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Research Article

# Characterization of pumpkin (*Cucurbita moschata* Duch. Ex. Poir.) germplasm through genetic variability, heritability and genetic advance

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**Abstract**
Twenty five pumpkin germplasm from the north eastern region were evaluated for twenty traits for the genetic variability, heritability and genetic advance. The results revealed that analysis of variance showed that there was a highly significant variation for all of the considered characters. In the present investigation, PCV was recorded higher than the GCV for all the characters indicating the considerable modifying effect of environment in the expression of all characters studied. The highest PCV and GCV was observed for vitamin A (PCV=86.27%, GCV=86.23%) followed by cavity length (PCV=35.52%, GCV=34.24%) and 100 seed weight (PCV=30.04%, GCV=29.37%). The maximum estimate of heritability (in the broad sense) recorded for vitamin A (100%) followed by cavity length (98%), carbohydrates (98%), 100 seed weight (96%) and fruit yield per plant (95%). The highest genetic advance as per cent of mean was observed for the characters vitamin A followed by cavity length, 100 seed weight and fruit yield per plant. Therefore, keeping the above point of view the genotypes could be select for the further breeding programme.

**Key words**
Variability, GCV, PCV, heritability, vitamin A content and genetic advance

## INTRODUCTION

Pumpkin (*Cucurbita moschata* Duch. Ex. Poir.) is the sexual propagated monoecious climbing vegetable (Mohsin *et al*., 2017) that belongs to the genus *Cucurbita* of the order Cucurbitales, family Cucurbitaceae, with chromosome number 2n= 40 (Martins *et al.,* 2015). Pumpkin is also known as Kashiphal or Sitaphal or Kaddu (Rana 2014). The primary centers of origin and domestication for cultivated *Cucurbita* species can be identified in various areas in Central and South America (Jeffrey, 1990) and the first domestication of *Cucurbita* dates back 8,000 to 10,000 years ago (Sanjur *et al*., 2002). It can grow well under various agro-ecological zones (Kiramana *et al*., 2017). Pumpkin is comparatively high in energy and carbohydrates, vitamins and minerals, especially rich in carotenoid pigments (Bose and Som, 1998).

North East India exhibits wide variability constitutes 8 states *viz*., Arunachal Pradesh, Assam, Manipur, Meghalaya, Mizoram, Nagaland, Sikkim and Tripura (Mena *et al.,* 2019). The region has mystic splendours and rich cultural tradition. It is widespread between 89.46° to 97.30° East longitude and 21.57° to 29.30° North latitude. The entire northeastern region is at a low level of economic development although it has a marvellous possibility to develop. Horticulture has been the most important sector in the region which is playing a significant role in determining the varying nature of agro-economic activities (Bhatt and Bujarbaruah, 2005).

The region has the highest accessibility to natural resources in the country. It is one of the 12 mammoth centers of biodiversity in the world (Arisdason and Lakshminarasimhan, 2016). The region has abundant potential for horticultural based systems. Genetic diversity within germplasm and populations of *Cucurbita* is high,

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including variation in shape, size and colour of fruits; the number and size of seeds; quality, colour and thickness of fruit flesh (Hernandez *et al.,* 2005) so that can be utilized in the breeding programme and by this way we can simply fulfil the gap by developing high yielding hybrid variety. Moreover, consideration based on the superiority and quality aspects of fruits is very inadequate in NER in India. So it is required for a breeder to develop high yielding as well as high quality varieties through selection (Akter *et al.,* 2013).

Availability of genetic diversity is a pre-requisite for any crop improvement programme. Genetic resources are a basic foundation block in any crop improvement programme (Suma *et al.,* 2019). These include a wide range of available genetic variability in the form of landraces, traditional cultivars, putative ancestor form, primitive cultivars, wild relatives' forms and related non-edible wild weedy species (Swarup, 2014). Genetic diversity has been considered as a requirement for obtaining high yielding progenies through the hybridization programme (Shivananda *et al*., 2013).

Heritability and genetic advance or genetic gain help in determining the influence of environment in expression of the characters and the extent to which improvement is potential after selection (Sultana *et al.,* 2015).

The achievement of any crop hybridization programme depends, to a large degree on the total genetic variability present in the population. Intensive efforts are needed particularly in the assortment of greater pumpkin genotypes because there is a wide genetic variability present in the existing genotypes (Aliu *et al.,* 2011). Therefore, the present study was undertaken to carry out the genetic variability, heritability, genetic advancement, diversity involvement of these traits towards the yield of pumpkin genotypes.

## MATERIALS AND METHOD

The experiment was conducted at Vegetable Research Farm, College of Horticulture and Forestry, (CAU) Pasighat, East Siang, Arunachal Pradesh, to study the characterization of pumpkin (*Cucurbita moschata* Duch. Ex. Poir.) germplasm through genetic variability, heritability and genetic advance in the northeastern state, India which is collected from the different states of northeast state (**Table 1**). The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Five seeds per replication were sown with a spacing of 3 x 1.3 m between row to row and plant to plant, respectively. The standard cultural practices as mentioned in the package of practices were followed to raise the healthy crop (Thamburaj and Singh, 2004).

For studying different genetic parameters and inter-relationships, twenty characters were taken into consideration. The mean values of data recorded for different traits were subjected to analysis of variance (Gomez and Gomez, 1984). The Genotypic Coefficients of variability and Phenotypic Coefficients of variability (GCV % and PCV %) were designed as per procedure (Burton and De-Vane, 1953) and the standards were categorized as low (0-10%), moderate (10-20%) and high (20% and above) as recommended by Sivasubramanian and Menon (1973). Heritability was considered using the prescription given by Singh and Chaudhary, (1985) and classified as low (0-30 %), moderate (30-60 %) and high (60 % and above) as agreed by Robinson *et al.* (1949). Genetic advance as a percentage of mean was calculated by the procedure given by Johnson *et al.* (1955), and the values were categorized as low (0-10 %), moderate (10-20 %) and high (more than 20 %).

## RESULTS AND DISCUSSION

The analyses of variance revealed that there is a significant variation was observed among the traits in the germplasm. Genotypic, phenotypic and error variance, and Genotypic Coefficient of Variation (GCV %), and Phenotypic Coefficient of Variation (PCV %), heritability (%), genetic advance (GA), in per cent of the mean are presented in **Table 2.** Phenotypic Coefficient of Variation (PCV) was advanced than the subsequent Genotypic Coefficient of Variation (GCV) for all the characters under study (Sultana *et al*., 2015). The ecological difference of the above behavior was observed to be very low representing that the environment had a very slight outcome on the observed phenotypic variation of the traits. These would also propose that the above traits have wide variation and improvement can be achieved through the obligation of selection on the behavior. The same result was reported by Aruah *et al.* (2010).

The perusal of the statistics presented in **Table 2** indicates that phenotypic coefficients of variability were moderately higher in degree than their subsequent genotypic coefficients of variability for all the characters. The highest estimates of phenotypic (PCV) and genotypic (GCV) coefficient of variation were observed for vitamin A (PCV=86.19%, GCV=86.12%) followed by cavity length (PCV=35.52%, GCV=34.24%), 100 seed weight (PCV=30.04%, GCV=29.37%), the number of seeds per fruit (PCV=26.09%, GCV=24.09%), node bearing first staminate flower (PCV=25.60%, GCV=18.36%), total fruit yield q/ha (PCV=24.74%, GCV=23.38%), average fruit weight (PCV=24.42%, GCV=22.16%), fruit yield per plant (PCV=24.22%, GCV=23.58%), the number of fruits per plant (PCV=24.07%, GCV=22.87%), flesh thickness (PCV=23.53%, GCV=20.16%) and Carbohydrate (PCV=20.97%, GCV=20.77%) However, the moderate estimates of PCV and GCV were recorded in case of total soluble solids (PCV=18.84%, GCV= 10.26%) followed by vine length (PCV=17.50%, GCV= 15.19%), equatorial circumference (PCV=16.89%, GCV=16.49%), the number of primary branches (PCV=15.25%, GCV=11.39%), node bearing first staminate flower (PCV=11.63%, GCV=5.76%) and polar circumference (PCV=11.63%, GCV=10.81%). The lowest estimates of PCV and GCV were recorded in case of days to first fruit harvest (PCV=6.580%, GCV= 5.88%), days to first staminate flower anthesis (PCV=4.32%, GCV=3.76%) and days to first staminate flower anthesis (PCV=3.15%, GCV= 2.30%).

**Table 1. Genotypes with their sources of collection**

| S. No. | Genotypes | Source | Coordinates of the places |
|---|---|---|---|
| 1. | CHFPUM-1 | A Landrace of Pasighat, Arunachal Pradesh | 28.07˚ N, 95.33˚ E |
| 2. | CHFPUM-2 | A landrace of Pasighat, Arunachal Pradesh | 28.07˚ N, 95.33˚ E |
| 3. | CHFPUM-3 | A landrace of Pasighat, Arunachal Pradesh | 28.07˚ N, 95.33˚ E |
| 4. | CHFPUM-4 | A landrace of Pasighat, Arunachal Pradesh | 28.07˚ N, 95.33˚ E |
| 5. | CHFPUM-5 | A landrace of Pasighat, Arunachal Pradesh | 28.07˚ N, 95.33˚ E |
| 6. | CHFPUM-6 | A landrace of Pasighat, Arunachal Pradesh | 28.07˚ N, 95.33˚ E |
| 7. | CHFPUM-7 | A landrace of IIVR,Varanasi (U.P.) | 25.28˚ N, 82.96˚ E |
| 8. | CHFPUM-8 | A landrace of Pasighat, Arunachal Pradesh | 28.07˚ N, 95.33˚ E |
| 9. | CHFPUM-9 | A landrace of Pasighat, Arunachal Pradesh | 28.07˚ N, 95.33˚ E |
| 10. | CHFPUM-10 | A landrace of Ziro, Arunachal Pradesh | 27.56˚ N, 93.83˚ E |
| 11. | CHFPUM-11 | A landrace of Aizawal Mizoram | 23˚43’38” N, 92˚43’4” E |
| 12. | CHFPUM-12 | A landrace of Aizawal Mizoram | 23˚43’38” N, 92˚43’4” E |
| 13. | CHFPUM-13 | A landrace of Aizawl Mizoram | 23˚43’38” N, 92˚43’4” E |
| 14. | CHFPUM-14 | A landrace of Aizawl Mizoram | 23˚43’38” N, 92˚43’4” E |
| 15. | CHFPUM-15 | A landrace of Imphal, Manipur | 24.80˚ N, 93.93˚ E |
| 16. | CHFPUM-16 | A landrace of Imphal, Manipur | 24.80˚ N, 93.93˚ E |
| 17. | CHFPUM-17 | A landrace of Imphal, Manipur | 24.80˚ N, 93.93˚ E |
| 18. | CHFPUM-18 | A landrace of Gangtok Sikkim | 27.33˚ N, 88.62˚ E |
| 19. | CHFPUM-19 | A landrace of Gangtok Sikkim | 27.33˚ N, 88.62˚ E |
| 20. | CHFPUM-20 | A landrace of Kohima Nagaland | 25.67˚ N, 94.10˚ E |
| 21. | CHFPUM-21 | A landrace of Kohima Nagaland | 25.67˚ N, 94.10˚ E |
| 22. | CHFPUM-22 | A landrace of Kohima Nagaland | 25.67˚ N, 94.10˚ E |
| 23. | CHFPUM-23 | A landrace of NDUAT, Faizabad (U.P.) | 26.77˚ N, 82.14˚ E |
| 24. | CHFPUM-24 | A landrace of Agartala, Tripura | 23.84˚ N, 88.62˚ E |
| 25. | CHFPUM-25 | A landrace of Agartala, Tripura | 23.84˚ N, 88.62˚ E |

Heritability estimates ranged from 100 to 25 per cent. In this investigation, higher heritability estimates were recorded for vitamin A (100%) followed by cavity length (98.00%), carbohydrates (98%), 100 seed weight (96%), fruit yield/plant (95%), the number of fruit/plant (90%), total fruit yield q/hectare (89%), polar circumference (86%), equatorial circumference (68%), the number of seed/fruit (85%), flesh thickness (84%), days to first fruit harvest (82%), average fruit weight (82%), days to first staminate flower anthesis (76%) and vine length (75%). Genetic advance or genetic gain was high for carbohydrate (203.95) followed by the number of seed/fruit (108.65) and total fruit yield q/ha (99.12). However, the equatorial circumference (18.86), polar circumference (12.18) and vitamin A (11.86) showed moderate genetic advance.

Genetic advance or genetic gain expressed as a percentage of the mean. The genetic gain was recorded higher for vitamin A (177.27%) followed by cavity length (69.98%), 100 seed weight (59.17%), fruit yield/plant (47.36%), the number of seed/fruit (45.82%), total yield q/hectare (45.50%), the number of fruit/plant (44.73%), carbohydrate (42.38%), average fruit weight (41.28%), flesh thickness (40.88%), equatorial circumference (33.33%), vine length (27.12%) and polar circumference (20.70%). However, the number of primary branches (17.53%), node bearing first staminate flower (14.07%), total soluble solid (12.06%) and days to first harvest (10.95%) showed a moderate genetic gain.

The high genotypic coefficient of variation (GCV) was observed for vitamin A, cavity length, 100 seed weight, the number of seeds/fruit, node bearing first staminate flower, total fruit yield, average fruit weight, fruit yield/plant number of fruit/plant, flesh thickness and carbohydrates. Variability among all the genotypes for these characters for making further improvement by selection. These outcomes were in conformity with Sultana *et al.* (2015), Kumar *et al.* (2011), Srikanth *et al.* (2017); Shrikant *et al.* (2017) and Kumar *et al*. (2017). However, the moderate GCV was recorded in case of total soluble solids, vine length equatorial circumference, node bearing first staminate flower and polar circumference. The estimates of these parameters are in line with the result of

Kumar *et al.* (2011), Shrikant *et al.* (2017) and Kumar *et al*. (2017). The lowest estimates of GCV were recorded in case of days to first harvest, days to first pistillate flower anthesis and days to first staminate flower anthesis. The estimates of these parameters are in line with the result of Kumar *et al.* (2011), Shrikant *et al.* (2017) and Kumar *et al*. (2017) and Wide variability present in experimental materials suggested that there are ample scopes for bringing out improvement in these characters.

**Table 2. Estimation of genetic parameters in 25 genotypes in pumpkin**

| S.No. | Characters | Mean ± SE(m) | Range | | Variance (%) | | Coefficient of variability (%) | | Heritability % | Genetic advance (GA) | GA as % of mean |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | Mini. | Max. | Phenotypic | Genotypic | PCV | GCV | | | |
| 1. | Vine length (m) | 7.63±0.38 | 6.36 | 11.36 | 1.78 | 1.34 | 17.50 | 15.19 | 75 | 2.07 | 27.13 |
| 2. | Number of primary branches | 10.95±0.64 | 8.06 | 13.63 | 2.77 | 1.54 | 15.25 | 11.39 | 56 | 1.92 | 17.53 |
| 3. | Days to first staminate flower anthesis | 61.27±0.74 | 58.53 | 63.50 | 3.68 | 2.04 | 3.15 | 2.30 | 54 | 2.17 | 3.54 |
| 4. | Days to first pistillate flower anthesis | 65.22±0.79 | 62.00 | 70.73 | 7.93 | 6.02 | 4.32 | 3.76 | 76 | 4.40 | 6.75 |
| 5. | Node bearing first staminate flower | 4.04±0.41 | 2.73 | 6.33 | 1.07 | 0.55 | 25.60 | 18.36 | 51 | 0.57 | 14.06 |
| 6. | Node bearing first staminate flower | 12.32±0.71 | 10.43 | 14.33 | 2.05 | 0.50 | 11.63 | 5.76 | 25 | 0.72 | 5.84 |
| 7. | Days to first fruit harvest | 86.90±1.38 | 70.20 | 103.33 | 31.88 | 26.12 | 6.50 | 5.88 | 82 | 9.53 | 10.97 |
| 8. | Number of fruits per plant | 2.66±0.12 | 1.43 | 3.73 | 0.41 | 0.37 | 24.07 | 22.87 | 90 | 1.19 | 44.74 |
| 9. | Polar circumference (cm) | 58.83±1.45 | 41.93 | 68.93 | 46.83 | 40.46 | 11.63 | 10.81 | 86 | 12.18 | 20.70 |
| 10. | Equatorial circumference (cm) | 56.57±1.05 | 33.93 | 78.30 | 90.38 | 87.04 | 16.89 | 16.49 | 86 | 18.86 | 33.34 |
| 11. | Flesh thickness (cm) | 3.40±0.19 | 2.33 | 5.16 | 0.64 | 0.54 | 23.53 | 20.16 | 84 | 1.39 | 40.88 |
| 12. | Cavity length (cm) | 11.76±0.30 | 5.93 | 23.56 | 16.48 | 16.28 | 35.52 | 34.24 | 98 | 8.23 | 69.98 |
| 13. | Number of seed per fruit | 237.12±13.1 | 134.33 | 401.10 | 3827.44 | 3263.08 | 26.09 | 24.09 | 85 | 108.65 | 45.82 |
| 14. | 100 seed weight (g) | 8.94±0.33 | 4.77 | 14.57 | 7.21 | 6,89 | 30.04 | 29.37 | 96 | 5.29 | 59.17 |
| 15. | Average fruit weight (kg) | 2.18±0.13 | 1.37 | 3.00 | 0.28 | 0.23 | 24.42 | 22.16 | 82 | 0.90 | 41.28 |
| 16. | Fruit yield per plant (kg) | 5.13±0.16 | 2.83 | 7.37 | 1.54 | 1.46 | 24.22 | 23.58 | 95 | 2.43 | 47.37 |
| 17. | Total fruit yield per hectare (q) | 219.16±10.18 | 121.7 | 314.77 | 2904.11 | 2592.90 | 24.74 | 23.38 | 89 | 99.12 | 45.50 |
| 18. | Total soluble solids ($^0$Brix) | 6.96±0.63 | 4.67 | 8.67 | 1.72 | 0.51 | 18.84 | 10.26 | 30 | 0.84 | 12.07 |
| 19. | Carbohydrates (mg/100g) | 481.14±7.90 | 126.00 | 559.50 | 10172.62 | 9985.36 | 20.97 | 20.77 | 98 | 203.95 | 42.39 |
| 20. | Vitamin A (mg/100g) | 6.63±0.11 | 0.52 | 14.57 | 33.21 | 33.18 | 86.27 | 86.23 | 100.00 | 11.86 | 177.28 |

Further, Johnson *et al.* (1955) reported that high heritability estimates along with high genetic gain or genetic advance were useful than heritability alone for efficient selection. Similarly, in the present experiment, the characters resembling vitamin A, cavity length, carbohydrates, 100 seed weight, fruit yield per plant, the number of fruit per plant, total fruit yield, polar circumference, equatorial circumference, the number of seed per fruit, flesh thickness, average fruit weight, days to first staminate flower anthesis, and vine length, high heritability with high genetic advance or genetic gain indicated that these characters are beneath additive gene effects and hence these characters are more dependable for effective selection (Panse, 1957). These results were in conformity with Kumar *et al.* (2017), Srikanth *et al.* (2017), Mahmud *et al.* (2016). High heritability joined with a moderate genetic gain was recorded for the number of primary branches/plant, node bearing first staminate flower, total soluble solids, and days to first fruit harvest reported with Kumar *et al*. (2017).

The characters like, vitamin A, cavity length, carbohydrates, 100 seed weight, fruit yield/plant, number of fruit/plant, total fruit yield, polar circumference, equatorial circumference, flesh thickness and average fruit weight recorded high heritability accompanied with a high genetic advance which indicated that these traits are under additive gene property and hence these characters are additional dependable for useful selection. Hence, the selection on the basis of these characters will be more effective and valuable for the improvement of this crop towards yield and quality production.

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