupled with high genetic gain were observed for seed yield/plant therefore this trait is more reliable for effective selection. High to moderate heritability coupled with high to low genetic gain were observed for seed yield/plant (g), 100 seed weight (g), seed area (mm^2), seed breadth (mm) and seed length (mm) indicating the prevalence of additive gene effect which in turn offers good scope for effective selection. The fruit yield per plant had significantly positive association with seed length, seed breadth, seed area, 100 seed weight and seed yield/plant indicating that these traits can be taken into consideration, while making the selection for yield and quality improvement in pumpkin. Seed area, seed yield/plant and 100 seed weight have maximum positive direct effect on marketable fruit yield/plant. Further, maximum positive indirect effects of seed breadth, seed length, 100 seed weight and seed yield/plant via seed area, thereby indicating the importance of these traits for yield and quality improvement in pumpkin through direct or indirect selection. For the traits, where selection is not effective, genetic divergence can play an important role on further partitioning of variability. In the present investigation, the cluster I and cluster IV were found more divergent for all seed traits. Hence, there will be more chances of getting transgressive segregants in F_2 generations from the crossing of genotypes from cluster I and cluster IV. Therefore, hybridization between the genotypes of these groups can be very effective for further improvement in pumpkin.

ACKNOWLEDGEMENT

Arvind Nagar is thankful to the ICAR, New Delhi for providing JRF. Authors are grateful to Director, ICAR-IARI for providing necessary facilities for this study.

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