



Assessment of Genetic Variability, Heritability and Expected Genetic Advance in Summer Squash (*Cucurbita pepo* L.)

Uzma Maqbool ^a, Asima Amin ^{a*}, Baseerat Afroza ^a,
Gowhar Ali ^b, Nageena Nazir ^c, Parveez Ahmad Sheikh ^d,
Ishfaq Abidi ^a, Gazal Nazir ^a, Faheema Mushtaq ^a,
Shahnaz Mufti ^a, Ummiyah Masoodi ^a, Rizwan Rashid ^a,
Feroz A Parray ^a, Berjes Zehra ^a and Mehnaz Rashid ^a

^a Division of Vegetable Science, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Srinagar-190025, Jammu and Kashmir, India.

^b Division of Genetics and Plant Breeding, SKUAST-K, Shalimar, Srinagar-190025, India.

^c Division of Agricultural Statistics, Shalimar, Srinagar-190025, Jammu and Kashmir, India.

^d Division of Plant Pathology, Shalimar, Srinagar-190025, Jammu and Kashmir, India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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*Corresponding author: E-mail: drshahasimaamin@gmail.com;

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ABSTRACT

An economically significant cucurbit crop prized for its culinary, medicinal and nutritional qualities is summer squash (*Cucurbita pepo* L.). For efficient selection and breeding of superior cultivars, it is essential to comprehend the degree of genetic variability, heritability and genetic advancement among genotypes. Using 40 different genotypes arranged in a randomized complete block pattern with three replications, the current study was carried out at the Vegetable Experimental Farm, SKUAST-Kashmir, Shalimar, during Kharif 2024. To separate phenotypic and genotypic variability, data on 22 morphological, yield and quality variables were collected and examined. Wide genetic diversity was confirmed by analysis of variance, which showed highly significant variations between genotypes for all variables using ANOVA. PCV values were marginally greater than GCV, indicating little environmental influence, according to estimates of the phenotypic and genotypic coefficients of variation. Fruit yield per plant, fruit yield per hectare, rind thickness, 100-seed weight, flesh thickness, fruit length, vitamin C content, total sugars, dry matter content and crude fiber all showed high heritability and high genetic advancement as a percentage of the mean. The fact that additive gene action essentially controls these features emphasizes how direct selection may be used to improve them. Interestingly, genotypes SKUA-SQ-5, SKUA-SQ-34, SKUA-SQ-17, SKUA-SQ-24 and SKUA-SQ-27 produced the highest no. of fruit per hectare. Overall, the results highlight the significance of utilizing the genetic diversity now in place to create commercially viable, high-yielding, nutritionally enhanced summer squash cultivars in temperate climates.

Keywords: Genetic variability; heritability; genetic advance; GCV; PCV; additive gene action; breeding potential.

1. INTRODUCTION

Summer squash, a warm-season vegetable crop with the chromosome number $2n = 2x = 40$, is botanically known as *Cucurbita pepo* L. Due to its monoecious nature, it is referred to by a number of colloquial names worldwide, including baby marrow in South Africa, courgette in America, marrow in Britain and Ireland, cucuzza in Saudi Arabia and zucchini in Italy. *Cucurbita pepo* L. is an economically significant taxon that is a member of one of the oldest genera in the Cucurbitaceae family (Tadmor et al., 2005). Although it is indigenous to Mexico and the eastern United States, it is commonly grown for its edible fruits in temperate, subtropical and tropical climates (Bisognin, 2002). Among cucurbits, this species is thought to have the highest fruit variability and is one of the most variable taxa in the genus. It is often called "summer squash," as the crop is collected when the fruits are still tender, the pericarp is glossy and smooth, and the seeds are still immature, allowing for commercial production and consumption worldwide (Garza et al., 1995). Summer squash (*Cucurbita pepo* L.) is very productive and has a quick growth cycle; it matures 40–50 days after seeding. It has an impressive range of morphologies and is the most commonly grown species in the genus *Cucurbita*. Acorn, zucchini, crookneck, scallop, straight neck and cocozelle are some of the main morphotypes.

Summer squash (*Cucurbita pepo* L.) is a hardy annual with prickly-haired petioles, orbicular, shallow- to deeply-lobed leaves, and a cross-pollination-dependent monoecious flowering system. It develops as a compact, bushy plant with relatively small tendrils in temperate and subtropical climates with mild summers. Known by various names, including bush squash, vegetable marrow, zucchini, Vilayati Kaddu, Chappan Kaddu, and Safed Kaddu (Thamburaj and Singh, 2001), the crop's primary economic significance stems from the ingestion of its tender fruits, which are prized for their great nutritional and therapeutic value. Numerous bioactive substances, including phenolics, flavonoids, amino acids, vitamins, carbohydrates, and vital minerals, especially potassium, are included in summer squash's nutritional profile (Gramza-Michałowska and Kulczyński, 2019). The fruits are also low in calories, with about 17 kcal per 100 g of fresh weight, and high in dietary fiber (Tamer et al., 2010). Summer squash is one of several species in the Cucurbitaceae family that have been shown to have a variety of pharmacological qualities, including anti-inflammatory, anti-hypertensive, antitumor, antimutagenic, immunomodulatory, antibacterial, anti hypercholesterolemic, intestinal antiparasitic, and antidiabetic effects (Kostalova et al., 2009). Summer squash's extremely low-calorie content makes it a good choice for diets aimed at weight loss (Fageria, 2012). Essential nutrients such as vitamins A, C, niacin, and folate, along with

dietary fiber, are abundant in squash and are known to lower the risk of cardiovascular disease, cancer, and inflammatory diseases like asthma and arthritis (Balluz et al., 2005).

Asia accounts for about half of the world's total area used for pumpkin and squash cultivation (Albrifcany, 2015). Squash and pumpkin production in India were estimated to reach 2,703.61 thousand metric tonnes in 2023–2024 (NHB, 2024). Approximately 3,200 hectares of summer squash are cultivated in the Kashmir region, yielding 64,800 tonnes annually (Anonymous, 2024). Widely cultivated throughout India, this cucurbit thrives in moderate, humid climates and is characterized by its rapid growth and early maturity. The recommended temperature range for its typical growth and development is 16–27 °C. Summer squash's capacity for crop diversification and sustainable production is further enhanced by its ability to adapt to a variety of soil types, including marginal and less fertile soils.

Analysing genetic diversity helps to comprehend the germplasm's genetic base and breeding potential. In order to reduce the amount of available genes and focus their efforts on fewer hybrid pairings, breeders can also exclude some parents by estimating genetic divergence (Fuzzato et al., 2002). A breeding program's ability to advance is largely dependent on the genetic variety found in germplasm. To comprehend this diversity, it is essential to examine the crop's biological characteristics. Numerous genes and environmental factors influence many economically important plant features; therefore, distinguishing between inherited and environmental variability is crucial. The significance of distinguishing between heritable and non-heritable components of phenotypic differences is emphasized by this. In particular, qualities with high genetic variability, heritability, and strong genetic gains require the use of genotypic and phenotypic variability coefficients to assess variations in attributes. Significant improvements in breeding programs result from selection, giving greater weight to traits with significant genetic diversity and heritability. Breeders can use heterosis to develop cultivars with particular qualities, such as resilience to biotic and abiotic stressors and quality enhancement. The ability of crops to adapt to different surroundings, particularly in the face of shifting climatic circumstances, depends on diversity. The need to find and isolate breeding lines with desirable horticultural

features, better quality, high production potential, and genetic variety is critical, given the economic potential of summer squash. These lines will be essential to future initiatives to improve summer squash, guaranteeing the crop's continued prosperity and sustainability. The most efficient method of increasing agricultural yield is genetic enhancement. Genetic resources must have qualities that contribute to productivity and quality for vegetable breeding programs (Balkaya et al., 2010; Gomes et al., 2020). Genetic divergence characteristics such as genetic progress and heritability give the optimal circumstances for selection (Kakeeto et al., 2019).

2. MATERIALS AND METHODS

The present investigation was conducted at the Vegetable Experimental Farm, Division of Vegetable Science, Faculty of Horticulture, SKUAST-K, Shalimar, Srinagar, Jammu and Kashmir, during the Kharif season of 2024. The experiment employed a randomized complete block design and consisted of 40 genotypes. These genotypes were assessed for a range of growth, yield, seed and quality characteristics. The experimental site is located 15 kilometres from Srinagar city, on the foothills of Zabarvan. Situated at latitude 340.14" North and longitude 740.86" East, the location is 1685 meters above mean sea level. The soil was alluvial, with neutral pH. One characteristic of the temperate environment is the mild summers. October has the lowest average temperature of 5.260°C, while August has the highest average temperature of 31.40°C. Rainfall is highest in April. The yield and yield-attributing parameters of forty genotypes of summer squash with distinct phenotypes, collected from diverse sources, were assessed during Kharif 2024. At the Vegetable Experimental Farm, Division of Vegetable Science, SKUAST Kashmir, Shalimar Srinagar, seeds were sown on April 23, 2024. Using a Randomized Complete Block Design (RCBD), three replications of the single-factor experiment were established. In each replication, five plants of each genotype were planted, with rows and plants separated by 2 x 1 m. During the growth and development stage, suggested cultural practices were followed in order to produce a healthy crop to record parameters like ion, with rows and plants spaced 2x1 m apart respectively. Data was recorded on 22 parameters viz., Node number at which first male flower appears, Node number at which first female flower appears, Days to appearance of first male flower, Days to appearance of first

female flower, Days to 1st Fruit Harvest, Days to Last Fruit Harvest, Number of Fruits/Plant, Average Fruit Weight (kg), Fruit Length (cm), Fruit Diameter (cm), Flesh Thickness (cm), Rind Thickness(mm), Flesh Weight (g), Fruit Yield/Plant (kg), Fruit Yield/ha (q), Total Sugars (%), Dry Matter content (%), Vitamin C content (mg/100g), TSS (0Brix), Crude Fibre content (%). Observations on various growth, yield traits and quality parameters were recorded from five randomly selected plants per genotype in each replication. The average data from these selected plants were used for statistical analysis. Analysis of variance for all characters was conducted following the method described by Panse and Sukhatme (1957). The treatment means were evaluated for significance at the 5% and 1% levels. Genotypic and phenotypic variance were calculated using the method proposed by Johnson et al. (1955). The magnitudes of the phenotypic coefficient of variation (PCV) and the genotypic coefficient of variation (GCV) for the parameters under study were calculated using the formula provided by Burton (1952). The estimates of PCV and GCV were classified into low, moderate and high according to Sivasubramanian and Madhavmenon (1973), 0 – 10% (Low), 10 – 20% (Moderate), and > 20% (High). The ratio of genotypic to phenotypic variance was used to determine the heritability (h^2) of yield and its constituent parts, which was then reported as a percentage. The calculation was carried out using the methodology described by Hanson et al. (1956), Johnson et al. (1955), and Burton and De Vane (1953). The estimates of broad sense heritability, expressed in percentage, were then categorized as low, moderate and high as suggested by Robinson et al. (1949), 0-30% (Low), 30-60% (Moderate), > 60% (High). Genetic advance at a 5 percent selection intensity was calculated using the procedure suggested by Lush (1940) and Johnson et al. (1955). R software was used at the Division of Agricultural Statistics, SKUAST-Kashmir, Shalimar, for all statistical analyses and calculations.

3. RESULTS AND DISCUSSION

The experiment was conducted at the Vegetable Experimental Farm, Division of Vegetable Science, Faculty of Horticulture, SKUAST-K, Shalimar, Srinagar, Jammu and Kashmir, during the Kharif season of 2024. The experiment employed a randomized complete block design and consisted of 40 genotypes.

These genotypes were assessed for a range of growth, yield, seed and quality characteristics. The results of the analysis of variance showed that all 22 traits exhibited significant variations between the genotypes, indicating that the germplasm under study had sufficient genetic diversity. The analysis of variance presented indicates that the mean sum of squares for treatments across all characters was highly significant, highlighting substantial variation among all treatments for each character examined. (Table 1a and 1b). Therefore, it provides a more efficient method for improving breeding material by selecting potential genotypes for the summer squash breeding program. The analysis of variance revealed that all forty genotypes differed significantly for every parameter, indicating that the germplasm under investigation exhibited considerable variability. Table 2 provides estimates of genetic variability, including mean, range, phenotypic variance (PV), genotypic variance (GV), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability, and genetic gain (genetic advancement as a percentage of the mean). There was significant diversity in the majority of the attributes examined in this study (Table 2). Most of the qualities analyzed in this study exhibited considerable variability. The node number at which the 1st male flower appears has a mean value of 1.74, ranging from 1 to 2.2. Similarly, the node number at which the 1st female flower appears has a mean of 4.47, with a range of 3 to 5.4. The days to the appearance of the 1st male flower averages 60.30 days, with a range of 56.4 to 64.3 days. While days to the appearance of the 1st female flower averages 62.72 days, ranging from 56.4 to 66.06 days. The days to the first fruit harvest occur after an average of 78.24 days, with variability from 75.34 to 82.44 days. The days to last fruit harvest average 109.56 days, ranging from 105.17 to 115.29 days. The average number of fruits per plant is 4.36, with a range of 3.2 to 4.36 fruits. The average fruit weight is recorded at 0.91 kg, with a range of 0.9 kg to 1.12 kg. The average fruit length is 33.62 cm, with a significant range from 19.03 cm to 43.21 cm. Fruit diameter has a mean value of 7.54 cm, ranging from 6.22 cm to 8.73 cm. Flesh thickness averages 1.89 cm, with variability between 1.16 cm and 2.51 cm. Rind thickness has a mean of 0.36 mm, ranging from 0.2 mm to 0.56 mm. While the flesh weight averages 746.56 g, with variability from 403.36 g to 926.33 g. The fruit yield per plant averages 4.00 kg, with a range from 2.35 kg to 6.35 kg, and the fruit

yield per hectare averages 200.48 q, ranging from 117.5 to 317.66 q. The number of seeds per fruit averages 188.15, with variability from 74.2 to 401.6 seeds and the 100-seed weight averages 25.03g, ranging from 17.26 g to 36.25 g. The total sugar content averages 2.32%, with a range of 1.5% to 4.73%. The dry matter content averages 6.84%, with a range of 4.2% to 9.65%. The vitamin C content averages 11.91 mg per 100 grams, with variability from 7.4 mg to 30.5 mg. Total soluble solids (TSS) have a mean of 8.25°Brix, with a range of 6.4°Brix to 11.36 °Brix, while crude fiber content has a mean of 1.85%, with variability from 1.6 % to 2.48%. The range of values found for the various qualities under investigation suggests that there is sufficient genetic variation, which is essential for improvement through selection. The degree of phenotypic variability is reflected in these range values, which are less accurate since they include environmental, genotypic, and genotype x environment interaction components, making it difficult to determine which trait is most variable. Additionally, a crop's phenotype is impacted by dominance (non-heritable), epistasis (non-allelic interactions), and additive gene effects (heritable). Consequently, in order to precisely ascertain the degree of variability present for each trait, the observed variability must be divided into phenotypic and genotypic coefficients of variation. These findings align with the results reported by Harika et al. (2012), Jain et al. (2016, 2017), Rambabu et al. (2017), Kumar et al. (2018), Khan et al. (2020), Rashid et al. (2020a), Sohi et al. (2021), Dubey et al. (2022), Bashir et al. (2024a), and Das et al. (2024).

The estimates of phenotypic variance exceeded the corresponding genotypic variance for all traits analyzed in this study. The highest phenotypic and genotypic variances were observed for the flesh weight (13781.98 and 13378.98, respectively). Significant variances were also noted for the number of seeds per fruit (7768.23 and 7629.99). Fruit yield per hectare exhibited substantial variances as well, with values of 2551.96 and 2329.45 for phenotypic and genotypic variance, respectively. The remaining traits showed comparatively lower values for both phenotypic and genotypic variances. Key measures of variability, such as genotypic and phenotypic coefficients of variation, are commonly employed to assess diversity within genetic populations. The relative values of these coefficients provide insights into the level of variability within a population. Consequently, the

phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated. The results indicated that PCV values were consistently higher than GCV values, suggesting that environmental influences on the expression of the studied traits were minimal. To achieve this, the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated, which are presented in Table 2. This was in agreement with the study of Sajid et al. (2022) in Summer Squash, Akter et al. (2013) in pumpkin, Rani et al. (2015), Rambabu et al. (2017) in bottle gourd (Deepthi et al., 2012; Rambabu et al., 2020). According to Sivasubramanian and Madhavamenon (1973), GCV and PCV are classified into three categories: low (0–10%), moderate (10–20%), and high (greater than 20%). Low values of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were noted for traits such as Days to First Fruit Harvest (1.86, 1.84), Days to Last Fruit Harvest (2.03, 1.96), Days to First Female Flower (3.33, 2.29), Days to First Male Flower (3.96, 2.87) and Fruit Diameter (7.78, 7.58). Moderate values of PCV and GCV were observed for TSS (14.06, 13.80), Average Fruit Weight (14.56, 14.52), Node Number at which the First Female Flower Appears (15.45, 14.90), Fruit Weight (15.72, 15.49), Fruit Length (16.01, 15.86), Crude Fiber (16.62, 15.91), Dry Matter Content (18.98, 18.96), No. of Fruits/ Plant (19.48, 18.83), Flesh Thickness (20.01, 18.32). High values of PCV and GCV were recorded for traits such as No. of Seeds/Fruit (46.84, 46.42), Total Sugars (39.12, 33.12), Ascorbic Acid (33.30, 33.12), Rind Thickness (30.24, 7.85), Node Number at which the First Male Flower Appears (27.47, 26.16), Fruit Yield/Hectare (25.19, 24.07), Fruit Yield/Plant (25.09, 23.97) and 100 Seed Weight (24.25, 23.81). The results were in tune with the findings of Sajid et al. (2022) in Summer Squash, Akter et al. (2013) in pumpkin, Bartaula et al. (2019) in cucumber and Sowmya et al. (2021) in bitter gourd.

The phenotypic and genotypic coefficients of variation were marginally greater, but otherwise they were almost the same. This demonstrates how environmental influences affect the characteristics being examined. Khan et al. (2020), Rashid et al. (2020c), Chandramouli et al. (2021), Damor et al. (2016), Rambabu et al. (2017), and Bashir et al. (2024a) have all reported similar results. More improvement through selection is possible for traits with moderate to high coefficients of variance. A wide

range of variability and high phenotypic and genotypic coefficients of variation indicate that these traits are quite sensitive to selection. Although the phenotypic coefficients were marginally greater than the genotypic ones, this slight discrepancy suggests that genetic variables account for the majority of the observed variation, with minimal environmental influence. These findings are consistent with those of Ahmad et al. (2019), Rashid et al. (2020c), Duhan et al. (2022), Rambabu et al. (2017), Damor et al. (2016), and Deepthi et al. (2016). The broad variability and high estimates indicate that traits with moderate to high coefficients of variation are well-suited for selective breeding programs, suggesting a great potential for genetic improvement through selection. Neither the genotypic nor the phenotypic coefficients of variation are useful in determining the amount of variation that is actually heritable, nor do they adequately reflect the degree of inheritance of the trait. The heritability of a trait can be trusted in this situation because it enables the breeder to discriminate between the environmental impact and general variability by determining the level of selection pressure that should be applied in a particular environment. The evaluation of environmental and heritable factors influencing observed phenotypic variation is made possible by it. When compared to the projected genetic gain, the evaluation of heredity has a considerable impact on the efficacy of character selection, as proposed by Panse and Sukhatme (1957) and Johnson et al. (1955). Furthermore, the amount of genetic gain directly correlates with the progress in selection. As a result, traits with high heritability and significant genetic gain experience the effects of selection more quickly. Additive gene effects are indicated by high heritability and high Genetic Advance as a Percentage of Mean (GAM), which raises the possibility of successful selection. Low GAM and high heritability point to the importance of non-additive gene interactions, where environmental factors, not genotype, cause high heritability, suggesting that selection for these traits may have limited effects. Additive gene effects control high GAM and low heritability; in these situations, selection can be successful since low heritability results from significant environmental influences. Low GAM and low heritability indicate that selection would be inefficient since environmental factors greatly influence the trait.

For every attribute, heritability was found to be high, surpassing 60 percent in the broadest

sense and varied between 47 and 99 percent, suggesting that the traits are less affected by environmental factors and are successfully passed on to the offspring. This suggests that a significant role of genetic constitution in character expression is involved, and selection based on phenotypic expression could therefore be trusted. In the case of summer squash, Sajid et al. (2022), Akter et al. (2013), Sultana et al. (2018), Emina et al. (2012), Prasanth et al. (2020), and Sowmya et al. (2021) found similar outcomes. When represented as a percentage of the mean, the attribute with the most significant genetic gain was No. of Seeds/Fruit, with a value of 94.78. This was followed by the Total Sugars (79.99), Ascorbic Acid Content (67.85), and Rind Thickness (52.86). Days to First Female Flower (3.25), Days to First Fruit Harvest (3.75), Days to Last Fruit Harvest (3.89), and the days until the first male bloom appeared (4.29), on the other hand, showed the lowest genetic gain (genetic advancement as a percentage of mean).

The traits including Node number at which the First Male Flower Appears, Node no. at which the First Female Flower Appears, Average Fruit Weight, , Fruit length, Flesh Weight, Flesh Thickness, Rind Thickness, No. of Fruits/Plant, Fruit Yield/Plant, Fruit Yield/Hectare, Number of Seeds/Fruit, 100-seed Weight, Total Sugars, Dry Matter Content, Ascorbic Acid Content, Total Soluble Solids (TSS) and Crude Fiber Content exhibited high heritability estimates along with high genetic advance as a percentage of the mean (GAM). This suggests that these variables are mostly controlled by additive gene activity, suggesting that yield-related traits can be significantly improved by selection. The results of Rambabu et al. (2017), Chandrashekhar et al. (2018), Kumar et al. (2020b), Rashid et al. (2020c), and Bashir et al. (2024a) are all in agreement with these findings.

Fruit yield/ha is a crucial characteristic that determines the commercial viability of a hybrid or variety. This feature should therefore be given top importance in any breeding effort. It was recommended that high-yielding cultivars might be chosen from the current collection due to the trait's high heritability and high genetic advancement as a percentage of mean. Islam et al. (2009), Kumari et al. (2018) in bitter melon, Damor et al. (2016), Rambabu et al. (2017) in bottle melon, Sajid et al. (2022) in summer squash, and Yadav et al. (2021) in cucumber all backed up this claim.

Table 1a. Analysis of variance for various agronomic characters in summer squash (*Cucurbita pepo* L.)

S. No.	Source of variation	d.f	Mean sum of squares																
			Fruit length (cm)	Fruit diameter (cm)	Flesh weight(g)	Flesh Thickness (cm)	Rind Thickness (mm)	No. of fruits /plants	Average fruit weight (Kg)	Fruit yield /plant (Kg)	Fruit yield /hectare(q)	Node no. at which first Male flower appear	Node no. at which first female flower appears	Days to first female flower	Days to first male flower	Days to first fruit harvest	Days to last fruit harvest	No. of seeds /fruit	100 Seed weight (g)
1.	Replication	2	0.64	0.045	1.79	0.095	0.004	0.090	0.000013	0.149	4.24	0.232	0.256	291.264**	189.381**	0.025	2.501	2.89	18.291*
2.	Treatment	39	85.94*	1.001*	40539.65*	0.384*	0.033*	2.082*	0.053*	2.851*	7210.86*	0.532*	1.201*	8.506*	11.734*	6.276**	14.254**	23028.222**	108.002**
3.	Error	78	0.51	0.01	4.02	0.02	0.001	0.047	0.000093	0.088	2.22	0.017	0.029	2.291	2.707	0.045	0.359	1.38	1.317

**= significant at 1%, *= Significant at 5%

Table 1b. Analysis of variance for various quality characters in summer squash (*Cucurbita pepo* L.)

S. No.	Source of Variation	d.f	Mean sum of squares				
			TSS (°Brix)	Ascorbic acid content (mg 100g-1)	Dry matter content (%)	Crude fiber (%)	Total sugar (%)
1.	Replication	2	0.268	0.019	0.029	0.002	0.043
2.	Treatment	39	3.946*	46.884*	5.060*	0.270*	2.476*
3.	Error	78	0.049	0.170	0.004	0.007	0.006

**= significant at 1%, *= Significant at 5%

Table 2. Estimates of mean, range, phenotypic variance, genotypic variance, phenotypic and genotypic coefficients of variation, heritability and genetic advance (as % of mean) for various characters in summer squash (*Cucurbita pepo* L.)

S. No.	Parameters	Mean	Range	Phenotypic variance (PV)	Genotypic variance (GV)	Phenotypic coefficient of variation (PCV)	Genotypic coefficient of variation (GCV)	Heritability H ₂ (broad sense)	Genetic gain (genetic advance as % of mean)
1	Fruit Length (cm)	33.63	19.03-43.21	28.99	28.47	16.01	15.86	0.98	32.39
2	Fruit Diameter (cm)	7.54	6.22-8.73	0.34	0.32	7.78	7.58	0.94	15.21
3	Flesh Weight(g)	1.89	403.36-926.33	13781.98	13378.98	15.72	15.49	0.97	31.44
4	Flesh Thickness(cm)	1.89	1.16-2.50	0.14	0.12	20.01	18.32	0.83	34.57
5	Rind Thickness(mm)	0.36	0.20-0.56	0.012	0.010	30.24	27.85	0.84	52.86
6	No. of Fruits /Plant	4.37	3.20-6.43	0.72	0.67	19.48	18.83	0.93	37.51
7	Average Fruit Weight	0.91	0.51-1.12	0.0178	0.0177	14.56	14.52	0.99	29.84
8	Fruit Yield /Plant	4.00	2.35-6.35	1.009	0.921	25.09	23.97	0.91	47.16
9	Fruit Yield/Hectare	200.49	2.35-6.35	2551.96	2329.45	25.19	24.07	0.91	47.37
10	Node No. at which First Male Flower Appears	1.58	1.03-2.26	0.18	0.17	27.47	26.16	0.81	51.32
11	Node No. at which First Female Flower Appears	4.19	3.00-5.40	0.42	0.39	15.45	14.90	0.92	29.60
12	Days to First Female Flower	62.72	59.16-66.06	4.36	2.07	3.33	2.29	0.47	3.25
13	Days to First Male Flower	60.30	56.40-64.30	5.71	3.00	3.96	2.87	0.52	4.29
14	Days to First Fruit Harvest	78.25	75.34-82.44	2.12	2.07	1.86	1.84	0.97	3.75
15	Days to Last Fruit Harvest	109.56	105.17-115.29	499	4.63	2.03	1.96	0.92	3.89
16	No.of Seeds/Fruit	188.15	74.20-401.60	7768.23	7629.99	46.84	46.42	0.98	94.78
17	100 Seed Weight	25.04	17.26-36.25	36.87	35.56	24.25	23.81	0.96	48.17
18	TSS (°Brix)	8.25	6.40-11.40	1.34	1.29	14.06	13.80	0.96	27.91
19	Ascorbic acid (mg / 100g)	11.91	7.40-30.50	15.74	15.57	33.30	33.12	0.98	67.85
20	Dry matter content (%)	6.84	4.20-9.65	1.69	1.68	18.98	18.96	0.99	39.00
21	Crude fiber content (%)	1.85	1.12-2.48	0.095	0.087	16.62	15.91	0.91	31.37
22	Total sugar (mg /100g)	2.32	1.12-4.73	0.829	0.823	39.12	38.97	0.99	79.99

4. CONCLUSION

It is apparent from the discussion above that there is considerable promise in combining the beneficial allelic resources found in these summer squash genotypes through a methodical breeding and selection process to create high-yielding recombinants with the desired features. Variance analysis showed significant differences among the genotypes for the various traits examined. The mean performance of the genotypes indicated that the highest fruit yield per hectare was observed in SKUA-SQ-5 (317.66), SKUA-SQ-34 (304.83), SKUA-SQ-17 (302), SKUA-SQ-24 (291.83) and SKUA-SQ-27 (270.33). The phenotypic coefficients of variation were marginally greater than the corresponding genotypic coefficients for all traits studied. High heritability alongside significant genetic gain (expressed as genetic advance as a percentage of the mean) was noted for traits such as the number of seeds per fruit, rind thickness, node number at which 1st male flower appears, fruit yield per hectare, fruit yield per plant, 100 seed weight, flesh thickness, number of fruits per plant, fruit length, flesh weight, total sugars, vitamin C content, dry matter content, crude fibre content and total soluble solids (TSS). This suggests a strong influence of additive gene action on these traits.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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