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RESEARCH ARTICLE

ASSESSING YIELD-ASSOCIATED TRAITS AND GENETIC DIVERSITY AMONG VARIOUS MAIZE (*ZEA MAYS L.*) ACCESSIONS

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ABSTRACT

Maize (*Zea mays L.*) is a globally important cereal crop, serving as a staple food, livestock feed, and industrial raw material, with immense economic and agricultural significance. However, maize productivity in Nepal remains constrained by limited genetic diversity, suboptimal genotype selection, and environmental variability, leading to inconsistent yields. To address this challenge, evaluating diverse maize genotypes under local conditions is essential for identifying high-yielding, stress-tolerance, and adaptable varieties. Therefore, this study was conducted in a farmer-managed agricultural field in Itahari, Sunsari, Nepal, to evaluate the genetic diversity and agronomic performance of twenty-four maize genotypes, aiming to identify high-yielding and adaptable varieties for sustainable production. The trial utilized a Randomized Complete Block Design (RCBD) with three replications, allowing for precise comparison across genotypes. Significant variations were observed in key vegetative and reproductive traits. RML152/RML96 demonstrated the tallest plant height, suggesting its potential for high biomass production, particularly in silage applications, although it requires careful management to avoid lodging. RH10, with its shorter stature and lower ear placement, showed strong resistance to lodging, making it suitable for regions prone to high winds or mechanical harvesting. RL35-1/RML2001 exhibited the highest number of grains per row, while RML142/RML17 had the highest thousand kernel weight, both indicating strong yield potential. The genotype RL284/RML146 emerged as the top performer, achieving the highest grain yield due to its favorable cob size, grain row count, and efficient nutrient utilization. Based on these findings, RL284/RML146, RL35-1/RML2001, and RML142/RML17 are recommended for cultivation in environments prioritizing high productivity.

KEYWORDS

Maize, Genotypes, Vegetative, Reproductive traits

1. INTRODUCTION

Maize (*Zea mays L.*) is globally recognized as one of the most significant cereal crops, serving as a fundamental component of human diets while also playing a crucial role as a raw material in various industries, including food processing, animal feed, and biofuel production (Yadav et al., 2024). As a member of the Poaceae family, maize is often designated the "queen of cereals" due to its remarkable genetic variability, adaptability to diverse agro-ecological conditions, and superior yield potential when compared to other staple crops such as rice and wheat (Jakhar et al., 2018; Ghimire et al., 2023). Nutritionally, maize holds great significance as it is an abundant source of carbohydrates, proteins, starch, fats, dietary fiber, vitamins, and essential minerals, making it an indispensable component of food security and nutritional well-being (Islam et al., 2020). Additionally, maize plays a multifaceted role within traditional farming systems, extending beyond human consumption to serve as a vital feedstock for livestock and poultry industries (Patel et al., 2024).

In 2019, global maize production reached approximately 1,050 million metric tons, with the United States emerging as the leading producer, contributing 33.23% of total output, followed by China, Brazil, Argentina, and Ukraine (World Data Atlas, 2020). In Bangladesh, maize ranks as the second most significant cereal crop after rice in terms of both economic value and byproduct utilization, positioning the country as the world's 23rd-largest maize producer, with production surging from 15.52 lakh metric tons in 2010 to 40.00 lakh metric tons by 2019; an impressive annual growth rate of 11.40% (World Data Atlas, 2020; BBS, 2019; Islam et al., 2020). Similarly, in Nepal, maize remains the second most widely cultivated staple crop after rice, occupying around 870,166 hectares or 28.15% of the country's total arable land, with its production spanning various agro-ecological regions, including the hills, mountains, and the Terai and Inner-Terai plains, underscoring its significance in national agricultural systems (Mehata et al., 2023; Yadav et al., 2024).

As the global demand for maize continues to escalate, owing to its diverse applications in food production, forage, oil extraction, and biofuel synthesis, the genetic diversity of maize landraces has been gradually diminishing due to their declining presence in farmers' fields. This loss threatens the availability of critical genetic resources essential for future breeding programs (Koirala et al., 2020). Evaluating the genetic diversity of maize germplasm is paramount for the identification of superior parental lines required for hybrid development and successful breeding initiatives (Anusha et al., 2022). The presence of extensive genetic variability is a fundamental prerequisite for achieving substantial genetic progress in applied breeding strategies. Similar to other crops, maize yield is an outcome of complex interrelated genetic and environmental factors, necessitating a thorough understanding of trait associations to enhance selection accuracy in breeding programs (Singh et al., 2005). Variability, which denotes the extent of phenotypic differences observed within a population, provides valuable insights into the genetic potential of maize and its adaptability to varying environmental conditions. A comprehensive assessment of this variability is essential for enhancing

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breeding efficiency and optimizing crop performance under different agro-climatic conditions (Melchinger et al., 2018). However, several abiotic stresses, particularly extreme temperatures, prolonged drought conditions, and nutrient deficiencies—pose significant challenges to maize cultivation and overall yield stability. Exposure to cold stress, defined by temperatures falling below 10°C, adversely affects photosynthetic efficiency and protein stability, ultimately reducing grain formation and yield potential (Yadav et al., 2024). Likewise, drought stress is a major constraint, particularly in rainfed maize-growing areas, where soil moisture depletion severely inhibits seed germination, root elongation, and grain-filling processes (Setimela et al., 2017). In addition to environmental stressors, maize production in Nepal is frequently compromised by a range of biotic threats, including fungal, bacterial, and viral pathogens, which substantially reduce crop productivity. The earliest documented research on maize diseases in Nepal dates to 1964–1965, during a period when improved maize cultivars were yet to be introduced (Manjunatha et al., 2018).

The rising demand for hybrid maize in Nepal underscores the necessity of developing region-specific hybrids with enhanced resistance to both biotic and abiotic stresses. Nevertheless, most currently available maize varieties—except for Poshilo Makai-1—are conventional cultivars with a lysine content as low as 2%, which is significantly below the recommended dietary threshold (Shrestha et al., 2015; Neupane et al., 2020). The introduction of hybrid maize in Nepal commenced in the 1980s through seed imports from India, followed by the initiation of domestic hybrid maize research in 1987 (Koirala et al., 2020). Despite these advancements, domestic maize production remains insufficient to meet the country's escalating demands, particularly for human consumption and livestock feed (Paudyal et al., 2001). Hybrid maize, characterized by its superior genetic attributes, presents an opportunity to enhance yield potential, nutritional quality, and resilience against environmental stressors (Rahman et al., 2017). On a global scale, maize accounts for approximately 19.5% of total caloric intake, emphasizing its vital role in addressing food security and mitigating nutritional deficiencies. Given these existing challenges and potential opportunities, it is imperative to identify high-yielding, stress-resilient maize genotypes that are well-suited to Nepal's diverse agro-climatic regions. Enhancing maize productivity necessitates a combination of conventional breeding and modern molecular approaches to accelerate genetic improvement and trait selection. Furthermore, the implementation of advanced agronomic practices; such as site-specific nutrient management, conservation tillage, and integrated pest and disease control for sustaining long-term productivity. Strengthening the efficiency of seed distribution networks and ensuring farmers' access to high-quality hybrid seeds will be pivotal in bridging the productivity gap and fulfilling national food security objectives (Yadav et al., 2024).

This study is designed to evaluate the agronomic performance of various maize cultivars to enhance productivity and resilience under diverse environmental conditions. The research findings will provide valuable insights for farmers, agricultural extension professionals, policymakers, and other stakeholders, contributing to the formulation of effective maize improvement strategies aimed at ensuring sustainable agricultural development.

2. Materials And Methods

2.1 Site Selection

The field experiment was conducted in a farmer-managed agricultural field in Itahari, Sunsari, situated within Province 1 of Nepal. Itahari, positioned in the eastern Terai region, is recognized for its highly fertile alluvial plains, making it a crucial hub for agricultural activities. The experimental site was located at an elevation of 130 meters above sea level, precisely at a latitude of 26°07'45" N and a longitude of 87°28'11" E. This region experiences a subtropical climate, characterized by significant annual precipitation and considerable temperature variability throughout the year. Climatic data indicate that Itahari receives an average annual rainfall of 1,435.3 mm, which ensures adequate moisture availability for agricultural production. The temperature regime in the area exhibits notable fluctuations, with recorded maximum temperatures soaring to 39.2°C and minimum temperatures plummeting to 11.8°C. Such pronounced thermal variations, coupled with high precipitation levels, create a dynamic agroecological environment conducive to assessing crop responses under varying climatic conditions. The geographical map of the research site is presented in Figure 1.

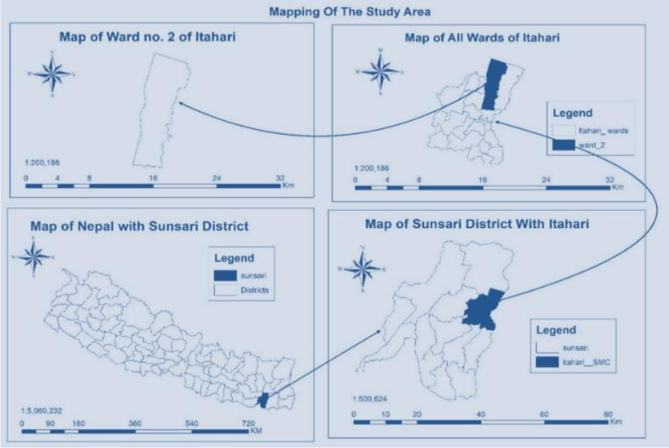

Figure 1: Geographical map of research site

2.2 Genotypes Details

Table 1: List of the maize accessions utilized in the study, together symbols

S. N	Symbol	Accessions
1	T1	RML36/RML2244
2	T2	RL35-1/RML2001
3	T3	RL284/RML146
4	T4	RML62/RML2
5	T5	RML147/cML430
6	T6	RH16
7	T7	RML2137/RL2118
8	T8	SULTAN
9	T9	RML14/RML76
10	T10	RML142/RML17
11	T11	RL252/RML98
12	T12	RML150/RL111
13	T13	RML32/cML613
14	T14	RML5/RML17
15	T15	RMl98/RML145
16	T16	RL143/RML96
17	T17	RML76/TZEIOR157
18	T18	RML152/RML96
19	T19	cML161/RML96
20	T20	RML187/RML96
21	T21	RL240/RML96
22	T22	RML145/TZEIO157
23	T23	RML108/RL2118
24	T24	RH10

2.3 Experimental Design and cultural Practices

The experimental site was meticulously organized using a Randomized Complete Block Design (RCBD), a highly effective statistical method commonly employed in agricultural research to control variability and enhance the reliability of results. The experiment involved twenty-four different genotype accessions, which were replicated three times to ensure statistical robustness which is presented in table 1. These genotypes were sourced from Rampur and planted in a total of 72 research plots. The study employed experimental plots, each encompassing an area of 12 m^2 with dimensions of 4 meters in length and 3 meters in width. The planting configuration was structured with rows positioned 75 centimeters apart, while the spacing between individual plants within a row was maintained at 25 centimeters. Furthermore, a 1-meter gap was allocated between distinct plot blocks, whereas individual

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plots within the same block were separated by a distance of 0.75 meters to ensure adequate spatial arrangement, facilitating optimal growth conditions and ease of management. Prior to snowing, the main field was thoroughly prepared. The soil was initially ploughed using a tractor to break up the ground, followed by harrowing to achieve a finer soil texture, which is crucial for uniform seedbed preparation. By adding farmyard manure to the soil throughout the field preparation process, organic enrichment was guaranteed.

Urea, diammonium phosphate (DAP), and muriate of potash (MOP) were applied at a prescribed dose of 120:60:40 NPK kg/ha as part of the fertilization program. The range of 20 to 25 kg/ha was the seed rate that was maintained. While nitrogen was provided gradually, with only half of the entire amount originally assimilated, phosphorus and potassium were applied as baseline dosage at the time of planting. Two equal parts of the remaining nitrogen were administered in succession, first during the knee-high growth phase and again during the pre-tasseling or silking stage. At the knee-high stage, earthing up was also done to promote root growth and plant stability. Manual weeding was carried out to eliminate any existing weeds that could compete with the crops for nutrients and water. Irrigation was managed according to the moisture requirements of the crop, ensuring that water stress did not affect plant growth. Regular monitoring of the plots was conducted to manage any emerging pests or diseases.

2.4 Data observations and collection

For data collection, five plants were randomly chosen from each of the 72 research plots to ensure a representative sample, with observations focusing on key yield-related parameters such as plant height, cob dimensions, phenological stages, and grain characteristics. Post-harvest assessments included measuring total field weight while adjusting for moisture content, alongside evaluating the thousand kernel weight at a standardized 12.5% moisture level to facilitate accurate yield comparisons. The formula used for calculating grain yield and thousand kernel weight is given below in equation 1 and equation 2 respectively which were also used to adjust the grain yield (tons/ha) at 15% moisture content (Yadav et al., 2024).

$$\textbf{Grain Yield (tons/ha)} = \frac{\text{F.W.(kg/plot)} \times (100 - \text{HMP}) \times \text{S} \times 10000}{(100 - \text{DMP}) \times \text{NPA} \times 1000} \times 100 \qquad (1)$$

Where,

F.W. = Fresh weight of ear in kg per plot at harvest

HMP = Grain moisture percentage at harvest

DMP = Desired moisture percentage, i.e., 15%

NPA = Net harvest plot area, m^2

S = Shelling coefficient, i.e., 0.8

$$\textbf{Test weight (1000 kernel weight)} = \frac{\text{Kernel weight} \times (100 - \text{moisture }\%)}{100 - 12.5} \qquad (2)$$

2.5 Statistical analysis

The data was initially organized sequentially for both replication and treatment blocks using MS Excel 2021 (Microsoft Corporation, Washington, USA). Following this, ANOVA was performed using statistical software (R Studio, Version 4.2.3, Boston, Massachusetts, USA). To assess differences in mean values across the treatments, Duncan's Multiple Range Test (DMRT) was employed, with a significance level set at 5%.

3. RESULTS

3.1 Plant Height

The study revealed significant variability in plant height (PH) among maize genotypes (figure 2), with values ranging from 140.60 cm (RH10) to 241.33 cm (RML152/RML96) and a grand mean of 201.04 cm. The genotype RML152/RML96 emerged as the tallest (241.33 cm), suggesting a strong genetic potential for biomass production, possibly due to enhanced gibberellin activity promoting stem elongation. In contrast, RH10 recorded the shortest height (140.60 cm), indicating a genetic predisposition toward reduced stature, which may be advantageous for high-density planting, lodging resistance, and mechanized harvesting. Other genotypes, such as RML284/RML146 (227.00 cm) and RML187/RML96 (224.33 cm), exhibited considerable height, demonstrating potential for breeding programs focused on increased biomass. Meanwhile, genotypes like RML36/RML2244 (209.33 cm) and RL240/RML96 (210.66 cm), which clustered around the grand mean, represent a balance between height and agronomic adaptability. The coefficient of variance (CV) of 8.333% and a standard error of mean (SEM) of ±2.932 indicate substantial genetic diversity, highlighting opportunities for selective breeding to optimize plant height for different agricultural applications. These findings underscore the importance of genotype selection in balancing biomass production, lodging susceptibility, and suitability for diverse agronomic conditions.

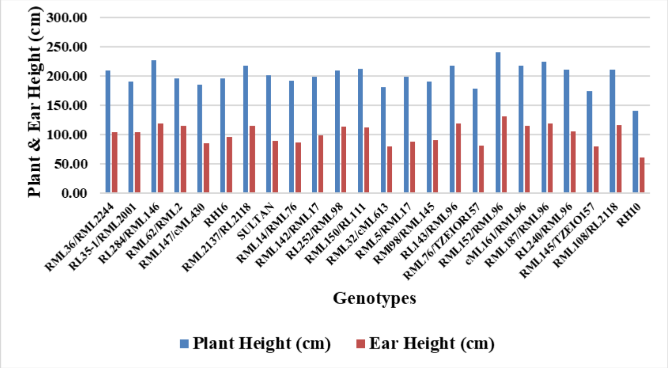

Figure 2: Graphical representation of plant height and ear height among different genotypes

3.2 Ear height

The study revealed significant variability in ear height (EH) among maize genotypes (figure2), ranging from 61.66 cm (RH10) to 131.66 cm (RML152/RML96), with a grand mean of 101.18 cm. The tallest ear height in RML152/RML96 (131.66 cm) suggests robust plant architecture, beneficial for light interception and yield potential but posing a higher lodging risk under adverse conditions. In contrast, RH10 (61.66 cm) exhibited the lowest ear height, enhancing stability and lodging resistance, making it ideal for wind-prone areas and mechanized harvesting. Other genotypes, such as RL143/RML96 (119.06 cm) and RML284/RML146 (118.66 cm), showed high ear placement, favoring deep rooting and water use efficiency. Meanwhile, moderate ear height genotypes like RML32/cML613 (80.53 cm) and RML145/TZEIO157 (79.53 cm) offer a balance between stability and yield potential. The high coefficient of variance (CV) of 14.997% and SEM of ±2.463 highlight significant genetic diversity, providing valuable opportunities for breeding programs targeting optimal ear height for different environments.

3.3 Days to anthesis (AD) & Silking

Anthesis days (AD) and silking days (SD) are critical phenological traits that influence reproductive efficiency, pollination success, and overall grain yield in maize presented in figure 3. In this study, significant variation was observed among genotypes, with AD ranging from 60.00 days in RH10 to 75.33 days in RML36/RML2244, and a grand mean of 68.23 days. Early flowering genotypes, such as RH10 (60.00 days) and RML108/RL2118 (64.33 days), may be advantageous in short-season environments or under drought stress, whereas late-flowering genotypes like RML36/RML2244 (75.33 days) exhibit extended vegetative growth, which can contribute to higher biomass accumulation but may also increase susceptibility to late-season stress. Similarly, SD varied from 63.66 days in RH10 to 79.00 days in RML36/RML2244, with a mean of 71.90 days. The shortest anthesis-silking interval (ASI) was observed in RH10, indicating effective synchronization between male and female flowering, which is crucial for optimal pollination and kernel set. In contrast, RML36/RML2244, with the longest ASI, may be more prone to pollination issues, particularly under stress conditions. Most genotypes exhibited a 3–5-day ASI, ensuring balanced flowering, which is essential for maximizing grain yield. The observed variations in AD and SD highlight the genetic diversity in flowering behavior, which can be strategically utilized in breeding programs to develop maize varieties suited to different agro-climatic conditions, ensuring improved yield stability and resilience under varying environmental constraints.

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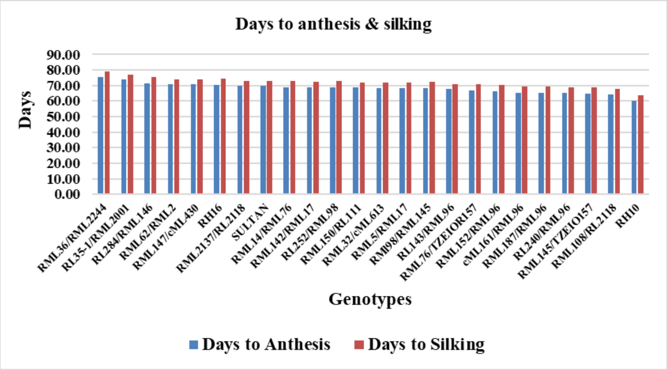

Figure 3: Graphical representation of days to anthesis and silking among different genotypes

3.4 Cob length

The study revealed significant variation in cob length (CL) among maize genotypes, ranging from 12.90 cm (RH10) to 19.45 cm (RML152/RML96), with a grand mean of 16.40 cm. The longest cob length observed in RML152/RML96 (19.45 cm) suggests strong genetic potential for high grain yield, likely due to efficient nutrient uptake and favorable ear development traits. In contrast, RH10 (12.90 cm) exhibited the shortest cob length, indicating a lower yield potential, which may be linked to its earlier maturity and shorter plant height. Genotypes such as RML2137/RL2118 (17.98 cm) and RML36/RML2244 (17.27 cm) also demonstrated considerable yield potential, making them strong candidates for breeding programs targeting improved cob size. Figure 4 presents the cob length and cob diameter in graphical form. The high coefficient of variance (CV) of 8.782% and SEM of ±0.363 highlight significant genetic diversity, emphasizing the influence of both genetic and environmental factors on cob length. This variability provides valuable opportunities for breeding programs to enhance yield traits and adaptability in maize genotypes.

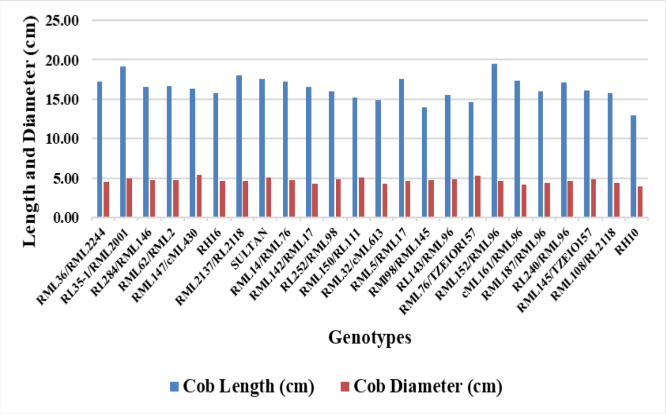

Figure 4: Graphical presentation of cob length and diameter among different genotypes

Table 2: Analysis of genotypes for agronomic traits:

Genotypes	PH (cm)	EH	AD	SD	CL (cm)
RML36/RML2244	209.33^{abcdef}	104.13^{abcde}	75.33^{a}	79.00^{a}	17.27^{abcde}
RL35-1/RML2001	190.46^{defg}	104.40^{abcde}	73.66^{ab}	77.00^{ab}	19.16^{ab}
RL284/RML146	227.00^{ab}	118.66^{ab}	71.33^{bc}	75.33^{bc}	16.61^{bcdef}
RML62/RML2	196.66^{bcdefg}	114.66^{abcd}	71.00^{bc}	74.00^{bcde}	16.69^{abcdef}
RML147/cML430	185.73^{defg}	85.66d^{ef}	70.66^{bc}	74.00^{bcde}	16.34^{bcdef}
RH16	195.66^{bcdefg}	95.66^{bcde}	70.33^{bcd}	74.33^{bcd}	15.74^{cdef}
RML2137/RL2118	218.06^{abcd}	115.13^{abcd}	69.66^{cde}	73.00^{cdef}	17.98^{abc}
SULTAN	202.13^{bcdefg}	89.33^{bcdef}	69.66^{cde}	72.66^{cdefg}	17.58^{abcd}
RML14/RML76	191.66^{cdefg}	86.60^{def}	69.00^{cdef}	73.00^{cdef}	17.18^{abcde}
RML142/RML17	198.73^{bcdefg}	99.20^{bcde}	69.00^{cdef}	72.33^{cdefgh}	16.51^{bcdef}
RL252/RML98	209.66^{abcdef}	113.66^{abcd}	68.66^{cdefg}	72.66^{cdefg}	16.04^{cdef}
RML150/RL111	212.66^{abcde}	112.33^{abcd}	68.66^{cdefg}	72.00^{cdefgh}	15.25^{cdefg}
RML32/cML613	181.26^{efg}	80.53^{e}f	68.33^{cdefgh}	72.00^{cdefgh}	14.84^{defg}
RML5/RML17	198.86^{bcdefg}	87.73^{cdef}	68.33^{cdefgh}	72.00^{cdefgh}	17.55^{abcd}
RMl98/RML145	190.33^{defg}	91.20^{bcde}	68.33^{cdefgh}	72.33^{cdefgh}	13.98^{fg}
RL143/RML96	217.80^{abcd}	119.06^{ab}	68.00^{cdefghi}	71.00^{defghi}	15.59^{cdef}
RML76/TZEIOR157	178.13^{fg}	82.00^{ef}	66.66^{defghi}	70.66^{defghi}	14.64^{efg}
RML152/RML96	241.33^{a}	131.66^{a}	66.33^{efghi}	70.33^{efghi}	19.45^{a}
cML161/RML96	217.66^{abcd}	114.66^{abcd}	65.33^{fghi}	69.33^{fghi}	17.39^{abcde}
RML187/RML96	224.33^{abc}	119.00^{ab}	65.33^{fghi}	69.33^{fghi}	16.03^{cdef}
RL240/RML96	210.66^{abcdef}	105.20^{abcde}	65.00^{ghi}	69.00^{ghi}	17.13^{abcde}
RML145/TZEIO157	174.46^{g}	79.53^{ef}	64.66^{hi}	68.66^{hi}	16.08^{cdef}
RML108/RL2118	211.80^{abcde}	116.66^{abc}	64.33^{i}	68.00^{i}	15.75^{cdef}
RH10	140.60^{h}	61.66^{f}	60.00^{j}	63.66^{j}	12.90^{g}
Grand mean	201.04	101.18	68.23	71.90	16.40
CV (%)	8.333	14.997	2.883	2.765	8.782
SEM (±)	2.932	2.463	0.422	0.412	0.223
F-test	***	***	***	***	***

Note: ***Significant at 0.1 % level of significance, CV: Coefficient of variance, SEM: standard error mean, AD: days to anthesis, SD: days to silking, PH: plant height, CL: Cob length

3.5 Cob diameter

Cob diameter (CD) is a vital yield component in maize presented in figure 4, directly influencing the number of rows of grains per ear and, consequently, the grain yield. In this study, cob diameter among the maize genotypes ranged from 3.98 cm to 5.38 cm, with a grand mean of 4.66 cm. This variation in cob diameter reflects the genetic diversity among the genotypes and their potential to influence grain yield through ear size. The genotype RML147/cML430 exhibited the largest cob diameter at 5.38 cm, indicating its potential for higher yield due to a larger ear size. Larger cobs typically support more rows of grains, which can directly translate into increased grain yield. The large cob diameter observed in RML147/cML430 suggests that this genotype may have favorable genetic traits for ear development, such as efficient nutrient allocation to the reproductive organs, which is crucial for maximizing yield. On the other hand, RH10 recorded the smallest cob diameter at 3.98 cm, indicating a lower yield potential compared to other genotypes. Smaller cobs generally have fewer rows of grains, which can result in lower overall grain yield. The small cob diameter in RH10 may be associated with its shorter plant stature and earlier maturity, which could limit the time available for resource accumulation and ear development. However, in environments where early maturity is a priority, the smaller cob diameter may be a trade-off for the benefits of avoiding late-season environmental stresses. Genotypes like RL35-

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1/RML2001 and RL252/RML98, with cob diameters of 4.96 cm and 4.78 cm respectively, demonstrated a balance between ear size and grain yield potential. These genotypes, while not having the largest cobs, still exhibited above-average cob diameters, indicating their suitability for environments where moderate ear size is preferred. The substantial cob diameter observed in these genotypes suggests they may possess genetic potential for both ear development and overall yield. The coefficient of variance (CV) of 8.298% for cob diameter highlights the moderate variability observed among the genotypes, reflecting the influence of both genetic and environmental factors on this trait. The standard error of mean (SEM) of ±0.053 further supports the reliability of the observed differences in cob diameter, indicating that these differences are statistically significant.

3.6 Number of Grain Rows per Ear (NGRPE)

Figure 5 represents the graphical form of number of grain rows per ear (NGRPE) is a key yield component in maize, contributing to the overall grain yield. In this study, the number of grain rows per ear among the maize genotypes ranged from 12.00 to 14.53, with a grand mean of 13.41. This variation in the number of grain rows reflects the genetic diversity among the genotypes and their potential to influence grain yield through ear architecture. The genotype cML161/RML96 recorded the highest number of grain rows per ear at 14.53, indicating its potential for higher yield due to a greater number of rows. A higher number of grain rows per ear generally translates to a greater number of grains, which directly impacts the overall grain yield. The high number of grain rows observed in cML161/RML96 suggests that this genotype may have favorable genetic traits for ear development and grain set. In contrast, the genotype RML32/cML613 had the lowest number of grain rows per ear at 12.00, indicating a lower yield potential compared to other genotypes. A lower number of grain rows generally results in fewer grains per ear, which can lead to a reduction in overall grain yield. The low number of grain rows in RML32/cML613 may be associated with its genetic makeup, which could limit its ability to produce a high number of grain rows. Genotypes such as RL284/RML146 and RML2137/RL2118, with grain rows per ear of 13.80 and 12.80 respectively, demonstrated a balance between ear architecture and grain yield potential. These genotypes, while not having the highest number of grain rows, still exhibited above-average values, indicating their suitability for environments where moderate ear size and grain yield are preferred. The coefficient of variance (CV) of 5.993% for the number of grain rows per ear highlights the relatively low variability observed among the genotypes, reflecting the stable expression of this trait across different environmental conditions. The standard error of mean (SEM) of ±0.110 further supports the reliability of the observed differences in the number of grain rows per ear, indicating that these differences are statistically significant.

3.7 Number Number of Grains per Row (NGPR)

The number of grains per row (NGPR) is another critical yield component in maize, directly influencing the total number of grains per ear and, consequently, the grain yield presented in figure 5. In this study, the number of grains per row among the maize genotypes ranged from 25.60 to 41.26, with a grand mean of 33.97. This significant variation in the number of grains per row reflects the genetic diversity among the genotypes and their potential to influence grain yield. The genotype RL35-1/RML2001 recorded the highest number of grains per row at 41.26, indicating its potential for high yield due to a greater number of grains per ear. A higher number of grains per row generally translates to a larger overall grain yield, as more grains are produced on each ear. The high number of grains per row observed in RL35-1/RML2001 suggests that this genotype may possess favorable genetic traits for grain set and development, making it a strong candidate for breeding programs focused on increasing grain yield. On the other hand, RH10 had the lowest number of grains per row at 25.60, indicating a lower yield potential compared to other genotypes. A lower number of grains per row generally results in fewer total grains per ear, which can reduce overall grain yield. The low number of grains per row in RH10 may be associated with its smaller cob diameter and overall ear size, which could limit the number of grains that can develop on each row. Genotypes such as RL252/RML98 and RMl98/RML145, with grains per row of 33.13 and 33.26 respectively, demonstrated a moderate number of grains per row, indicating their potential for stable grain yield under varying environmental conditions. These genotypes, while not having the highest number of grains per row, still exhibited above-average values, suggesting their suitability for environments where moderate grain yield is preferred. The coefficient variance (CV) of 7.554% for the number of grains per row reflects the moderate variability observed among the genotypes, indicating the influence of both genetic and environmental factors on this trait. The standard error of mean (SEM) of ±0.433 further supports the reliability of the observed differences in the number of grains per row, indicating that these differences are statistically significant.

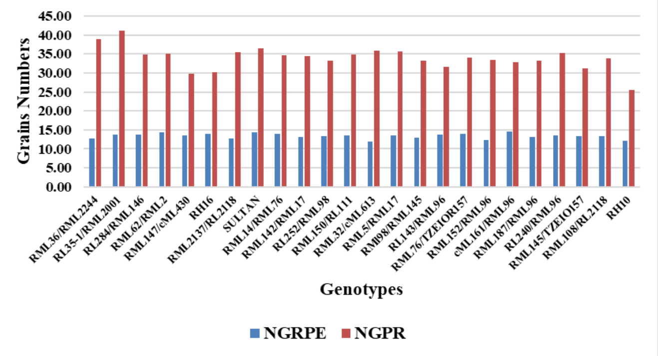

Figure 5: Graphical presentation of Number of grains rows per ear (NGRPE) and grains per row (NGPR)

3.8 Thousand Kernel Weight (TKW)

Thousand kernel weight (TKW) is a key yield component in maize, reflecting the size and weight of the grains. It is a critical determinant of grain yield and quality. In this study, the TKW among the maize genotypes ranged from 0.032 kg to 0.067 kg, with a grand mean of 0.047 kg. This variation in TKW reflects the genetic diversity among the genotypes and their potential to influence grain yield and quality. The genotype RML142/RML17 recorded the highest TKW at 0.067 kg, indicating its potential for producing larger and heavier grains. Higher TKW generally reflects better grain filling and development, which can lead to higher overall grain yield and improved grain quality. The high TKW observed in RML142/RML17 suggests that this genotype may possess favorable genetic traits for nutrient allocation to the grains, resulting in larger and heavier seeds. In contrast, the genotype RML14/RML76 had the lowest TKW at 0.032 kg, indicating a lower grain weight compared to other genotypes. Lower TKW generally reflects smaller and lighter grains, which can reduce overall grain yield and affect grain quality. The low TKW in RML14/RML76 may be associated with its genetic makeup, which could limit its ability to produce large, well-filled grains. Genotypes such as RML147/cML430 and RML5/RML17, with TKWs of 0.056 kg and 0.057 kg respectively, demonstrated a balance between grain weight and overall yield potential. These genotypes, while not having the highest TKW, still exhibited above-average values, indicating their suitability for environments where moderate grain size and quality are preferred. The coefficient of variance (CV) of 20.605% for TKW highlights the high variability observed among the genotypes, reflecting the significant influence of both genetic and environmental factors on this trait. The standard error of mean (SEM) of ±0.001 further supports the reliability of the observed differences in TKW, indicating that these differences are statistically significant.

3.9 Grain yield (GY)

Grain yield (GY) is the ultimate measure of a maize genotype's productivity which is displayed in graphical form in figure 6, reflecting the combined effect of various yield components such as cob diameter, number of grain rows per ear, number of grains per row, and thousand kernel weight. In this study, grain yield among the maize genotypes ranged from 5341.567 kg/ha to 10931.067 kg/ha, with a grand mean of 8355.79 kg/ha. This significant variation in grain yield reflects the genetic diversity among the genotypes and their potential to influence overall productivity. The genotype RL284/RML146 recorded the highest grain yield at 10931.067 kg/ha, indicating its potential for high productivity. High grain yield generally reflects a combination of favorable traits such as large cob size, high number of grains per ear, and heavy grains. The high grain yield observed in RL284/RML146 suggests that this genotype may possess a favorable genetic combination for yield traits, making it a strong candidate for breeding programs aimed at improving maize productivity. In contrast, RML14/RML76 had the lowest grain yield at 5341.567 kg/ha, indicating a lower productivity compared to other genotypes. Lower grain yield generally reflects a combination of less favorable yield components, such as smaller cob size, fewer grains per ear, and lighter grains. The low grain yield in RML14/RML76 may be associated with its lower thousand kernel weight and overall smaller ear size, which could limit its ability to produce high yields. Genotypes such as RML36/RML2244 and RML108/RL2118, with grain yields of 10570.733 kg/ha and 10597.533 kg/ha respectively, demonstrated a balance between various yield components, resulting in high productivity. These genotypes, while not having the highest grain yield, still exhibited above-average values, indicating their suitability for environments where high yield is a priority. The coefficient of variance (CV) of 17.006% for grain yield highlights the moderate variability observed among the genotypes, reflecting the influence of both genetic and environmental factors on this trait. The standard error of mean (SEM) of ±222.384 further supports the reliability of the observed differences in grain yield, indicating that these differences are statistically significant. Overall, the significant variation observed in the yield components and grain yield among the maize genotypes highlights the importance of selecting genotypes with favorable traits for specific environments. The results of this study provide valuable insights into the genetic potential of these genotypes for improving maize productivity, which can guide breeding programs and crop management practices aimed at increasing maize yields.

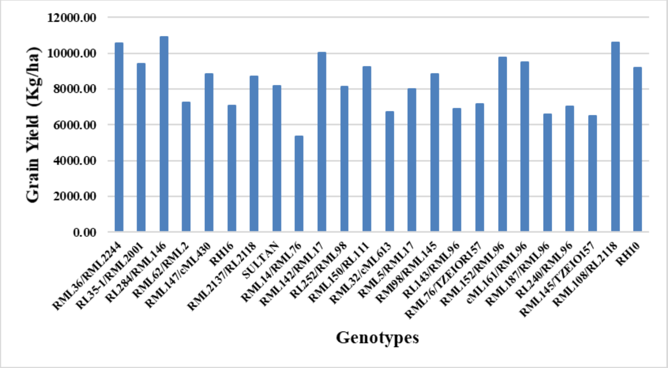

Figure 6: Graphical representation of grains yields among different genotypes

Table 3: Analysis of genotypes for agronomic traits

Genotypes	CD (cm)	NGRPE	NGPR	TKW	GY (Kg/ha)
RML36/RML2244	4.48^{cde}	12.66^{cde}	38.80^{ab}	0.046^{bcdefg}	10570.733^{ab}
RL35-1/RML2001	4.96^{abc}	13.73^{abc}	41.26^{a}	0.050^{abcdefg}	9422.033^{abcde}
RL284/RML146	4.70^{abcde}	13.80^{abc}	34.93^{bcdef}	0.036^{efg}	10931.067^{a}
RML62/RML2	4.67^{abcde}	14.40^{ab}	35.06^{bcde}	0.046^{bcdefg}	7245.967^{cdefg}
RML147/cML430	5.38^{a}	13.46^{abcde}	29.86^{f}	0.056^{abcd}	8821.133^{abcdef}
RH16	4.60^{bcde}	13.86^{abc}	30.13^{ef}	0.043^{bcdefg}	7091.167^{defg}
RML2137/RL2118	4.62^{abcde}	12.80^{bcde}	35.46^{bcd}	0.050^{abcdefg}	8689.733^{abcdef}
SULTAN	5.02^{abc}	14.40^{ab}	36.53^{bc}	0.055^{abcd}	8191.567^{abcdef}
RML14/RML76	4.70^{abcde}	14.00^{abc}	34.66^{bcdef}	0.032^{g}	5341.567^{g}
RML142/RML17	4.30^{cde}	13.20^{abcde}	34.53^{bcdef}	0.067^{a}	10029.933^{abc}
RL252/RML98	4.78^{abcd}	13.33^{abcde}	33.13^{cdef}	0.049^{abcdefg}	8141.633^{abcdef}
RML150/RL111	5.03^{abc}	13.60^{abcd}	34.93^{bcdef}	0.052^{abcdef}	9241.867^{abcdef}
RML32/cML613	4.29^{cde}	12.00^{e}	35.93^{bcd}	0.039^{cdefg}	6723.800^{efg}
RML5/RML17	4.62^{abcde}	13.46^{abcde}	35.73^{bcd}	0.057^{ab}c	7999.733^{bcdefg}
RMl98/RML145	4.68^{abcde}	12.93^{abcde}	33.26^{cdef}	0.0460^{bcdefg}	8823.700^{abcdef}
RL143/RML96	4.83^{abcd}	13.73^{abc}	31.66^{cdef}	0.043^{bcdefg}	6923.533^{efg}
RML76/TZEIOR157	5.27^{ab}	14.00^{abc}	34.06^{bcdef}	0.034^{fg}	7182.900^{defg}
RML152/RML96	4.62^{abcde}	12.40^{cde}	33.33^{cdef}	0.060^{ab}	9759.267^{abcd}
cML161/RML96	4.16^{de}	14.53^{a}	32.80^{cdef}	0.044^{bcdefg}	9505.167^{abcde}
RML187/RML96	4.40^{cde}	13.20^{abcde}	33.20^{cdef}	0.037^{defg}	6577.333^{fg}
RL240/RML96	4.64^{abcde}	13.60^{abcd}	35.26^{bcd}	0.054^{abcde}	7047.967^{defg}
RML145/TZEIO157	4.78^{abcd}	13.33^{abcde}	31.26^{def}	0.041^{bcdefg}	6500.800^{fg}
RML108/RL2118	4.43^{cde}	13.33^{abcde}	33.86^{bcdef}	0.049^{abcdefg}	10597.533^{ab}
RH10	3.98^{e}	12.13^{de}	25.60^{g}	0.046^{bcdefg}	9178.833^{abcdef}
Grand mean	4.66	13.41	33.97	0.047	8355.79
CV (%)	8.298	5.993	7.554	20.605	17.006
SEM (±)	0.053	0.110	0.433	0.001	222.384
F-test	*	*	**	**	**

CD: Cob diameter, NGRPE: No. of grains rows per ear, NGPR: No. of grains per row, TKW: 1000 seed weight, GY: Grains yield

4. DISCUSSION

The substantial variability in plant height (PH) observed in this study, ranging from 140.60 cm to 241.33 cm, reflects the genetic diversity among maize genotypes. RML152/RML96 (241.33 cm) exhibited the greatest height, which may be advantageous in silage production due to increased biomass. However, as noted by taller plants can be more susceptible to lodging, especially in adverse weather conditions (Hammer et al., 2009). Conversely, shorter genotypes like RH10 (140.60 cm) provide greater stability and are more suitable for wind-prone regions and mechanized harvesting, aligning with the findings of (Zhang et al., 2018). The observed coefficient of variance (CV) of 8.333% highlights significant genetic and environmental influence on PH, reinforcing the importance of genotype selection based on environmental conditions. Similarly, ear height (EH), which ranged from 61.66 cm (RH10) to 131.66 cm (RML152/RML96), plays a crucial role in plant architecture and lodging susceptibility.

While higher EH, as observed in RML152/RML96 (131.66 cm), can indicate greater biomass and potential yield, it also increases lodging risk (Tollenaar and Wu, 1999). In contrast, RH10's low EH (61.66 cm) enhances lodging resistance, as supported by (Stewart et al., 2003). The variation in EH underscores the need for balancing ear placement to optimize both yield potential and plant stability in different environments. The observed variation in days to anthesis (AD), from 60.00 to 75.33 days, highlights the adaptability of maize genotypes to different growing seasons. RH10 (60.00 days) was the earliest to flower, making it ideal for short growing seasons or drought-prone areas, consistent with the findings of (Edmeades et al., 1993). In contrast, RML36/RML2244 (75.33 days) exhibited late anthesis, suggesting suitability for longer growing seasons, where extended vegetative growth can lead to greater biomass and yield.

The low CV of 2.883% indicates that flowering time is relatively stable, supporting in their assertion of the genetic control of anthesis (Hallauer et al., 2010). Similarly, early-silking genotypes like RH10 (63.66 days) ensure better pollination synchronization, as emphasized by whereas late-silking genotypes like RML36/RML2244 (79.00 days) are better suited for regions with prolonged rainfall, although they may be vulnerable to unpredictable weather (Campos et al., 2004; Russell, 1984). Cob length (CL), a critical determinant of grain yield, ranged from 12.90 cm (RH10) to 19.45 cm (RML152/RML96), with a grand mean of 16.40 cm. Longer cobs, as seen in RML152/RML96 (19.45 cm), suggest a higher kernel count and potential for greater yield, aligning with who noted a positive correlation between cob length and grain yield (Fischer et al., 2009). Conversely, RH10 (12.90 cm) had the shortest cob length, likely due to its shorter growing period and smaller stature. Moderate-length cobs in RML2137/RL2118 (17.98 cm) and RML36/RML2244 (17.27 cm) indicate a balance between ear size and plant adaptability, making them valuable for breeding programs targeting yield improvement.

The high CV of 8.782% underscores the genetic influence on cob length, offering opportunities for trait optimization in breeding. Cob diameter (CD) significantly influences kernel number and, consequently, yield. The largest CD (5.38 cm) in RML147/cML430 supports the findings of who reported that larger cobs result in higher grain yield due to increased kernel rows (Agung et al., 2020). In contrast, RH10 (3.98 cm) had the smallest cob diameter, aligning with who found that smaller cobs generally produce lower grain yields (Sibiya et al., 2019). Moderate cob diameters in RL35-1/RML2001 (4.96 cm) and RL252/RML98 (4.78 cm) suggest a balance between ear size and adaptability, a trend also observed by (Wende et al., 2021). The number of grain rows per ear (NGRPE) ranged from 12.00 to 14.53, with cML161/RML96 (14.53) exhibiting the highest value, reinforcing who noted that higher NGRPE correlates with greater yield potential (Badu-Apraku et al., 2020). Conversely, RML32/cML613 (12.00) recorded the lowest NGRPE, consistent with who found that fewer grain rows often lead to reduced yield (Moles et al., 2019).

Genotypes like RL284/RML146 (13.80) and RML2137/RL2118 (12.80) exhibited moderate NGRPE, balancing ear architecture with grain yield potential, supporting Prasanna et al. (2021). The number of grains per row (NGPR) ranged from 25.60 to 41.26, with RL35-1/RML2001 (41.26) recording the highest value, reinforcing who found that higher NGPR contributes significantly to total grain yield (Xia et al., 2019). Conversely, RH10 (25.60 NGPR) had the lowest value, supporting who observed that genotypes with fewer grains per row generally yield less (Khamis et al., 2020). Moderate NGPR values in RL252/RML98 (33.13) and RMl98/RML145 (33.26) suggest their potential for stable grain yield, aligning with (Kim et al., 2019). Thousand kernel weight (TKW), a key indicator of grain size and weight, varied from 0.032 kg (RML14/RML76) to 0.067 kg (RML142/RML17), with RML142/RML17 showing superior grain weight, aligning with who noted that higher TKW is associated with better grain quality and yield (Kamara et al., 2020).

Conversely, RML14/RML76 (0.032 kg) had the lowest TKW, consistent with who reported that lower TKW leads to reduced grain quality and yield (Semagn et al., 2021). Moderate TKW in RML147/cML430 (0.056 kg) and RML5/RML17 (0.057 kg) suggests their suitability for diverse environments, supporting (Amegbor et al., 2019). Grain yield (GY), the ultimate measure of maize productivity, ranged from 5341.567 kg/ha (RML14/RML76) to 10931.067 kg/ha (RL284/RML146). RL284/RML146 recorded the highest GY, aligning with who reported that high yield results from a combination of favorable traits (Wende et al., 2021). Conversely, RML14/RML76 (5341.567 kg/ha) had the lowest yield, consistent with who noted that genotypes with lower GY often have less favorable yield components (Masuka et al., 2017). Moderate-yielding genotypes like RML36/RML2244 (10570.733 kg/ha) and RML108/RL2118 (10597.533 kg/ha) highlight the importance of balancing yield components, supporting (Shiri et al., 2020).

In summary, the study highlights substantial genetic variability among maize genotypes in key agronomic traits, reinforcing the importance of targeted breeding programs to optimize yield, lodging resistance, and adaptability. The observed differences in plant height, ear placement, flowering time, cob characteristics, and grain weight align with previous studies and offer valuable insights for developing high-yielding, climate-resilient maize varieties (Badu-Apraku et al., 2019; Prasanna et al., 2021).

5. CONCLUSION

This study underscores the significant genetic diversity among maize genotypes, highlighting notable differences in plant height, ear placement, flowering time, cob characteristics, and grain yield. RML152/RML96 stands out for its tall stature and high biomass potential, making it a strong candidate for silage production, though its lodging risk necessitates careful management. Conversely, RH10, characterized by shorter height and lower ear placement, exhibits exceptional lodging resistance, making it particularly suitable for wind-prone regions and mechanized harvesting. Genotypes such as RL35-1/RML2001, with the highest number of grains per row, and RML142/RML17, which recorded the greatest thousand kernel weight, demonstrate strong grain yield potential. However, RL284/RML146 emerges as the most productive genotype overall, boasting larger cob size, more grain rows per ear, and efficient nutrient utilization, making it ideal for high-yield environments. In contrast, RML14/RML76, with its lower grain yield, may be less suitable for regions prioritizing high output. Based on these findings, RL284/RML146, RL35-1/RML2001, and RML142/RML17 are recommended as the most promising genotypes for cultivation due to their superior yield attributes and adaptability across diverse environmental conditions.

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