Original Research Article

Assessment of genetic variability, heritability and genetic advance for yield and related traits in pumpkin (*Cucurbita moschata* Duch ex Poir)

Abstract

A study on pumpkin genotypes was conducted at Vegetable Research Farm of Banda University of Agriculture and Technology during the 2022 *Kharif* season. A Randomized Block Design with three replications was used to evaluate 18 pumpkin genotypes. The aims of the study were to assessing genetic variability, performance of genotypes, variation coefficients, heritability and percentage genetic advance for pumpkin genotypes.The mean sum of squares attributed to genotypes exhibited significant differences ($p < 0.01$) across all characters, indicating pronounced genetic variability. Furthermore, phenotypic (PCV) and genotypic (GCV) coefficients of variation were remarkably high for most quantitative traits male/female bud ratio(PCV=37.90% and GCV=37.65%)followedbypericarp/seedballratio(PCV=31.39%and GCV= 31.07%)fruityield(PCV=27.48%and GCV= 26.22%),vine length (PCV=22.14% and GCV=21.85%)and leaf area(PCV=20.73% and GCV=20.31%).The investigation demonstrated high heritability (h^2) and genetic advance (GA) for the majority of assessed traits namely male/female bud ratio (98.65%) followed by pericarp/seed ball ratio (98.02%), vine length(97.35%), leaf area (95.95%). The genotypes VRPK-22-04, Kashi Harit and Arka Chandan exhibited superior yield performance. Notably, VRPK-2201 and VRPK-02-07 displayed accelerated maturity and satisfactory yields, rendering them suitable cultivars for the Bundelkhand region.

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Keywords: gcv, heritability, pcv, pumpkin, variability

Introduction

Pumpkin (*Cucurbita moschata* Duchesne ex Poir.)is a vital cucurbitaceous vegetable crop native to Northern and Southern America and consisting $2n = 2x=40$ chromosome number (Martins *et al.*, 2015). Among the 27 *Cucurbita* species, five are cultivated *viz.*,*Cucurbita argyrosperma*, *Cucurbita moschata*, *Cucurbita maxima*, *Cucurbita pepo*, and *Cucurbita ficifolia*. Globally, *C. moschata*, *C. maxima* and *C. pepo* are the most widely grown species (OECD, 2016). In India, pumpkin is a versatile crop, with vine tips, leaves and flowers being consumed alongside the fruit. Pumpkin serves as a rich source of energy, carbohydrates, carotenoid pigments and essential minerals (Pandey et al., 2003).

Pumpkin exhibits distinctive morphological features, including an angular, five-ridged stem without hairs, trailing and branched vines that strike roots at nodes and deeply or shallowly lobed leaves. Fruits possess diuretic and vermifuge properties, while seeds are non-bitter, tasty and nutritious. The corolla exhibits a campanulate shape, characterized by gamopetaly and lobation. The plant's reproductive strategy involves monoecy, facilitating high levels of cross-pollination through entomophily, with each flower bearing three anthers. The term “pumpkin”originates from the Greek word “pepon,” meaning “large melon” or something round and large. Globally, China and India lead pumpkin production, followed by the U.S., Egypt, Mexico, Ukraine, Cuba, Italy, Iran and Turkey (Ferriol and Pico, 2008).In India, Madhya Pradesh is the leading state for pumpkin cultivation (NHB, 2022).

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Genetic variability is crucial for formulating effective breeding strategies to develop new vegetable varieties, particularly in pumpkin which exhibits immense potential and diversity in India. Key parameters like genotypic and phenotypic coefficient of variation, heritability, and character associations guide breeding strategies. The study assessed genetic variability in pumpkin genotypes through genotypic and phenotypic coefficients of variation, heritability, and genetic advance as a percentage of the mean for different traits. It is crucial for designing an effective breeding strategy to harness the inherent variability of a population. In a modern and industrialized vegetable industry, there is a constant need for new varieties, and germplasm serves as the foundation for their development. The extent and nature of genetic variability are fundamental for breeders in any crop improvement program. A population with greater variability increases the likelihood of successfully selecting desirable traits. Pumpkin exhibits significant potential and wide diversity in India, particularly in traits such as fruit shape, size, and yield. In light of these factors, the current study focuses on assessing the genetic variability of quantitative traits using parameters such as phenotypic and genotypic coefficients of variation, heritability and genetic advance.

Materials and Methods

The present investigation was carried out at the Instructional Farm of Department of Vegetable Science, College of Horticulture, Banda University of Agriculture and Technology, Banda, Uttar Pradesh, India during *Kharif*, 2022-23.This study was employed in Randomized Complete Block Design (RCBD) with three replications for each genotype. Seeds (2-3 per hill) of each genotypes were sown on ridges, with a spacing of 2.5m x 1m apart, following recommended agronomic practices. Data collection focused on ten quantitative traits. Mean values from five randomly selected plants per germplasm per replication were used for analysis. The analysis of variance (ANOVA) for the experimental design followed the standard procedure outlined by Panse and Sukhatme (1984). Genotypic (GCV) and Phenotypic Coefficients of Variation (PCV) were calculated using Burton and De-Vane's (1953) formulas. Heritability (broad sense) and genetic advance were computed according to Hanson et al.'s (1956) methods. Genetic gain, expressed as a percentage ratio of genetic advance to population mean, was calculated using Johnson et al.'s (1955) approach.

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Results and Discussions

Analysis of variance (ANOVA) for 18 traits revealed substantial genetic variation, partitioning total variability into genotype and residual sources. Highly significant mean squares (p <0.01) due to genotypes (Table 1) indicated significant differences among genotypes for all yield and yield-related characteristics. The presence of significant genetic variation provides a foundation for effective selection and breeding programs aimed at improving yield and yield-related traits. The genetic diversity observed among genotypes offers opportunities for exploiting heterosis, thereby enhancing crop productivity. The results also highlight the potential for genetic improvement of pumpkin through selective breeding, targeting specific traits such as fruit weight, size and yield.

Table 1. Analysis of variance for growth and yield parameters in Pumpkin genotypes.

Sourceof variation	Replications	Treatments	Error
DF	2	17	34
Numberofprimarybranches per plant	0.009	0.105**	0.016
Male/Femalebudratio	0.03	24.86**	0.110
Internodallength(cm)	0.021	1.520**	0.203
Nodenumber,atfirstfemaleflower appear	0.064	11.332**	0.733
Nodenumberat first,male flower appear	0.061	6.979**	0.111
Fruitweight(kg)	0.001	0.326**	0.021
Pericarp/seedballratio	0.004	20.257**	0.135
Vinelength(cm)	59.37	5768.32**	51.810
Leafarea(cm^2)	16.78	11212.42**	155.64
Daysforfirst maleflower anthesis(DAS)	0.35	116.05**	3.420
Daysforfirstfemale floweranthesis(DAS)	2.29	99.69**	4.520
Number offruits perplant	0.147	0.419**	0.132
Fruitpolardiameter(cm)	0.742	9.315**	0.708
Peripheralthicknessoffruit(cm)	9.81	116.47**	14.700
Daysforfirstfruitharvest(DAS)	0.36	449.19**	9.480
Fruitpericarpthickness (cm)	0.017	0.339**	0.041
TSS(°brix)	0.014	0.895**	0.032
Fruityield(q/ha)	4.48	9098.34**	288.23

***,**significantat5%and1%level,respectively**

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Comment [r6]: “Node number at which the first male flower appears” would be better instead “Node number at first, male flower appear”. Remove ,

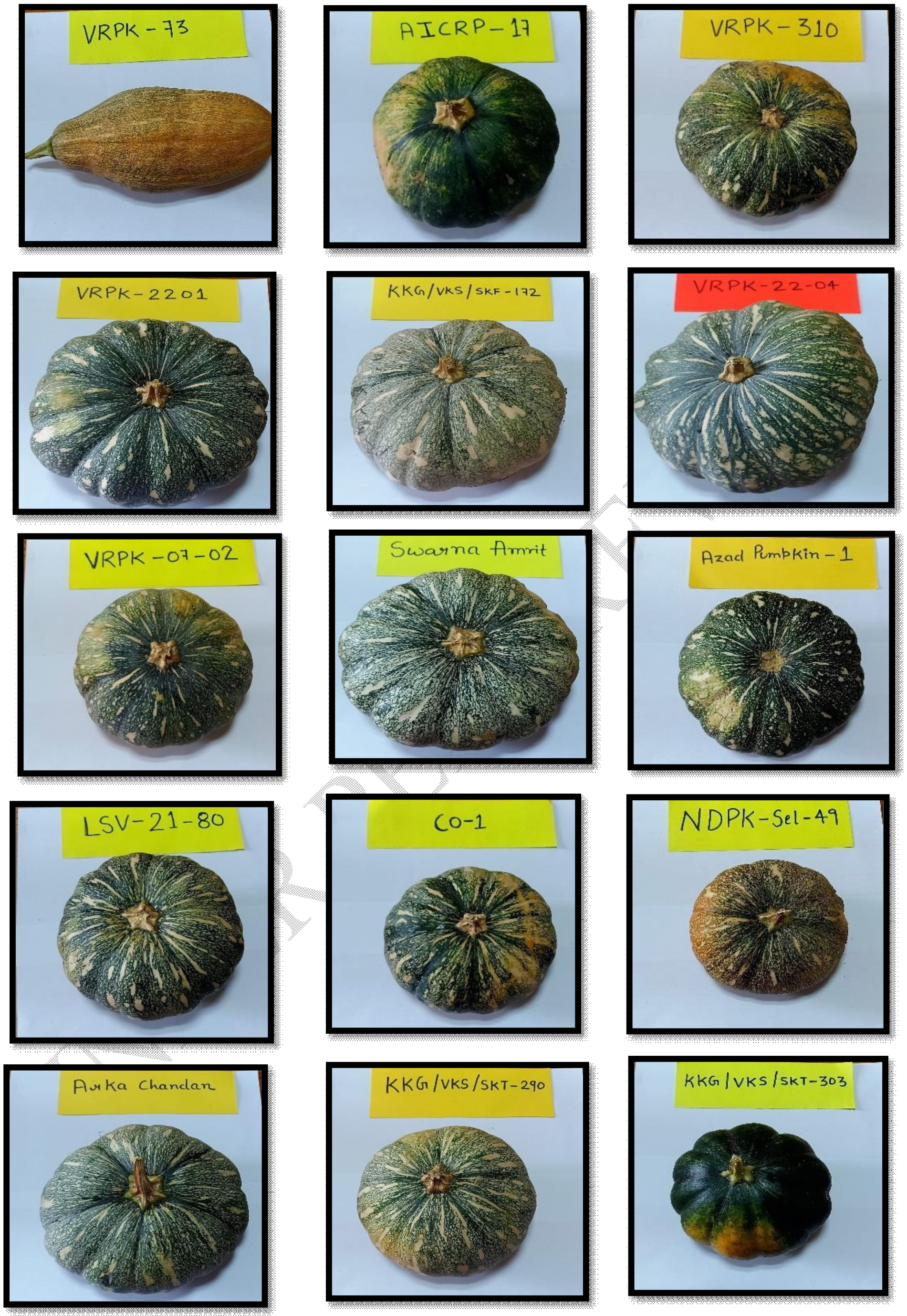

Figure 1: Morphological variation among fruits of different genotypes

The mean performances of 18 pumpkin genotypes, evaluated across 18 characters, are presented in Table 2, exhibiting a broad spectrum of variability for all assessed traits. In terms of phenological parameters the earliness of 18 okra genotypes was evaluated based on node number at first female flower appearance, node number at first staminate flower anthesis, days to first male flower anthesis, days to first pistillate flower anthesis and days to first fruit harvest.Among all the 18 genotypes node number first female flower appear ranged from 18.33 to 25.93 with a general mean value of 21.27 nodes over the genotypes. Lowest node number at first female flower appear was recorded in VRPK-2201 (18.33) whereas highest in the genotype Azad Pumpkin-1 (25.93). In contrast, node number at first staminate flower appear ranged from 5.93 to 12.47 with a mean value of 8.74 nodes over the genotypes. Lowest node number at first male flower appear was recorded in VRPK-310 (5.93) whereas highest in BUP-18-1 (12.47). The extent of variation for days to first male flower anthesis was 37.87 days to 60.67 days with general mean of 44.61 days. The value for days to first pistillate flower anthesis ranged from 47.60 (VRPK- 310) to 69.67days (CO-1) with general mean of 51.66 days.The perusal of the data indicated that the genotype Kashi Basant was found to be earlier as exhibited minimum number of days (56.33) in respect of days to first fruit harvest, whereas VRPK-73 was observed as late maturing genotype having the value 102.17 days.In the context of vegetative or growth parameters the 18 okra genotypes exhibited significant variability in vegetative growth characteristics. Primary branches per plant were ranged from 3.46 (CO-1) to 4.07 (LSV-21-80) with the general mean of the character was 3.76 primary branches.The internodal length for all theeighteen genotypes varied from 9.27 cm (Narendra Amrit) to 11.53 cm (KKG/VKS/ SKT-290 & BUP 18-1) with general mean of 10.67 cm.The vine length value (cm) ranged from 138.00 cm (VRPK-73) to 273.33 cm (KKG/VKS/SKT-303) with general mean of the character was 199.79 cm. The leaf area (cm^2) in eighteen genotypes ranged from 190.70cm^2 (LSV-21-80) to 409.67cm^2 (VRPK-22-04). The general mean of the character was recorded 298.91cm^2.As far as fruit and yield parameters are concern the 18 okra genotypes demonstrated substantial variability in yield-related traits.The male/female bud ratio for all the eighteen genotypes ranged from 4.44 (KKG/VKS/SKT-290) to 14.21 (Azad Pumpkin- 1) with the mean value of 7.631.Fruit weight ranged from 1.41 kg (CO-1) to 2.58 kg (VRPK-73) with general mean of 1.77 kg.The genotypes VRPK-73 had the maximum average fruit weight (2.58 kg) whereas CO-1 (1.41 kg) registered lesser fruit weight.The pericarp/seed ball ratio for all the eighteen genotypes ranged from 4.76 (VRPK-22-04) to14.27 (KKG/VKS/SKT-303) with mean value of 8.33. The genotype VRPK-22-04 exhibited maximum number of fruits per plant (6.60) and ranged from 5.33 (Kashi Basant) to 6.60 (VRPK-22-04) with general mean of 5.92 fruits.In terms of polar diameter VRPK-22-4 had the maximum polar diameter (16.09 cm) whereas Azad pumpkin-1 reported minimum of 9.42 cm.The value of peripheral thickness of fruit ranged from 34.67cm to 58.87 cm with the mean value of 49.42 cm.A comparison of mean values evinced that the genotype VRPK-22-4 exhibited the maximum pericarp thickness having the value 3.38 mm whereas minimum (2.51 mm) was recorded in LSV -21-80 with the mean value of 2.40 mm. The genotype VRPK-22-04 produced the highest yield (338.11q/ha) followed by Kashi Harit (270.04), VRPK-2201 (256.08) and VRPK-73 (249.03 q/ha), whereas the genotype KKG/VKS/SKT-290 exhibited minimum yield (128.19 q/ha). The TSS for all the eighteen genotypes ranged from 3.17ºB to 4.93ºB. The general mean of the character was recorded 4.46 ºB.**Ahmed *et al.*(2011), Shrikanth *et al.*(2017)**and **Rai *et al.*(2023)**has also observed sufficient morphological variability in pumpkin during their study.

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Table 2. Mean performance of eighteen genotypes of pumpkin for eighteen characters.

Genotypes	Number of primary branches per plant	Male/ Female bud ratio	Internodal length (cm)	Node number, at first female flower appear	Node number, at first male flower appear	Fruit weight (kg)	Pericarp/seed ball ratio	Vine length (cm)	Leaf area (cm²)	Days for first male flower anthesis (DAS)	Days for first male flower anthesis (DAS)	No of fruit s per plan t	TSS (ºbrix)	Fruit polar diameter (cm)	Peripheral thickness of fruit (cm)	Days for first fruit harvest (DAS)	Fruit pericarp thickness (cm)	Fruit yield (q/ha))
KKG/VKS/SK T-290	3.93	4.44	11.53	21.53	8.60	1.50	6.64	182.07	201.33	45.13	51.00	5.53	3.87	10.67	34.67	58.33	2.25	128.19
KKG/VKS/SKT-303	3.60	6.03	9.73	25.00	8.80	1.54	14.27	273.33	190.70	41.20	52.60	5.67	4.71	11.86	46.73	79.60	2.20	158.92
VRPK-2201	3.67	5.38	10.73	18.33	8.40	2.00	6.59	156.33	243.70	50.00	52.53	6.53	3.89	13.09	50.07	80.40	2.39	256.08
VRPK-310	3.93	9.37	10.87	21.93	5.93	1.57	5.23	197.13	333.51	37.87	47.60	5.93	3.90	10.44	45.93	65.93	2.16	163.71
KKG/VKS/SK F-172	3.67	12.47	11.13	21.60	7.77	1.60	9.44	225.33	357.77	42.80	48.00	5.53	4.89	10.01	47.27	80.20	2.25	180.91
Azad Pumpkin-1	3.48	14.21	11.23	25.93	11.27	1.73	8.82	266.33	246.11	41.20	50.13	5.73	4.90	9.42	54.07	61.33	2.41	185.13
Pusa vishwas	3.53	8.72	10.53	19.80	9.33	1.71	6.62	172.07	351.40	41.20	51.53	5.87	4.29	11.29	36.33	80.73	2.24	177.34
Arka chandan	3.93	5.17	11.27	20.60	7.80	2.11	7.64	228.67	273.55	41.40	48.20	6.22	4.77	14.45	53.67	63.33	3.16	256.55
VRPK-22-04	3.87	5.33	9.40	19.13	9.00	2.50	4.76	248.73	362.55	40.87	49.00	6.60	3.17	16.09	58.87	91.33	3.38	338.11
VRPK-73	3.87	4.70	10.40	20.60	7.40	2.58	6.80	138.00	409.67	57.33	61.67	6.13	3.87	13.31	53.63	102.17	2.42	249.43
CO-1	3.46	8.57	11.47	22.20	9.07	1.41	11.57	142.67	256.56	60.67	69.67	5.93	4.93	11.29	49.07	80.80	2.21	177.00
Kasi Basant	3.49	11.43	10.87	22.13	8.20	1.51	5.43	236.60	371.57	41.93	48.27	5.33	4.81	11.31	47.00	56.33	2.43	184.77

Genotypes	**Number of primary branches per plant**	**Male/ Female bud ratio**	**Internodal length (cm)**	**Node number, at first female flower appear**	**Node number, at first male flower appear**	**Fruit weight (kg)**	**Pericarp/seed ball ratio**	**Vine length (cm)**	**Leaf area (cm²)**	**Days for first male flower anthesis (DAS)**	**Days for first male flower anthesis (DAS)**	**No of fruit s per plan t**	**TSS (ºbrix)**	**Fruit polar diameter (cm)**	**Peripheral thickness of fruit (cm)**	**Days for first fruit harvest (DAS)**	**Fruit pericarp thickness (cm)**	**Fruit yield (q/ha))**
VRPK-07-02	3.80	4.74	11.13	20.47	9.53	1.78	6.87	139.00	292.22	40.80	47.93	5.60	4.89	13.14	51.07	80.47	2.47	253.07
LSV-21-80	4.07	8.07	10.80	21.73	9.80	1.69	11.78	226.00	337.52	50.67	48.27	5.47	4.86	11.26	52.67	64.33	2.15	161.61
Kashi Harit	3.93	7.00	10.00	22.67	8.40	1.77	8.83	149.67	262.82	41.37	48.33	6.33	4.86	12.55	56.00	80.80	2.46	270.04
Narendra Amrit	3.73	9.46	9.27	20.00	9.00	1.57	9.51	190.33	277.45	41.00	50.87	5.87	4.85	9.76	47.20	76.40	2.18	149.24
BUP-18-1	3.90	6.29	11.53	19.40	12.47	1.56	11.36	200.33	277.51	46.67	47.73	5.87	3.90	10.51	50.27	62.33	2.21	181.52
NDPV-sel-49	3.73	5.96	10.13	19.80	6.53	1.77	7.86	223.67	334.44	40.80	56.47	6.33	4.89	13.31	55.07	80.20	2.24	248.64
Mean	3.76	7.63	10.67	21.27	8.74	1.77	8.33	199.79	298.91	44.61	51.66	5.92	4.46	11.88	49.42	74.72	2.40	206.68
Min	3.46	4.44	9.27	18.33	5.93	1.41	4.76	138.00	190.70	37.87	47.60	5.33	3.17	9.42	34.67	56.33	2.15	128.19
Max	4.07	14.21	11.53	25.93	12.47	2.58	14.27	273.33	409.67	60.67	69.67	6.60	4.93	16.09	58.87	102.17	3.38	338.11
SE(d)	0.10	0.28	0.37	0.70	0.27	0.12	0.30	5.88	10.19	1.51	1.74	0.30	0.15	0.69	3.13	2.51	0.17	13.86
C.D. at 5%	0.21	0.56	0.75	1.43	0.56	0.24	0.61	12.00	20.79	3.08	3.54	0.61	0.30	1.40	6.39	5.13	0.34	28.29
C.V. (%)	3.40	4.41	4.23	4.03	3.82	8.21	4.42	3.60	4.17	4.15	4.12	6.14	4.04	7.08	7.76	4.12	8.45	8.21

Anunderstanding of the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h²), and genetic advance (GA) is crucial for breeders to optimize vegetable breeding strategies. Genetic variability, the fundamental basis for selection, determines the potential for trait improvement.High genetic variability within breeding materials enhances the scope for selection-driven improvement. Conversely, limited variability restricts the breeding program's effectiveness.Effective utilization of genetic variability is pivotal for developing superior vegetable cultivars. By leveraging genetic diversity, breeders can accelerate progress toward improved yield, quality, and resilience.Assessing genetic components of variability in the total variation is crucial before exploiting variability for genetic improvement. Additive genetic variance represents the constant heritable portion of total variation. To evaluate existing variability in the germplasm, genotypic (GCV) and phenotypic coefficients of variation (PCV) were computed (Table 3). Notably, PCV exceeded GCV for all characters, indicating significant environmental influence on trait expression. This disparity suggests that environmental factors substantially modify genetic expression, masking the underlying genetic potential.**Singh *et al.*(2019); Srikanth**, ***et al.*(2017), andSultana*et al.*(2015)** also mentioned the higher PCV than the GCV.

PCV ranged from 5.69% (number of primary branches perplant) to 37.90% (male female bud ratio). Genotypic coefficient of variance varied from4.57% (number of primary branches per plant) to 37.65% (Male/Female bud ratio). Ingeneral, considering the estimates of genotypic and phenotypic variance separately, it wasnoticedthatallthesetraitsshowedcomparativelyhighervaluesofphenotypicvariancethan their corresponding genotypic variance.The high estimate (>20%) of phenotypic and genotypic (PCV and GCV) were recorded for male/female budratio(PCV=37.90% and GCV=37.65%)followedbypericarp/seedballratio(PCV=31.39%and GCV= 31.07%)fruityield(PCV=27.48%and GCV= 26.22%),vine length (PCV=22.14% and GCV=21.85%)and leaf area(PCV=20.73% and GCV=20.31%).These traits are demonstrated minimal environmental influence in comparison to others traits and indicating strong genetic control and potential for significant selection response (Nagar et al., 2017). This suggests that breeding efforts can effectively harness genetic variation to drive improvement. Previous studies of **Samadia 2011;Kumar *et al.*2017; Karthick *et al.*2019; Sundharaiya*et al.* 2019** have consistently reported high phenotypic (PCV) and genotypic (GCV) coefficient of variation estimates for these traits, highlighting their potential for genetic enhancement.Moderate estimate(10%-20%) of PCV and GCV werenoted forfruitweight(PCV=19.79%and GCV=18.00%) followed by node number, at first male flower appear(PCV=17.73%and GCV= 17.31%), fruit harvest(PCV=16.72% and GCV= 16.20%), fruit polar diameter (PCV=15.93%and GCV= 14.26%), pericarp thickness (PCV=15.60% and GCV=13.12%),daysforfirstdaysforfirstmaleflоweranthesis(PCV=14.35%and GCV=13.74%), peripheral thickness of fruit(PCV=14.11%and GCV=11.79%), TSS (PCV=12.69% and GCV=12.03%) anddays for first female flower anthesis (PCV=11.65% and GCV=10.90%).ThemoderateestimatesofPCVandGCVforthese characterswerealsoreportedearlierby**Punitha(2000)andSahithya(2001)**.Theoccurrence of moderate values for these traits reveals the reasonable scope of improvement through

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selection. While, the low estimate (<10%) ofphenotypic coefficients of variation were observed for node number, at first female flowerappear(PCV=9.71% GCV=8.84%) followed by number of fruits per plant (PCV=8.07% GCV= 5.23%), internodallength(PCV=7.51% GCV=6.21%) andnumberof primarybranches perplant(PCV=5.69% and GCV=4.57%). These characters offer little scope for improvement by selection. (**Karthick *et al.* 2019**) and (**Kumar *et al*. 2007**)also observed low PCV and GCV for these characters.

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Table 3 presents the estimated heritability and genetic advance data for various characters, providing valuable insights into the genetic architecture of the traits. Heritability estimates (h²) quantify the proportion of genetic variation contributing to total phenotypic variation, serving as a crucial indicator of the potential for genetic improvement through selection. Heritability assesses the extent to which genetic factors influence trait expression, determining the effectiveness of selective breeding.The effectiveness of selection in achieving genetic progress depends on three crucial factors: heritability, genetic variation, and selection pressure. While heritability indicates potential for genetic improvement, actual progress relies on sufficient genetic diversity within the breeding population and the intensity of selection applied. Optimal breeding outcomes require balancing high heritability with adequate genetic variation and moderate selection pressure. Neglecting these factors can limit genetic progress or render selection inefficient.Thehighheritability (>75%)wasexpressedbymale/female bud ratio (98.65%) followed by pericarp/seed ball ratio (98.02%), vine length(97.35%), leaf area (95.95%), node number, at first male flower appear(95.36%), days forfirstfruitharvest(93.93%),daysforfirstmalefloweranthesis(91.64%),fruityield(91.06%), TSS (89.91%), days for first female flower anthesis (87.52%), node number, atfirstfemaleflowerappear(82.82%),fruitweight(82.77%)andfruitpolardiameter(80.21%) whereas, moderate heritability (50-75%) was expressed by pericarp thickness(70.67%), peripheral thickness of fruit(69.76%), internodal length (68.37%) and numberof primarybranches per plant(64.37%).The high heritability estimates observed in these traits indicate additive gene action, suggesting that selection based on these characters will effectively lead to crop improvement **(Ullah *et al.* 2011).** However, combining high heritability estimates with high genetic advance enhances the reliability of predicting individual responses to selection **(Ibrahim and Hussein, 2006).** Given the high heritability of these traits, considering them during selection will ensure their enhanced expression in subsequent generations. This finding aligns with previous research by **Singh *et al.* (2019)** and **Chaudhari *et al.* (2017),** highlighting the importance of these traits in breeding programs.

The highest genetic advance (>20) was expressed by leaf area (122.50) followed byfruit yield (106.53), vine length (88.73), days for first fruit harvest (24.17) while moderategenetic advance (10-20) was expressed by days for first female flower anthesis (10.85) andperipheralthicknessoffruit(10.02).Lowgeneticadvance(<10)wasexpressedbymale/female bud ratio (5.88) followed by pericarp/seed ball ratio (5.28), node number, atfirst female flower appear(3.52), fruit polar diameter (3.13), node number, at first maleflower appear(3.04), internodal length (1.13), TSS (1.05), fruit weight (0.60), pericarpthicknesss(0.55), number offruit per plant (0.41)andprimarybranches (0.28).

Genetic advance in percent of mean (>20%) for different characters have beenpresented in table 3. The genetic advance as percent of mean was observed to be thehighest formale/female bud ratio (77.02%) followed by pericarp/seed ball ratio (63.38%),and fruit yield (51.54%). High genetic advance as percent of mean were also observed invinelength(44.41%),leafarea(40.98%),nodenumber,atfirstmaleflowerappear(34.83%), fruit weight (33.74%), days for first fruit harvest (32.35%), male female ratio(27.09%), fruit polar diameter (26.32%), TSS (23.50%), pericarp thickness (22.71%),daysforfirstfemalefloweranthesis(21.01%),andperipheralthicknessoffruit(20.28) whereas moderate genetic advance in percent of mean (10-20%) was expressed by nodenumber,atfirstfemaleflowerappear(16.57),internodallength(10.58).Lowgeneticadvance(<10%)wasexpressedbynumberofprimary branchesperplant(7.55)andnumberof fruit per plant(6.98).

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In present study high heritability coupled with the high genetic advance in percentof mean were noted for male/female bud ratio followed by pericarp/seed ball ratio, vinelength, leaf area, node number, at first male flower appear, days for first fruit harvest, daysfor first male flower anthesis, fruit yield, TSS, days for first female flower anthesis, fruitweightand fruit polardiameter.The combination of high heritability and substantial genetic advance in key yield-attributing traits presents a promising opportunity for rapid genetic improvement. This indicates that these traits are largely governed by additive gene action, making them highly responsive to selective breeding.Studies have consistently shown high heritability coupled with substantial genetic advance in fruit yield and yield-attributing traits (Pandey et al., 2007;Shah et al., 2018; Ratnakar et al., 2018; Sundharaiya et al., 2019). This concurrence suggests a strong genetic basis for these traits, making them amenable to selective breeding.

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Table 3. Estimates of range, phenotypic, genotypic variances, co-efficient of variation, heritability and genetic advance as percent of mean for the 18 characters in pumpkin germplasm

Characters	Mean	Min	Max	Var(g)	Var(p)	Heritability (h^2)(%)	Genetic Advance (GA)	Geneticadvance aspercentof Mean	Genotypicco-efficientof variation GCV(%)	Phenotypicco-efficient ofvariation PCV(%)
Numberofnumber ofprimarybranchesperplant	3.76	3.46	4.07	0.03	0.05	64.37	0.28	7.55	4.57	5.69
Male/Femalebudratio	7.63	4.44	14.21	8.25	8.36	98.65	5.88	77.02	37.65	37.90
Internodallength(cm)	10.67	9.27	11.53	0.44	0.64	68.37	1.13	10.58	6.21	7.51
Nodenumber,atfirstfemaleflowerappear	21.27	18.33	25.93	3.53	4.27	82.82	3.52	16.57	8.84	9.71
Nodenumber,atfirstmaleflowerappear	8.74	5.93	12.47	2.29	2.40	95.36	3.04	34.83	17.31	17.73
Fruitweight(kg)	1.77	1.41	2.58	0.10	0.12	82.77	0.60	33.74	18.00	19.79
Pericarp/seedballratio	8.33	4.76	14.27	6.71	6.84	98.02	5.28	63.38	31.07	31.39
Vinelength(cm)	199.79	138.00	273.33	1905.50	1957.31	97.35	88.73	44.41	21.85	22.14
Leafarea(cm^2)	298.91	190.70	409.67	3685.59	3841.23	95.95	122.50	40.98	20.31	20.73
Daysforfirstmalefloweranthesis(DAS)	44.61	37.87	60.67	37.54	40.97	91.64	12.08	27.09	13.74	14.35
Daysforfirstfemalefloweranthesis(DAS)	51.66	47.60	69.67	31.72	36.25	87.52	10.85	21.01	10.90	11.65
Nooffruitsperplant	5.92	5.33	6.60	0.10	0.23	42.02	0.41	6.98	5.23	8.07
TSS(°brix)	4.46	3.17	4.93	0.29	0.32	89.91	1.05	23.50	12.03	12.69
Fruitpolardiameter(cm)	11.88	9.42	16.09	2.87	3.58	80.21	3.13	26.32	14.26	15.93
Peripheralthicknessoffruit(cm)	49.42	34.67	58.87	33.92	48.63	69.76	10.02	20.28	11.79	14.11
Daysforfirstfruitharvest	74.72	56.33	102.17	146.57	156.05	93.93	24.17	32.35	16.20	16.72
Pericarpthickness(cm)	2.40	2.15	3.38	0.10	0.14	70.67	0.55	22.71	13.12	15.60

Comment [r13]: Remove “ number off”

Fruityield(q/ha)	206.68	128.19	338.11	2936.70	3224.93	91.06	106.53	51.54	26.22	27.48

Conclusions

In conclusion, the present study revealed a significant level of variation among the pumpkin genotypes, suggesting ample potential for improving pumpkin cultivars through selection. Among the eighteen genotypes evaluated VRPK-22-04 demonstrated the highest yield. Other two varieties Kashi Harit and Arka Chandan also perform well in this region. These genotypes shows promise for large-scale cultivation among farmers. However, before its widespread adoption, further validation through multi-locational trials is essential to ensure its adaptability and stability across different environments.

Comment [r14]: Remove “s”

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Comment [r15]: Correct spelling: Bangladesh

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