Research Article:

EVALUATION OF MAIZE GENOTYPES FOR AGRO-MORPHOLOGICAL AND YIELD TRAITS UNDER MID-HILL CONDITIONS OF NEPAL

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Received date: 09 September 2025, Accepted date: 26 December 2025
DOI: https://doi.org/10.3126/jafu.v6i2.88462

ABSTRACT

The present study was conducted to evaluate the extent of agro-morphological variability, heritability, and genetic advance among nine maize genotypes, with the aim of identifying traits useful for yield improvement. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. The plot size was 3m×2.5m with the spacing of 60cm×25cm and the experiment was carried out from June 2019 to October 2019. Data were recorded on key phenological, morphological, and yield-related traits, including plant height, ear height, days to 50% tasseling and silking, anthesis–silking interval, ear and plant aspects, yield components, and grain yield. Data were analyzed through R-Studio. Analysis of variance revealed significant differences among genotypes for most of the traits studied, indicating the presence of sufficient genetic variability. Grain yield varied widely, ranging from 4.12 to 9.65 t ha^{-1}, with a mean yield of 6.69 t ha^{-1}. For most of the traits, the value of genotypic coefficient of variation (GCV) was close to the phenotypic coefficient of variation (PCV), suggesting that the observed variation was largely governed by genetic factors with minimal environmental influence. High heritability (≥0.80) was observed for days to 50% tasseling, days to 50% silking, ear height, and number of ears per plot. Among these traits, ear height exhibited high heritability coupled with substantial genetic advance, indicating the predominance of additive gene action. The high heritability and genetic advance observed in several traits are particularly important because the evaluated genotypes mainly consisted of hybrids and released varieties, which are generally expected to show reduced variability. The presence of high heritable variation in these materials suggests that further genetic improvement through selection is feasible. Therefore, ear height emerged as a reliable selection criterion for improving grain yield and overall performance in maize breeding programs.

सारांश

यस अध्ययनको उद्देश्य नौ वटा मकैका जातहरूको विभिन्न गुणहरू र उत्पादनमा भएको भिन्नतालाई मूल्याङ्कन गर्नु थियो । यो परीक्षण अनियमित पूर्ण ब्लक ढाँचामा तीन पटक दोहोर्‍याई गरिएको थियो । विभिन्न गुणहरू जस्तै घोगाको लम्बाई; बोटको उचाई; ५०% चमारा निस्कने दिन; ५०% जुंगा निस्कने दिन; चमरा र जुँगा निस्कने दिनको अन्तराल; बोट, घोगा तथा खोसेलाको स्वरूप; सङ्कलित घोगाको संख्या; प्लटमा बोटको संख्या; प्लटमा घोगाको संख्या; पाँच घोगाको तौल; प्रति घोगा दानाको पङ्क्तिको संख्या; घोगाको व्यास; टुप्पासम्म घोगाको लम्बाई; हजार दानाको तौल र मकैको उत्पादनको अभिलेख राखिएको थियो । प्रसरण विश्लेषणले अधिकांश गुणहरूमा जातहरू बिच साङ्ख्यिक रूपमा उल्लेख्यपूर्ण फरक देखायो । यस अध्ययनमा अधिकतम उत्पादन ९.६५ टन/हेक्टर र न्यूनतम ४.१२ टन/हेक्टर पाइयो भने औसत उत्पादन ६.६९ टन/हेक्टर थियो । अधिकांश गुणहरूमा आनुवंशिक गुणक भिन्नता (GCV) र रूपगत गुणक भिन्नता (PCV) बिच कम मात्रामा फरक देखियो । ५०% चमरा निस्कने दिन, ५०% जुंगा निस्कने दिन,

घोगाको लम्बाई र प्लटमा घोगाको संख्या जस्ता गुणहरूमा उच्च वंशाणुगतता (≥०.८) पाइयो । वंशानुगतता र आनुवांशिकी प्रगति अनुसार मकैको घोगाको लम्बाईलाई प्रत्यक्ष रूपमा चयन गरेर हाइब्रिड मकैको सुधार गर्न सकिन्छ ।

Keywords: Agromorphological traits, grain yield, heritability, maize yield parameters

INTRODUCTION

Maize is one of the world's most important food crops, alongside rice and wheat, providing over 30% of the dietary calories for more than 4.5 billion people across 94 developing countries (Shiferaw et al., 2011). In terms of area and production, it is the second most important cereal crop after rice in Nepal (MoALD, 2024). It is cultivated on 0.98 million hectares of land, producing 3.1 million tons with a productivity of 3.15 t/ha (MoALD, 2024). It is a highly preferred crop due to its adaptability, as it can be cultivated in nearly all seasons and regions. Maize production in Nepal has increased from 0.83 million tons in 1970 to 2.65 million tons in 2019 with an average annual rate of 2.73% (Ghimire et al., 2018). Mid hills occupy 70%, terai occupy 22% and high hills occupy 8% of the total area under maize production. Maize contributes approximately 9.5% to Nepal's Agricultural Gross Domestic Product (Ghimire et al., 2018). For many farmers in the hills of Nepal, cultivating maize is an essential part of their way of life (Adhikari, 2000). Due to yield advantage hybrid maize varieties are becoming popular in Nepal. It is estimated that hybrids can produce 25-30% higher grain yield as compared to open-pollinated varieties.

The number of ears per plant, the number of kernels per row, the number of kernel rows per ear, and the thousand-kernel weight influence the grain yield (Viola et al., 2003). These components collectively determine the grain yield. Traits such as ear length, ear diameter, grain number per ear, and 1000-kernel weight exhibit a strong positive correlation with grain yield, indicating their critical role in yield determination (Reddy et al., 2022). Focusing on these positively correlated traits, breeders can make informed decisions that help in the improvement of complex traits, and ultimately leads to more efficient and targeted breeding programs (Zeng et al., 2022).

Developing high-yielding hybrid varieties better than existing open-pollinated, synthetic, or composite varieties is one of the major objectives of the maize breeding programs because it has a yield advantage, due to which it is popular among the farming community (Patel et al., 2020). In the case of Nepal, testing of most released varieties is conducted at a research station only, resulting in a gap in extension services. Directly planting in the farmer's field without pre-testing of the hybrid varieties might lead to lower yield than expected (Gurung et al., 2011). Many hybrid maize varieties are available in the Nepali market, offering diverse choices for farmers, but choosing a suitable variety is difficult due to diverse agro-ecological conditions. In crop improvement, genetic variation and its analysis are very crucial components for the selection of desirable genotypes with suitable characters (Dudley & Moll, 1969). Maintaining a suitable level of genetic variability for economically significant traits plays a crucial role in the hybrid maize breeding program. Heritability and genetic gain help to estimate the genetic gain under selection. Multivariate analysis based on principal component analysis helps to understand the genetic diversity among different genotypes (Brown-Guedira, 2000).

Due to the limited research, evaluation, and understanding of maize varieties adapted to the mid-hill regions of Nepal (Neupane et al., 2020), this study was undertaken to assess the genetic variability among diverse maize genotypes, including hybrids, focusing on phenological traits, agro-morphological characteristics, and yield-related attributes. The findings are expected to aid maize breeding programs by identifying promising genotypes with desirable traits for future varietal development and recommendations.

RESEARCH METHODS

Nine maize genotypes were included in this study. They were obtained from the Agriculture Botany Division NARC, Khumaltar, Nepal. The plant materials tested were 5 hybrids (KWM-93*KWM-91, Khumal Hybrid-2, and chinese hybrids; LPM-163, LPM-166, LPM-153), 4 released varieties (Deuti, Manakamana-3, Manakamana-7 and Manakamana-4 as a local check). The field experiment was conducted at the research farm of the Valley Agriculture Campus, Jharuwarasi, Lalitpur, Nepal, from June to October 2019. The site is located at 27°37′ N latitude and 85°20′ E longitude, at an altitude of 1,349 m above sea level, and is characterized by moderate to high rainfall. The soil of the experiment field was silty loam. The experimental design was Randomized Complete Block Design(RCBD) with three replications. The plot size was 3m×2.5m with the spacing of 60cm×25cm—the total number of plants per plot was 50 with 10 rows each containing 5 plants. The fertilizer was applied at the rate of 120:60:40 NPK kg/ha. Half dose of nitrogenous fertilizer and full dose of phosphorus and potash was applied as basal dose and remaining half dose of nitrogenous fertilizer was applied in two split doses, that is, in knee height stage and tasseling stage. Irrigation was supplied as per the need of the crop.

For the purpose of data recording, in each plot, ten plants from the middle rows were randomly selected. Different phenological traits (days to 50% tasseling, days to 50% silking, anthesis silking interval), agromorphological traits (plant aspect, ear aspect, husk cover, number of ear harvested, number of plant per plot, number of ear per plot, ear height, and plant height), and yield attributing traits (five ear weight, number of kernel row per ear, ear diameter, ear length, ear length up to tip, thousand-grain weight, grain yield) were recorded.

Before performing the analysis of variance (ANOVA), the assumption of homogeneity of variance was tested. Analysis of variance (ANOVA) and mean comparisons were performed using RStudio software (version 4.3.1) at a 5% level of significance ($p \leq 0.05$). The least significant difference (LSD) was used to compare and separate genotype means following a significant ANOVA. Principal component analysis (PCA) was carried out by using FactoExtra, FactoMineR and Gridextra packages of R software. A hierarchical cluster dendrogram was conducted using average linkage method and Euclidean distance from the Dendextend package.

All the components of the variance, heritability, and genetic advance components were computed as the calculation described by Baye (2002). Genotypic, phenotypic, and error variance were calculated as follows:

$$GV = \frac{(MSG\text{-}MSE)}{r}$$

$$EV = MSE$$

$$PV = GV + EV$$

Where, MSG, MSE and r are the mean sum of squares of genotypes, error and number of replication respectively. Phenotypic (PCV) and genotypic (GCV) coefficient of variation were calculated as follows:

$$\mathrm{PCV} = \sqrt{(\frac{PV}{\underline{X}})} \times 100$$

$$\mathrm{GCV} = \sqrt{(\frac{GV}{\underline{X}})} \times 100$$

where PV, GV and are the phenotypic variances, genotypic variances and grand mean of traits of the genotypes, respectively. Broad sense heritability (H_{bs}) was expressed as the ratio between GV and PV. Genetic advance (GA) expected and genetic advance as a percent of mean (GAM) assuming selection of 5% of the genotypes were estimated as:

$$GA = K(S_p)H_{bs}$$

$$GCV = \sqrt{(\frac{GV}{\underline{X}})} \times 100$$

where K is constant (assuming top 5% selection, value of K is 2.06), Sp is the phenotypic standard deviation, Hbs is heritability ratio and is the grand mean of traits of genotypes.

RESULTS AND DISCUSSION

Analysis of variance

The analysis of variance revealed significant differences among the maize genotypes for most phenological and yield-related traits, including grain yield, indicating the presence of substantial genetic variability among the tested genotypes (Table1 and Table 2). Such variability is essential for effective selection and genetic improvement in maize breeding programs. In contrast, traits such as anthesis–silking interval, plant aspect, ear aspect, husk cover, number of plants per plot, ear diameter, and thousand-grain weight exhibited non-significant differences, suggesting a relatively narrow genetic base or greater environmental influence on these traits under the experimental conditions. Grain yield, being a complex trait governed by the interaction of multiple genetic and environmental factors, showed considerable variation among the genotypes. The observed variability in grain yield supports the findings of Raut et al. (2017), who reported significant yield differences among maize genotypes under field conditions. Similarly, Gaire (2013) documented highly significant genotypic differences for grain yield and its contributing traits, reinforcing the reliability of the present results.

Phenological traits

Male flower appeared earlier in LPM-153(60 days) and late in Deuti (76.33 days) with the mean value of 67.22 days, similarly, female flower appeared earlier in LPM-153(61.66 days) and appeared late in Deuti (79.66 days), with the average days to 50% silking of 70 days. Both days to 50% tasseling and days to 50% silking showed highly significant differences among the tested genotypes, indicating substantial genetic diversity for these phenological traits. This variation provides opportunities for selecting maize varieties suited to both early- and late-maturing production environments. The finding is consistent with the result of (Khan et al., 2017; Prasai et al., 2015; Sharma et al., 2018). In contrast, anthesis–silking interval (ASI) was non-significant among the genotypes, suggesting synchronized male and female flowering. A stable and shorter ASI is generally associated with reduced reproductive stress, improved pollination efficiency, and greater yield stability under field conditions. It aligns with the results of Kandel et al. (2019), although Bhusal et al. (2017) reported significant variation in ASI among the fifty-five maize inbred lines. Early-flowering genotypes are generally associated with reduced yield potential owing to shorter vegetative growth periods, while late-flowering genotypes may express either enhanced or diminished yield depending on prevailing environmental conditions and resource availability. Consequently, flowering phenology should be evaluated alongside yield performance when selecting genotypes for targeted agro-ecological environments.

Agromorphological traits

The non-significant differences among genotypes for ear aspect suggest uniformity in this trait and indicate its stability under the tested environmental conditions. This finding implies that the evaluated genotypes possess comparably desirable ear characteristics, which is consistent with earlier reports by Kandel et al. (2018, 2019). Although traits such as number of plants per plot, husk cover, and plant aspect did not show significant genotypic variation, they remain important selection criteria in maize breeding due to their influence on crop establishment, ear protection, and overall plant performance. The number of ears harvested per plot varied from 19.66 in Deuti to 28 in LPM-166, with a mean of 23.74, while the number of ears per plot ranged from 35.66 (Deuti) to 47 (LPM-166), averaging 42.33. The highly significant variation observed for the number of ears per plot reflects differences in prolificacy among the genotypes, which is a key contributor to grain yield. This result corroborates the findings of Sharma et al. (2018), who reported significant variability in prolificacy among promising maize genotypes. Ear height differed significantly among genotypes, ranging from 77 cm in LPM-153 to 125 cm in Manakamana-3, with a mean of 106.07 cm. Variation in ear height is agronomically important as it influences yield potential, lodging resistance, and harvesting efficiency. The significant genotypic effect on ear height observed in this study is well supported by previous reports (Khan et al., 2017; Kharel et al., 2017; Prasai et al., 2015; Silva et al., 2016), reinforcing the robustness of the present findings. Plant height also exhibited significant genotypic variation, with values ranging from 207.00 cm in LPM-153 to 250.66 cm in KWM-93* KWM-91 and an overall mean of 231.66 cm. Such variability in plant height offers opportunities for selecting genotypes with desirable canopy architecture, improved photosynthetic efficiency, optimal biomass production, and enhanced lodging resistance. These results are in agreement with earlier studies by Golam et al. (2011) and Mecha et al. (2017), further validating the observed trends.

Yield traits

The mean weight of five ears was 0.99 kg, ranging from 0.71 kg in LPM-153 to 1.23 kg in KWM-93* KWM-91. Significant genotypic differences were observed for five-ear weight, indicating substantial variability in ear productivity among the tested genotypes. Variation in ear weight is agronomically important, as it directly reflects assimilate partitioning efficiency and contributes substantially to overall grain yield and biomass value for food and feed purposes. The present findings are in agreement with those of Kharel et al. (2017), who reported significant genotypic variation in ear weight, although Golam et al. (2011) observed non-significant differences for this trait under different experimental conditions, suggesting environmental and genetic influences on ear weight expression. The number of kernel rows per ear ranged from 14.02 in Deuti to 16.66 in LPM-163, with a mean value of 14.44. This trait exhibited significant genotypic variation, indicating the presence of exploitable genetic diversity among the tested maize genotypes. Variation in kernel row number is of particular agronomic importance, as it is a key yield component that directly influences the potential number of kernels per ear and, consequently, final grain yield. Genotypes with a higher number of kernel rows are therefore desirable for yield improvement programs. The present results are consistent with the findings of Munawar et al. (2013), who also reported significant variation in kernel row number among maize genotypes. Furthermore, the highly significant differences observed by Izzam et al. (2017) and Kharel et al. (2017) reinforce the importance of this trait as a reliable selection criterion in maize breeding, although the magnitude of variation may differ depending on genetic background and environmental conditions. Ear diameter did not exhibit significant genotypic variation, indicating relative uniformity of this trait among the evaluated genotypes under the experimental conditions. This observation is consistent with the findings of Sharma et al. (2018), although Khan et al. (2017) reported highly significant differences for ear diameter, suggesting that the expression of this trait may be influenced by genetic background and environmental factors. In contrast, ear length showed substantial variability among genotypes, ranging from 13.68 cm in LPM-153 to 17.97 cm in KWM-93*KWM-91, with a mean value of 15.90 cm. Similarly, ear length up to the tip varied significantly, with the highest value recorded in KWM-93* KWM-91 (19.17 cm) and the lowest in LPM-153 (14.89 cm), averaging 17.13 cm. Significant differences for these traits indicate their potential usefulness as selection criteria, as longer ears generally accommodate more kernels and contribute positively to grain yield. These findings are in agreement with Sharma et al. (2018), while Izzam et al. (2017) and Kharel et al. (2017) reported highly significant variation for ear length among diverse maize genotypes. Thousand grain weight did not show the significant differences between the genotypes, suggesting the uniform grain weight of the tested genotypes, Golam et al. (2011) and Kandel et al. (2019) also reported the similar finding. The mean grain weight was 6.69 kg/ha, with the highest yield in KWM-93*KWM-91 9.65 kg/ha) followed by Khumal Hybrid-2 (8.22 t/ha) and the lowest in LPM-153 (4.12 kg/ha). This wide yield variation underscores the strong influence of genotype on productivity and aligns with the findings of Aman et al. (2020), as well as earlier reports by Golam et al. (2011), Raut et al. (2017), Reddy et al. (2022), and Silva et al. (2016). Most of the evaluated genotypes outperformed the check variety Manakamana-4 in terms of grain yield, with the exception of LPM-153, which was inferior for several yield-related traits. The superior performance of KWM-93*KWM-91 can be attributed to its favorable expression of multiple yield-contributing traits, including higher five-ear weight, longer ear length, and greater ear length up to the tip. This suggests that the combined effect of these traits played a key role in enhancing grain yield, highlighting their importance in maize genotype selection and breeding programs.

Table 1. Plant Height and Phenological traits of Maize genotypes (2019)

Genotypes	DT	DS	ASI	EH	PH	PA	EA	HC	HE
Deuti	76.33^{a}	79.66^{a}	3.33	114.00^{ab}	240.00^{ab}	2.33	2.66	1.66	19.66^{d}
KWM-93*KWM-91	73.00^{b}	76.00^{b}	3.00	114.33^{ab}	250.66^{a}	1.66	1.00	1.00	24.66^{abc}
LPM-163	61.00^{d}	64.00^{d}	3.00	86.66^{c}	215.00^{bc}	1.66	1.33	1.66	25.00^{abc}
Khumal Hybrid-2	66.66^{c}	69.00^{c}	2.33	120.33^{ab}	233.00^{abc}	1.33	1.33	1.33	25.66^{ab}
Manakamana-3	68.00^{c}	70.66^{c}	2.66	125.00^{a}	252.66^{a}	2.00	1.33	1.66	21.00^{cd}
LPM-166	67.66^{c}	70.00^{c}	2.33	104.33^{b}	229.33^{abc}	1.66	2.00	1.33	28.00^{a}
Manakamana-4	66.00^{c}	70.00^{c}	4.00	105.66^{b}	227.00^{abc}	2.66	2.33	2.00	21.33^{cd}
LPM-153	60.00^{d}	61.66^{d}	1.66	77.00^{c}	207.00^{c}	2.66	2.33	2.00	24.66^{abc}
Manakamana-7	66.33^{c}	69.00^{c}	2.66	107.33^{b}	230.33^{abc}	1.66	1.66	1.33	23.66^{bc}
Mean	67.22	70.00	2.77	106.07	231.66	1.96	1.77	1.55	23.74
SEm±	0.44	0.50	0.19	2.57	4.67	0.19	0.19	0.15	0.56
CV%	2.34	2.50	27.15	8.40	6.29	38.73	39.21	36.30	8.80
LSD (0.05)	2.72***	3.03***	1.30^{NS}	15.42***	25.22*	1.31^{NS}	1.20^{NS}	0.97^{NS}	3.61**

Note: EH= ear height (cm), PH =plant height (cm), DT= days 50% tasseling, DS= days to 50% silking, ASI= anthesis silking interval (days), PA= plant aspect, EA= ear aspect, HC=husk cover, HE= number of ear harvested, SEM= standard error of mean, CV= coefficient of variation, LSD= least significant difference

NS, *, **, *** = Non-significant, significant at 0.05, 0.01 and 0.001 level, respectively

Table 2. Grain yield, agromorphological traits and yield attributing traits of Maize genotypes (2019)

Genotypes	NPP	NEP	EW	NOR	ED	EL	ELT	TGW	GY
Deuti	43.66	35.66^{d}	0.95^{abc}	12.66^{c}	4.28	14.02^{c}	15.62^{cd}	407.33	5.61^{bc}
KWM-93*KWM-91	47.33	42.00^{bc}	1.23^{a}	14.66^{abc}	5.08	17.97^{a}	19.17^{a}	448.66	9.65^{a}
LPM-163	46.33	43.00^{abc}	1.02^{ab}	16.66^{a}	4.66	15.71^{abc}	16.10^{bcd}	393.33	6.92^{abc}
Khumal Hybrid-2	48.66	45.33^{ab}	1.10^{ab}	13.33^{bc}	4.62	16.77^{ab}	18.10^{ab}	437.33	8.22^{ab}
Manakamana-3	47.66	42.66^{abc}	1.14^{a}	14.00^{bc}	4.92	17.32^{ab}	18.29^{ab}	473.33	7.15^{abc}
LPM-166	49.33	47.00^{a}	0.99^{ab}	15.33^{ab}	4.67	15.10^{bc}	16.88^{abcd}	338.00	6.92^{abc}
Manakamana-4	44.66	40.33^{c}	0.82^{bc}	13.33^{bc}	4.42	16.92^{ab}	17.97^{abc}	380.66	4.84^{bc}
LPM-153	46.66	43.00^{abc}	0.71^{c}	14.66^{abc}	4.30	13.68^{c}	14.89^{d}	332.66	4.12^{c}
Manakamana-7	47.00	42.00^{bc}	0.99^{ab}	15.33^{ab}	4.70	15.92^{abc}	17.19^{abcd}	368.66	6.74^{abc}
Mean	46.81	42.33	0.99	14.44	4.63	15.93	17.13	397.77	6.69
SEm±	0.80	0.85	0.043	0.39	0.08	0.366	0.35	21.41	0.46
CV%	5.33	5.73	14.63	8.93	6.77	8.28	7.29	19.47	26.97
LSD(0.05)	4.32^{NS}	4.20**	0.25*	2.33**	0.54^{NS}	2.28*	2.16*	134.0^{NS}	3.12*

Note: NPP= number of plant per plot, NEP= number of ear per plot, EW= five ear weight(kg), NOR= number of kernel row per ear, ED= ear diameter (cm), EL= ear length (cm), ELT= ear length up to tip (cm), TGW= thousand grain weight (gm), GY= grain yield (t/ha), SEM= standard error of mean, CV= coefficient of variation, LSD= least significant difference

NS, *, ** = Non-significant, significant at 0.05, 0.01 level, respectively

Phenotypic and genotypic coefficient of variation

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are crucial genetic parameters that help to find out the extent of genetic variability and influence of the environment on various traits. It further serves in the effective selection of desirable traits for crop improvement. Higher differences between PCV and GCV indicate the higher environmental influence (Bello et al., 2012). In the present study, the differences between GCV and PCV were generally small for most traits, suggesting that the observed phenotypic variability was largely governed by genetic factors with minimal environmental interference. As expected, PCV values were slightly higher than GCV for all traits (Table 3), reflecting the combined effect of genetic and environmental components on phenotypic expression. Similar trends have been reported by Ferdoush et al. (2017), Jilo et al. (2018), Rahman et al. (2018), and Korsa et al. (2024), supporting the consistency of the present findings. Moreover, the wide range of GCV and PCV values observed across traits indicates the presence of substantial variability among the evaluated genotypes, which can be effectively exploited for selection and genetic improvement in maize breeding programs. High estimates of both PCV and GCV were recorded for ear aspect, grain yield, and anthesis–silking interval, indicating the presence of substantial variability for these traits and suggesting that selection could be effective in improving them. High GCV, in particular, reflects a strong genetic contribution to phenotypic expression, thereby enhancing the prospects of achieving genetic gain through selection. In contrast, traits such as husk cover, thousand-grain weight, plant aspect, and ear aspect exhibited relatively large differences between PCV and GCV, implying a greater influence of environmental factors on their expression. A pronounced disparity between PCV and GCV for ear aspect implies that selection based solely on phenotypic performance for ear aspect may be less reliable, and breeders should consider evaluating this trait across multiple environments or generations to accurately capture its genetic potential. A similar result has also been reported by Neupane et al. (2020), while a similar trend for plant aspect was documented by Jilo et al. (2018). Furthermore, Neupane et al. (2020) reported high GCV values for ear aspect and anthesis–silking interval, which supports the present findings. High PCV values for ear aspect and grain yield were likewise observed by the same authors, reinforcing the consistency of these results.

The present study observed high GCV and PCV for grain yield and moderate values for ear height, which aligns with the findings of Yadesa et al. (2022), indicating substantial genetic variability for these traits. High PCV values for grain yield and anthesis–silking interval reported by Jilo et al. (2018) further support the observed variability in these key agronomic traits. In contrast, low GCV and PCV estimates for days to 50% tasseling and silking, consistent with Bello et al. (2012) and Korsa et al. (2024), suggest that these phenological traits are relatively stable and less influenced by environmental factors. However, the higher variability reported by Saboor et al. (2018) for the same traits highlights the potential impact of genotype and environmental conditions on trait expression. Interestingly, while Bello et al. (2012) and Saboor et al. (2018) documented high variability for plant height, the current study observed comparatively lower GCV and PCV values, underscoring the role of genetic background and local environmental factors in shaping trait performance.

Low GCV values for number of kernel rows per ear and days to 50% silking, as reported by Jilo et al. (2018), are consistent with the present findings, indicating limited genetic variability for these traits. The same study reported moderate GCV values for anthesis–silking interval and ear height, which aligns with the variability patterns observed in this investigation. These trends in GCV and PCV highlight the importance of accounting for both genetic and environmental influences when selecting traits for maize improvement, ensuring more effective and reliable breeding decisions.

Heritability and genetic advance

The heritability estimates for most traits ranged from 0.51 for ear aspect to 0.97 for days to 50% tasseling and silking, with exceptions observed for number of plants per plot (0.35), plant aspect (0.18), husk cover (0.04), and thousand-grain weight (0.15). High heritability (≥0.8) was recorded for days to 50% tasseling, days to 50% silking, ear height, and number of ears per plot, indicating that the majority of variation in these traits is genetically controlled, with minimal environmental influence, and suggesting that direct selection would be highly effective. Traits with heritability above 0.8 are expected to provide substantial genetic gain upon selection (Rocha et al., 2019). Moderate heritability (0.50–0.79) was observed for number of harvested ears, ear length, ear weight, plant height, number of kernel rows per ear, grain yield, anthesis–silking interval, and ear diameter, implying that genetic improvement for these traits is feasible through careful phenotypic selection, heterosis breeding, or hybridization, which is agreement with (Jilo et al., 2018). In contrast, low heritability (<0.3) for husk cover, thousand-grain weight, and plant aspect indicates strong environmental influence, limiting the effectiveness of selection for these traits.The high heritability observed for days to 50% tasseling and silking, as well as plant height in the present study, is consistent with the findings of Korsa et al. (2024) and Saboor et al. (2018), indicating strong genetic control of these traits. Moderate heritability for grain yield, plant height, ear diameter, and number of kernel rows per ear aligns with the reports of Yadesa et al. (2022), while Korsa et al. (2024) and Saboor et al. (2018) also documented moderate heritability for grain yield, ear length, and kernel row number. Similarly, Jilo et al. (2018) reported moderate heritability for plant height, ear length, and grain yield, supporting the potential for improvement through selection. High heritability for various yield-contributing traits in maize has also been documented by Ogunniyan and Olakojo (2014), further corroborating the reliability of these traits for breeding programs. Overall, these results underscore that traits with high heritability can be effectively targeted for direct selection, whereas traits with moderate heritability may benefit from hybridization or heterosis breeding strategies.

Genetic advance of most of the traits was more than one, excluding anthesis silking interval, plant aspect, ear aspect, husk cover and ear weight. High genetic advance (>20%) was observed in ear height and plant height. While, high value of GAM (>20%) was observed in ear aspect, grain yield, anthesis-silking interval, ear height and ear weight, indicating additive gene action and which can be selected in early generations. Moderate GAM (10-20%) was observed in the number of harvested ears, days to 50% silking, days to 50% tasseling, ear length, number of ear per plot and number of kernel rows per ear. Plant height, plant aspect, ear diameter, thousand grain weight, number of plants per plot and husk cover showed low GAM value (<10%). High genetic advance as a percentage of mean (GAM) for grain yield has been reported by Korsa et al. (2024) and Yadesa et al. (2022), while Jilo et al. (2018) also observed high GAM for both grain yield and ear height. Moderate GAM for ear length was reported by Korsa et al. (2024). In the present study, most traits exhibited high heritability coupled with moderate to high GAM, suggesting that additive gene action predominantly governs their inheritance. Specifically, the GAM for grain yield was 31.86%, indicating that the mean grain yield could potentially increase by 2.13 t/ha—from 6.69 t/ha to 8.82 t/ha—following a single cycle of selection. This highlights the effectiveness of selection for improving grain yield and other yield-contributing traits in maize breeding programs.

Table 3. Estimates of environmental variance (EV), phenotypic variance (PV), genotypic variance (GV), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (H_{bs}), genetic advance (GA), and genetic advance as a percent of mean (GAM) for growth, yield and yield attributing traits of maize genotypes (2019)

Traits	Mean	EV	PV	GV	PCV	GCV	H_{bs}	GA	GAM
Days to 50% tasseling	67.22	0.83	26.33	25.50	7.63	7.51	0.97	10.24	15.23
Days to 50% silking	70.00	1.03	29.67	28.64	7.78	7.65	0.97	10.83	15.47
Anthesis silking interval	2.78	0.19	0.44	0.25	23.98	18.15	0.57	0.79	28.31
Plant height	231.67	70.67	223.56	152.89	6.45	5.34	0.68	21.06	9.09
Ear height	106.07	26.47	239.91	213.44	14.60	13.77	0.89	28.39	26.76
Number of plant per plot	46.81	2.08	3.20	1.12	3.82	2.26	0.35	1.29	2.75
Number of ear per plot	42.33	1.97	10.06	8.09	7.49	6.72	0.80	5.25	12.41
Plant aspect	1.96	0.19	0.23	0.04	24.71	10.41	0.18	0.18	9.04
Ear aspect	1.78	0.16	0.33	0.17	32.44	23.25	0.51	0.61	34.34
Husk cover	1.56	0.11	0.11	0.00	21.37	4.36	0.04	0.03	1.83
Ear weight	1.00	0.01	0.03	0.02	15.97	13.56	0.72	0.24	23.71
Number of harvested ear	23.74	1.46	6.88	5.43	11.05	9.81	0.79	4.26	17.95
Number of kernel row per ear	14.44	0.56	1.56	1.00	8.64	6.93	0.64	1.65	11.44
Ear diameter	4.63	0.03	0.07	0.04	5.73	4.18	0.53	0.29	6.28
Ear length	15.94	0.58	2.15	1.57	9.20	7.86	0.73	2.20	13.83
Ear length up to tip	17.14	0.52	1.95	1.43	8.15	6.97	0.73	2.11	12.29
Thousand grain weight	397.78	1999.70	2365.90	366.20	12.23	4.81	0.15	15.51	3.90
Grain yield	6.69	1.09	2.83	1.74	25.13	19.71	0.62	2.13	31.86

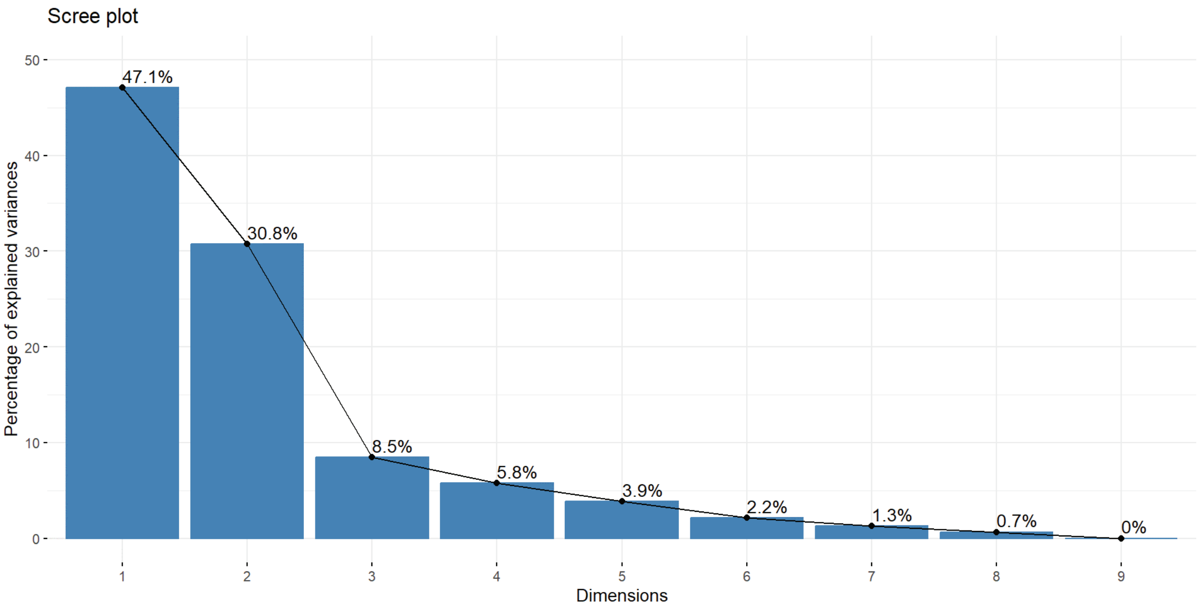

Fig. 1. Scree plot of principal component analysis showing dimension-wise percentage of explained variances

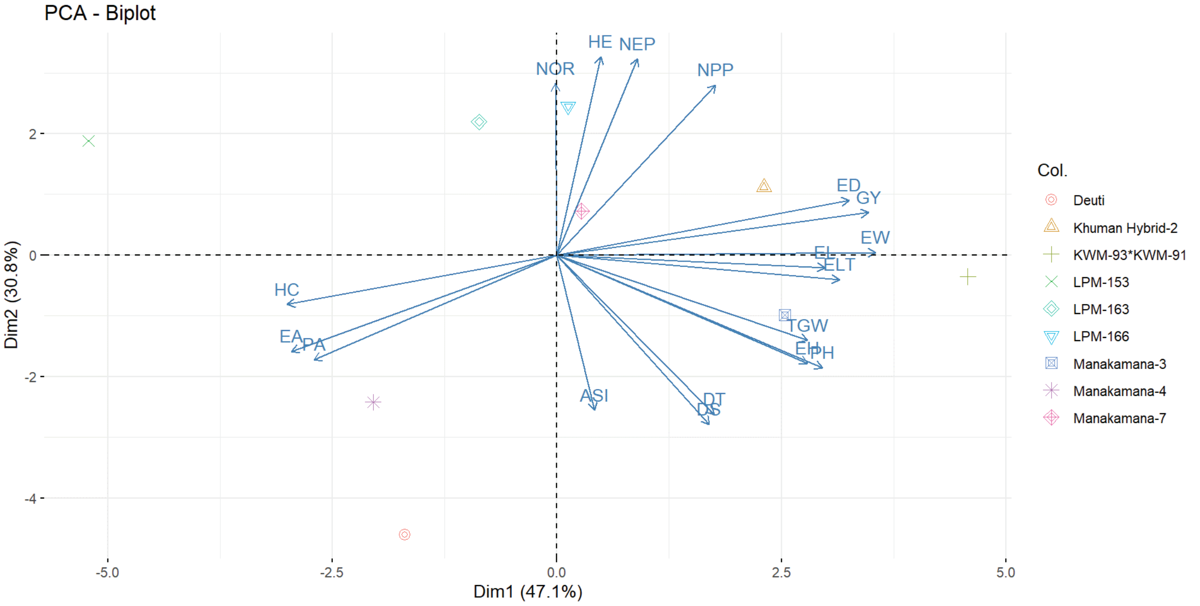

Fig. 2. Biplot of the larger PCs of maize genotypes tested in this study

Principal Component Analysis

Principal Component Analysis (PCA) is widely used in genetic diversity and breeding research to reduce data dimensionality, identify the most influential traits, and visualize relationships among genotypes, thereby supporting effective trait-based selection and breeding decisions (Ratnam & Latha, 2024). First four principal compnents (PCs) with eigenvalues greater than one accounted for 92.03% of the total phenotypic variations (Figure 1). Genotypic diversity and trait diversity, and their association, was explained by PCA-biplot (Figure 2). Patel et al. (2020) reported 76.25% of total variability explained by six PCs, while Yadesa et al. (2022) reported 64% of cumulative variance. The first principal component(PC-1) explained 35.55% of the variance and was positively associated with traits such as ear weight, grain yield, ear diameter, ear length, plant height, and ear height, while, negatively associated with husk cover, ear aspect, and plant aspect (Table 4), result from the Patel et al. (2020) aligns with our finding for ear height, plant height, ear diameter and ear length. Yadesa et al. (2022) also described the yield-related traits in PC-1. The contribution of PC1, 25.99% was explained by (Patel et al., 2020). So, PC-1 represents yield and ear-size related traits; larger ear, heavier grain yield, and better plant and ear structure (aspects are coded lower is better).

The second component (PC-2) explained 30.8% of variance, associated positively with traits such as number of harvested ear, number of ear per plot, number of kernel row per ear, number of plant per plot, and negatively with days to 50% silking, days to 50% tasseling and anthesis silking interval. PC-2 showed the earliness and plant/ear population traits, indicating high PC2 scores flower earlier and have more ears. Patel et al. (2020) reported that 19.85% of the total variation contributed by PC-2 and explained days to 50% silking, tasseling and anthesis silking interval in PC-2. Yadesa et al. (2022) reported the positive association of days to tasseling and silking in PC-2, which is in contrast to our finding.

The third principal component (PC-3) explained 8.5% of the variance and was positively associated with ear length, husk cover, and anthesis silking interval, while negatively associated with days to tasseling, silking, and ear aspect. PC-3 was related to reproductive synchrony and ear size. 9.36% variation contribution of PC-3 was reported by (Patel et al., 2020).

Table 4. Principal component analysis of phenological, agromorphological and yield traits of maize genotypes (2019)

Dimensions	**PC-1**	**PC-2**	**PC-3**	**PC-4**
Eigenvalue	8.471	5.536	1.522	1.038
Variance(%)	47.06	30.75	8.45	5.76
Cumulative variance(%)	47.06	77.81	86.26	92.03
Variables	**Coefficient vectors**			
Days to 50% tasseling	0.164	-0.304	-0.389	-0.099
Days to 50% silking	0.159	-0.323	-0.329	-0.136
Anthesis silking interval	0.039	-0.297	0.309	-0.351
Plant height	0.277	-0.216	-0.077	0.121
Ear height	0.262	-0.207	-0.097	0.318
Number of plant per plot	0.166	0.324	-0.155	0.351
Number of ear per plot	0.084	0.374	-0.012	0.318
Plant aspect	-0.253	-0.200	0.192	0.160
Ear aspect	-0.277	-0.184	-0.251	0.109
Husk cover	-0.281	-0.095	0.343	0.223
Ear weight	0.333	0.004	-0.014	-0.130
Number of harvested ear	0.046	0.379	-0.228	-0.021
Number of kernel row per ear	-0.002	0.328	0.133	-0.547
Ear diameter	0.305	0.105	0.159	-0.127
Ear length	0.280	-0.024	0.419	0.094
Ear length up to tip	0.295	-0.047	0.248	0.196
Thousand grain weight	0.262	-0.163	0.218	0.128
Grain yield	0.325	0.081	-0.085	-0.160

Hierarchical Clustering and Dendrogram

Cluster analysis is a powerful statistical technique used to group genotypes based on their similarities, such that genotypes within the same cluster are more similar to each other than to those in different clusters (Sharma, 1995). It provides a valuable framework for visualizing genetic relationships, identifying distinct groups, facilitating trait-based selection, simplifying multi-trait analysis, and guiding the planning of future plant breeding programs. Clustering is useful in reducing the number of genotypes to be tested in the future evaluation because varieties listed in the same cluster share similar characteristics (Patel et al., 2020). The optimum number of clusters was determined by using the average Silhouette method in R, which identified three clusters at 80% similarity (Figure 3 and Table 7). Grouping into three clusters of ten hybrid maize genotypes by Kandel et al. (2019) aligns with our findings. Rahman et al. (2018) reported four clusters from their study on fifteen different maize genotypes, including hybrid varieties. In the study of sixty maize inbred lines Shrestha (2013) identified six clusters with significant amounts of variability.

Clusterwise trait characteristics and their contribution are summarized in Table 5. Cluster I consisted four genotypes. Genotypes in this cluster showed moderate yield, earliness in tasseling and silking days, higher number of harvested ear, shorter plant and ear height, and higher kernel row per ear. Notably, higher harvested number of ear in LPM-166 and highest number of kernel row per ear in LPM -163. Cluster II contained 3 genotypes, with superior in terms of yield and yield attributing traits; thousand grain yield, longer ear, heavier ear, larger ear diameter. Higher ear weight, highest thousand grain weight in Cluster II was reported by (Kandel et al., 2019), which aligns with our findings. It also contained a better ear aspect, husk cover and plant aspect. Notably, KWM-93*KWM-91 had the highest grain yield and Manakamana-3 had the highest value of thousand grain weight. Cluster III consisted of the genotypes with late tasseling and silking days and lowest yield. Notably, longest days of tasseling and silking was observed in Deuti.

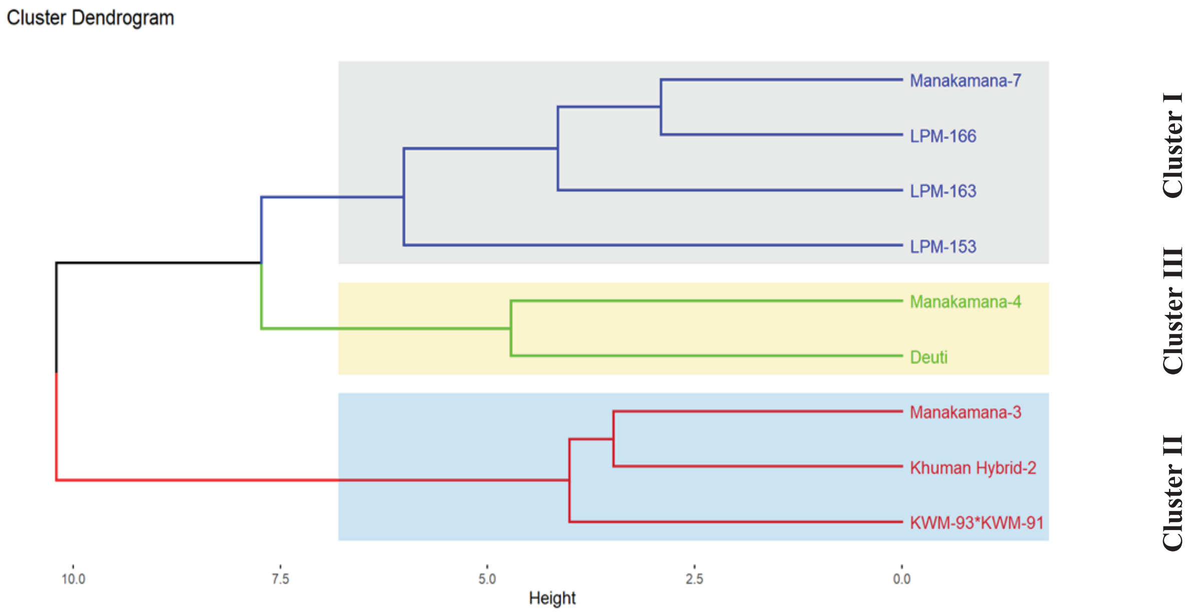

Fig. 3. Hierarchical cluster dendrogram with Euclidean distance and average method

Table 5. Cluster means of phenological, agromorphological and yield traits of maize genotypes (2019)

Variables	Cluster I	Cluster II	Cluster III
Days to 50% tasseling	63.75	69.22	71.17
Days to 50% silking	66.17	71.89	74.84
Anthesis silking interval	2.42	2.67	3.67
Plant height	220.42	245.45	233.50
Ear height	93.83	119.89	109.84
Number of plant per plot	47.33	47.89	44.17
Number of ear per plot	43.75	43.33	38.00
Plant aspect	1.92	1.67	2.50
Ear aspect	1.83	1.22	2.50
Husk cover	1.58	1.33	1.84
Ear weight	0.93	1.16	0.89
Number of harvested ear	25.34	23.78	20.50
Number of kernel row per ear	15.50	14.00	13.00
Ear diameter	4.59	4.87	4.36
Ear length	15.11	17.35	15.48
Ear length up to tip	16.27	18.52	16.80
Thousand grain weight	358.17	453.11	394.00
Grain yield	6.19	8.34	5.23

Table 6. Intra and intercluster distance (diagonal values are intra and off diagonal are inter cluster distance)

Cluster No.	I	II	III
I	4.72	6.9	6.49
II		4.01	5.89
III			6

Table 7. Grouping of genotypes based on studied traits

Cluster I	Cluster II	Cluster III
LPM-153	KWM-93*KWM-91	Deuti
LPM-163	Khumal Hybrid-2	Manakamana-4
LPM-166	Manakamana-3	
Manakamana-7		

Among the three clusters, cluster I contained more genotypes namely, LPM-153, LPM-163, LPM-166 and Manakamana-7. Cluster II contained KWM-93*KWM-91, Khumal Hybrid-2, and Manakamana-3, while cluster III contained only two genotypes; Deuti and Manakamana-4 (Table 7). The highest intercluster distance was observed between cluster I and cluster II, suggesting greater dissimilarity between them and the possibility of hybridization for the production of a single cross hybrid or double cross hybrid by crossing the genotypes between cluster I and cluster II. The lowest intercluster distance was observed between cluster II and cluster III, indicating more similarity between them (Table 6). The lowest intracluster distance was observed in cluster II, and the highest intracluster distance was observed in cluster III.

CONCLUSION

The significant differences observed among the genotypes for most traits indicate substantial genetic variability, which is vital for the success of future maize breeding strategies. Comparing hybrids with both local and improved varieties is important, as it provides a benchmark to evaluate the performance advantage of new genotypes under the same environmental conditions. Yield is a complex, polygenic trait and it is influenced by various agro-morphological characteristics. In this study, all the tested varieties outperformed the check variety Manakamana-4, except LPM 153, indicating the high yield potential of these genotypes. The small gap between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) indicated low environmental influences. Presence of high PCV, GCV, heritability with high genetic advance as percentage of mean (GAM) in studied traits offers variability for the selection. From cluster analysis, genotypes were grouped into three clusters. Cluster II consisted of high yielding genotypes alongwith yield related traits. High heritability coupled with high genetic advance was observed for ear height, making it an ideal trait for direct selection and moderate heritability with high GAM was observed for anthesis silking interval, ear aspect, ear weight and grain yield. Furthermore, the top-performing hybrids KWM-93* KWM-91 and Khumal Hybrid-2 should be evaluated across multiple locations and seasons to validate their performance stability. Overall, this finding supports the hybrid maize breeding program in Nepal by incorporating genetic diversity, trait-based selection, and agro-ecologically targeted adaptation.

ACKNOWLEDGEMENTS

The author thanks Agriculture Botany Division, Khumaltar, Lalitpur for providing with planting materials and Dr. Shambhu Khatiwada for constructive suggestions during the experiment.

CONFLICT OF INTEREST

The author declares no conflict of interests

ETHICS APPROVAL

Author ensures that research submitted complies with relevant ethical standards and legal requirements.

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