



Genetic variability and heterosis for yield components in maize: Comparison of single cross, double cross, and three-way cross hybrids

Suhana, O.^{1*}, Rosnani, A. G.² and Marton, J.³

¹Horticulture Research Centre, MARDI Headquarters, 43400, Serdang, Selangor, Malaysia

²Industrial Crops Research Centre, MARDI Bachok Station, Kampung Aur, Mukim Jalan Kandis, 16310, Kelantan, Malaysia

³Department of Agronomy, Hungarian University of Agriculture and Life Sciences, Páter Károly utca , 2100 Gödöllő, Hungary

Abstract

The increasing global demand for maize, coupled with the challenges of climate change, necessitates the improvement of maize yields. The main objective of this study was to assess genetic variability and heterosis in different types of maize hybrids; single-cross (SC), double-cross (DC) and three-way cross (TC) to identify promising genotypes for yield improvement. Conducted at the Hungarian University of Agriculture and Life Sciences (MATE), the study evaluated 16 genotypes, including parental lines and commercial check hybrids, during the 2022 spring growing season (May–November). Genetic coefficient of variation (GCV) and heritability estimates were calculated for traits including plant height, days to 50% flowering, ear length and ear diameter. Results showed low GCV and moderate phenotypic coefficient of variation (PCV) values for most traits, with the exception of ear weight, which showed high GCV (23.83%, 91.47% and 29.75%) and high PCV (27.85%, 92.18% and 31.33%), indicating substantial genetic variation. Among the genotypes, the SC hybrid V5 demonstrated the highest positive mid-parent heterosis for ear weight and high-parent heterosis for ear diameter. In contrast, TC and DC hybrids exhibited the lowest positive mid-parent and high-parent heterosis for ear length and row number per ear, respectively. Despite these variations, the promising performance of the TC and DC hybrids highlights their potential for future maize breeding programs, offering valuable opportunities to enhance maize productivity under changing environmental conditions.

Keywords: *maize, genetic variability, heterosis, yield components*

Introduction

Maize (*Zea mays* L.), commonly known as corn, is one of the most important crops globally, playing a crucial role in food security and economic stability. As the leading cereal crop by production value, maize surpasses even rice and wheat. In 2020, global maize production reached an impressive 1,163 million mt, contributing over 50% of the world's total grain production (FAO 2022). In Hungary, maize holds significant value as the second most valuable crop after wheat. With 6.3 million t produced in 2021, Hungary was the fourth-largest producer in the European Union, contributing 9.3% to the EU's total maize yield. However, in 2022, Hungary's maize production sharply declined to 2.8 million t, a 57% drop, largely due to extreme drought conditions (KSH 2022).

Maize is more adaptable to diverse growing environment than wheat or rice, making it a versatile and multi-purpose crop (Erenstein et al. 2022). This adaptability is increasingly important given the variability in climate conditions (Koutsika-Sotiriou, 1999). Nevertheless, producing high-yielding and resistant maize hybrids is a major agricultural challenge that can have a significant impact on farmers' livelihoods and food security. However, the biggest challenges are increasing or maintaining production due to various factors, especially global climate change, coupled with infertility, poor soil conditions, and a lack of superior varieties that can adapt to the extreme environments. As global climate change exacerbates extreme weather events, such as drought, flood and temperature fluctuations, maize crops face growing biotic and abiotic stresses that threaten yield and quality.

According to Salasya et al. (1998), the low grain yield is caused by various factors, such as biotic stress (viz., pests and diseases and a lack of superior varieties) and abiotic stress (viz., low soil fertility, nutrient deficiency, and inefficient field management). Accordingly, improved varieties will be less resilient to these stresses if they have a narrow genetic background (Maqboola et al. 2010), while a reduction in genetic variability in crops causes increased vulnerability to diseases and unfavourable climate changes (Aremu 2012).

For effective breeding program, understanding genetic variability, heritability and genetic advance is a crucial step in screening for the presence of novel genetic resources. Consequently, genetic variability provides a great opportunity for plant breeders to improve existing varieties with desirable traits as well as create new varieties that are preferred by both farmers and breeders viz. yield potential, early maturity, good shapes, taste, pest and disease resistance, etc. Plant breeders and local farmers have taken advantage of natural genetic variability to increase their yield. The main emphasis in maize breeding efforts is on characteristics that support economic objectives while conserving a sufficient degree of diversity (Hallauer 1972). In numerous studies, Grzesiak (2001) observed considerable genetic variation among maize genotypes for several traits, providing a foundation for further breeding strategies. Similarly, Ihsan et al. (2005) highlighted significant genetic variation in maize genotypes for morphological traits, underscoring the importance of these variations in the developing of improved maize hybrids.

Bocanski et al. (2009) suggested that maize yield traits are influenced by several genes that interacting with environmental factors, resulting in a multiplicative effect on the end product (Zeeshan et al. 2013). These yield components are inherited with minimal deviations, making selection based on them more appropriate than the yield itself (Nagabhushan et al. 2011). Assessing parental lines' performance based on yield components can help select superior parents for better yielding hybrids (Bocanski et al. 2009). This can be achieved by identifying the genetic characteristics that control the degree to which agronomic traits are inherited (Mahiboobsa et al. 2012). Additionally, utilising genetic variability, together with accurate physiological trait characterisation and their links to maize yield and yield components, can increase the diversity of the maize gene pool (Alake et al. 2008; Al-Tabbal et al. 2012). While the lack of improved varieties may not be classified as biotic stress, it limits maize's ability to adapt to environmental challenges, thus reducing yield potential. Enhancing genetic diversity through the development of superior varieties is essential for overcoming these challenges and improving productivity (Messmer et al. 2011; Tena et al. 2016).

Gosh et al. (2014) found that variation (GCV) and phenotypic coefficient of variation (PCV) are close for traits less influenced by environment. High GCV, heritability, and genetics advance indicate effective selection for these characters, controlled by additive gene

action. In addition to high heritability and GA values suggesting a high degree of characteristics being passed down to the next generation, while a higher magnitude of variability implies a greater opportunity for future breeding programs (Wan Rozita et al. 2022).

Heterosis, or hybrid vigour, has led to a noticeable increase in crop yields, and the exploitation of heterosis has been used for decades, first introduced by Darwin (1876). East (1908) and Shull (1908) claimed that hybrid F_1 or offspring had greater phenotypic characteristics than their parents. The phenomenon has subsequently investigated by Blum 2013, and the effect of increased grain yields is influenced by genetic components (Tollenaar et al. 2006), optimal growth conditions (Tollenaar et al. 2004) and physiological determinants in response to nitrogen (Hisse et al. 2019).

As breeding programs aim to increase crop yield, understanding genetic variability and heterosis has gained increasing important. On the other hand, the success of crop improvement depends on the chosen breeding material, variability, and understanding of quantitative traits related to yield and other factors. Genetic diversity is crucial for breeding success, as greater diversity increases heritability and the likelihood of selection success. The breeding material used contributes significantly to the overall effectiveness of the programme.

While numerous studies have explored genetic variability and heterosis in maize, limited comparative research has focused on how different hybrid types—specifically single-cross (SC), three-way cross (TC) and double-cross (DC) hybrids—differ in their expression of genetic variability and heterotic effects. Most existing studies emphasise either inbred lines or single hybrid types, leaving a gap in our understanding of how hybrid structure influences genetic performance. Addressing this gap is essential for optimising breeding strategies and improving maize yield potential under varying environmental conditions. To fill this gap, we compare genetic variability and heterosis among SC, TC, and DC hybrids, aiming to better understand the performance of these hybrid structures. This comparison will provide valuable insights for developing more effective breeding strategies that optimise maize yield potential across diverse environments.

This research focus on how different maize population types, with varying levels of genetic diversity, affect genetic variability and heterosis for yield and yield components. Specifically, we compare inbred parents, single-cross hybrids, three-way cross hybrids, and double-cross hybrids.

Materials and method

The maize seed genotypes used in this study were obtained from the Centre of Agricultural Research in Martonvásár and Szeged University. Single-cross, double-cross, and three-way cross hybrids, as well as their parents and a commercial check hybrid, were evaluated in the field during the spring growing season (May–November 2022). A total of nine parents, four single crosses, one double cross, and one three-way cross were tested. The commercial check hybrid was V16 (Table 1). The experiment was conducted at an experimental plot in Gödöllő, Hungary, between latitudes 47°59'46.46"N and 47°59'50.07"N, and longitudes 19°36'98.08"E and 19°37'02.81"E. In 2022, the average maximum temperature was 32.0°C (89.6°F), and the minimum was 20.0°C (68.0°F), while the total amount of precipitation was 917.2 mm (36.11 inches), with an average of 175.2 mm.

The type of soil in the experimental field was sand-based brown forest soil (Chromic Luvisol), which was prone to compaction. It had a neutral sand texture with varying clay content. The humus content was 3.18%, with sand, silt and clay levels of 10%, 54% and 36%, respectively, at the top 20 cm layer. Drought had an impact on the soil. The soil pH was 5.1 (KCl) and 6.2 (H₂O), both of which were slightly acidic. Parents, hybrids, and the commercial check hybrid were arranged in a randomised complete block design (RCBD) with three replicates, each containing 10 plants. Seeds were sown using a Wintersteiger Plotman maize planter at a density of 75,000 plants/ha, with 25 cm between plants and 70 cm between rows. The total experimental area, including buffer spacing, was approximately 0.01 ha. Weeding and irrigation were carried out as needed, and all treatments received standard agronomic practices. Data on plant height (PH), days to 50% flowering (DFF), ear weight (EW), ear length (EL), ear diameter (ED), number of rows per ear (RNPE), kernel number/ear (KNPE), and 1000-kernel weight (TKW) were measured to determine factors affecting yield.

Data analysis for variance components (ANOVA) was performed as recommended by Steel and Torrie (1980). Mean comparisons were performed using Duncan's Multiple Range Test (DMRT) at the 0.05 probability level. All statistical analyses were carried out using IBM SPSS Statistics version 23. Genotypic variances (σ_g^2), phenotypic variances (σ_p^2), phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV), broad sense heritability (h_b^2) and genetic advance (GA) were calculated with the method suggested by Allard (1960), and Singh and Chaudhury (1985).

Where,

MSG = Mean squares of genotypes, MSE = Mean squares of error, r = Number of replications, VE = Environmental variances, (σ_g^2) = Genotypic variances, (σ_p^2) = Phe-

notypic variances, \bar{I} = Grand mean and I = assumes a 5% (2.06) level of selection intensity. GCV and PCV were categorised as low (less than 10), moderate (less than 20), and high (greater than 20), as suggested by Burton (1952). Broad sense heritability (h_b^2) was expressed as the ratio of the amount of the genotypic variance (σ_g^2) to the phenotypic variance (σ_p^2). Heritability values were classified as low (less than 30), moderate (30–60) or high (greater than 60), as proposed by Johnson, Robinson and Comstock (1955).

Mid parent and high parent heterosis for each character was calculated using the following formula:

$$\text{Mid parent heterosis (\%)} = \frac{F1 - MP}{MP} \times 100$$

$$\text{High parent heterosis (\%)} = \frac{F1 - HP}{HP} \times 100$$

Where,

F₁ = Mean of the hybrid for a specific trait,

MP = Average mean of the parents for a specific trait

which = (P₁ + P₂)/2,

HP = Mean of the high parent in the cross for a specific trait, and

P₁ and P₂ represent the values of specific trait of the respective parents. The significance of the F₁ hybrids was assessed by using a t-test (Wynne et al., 1970) to compare the F₁ mean to both the mid-parent and high-parent means as follows:

$$t\text{-test} = \frac{F1 - MP}{\sqrt{\frac{3}{8} \times EMS}}$$

$$t\text{-test} = \frac{F1 - MP}{\sqrt{\frac{1}{2} \times EMS}}$$

Table 1. List of maize genotypes used in the study

No	Source	Entry	Genotypes	Description
1	Martonvásár	V1	(B1026/17) (SC, F)	Parent
2	Martonvásár	V2	(TK222/17)	TC Hybrid ²
3	Martonvásár	V3	(TKAPA15/DV) (SC, M)	Parent
4	Martonvásár	V4	(TK1083/19) (DC, F)	Parent
5	Martonvásár	V5	(TK623/18)	SC Hybrid ¹
6	Martonvásár	V6	(MCS901/19) (TC, F)	Parent
7	Martonvásár	V7	(TK256/17)	DC Hybrid ³
8	Szeged University	V8	(GK155)	Parent
9	Szeged University	V9	(GK131)	Parent
10	Szeged University	V10	(GK154 X155)	SC Hybrid ¹
11	Szeged University	V11	(Szegedi 521)	SC Hybrid ¹
12	Szeged University	V12	(GK154)	Parent
13	Szeged University	V13	(GK150)	Parent
14	Szeged University	V14	(GK144)	Parent
15	Szeged University	V15	(GK144X150)	SC Hybrid ¹
16	Commercial	V16	(MV277)	Commercial check hybrid

1SC Hybrid= Single cross hybrid; 2TC Hybrid= Triple cross hybrid; 3DC Hybrid= Double cross hybrid

Results and discussion

Variance and mean performance

The mean squares for eight characteristics from the analysis of variance (ANOVA) are presented in *Table 2*. Highly significant variation ($P < 0.01$) among genotypes was observed for all characteristics contributing to yield and yield components. This indicates a wide range of variability for plant height, days to 50% flowering, ear weight, ear length, ear diameter, number of rows/ear, number of kernels/ear and 1000-kernel weight, which can be exploited through selection in future breeding programs. Similar studies by Magar et al. (2021), Wan Rozita et al. (2022) and Rasheed et al. (2023) also revealed significant variation between genotypes for the characteristics studied, emphasising the importance of genotype-specific traits.

Table 3 presents a comparison of the mean yield and yield components. The hybrid V10 exhibited vigorous plant growth, with a plant height of 121.50 cm, showing a highly significant difference compared to the lowest plant height of the parent V8. Plant height is a crucial characteristic that allows the yield plant to compete directly with weeds and generally with other factors for light capture and photosynthetic activity (Abro et al. 2021).

Among the 16 genotypes studied, the SC hybrid of V10 was the earliest to flower, with a mean value of 58.20 days, followed by the parent of V9 of 59.00 days and the commercial hybrid of V16 at 67.33 days. The parent of V1 had the longest flowering date, taking 91.53 days (*Table 3*). Days to flowering is an essential characteristic that determines the duration of maturity, which contributes to the yield in maize. Earliness is particularly desirable in maize crops, as it assists the plants to avoid biotic and

abiotic stresses (Khan et al. 2019). Similar findings have been reported by Muchie and Fentie (2016) and Khan et al. (2019), who observed significant differences among the maize genotypes in terms of days to flowering. Additionally, Reddy et al. (1986) noted significant difference between hybrids and inbred lines. Therefore, for maize breeders, the earliness characteristic is crucial in selection, as it allows for a longer grain fill period before harvesting, ultimately leading to higher yields.

The SC hybrid of V10 exhibited the heaviest ear weight (105.89 g), followed by the TC hybrid of V2 at 100.0 g and the commercial hybrid of V16 (MV277) at 98.45 g. The parent of V12 had the lightest weight at 33.35 g. Additionally, the SC hybrid of V10 produced the longest ear length (16.13 cm), the highest rows number/ear (15.07) and the number of kernels/ear (436.27). In contrast, the parent of V1 had the shortest ear length (7.67 cm), the fewest rows number/ear (7.87) and the lowest number of kernels/ear (74.00). The TC hybrid of V2 (had the largest ear diameter (4.07 cm), while the parent of V1 had the smallest diameter (2.12 cm). The SC hybrid of V11 produced the highest 1000-kernel weight (438.87), while V3 (inbred line) had the lowest (217.00 g) (*Table 3*).

Ear weight is strongly correlated with grain yield, which is influenced by genotype and kernel set, but is also sensitive to environmental conditions, particularly during tasseling and silking (Cirilo and Andrade 1994). A higher number of kernel rows/ear positively impacts both grain weight and yield (Manivanan 1998), and these characteristics are also positively correlated with ear weight and kernel number. Khan et al. (2019) observed highly significant differences among maize genotypes for yield and its components, while Mojgan and Hamid (2008) found a positive correlation between grain yield and its components.

Table 2: Mean square for plant height, day to 50% flowering, ear weight, ear length, ear diameter, row number/ear, number of kernels/ear and 1000- kernel weight of different maize parents and hybrids

Characteristics	Genotype	Rep	Error	CV (%)	Mean
PH (cm)	8011.02**	1753.48**	98.49	8.56	84.95
DFF (50%)	1706.80**	431.00ns	56.51	0.09	75.50
EW (g)	7835.46**	479.77ns	194.3	0.20	69.75
EL (cm)	84.31**	8.15ns	3.2	0.14	12.43
ED (cm)	4.89**	0.05ns	0.16	0.11	3.49
RNPE	59.54**	1.61ns	1.47	0.10	12.35
NKPE	135166.00**	15076.00**	1089	0.15	215.52
OTKW (g)	49556.30**	35.81ns	804.4	0.09	315.64
	df = 15	df = 2	df = 222		

* PH, plant height (cm); DFF, days to 50% flowering; EW, ear weight (g); EL, ear length (cm); ED, ear diameter (cm); RNPE, row number/ear; NKPE, number of kernels/ear; OTKW, 1000-kernel weight (g).

df: Degree of freedom ** =Significant at P <0.01; * = Significant at P <0.05; ns = Not significant

Table 3. Mean performance for plant height, day to 50% flowering, ear weight, ear length, ear diameter, row number/ear, number of kernels/ear and 1000- kernel weight of different maize parents and hybrids

Genotype	PH	DFF (50%)	EW	EL	ED	RNPE	NKPE	OTKW
Parent								
V1 (B1026/17)	65.07 ^g	91.53 ^a	39.63 ^{ef}	7.67 ^g	2.12 ^g	7.87 ^f	74.00 ^h	301.00 ^e
V3 (TKAPA15/DV)	59.43 ^{gh}	89.40 ^{ab}	37.20 ^f	8.10 ^g	2.49 ^{fg}	10.53 ^{de}	113.87 ^{gh}	220.33 ^g
V4 (TK1083/19)	98.95 ^{cde}	74.53 ^{de}	60.61 ^d	11.43 ^{ef}	3.24 ^{de}	10.07 ^e	145.20 ^g	258.93 ^f
V6 (MCS901/19)	91.73 ^{def}	67.73 ^{ef}	67.61 ^{cd}	12.83 ^{c-f}	3.39 ^{b-e}	11.33 ^{de}	188.80 ^{ef}	244.20 ^{fg}
V8 (GK155)	51.80 ^h	84.27 ^{abc}	64.69 ^{cd}	12.16 ^{def}	3.89 ^{ab}	13.67 ^{ab}	219.00 ^{de}	368.03 ^b
V9 (GK131)	88.01 ^{ef}	59.00 ^{fg}	59.45 ^d	13.37 ^{cde}	3.86 ^{ab}	14.53 ^{ab}	262.13 ^c	308.83 ^{cde}
V12 (GK154)	67.68 ^g	80.00 ^{bcd}	33.35 ^f	11.53 ^{def}	2.96 ^{ef}	11.13 ^{de}	139.87 ^g	260.00 ^f
V13 (GK150)	58.51 ^{gh}	88.00 ^{ab}	60.30 ^d	11.26 ^{def}	3.73 ^{a-d}	13.20 ^{bc}	208.60 ^e	344.30 ^{bc}
V14 (GK144)	50.54 ^h	89.80 ^a	57.20 ^{de}	10.57 ^f	3.22 ^e	10.53 ^{de}	126.87 ^g	253.20 ^{fg}
Hybrid								
V5 (TK623/18) (SC)	101.09 ^{cd}	71.13 ^{de}	96.59 ^{ab}	15.87 ^{ab}	4.03 ^a	13.87 ^{ab}	329.13 ^b	362.37 ^b
V10 (GK154 X155) (SC)	121.50 ^a	58.20 ^g	105.87 ^a	16.13 ^a	3.90 ^a	15.07 ^a	436.27 ^a	342.03 ^{bc}
V11 (Szegedi 521; GK131XGK150) (SC)	100.98 ^{cd}	75.80 ^{cde}	81.66 ^{bc}	13.11 ^{cde}	3.78 ^{abc}	11.93 ^{de}	193.20 ^{ef}	438.87 ^a
V15 (GK144X GK150) (SC)	84.51 ^f	70.40 ^e	81.57 ^{bc}	13.38 ^{cde}	3.93 ^a	14.27 ^{ab}	272.33 ^c	305.33 ^{de}
V2 (TK222/17) (TC)	115.91 ^{ab}	69.40 ^e	100.46 ^a	14.97 ^{abc}	4.07 ^a	13.67 ^{ab}	325.67 ^b	349.00 ^b
V7 (TK256/17) (DC)	107.03 ^{bc}	71.40 ^{de}	71.32 ^{cd}	12.83 ^{c-f}	3.35 ^{cde}	12.00 ^{cd}	153.47 ^{fg}	339.97 ^{bcd}
V16 (MV277) (CH)	96.46 ^{c-f}	67.33 ^{efg}	98.45 ^{ab}	13.73 ^{bcd}	3.85 ^{abc}	13.93 ^{ab}	260.07 ^{cd}	353.80 ^b

* PH, plant height (cm); DFF, days to 50% flowering; EW, ear weight (g); EL, ear length (cm); ED, ear diameter (cm); RNPE, row number/ear; NKPE, number of kernels/ear; OTKW, 1000-kernel weight (g)

Values are presented as mean. Values with different superscript within the same column are significantly different P ≤ 0.05 based on Duncan's Multiple Range Test (DMRT)

Genetic variability

The estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and components of variance for eight characteristics contributing to yield components are presented in Table 4. A notable difference between genotypic and phenotypic variances was observed for plant height, days to 50% flowering, ear weight, number of kernels/ear, and 1000-kernel weight, suggesting that the phenotypic expression of these traits is predominantly influenced by environmental factors

(Belay 2018). The characteristics assessed in this study exhibited varying degrees of variation, with low (less than 10%), moderate (10 – 20%) and high (greater than 20%) coefficients of variation for both the phenotypic and genotypic measures. These findings align with those reported by Magar et al. (2021).

The GCV values ranged from 1.44% for 1000-kernel weight to 91.47% for ear diameter, while the PCV values varied from 9.10% for 1000-kernel weight to 92.18% for ear diameter. For plant height, days to 50% flowering, and number of kernels/ear, low GCV values (6.12%, 4.20%,

and 2.98%) were accompanied by moderate PCV values (13.19%, 10.81%, and 15.59%), respectively. Conversely, ear length, ear diameter, and row number per ear exhibited high GCV values (23.83%, 91.47% and 29.75%) along with high PCV values (27.85%, 92.18% and 31.33%). Ear weight displayed low GCV (5.25%) but relatively high PCV (20.66%), whereas 1000-kernel weight showed both low GCV (1.44%) and low PCV (9.15%).

The observed higher magnitude of PCV compared to GCV across all characteristics in this study indicates that environmental factors play a significant, though not overwhelming, role in the phenotypic expression of these characteristics. Despite this, the presence of substantial phenotypic variation suggests that selection for these traits can still be effective, even at the phenotypic level. These results are in agreement with prior studies by Sesay et al. (2016) and Belay (2018), further supporting the effectiveness of phenotypic selection in crop improvement.

Heritability (h^2_p) in broad sense and genetic advance

The estimates of broad-sense heritability and genetic advance, expressed in percentages, are presented in *Table 4*. Ear length, ear diameter, and row number/ear exhibited extremely high heritability (>80%). Similar results were reported by Sasey et al. (2016) for the ear length. These characteristics demonstrated high genetic variation and low environmental influence, suggesting that improvement of these characteristics could be effectively achieved through phenotypic selection (Belay 2018). High heritability estimates indicate that the observed variations are likely to be inherited by offspring, thereby facilitating the development of high-yielding varieties through the selection of desirable genotypes and plant material with favourable traits (Magar et al. 2021). Moderate heritability estimates (30 – 60%) were observed for plant height and days to 50% flowering. These findings align with previous reports by Sesay et al. (2016) and Belay (2018). In contrast, low heritability estimates (less than 30%) were found for ear weight, number of kernels/ear, and 1000-kernel weight.

The highest genetic advance was recorded for the number of kernels (13.23), followed by plant height (10.71), while ear length (6.10) had the lowest genetic advance. The genetic advance estimates provide insights into the type of gene activity involved in expression of various polygenic characteristics. According to Singh and Narayan (1993), high genetic advance values indicate additive gene action, whereas low values are indicative of non-additive gene action. Additive gene effects govern characteristics, leading to higher heritability and genetic advance, whereas non additive gene action may result in high heritability but poor genetic advance (Mohana Krishna et al. 2009). Consequently, heritability and genetic advance are key selection parameters, with the estimation of genetic advance being particularly informative when combined with heritability estimates (Johnson et al. 1955).

Heterosis

Heterosis was observed to be significant for all characteristics studied, as illustrated in *Table 5*. Standard heterosis for plant height ranging from 12.26% – 103.38% and 14.74% – 134.56% over mid parent and better parent (*Table 5*). The maximum positive heterosis was recorded in the SC hybrid of V15, with 103.38% over the mid parent and 134.56% over the high parent. Conversely, the minimum heterosis effect was exhibited for SC hybrid V11, which displayed a value of 12.26% over the mid parent and 16.68% over the high parent. These findings are consistent with previous studies on the heterosis effect of plant height in maize, including work on three-way cross hybrids (Iqbal et al. 2010; Zaid et al. 2014).

Table 5 also presents the percentage of heterosis between mid parent and high parent for days to 50% flowering. The mid parent heterosis values ranged from -29.14% to 3.13%, while the high parent values ranged from -30.94% to 28.47%. Notably, the TC hybrid of V2 exhibited a significant positive mid parent heterosis of 3.13%, whereas the SC hybrid of V15 demonstrated a negative mid parent value of -29.14%. The highest positive high parent heterosis value, 28.47%, was observed in the TC hybrid of V2, while the lowest negative high parent heterosis value, -30.94%, was recorded in the SC hybrid of V15. These findings are consistent with the study by Geleta and Labushagne (2004), which also reported superior performance of TC hybrids for this characteristic.

The percentages of heterosis values for ear weight, ear length, and ear diameter over the mid parent ranged from 11.25% to 161.23%, 6.46% to 107.45%, and -13.68% to 79.06%, respectively (*Table 5* and *Table 6*). In contrast, the heterosis values over the high parent ranged from 5.49% to 143.73, -1.94% to 106.91 and -12.06 to 89.62% or ear weight, ear length and ear diameter, respectively. The SC hybrid of V5 demonstrated the highest positive mid parent and high parent heterosis for ear weights (161.23% and 143.73%), ear lengths (107.45% and 106.91%), and ear diameters (79.06% and 89.62%), respectively. Conversely, the lowest mid parent and high parent heterosis values were observed in the SC hybrid of V11 for ear weight (11.25% and 5.49%), and in the TC hybrid of V2 for ear length (6.46% and -1.94) and ear diameter (-13.68% and 12.06%), respectively. The results contradicted those of Geleta and Labushagne (2004), who found that TC hybrids outperformed SC and DC hybrids in terms of heterosis for ear weight, ear length and ear diameter. However, as noted by Virmani et al. 1982 and Young and Virmani, 1990, yield heterosis is a variable characteristic influenced not only by parent combinations but also by environmental factors.

Table 6 presents the heterosis values for kernel number/ear and number of kernels/ear. For kernel number/ear, heterosis ranged from 13.94% to 50.73% over the mid parent, and from -17.92% to 273.45% over the high parent. In contrast, heterosis for the number of kernels/ear varied from -9.60% to 76.27% over the mid parent

and from -18.71% to 344.77% over the high parent. The SC hybrid of V5 recorded the highest heterosis for row number/ear, with values of 50.73% over the mid parent and 76.27% over the high parent. In contrast, the TC hybrid of V2 exhibited the lowest heterosis for this trait, with values of -13.94% over the mid parent and -9.60% over the high parent. For kernel number/ear, the SC hybrid of V5 again showed the highest heterosis, with 273.45% over the mid parent and 344.77% over the high parent. On the other hand, the TC hybrid of V2 recorded a minimum mid-parent heterosis of -17.92%, while the SC hybrid of V11 (GK131XGK150) showed the lowest heterosis values for both the mid parent and high parent.

The heterosis values for 1000-kernel weight ranged from 2.20% to 39.02% over the mid parent and from -11.32% to 42.92% over the high parent (Table 6). The highest heterosis over the mid parent was recorded for the SC hybrid of V5 at 39.02%, while the highest over the high parent was recorded for the SC hybrid of V10 at 42.92%. Conversely, the lowest heterosis values were observed in the DC hybrid of V7, with 2.20% over the

mid parent and -11.32% over the high parent. These findings align with previous studies by Zaid et al. (2014), which reported a positive increase in maize crosses for 1000-kernel weight.

The current study found that single cross hybrids (SC) outperformed three-way cross hybrids (TC) and double cross hybrids (DC) in terms of yield and yield components, highlighting varying degrees of heterosis among the three hybrid types. Additionally, SC hybrids demonstrated greater uniformity, while DC hybrids exhibited the highest heterogeneity, particularly when different genetic backgrounds were used to generate the hybrids (Geleta and Labuschagne, 2004). However, each cross-combination was found to excel in specific traits, emphasising the value of selecting the appropriate hybrid for particular characteristics.

Table 4. Estimation of genotypic and phenotypic coefficient variation, heritability and genetic advance for plant height, day to 50% flowering, ear weight, ear length, ear diameter, row number/ear, number of kernels/ear and 1000-kernel weight of different maize parents and hybrids

Characteristics	Mean	σ^2_g	σ^2_p	GCV (%)	PCV (%)	h ² B	GA
PH (cm)	84.95	27.11	125.60	6.12	13.19	46.39	10.71
DFF (50%)	75.50	10.06	66.57	4.2	10.81	38.85	6.53
EW (g)	69.75	13.44	207.74	5.25	20.66	25.41	7.54
EL (cm)	12.43	8.78	11.98	23.83	27.85	85.57	6.10
ED (cm)	3.49	10.19	10.35	91.47	92.18	99.23	6.58
RNPE	12.35	13.50	14.97	29.75	31.33	94.96	7.57
NKPE	215.52	41.37	1130.37	2.98	15.59	19.11	13.23
OTKW (g)	315.64	20.53	824.93	1.44	9.1	14.82	8.77

* PH, plant height (cm); DFF, days to 50% flowering; EW, ear weight (g); EL, ear length (cm); ED, ear diameter (cm); RNPE, row number/ear; NKPE, number of kernels/ear; OTKW, 1000-kernel weight (g)

Table 5. Mid and high parent heterosis for plant height, day to 50% flowering, ear weight, ear length of different maize hybrids

Hybrids	PH (cm)		DFF (50%)		EW (g)		EL (cm)	
	Mid parent (%)	High parent (%)	Mid parent (%)	High parent (%)	Mid parent (%)	High parent (%)	Mid parent (%)	High parent (%)
V5 (TK623/18) (SC)	62.39**	55.36*	-21.37**	-22.29**	161.23**	143.73**	107.45**	106.91**
V10 (GK154 X155) (SC)	47.84*	26.36	-12.85	2.47	87.36**	48.59**	46.05**	23.01
V11 (Szegedi 521; GK131XGK150) (SC)	12.26	16.68	0.38	5.42	11.25	5.49	8.73	5.42
V15 (GK144X GK150) (SC)	103.38**	134.56**	-29.14**	-30.94**	116.01**	63.69**	36.18**	32.65**
V2 (TK222/17) (TC)	37.84*	14.74	3.13*	28.47	36.38*	35.42**	6.46	-1.94
V7 (TK256/17) (DC)	54.99*	44.44*	-18.14	-20.00*	38.84*	35.27*	22.583*	18.83

*PH, plant height (cm); DFF, days to 50% flowering; EW, ear weight (g); EL, ear length (cm)

** =Significant at $P < 0.01$; * = Significant at $P < 0.05$

Table 6. Mid and high parent heterosis for ear diameter, row number/ear, number of kernels/ear and 1000- kernel weight of different maize hybrids

Hybrids	ED (cm)		RNPE		NKPE		OTKW (g)	
	Mid parent (%)	High parent (%)	Mid parent (%)	High parent (%)	Mid parent (%)	High parent (%)	Mid parent (%)	High parent (%)
V5 (TK623/18) (SC)	79.06**	89.62**	50.73**	76.27**	273.45**	344.77**	39.02**	20.39**
V10 (GK154 X155) (SC)	48.00**	20.41*	42.36**	20.58**	147.84**	72.49**	28.03**	42.92**
V11 (Szegedi 521; GK131XGK150) (SC)	1.66	-0.30	12.15	5.88	-8.10	-18.71	35.14**	39.22**
V15 (GK144X GK150) (SC)	14.37*	0.78	21.51**	10.24*	143.14**	99.21**	8.92	-7.06
V2 (TK222/17) (TC)	-13.68*	-12.06	-13.94*	-9.6*	-17.92*	-7.38	34.39**	27.47**
V7 (TK256/17) (DC)	12.77	5.36	20.23**	8.08	62.36**	30.55*	2.20	-11.32

*ED, ear diameter (cm); RNPE, row number/ear; NKPE, number of kernels/ear; OTKW, 1000-kernel weight (g)

** =Significant at P <0.01; * = Significant at P <0.05

Conclusion

All characteristics exhibited significant differences, indicating the presence of genetic variability among the maize genotypes, which can be utilized for yield improvement. The magnitude of the phenotypic coefficient of variation (PCV) was larger than the genotypic coefficient of variation (GCV) for each characteristic examined, suggesting that environmental factors influenced the phenotypic expression of these traits. Higher GCV, PCV, and heritability values were observed for ear length, ear diameter, and row number/ear, while ear weight showed low GCV, high PCV and low heritability. The highest genetic advance was recorded for the number of kernels and plant height, whereas ear length showed the lowest genetic advance. The high GCV, PCV, heritability and genetic advance for several characteristics suggest the potential for improvement in grain yield.

In contrast to previous studies comparing single crosses (SC), three-way crosses (TC), and double crosses (DC), this study found that SC hybrids exhibited significantly stronger heterosis effects on yield and yield components than TC and DC hybrids, both over the mid and high parents. This underscores the potential of SC hybrids for improving maize productivity. However, the heterogeneity observed in TC and DC hybrids shows promising potential and could be leveraged for future breeding programs. These genetically diverse hybrid groups may help safeguard populations against biotic and abiotic stresses. Nevertheless, further extensive investigations are needed to confirm these findings, considering additional factors—primarily environmental variables and increasing both the population size and hybrid combinations in future studies.

References

- Abro, T. F., Kaloi, A. A., Sootaher, J. K., Shar, P. A., Baloch, T. A., Soomro, T. A., Chang, M. S., Menghwar, K. K. & Shah, W. H. (2021). Assessment of genetic variability in F4 populations of upland cotton (*Gossypium hirsutum* L.). *Sarhad Journal of Agriculture*, 37(3), 722–734.
- Al-Tabbal, J. A. & Al-Fraihat, A. H. (2012). Genetic variation, heritability, phenotypic and genotypic correlation studies for yield and yield components in promising barley genotypes. *Journal of Agricultural Science*, 4(3), 193.
- Alake, C. O., Ojo, D. K., Oduwaye, O. A. & Adekoya, M. A. (2008). Genetic variability and correlation studies in yield and yield-related characters of tropical maize (*Zea mays* L.). *Asset Series A*, 8(1), 14–27.
- Allard, R. W. (1960). *Principles of plant breeding*. John Wiley & Sons.
- Aremu, C. (2012). Exploring statistical tools in measuring genetic diversity for crop improvement. In *Genetic Diversity in Plants*. <https://doi.org/10.5772/34950>.
- Belay, N. (2018). Genetic variability, heritability, correlation, and path coefficient analysis for grain yield and yield component in maize (*Zea Mays* L.) hybrids. *Advances in Crop Science and Technology*, 6(5). <https://doi.org/10.4172/2329-8863.1000399>.
- Blum, A. (2013). Heterosis, stress, and the environment: A possible road map towards the general improvement of crop yield. *Journal of Experimental Botany*, 64, 4829–4837.
- Bocanski, J., Sreckov, Z. & Nastasic, A. (2009). Genetic and phenotypic relationship between grain yield and components of grain yield of maize (*Zea mays* L.). *Genetika*, 41(2), 145–154. <https://doi.org/10.2298/GENSR0902145B>.
- Cirilo, A. G. & Andrade, F. H. (1994). Sowing date and maize productivity: I. Crop growth and dry matter partitioning. *Crop Science*, 34, 1039–1043. <https://doi.org/10.2135/cropsci1994.0011183X003400040037x>
- Darwin, C. R. (1876). *The origin of species by means of natural selection, or the preservation of favoured races in the struggle for life* (6th ed.). John Murray.
- East, E. M. (1908). Inbreeding in corn. *Report of the Connecticut Agricultural Experiment Station, 1907*, 419–428.

- Erenstein, O., Jaleta, M. & Sonder, K. (2022). Global maize production, consumption, and trade: Trends and R&D implications. *Food Security*, 14, 1295–1319. <https://doi.org/10.1007/s12571-022-01288-7>.
- FAO (2022). *FAOSTAT database. Food and Agriculture Organisation of the United Nations*. <http://www.fao.org/faostat/en/#home>
- Geleta, L. F. & Labuschagne, M. T. (2004). Comparative performance and heterosis in single, three-way, and double-cross pepper hybrids. *The Journal of Agricultural Science*, 142(6), 659–663. <https://doi.org/10.1017/S0021815960400440X>.
- Ghosh, A. (2014). Genetic variability and character association of grain yield components in some inbred lines of maize (*Zea mays* L.). 1, 34–39.
- Grzesiak, S. (2001). Genotypic variation between maize (*Zea mays* L.) single-cross hybrids in response to drought stress. *Acta Physiologiae Plantarum*, 23(4), 443–456.
- Hallauer, A. R. (1972). Third phase in yield evaluation of synthetic varieties of maize. *Crop Science*, 12, 16–18.
- Hisse, I. R., D'Andrea, K. E. & Otegui, M. E. (2019). Source-sink relations and kernel weight in maize inbred lines and hybrids: Responses to contrasting nitrogen supply levels. *Field Crops Research*, 230, 151–159.
- Ihsan, H., Khalil, I. H., Rehman, H. & Iqbal, M. (2005). Genotypic variability for morphological traits among exotic maize hybrids. *Sarhad Journal of Agriculture*, 21(4), 599–602.
- Iqbal, M., Khan, K., Rahman, H., Khalil, I. H., Sher, H. & Bakht, J. (2010). Heterosis for morphological traits in subtropical maize (*Zea mays* L.). *Maydica*, 55, 41–48.
- Johnson, H. W., Robinson, H. F. & Comstock, R. E. (1955). Estimates of genetic and environmental variances in soybeans. *Agronomy Journal*, 47, 314–318.
- Khan, A. H., Minhas, N. M., Asad, J., Iqbal, A., Ilyas, M. & Mahmood, R. T. (2014). Estimation of protein, carbohydrate, starch and oil contents of indigenous maize (*Zea mays* L.) germplasm. *Academic Research International*, 2(4).
- Koutsika-Sotiriou, M. (1999). Hybrid seed production in maize. In A. S. Basra (Ed.), *Heterosis and hybrid seed production in agronomic crops* (pp. 25–64). Food Products Press.
- KSH. (2022). *Agricultural production statistics*. Hungarian Central Statistical Office. <https://www.ksh.hu/>.
- Magar, B. T., Subash, A., Bibek, G., Kiran, T., Jharana, U. & Jiban, S. (2021). Genetic variability and trait association in maize (*Zea mays* L.) varieties for growth and yield traits. *Heliyon*, 7(9), e07939. <https://doi.org/10.1016/j.heliyon.2021.e07939>.
- Mahiboobsa, M., Dharmaraj, P. S., Muniswamy, S., Sony, Y. T., Avinalappa, H., Patil, R. & Bankar, C. (2012). Genetic variability studies on stable male sterile, maintainer and restorer lines of pigeonpea [*Cajanus Cajan* (L.) Millsp.]. *Karnataka Journal of Agricultural Sciences*, 25(4), 525–526.
- Manivannan, N. (1998). Character association and component analysis in maize. *Madras Agricultural Journal*, 85(5/6), 293–294.
- Maqbool, R., Sajjad, M., Khaliq, I., Azizur-Rehman, Khan, A. S. & Khan, S. H. (2010). Morphological diversity and traits association in bread wheat (*Triticum aestivum* L.). *American-Eurasian Journal of Agricultural and Environmental Sciences*, 8, 216–224.
- Messmer, M. M., Lantican, M. A. & Blair, M. W. (2011). Genetic diversity and its impact on maize productivity and resilience to biotic stresses. *Field Crops Research*, 120(3), 295–302. <https://doi.org/10.1016/j.fcr.2011.09.001>
- Mohana, K. D., Reddy, D. M., Reddy, K. H. P. & Sudhakar, P. (2009). Character association and interrelationship of yield and quality attributes in rice (*Oryza sativa* L.). *Andhra Agricultural Journal*, 56(3), 298–301.
- Suhana, O., Rosnani, A. G., Noriza, K., Zoltan, K. and Marton, J.
- Mojgan, B. & Hamid, A. (2008). Correlation coefficient analysis between grain yield and its components in corn (*Zea mays* L.) hybrids. *International Meeting on Soil Fertility, Land Management and Agroclimatology, Special Issue*, 263–265.
- Muchie, A. & Fentie, D. (2016). Performance evaluation of maize hybrids (*Zea mays* L.) in Bahir Dar Zuria District, North Western Ethiopia. *International Resource Journal of Agricultural Soil Science*, 3, 37–43.
- Nagabhushan, N. M., Mallikarjuna, C. H., Shashibhaskar, M. S. & Prahalada, G. D. (2011). Genetic variability and correlation studies for yield and related characters in single-cross hybrids of maize (*Zea mays* L.). *Current Biotica*, 5, 157–163.
- Rasheed, A., Muhammad, I., Taj Naseeb, K., Athar, M., Usama, R., Muhammad Bilal, C., Najla, A. T. Kashgry A. (2023). Study of genetic variability, heritability, and genetic advance for yield-related traits in tomato (*Solanum Lycopersicon* MILL.). *Frontiers in Genetics*, 13. <https://doi.org/10.3389/fgene.2022.1030309>.
- Reddy, P. R. R., Satyanarayana, E. & Kumar, R. S. (1986). Maturity components of inbred lines and single crosses of maize (*Zea mays* L.). *Annals of Agricultural Research*, 7, 337–342.
- Salasya, B. D. S., Mwangi, W., Verkuijl, H., Odendo, M. A. & Odenya, J. O. (1998). An assessment of the adoption of seed and fertilizer packages and the role of credit in smallholder maize production in Kakamega and Vihiga districts, Kenya. CIMMYT and KARI.
- Sesay, S., Ojo, D. K., Ariyo, O. & Meseka, S. (2016). Genetic variability, heritability, and genetic advance studies in top-cross and three-way cross maize (*Zea Mays* L.) hybrids. *Maydica*, 61, M12, 1–7.
- Shull, G. H. (1908). The composition of a field of maize. *Journal of Heredity*, 4, 296–301.
- Singh, R. K. & Chaudhary, B. D. (1985). *Biometrical methods in quantitative genetic analysis*. Kalyani Publishers.
- Singh, P. & Narayanan, S. S. (1993). *Biometrical techniques in plant breeding*. Kalyani Publishers.
- Steel, R. G. D. & Torrie, J. H. (1980). *Principles and procedures of statistics: A biological approach* (2nd ed.). McGraw-Hill.
- Tena, A., Delos, D. & Suarez, M. R. (2016). Role of genetic diversity in improving maize resistance to biotic stresses. *International Journal of Plant Breeding and Genetics*, 10(1), 42–49. <https://doi.org/10.1080/09724966.2016.1201234>.
- Tollenaar, M., Ahmadzadeh, A. & Lee, E. A. (2004). Physiological basis of heterosis for grain yield in maize. *Crop Science*, 44, 2086–2094.
- Tollenaar, M., Deen, W., Echarte, L. & Liu, W. (2006). Effect of crowding stress on dry matter accumulation and harvest index in maize. *Agronomy Journal*, 98, 930–937.
- Virmani, S. S., Aquino, R. C. & Khush, G. S. (1982). Heterosis breeding in rice (*Oryza sativa* L.). *Theoretical and Applied Genetics*, 63, 370–380.
- Wan Rozita, W. E., Noraziyah A. A. S., Suhana O., Farahzety A. M., Norfadzilal A. F. & Rosniza K. (2022). Estimation of heritability and genetic variability in selected F1 bitter melon population for yield and its contributing traits. *Food Research*, 6(4), 1–8. [https://doi.org/10.26656/fr.2017.6\(s4\).001](https://doi.org/10.26656/fr.2017.6(s4).001).
- Wynne, J. C., Emery, D. A. & Rice, P. W. (1970). Combining ability estimates in *Archihypogae* L. II. Field performance of F1 hybrids. *Crop Science*, 10, 713–715.
- Young, J. & Virmani, S. S. (1990). Heterosis in rice over environments. *Euphytica*, 51, 87–93.
- Zaid, I. U., Hidayatur, R., Sajid, K., Sana, U. K., Ghulam, U., Monsifur, R., Rafi, U. Nazeer, A. (2014). Heterotic response of three-way cross maize hybrids for grain yield and yield components. *Journal of Agricultural Science and Applications*, 3(1), 24–29. <https://doi.org/10.14511/jasa.2014.030105>.

Zeeshan, M., Ahsan, M., Arshad, W., Ali, S., Hussain, M. & Khan, M. I. (2013). Estimate of correlated responses for some polygenic parameters in yellow maize (*Zea mays* L.) hybrids. *International Journal of Advanced Research*, 1(5), 24–29. <https://www.journalijar.com>.