

Research Article

Agromorphological Characterization of Maize Hybrids and Estimation of Genetic Parameters in Mid-Hills of Far-West Nepal

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The experiment was laid out in alpha-lattice design with two replicates of each genotype which comprised twenty-three heat-tolerant maize hybrids received from CIMMYT-Mexico and three check varieties. These treatment genotypes were evaluated at the Agronomy farm, Gokuleshwor College, Baitadi, Nepal, during the spring season of 2021. ZH191065 and ZH191158 were found to be the tallest (307.2 cm) and the shortest (227.6 cm) genotypes, respectively. High heritability (>60%) with high genetic advances in most traits, ensures the predominance difference of the genetic components observed among accessions. The presence of differences among genotypes showed that selection is possible by evaluating the days of 50% anthesis, days of 50% silking, anthesis-silking interval, number of ears per plant, number of grains per row, number of rows per cob, cob length, cob diameter, and grain yield; most of these evaluated morphological traits were found highly correlated with grain yield of varieties, suggesting that indirect selection achieves improvement for high yield. Based on yield ranks, ZH 19782, ZH 19961, and DKC 9108 could be promoted as potential higher-yielding heat-tolerant maize hybrids for Nepal.

1. Introduction

Globally, maize production is the highest followed by wheat and rice [1]. Maize (*Zea mays*), also called corn, is believed to have originated in central Mexico 7000 years ago from wild grass, and Native Americans transformed maize into a better source of food. Maize contains approximately 72% starch, 10% protein, and 4% fat, supplying an energy density of 365 Kcal/100 g [2]. The world's leading top three maize-producing countries are the United States, China, and Brazil, producing approximately 563 of the 717 million metric tons/year [2].

Maize is serving as a staple food for consumption in the mid-hills of Nepal where food insecurities are major challenges. Maize ranks second after rice in terms of production and area coverage in Nepal. Maize crops are cultivated from March to May depending upon the distribution of rainfall. Maize productivity has been decimated (2.67 t/ha) in Nepal even though maize crop expansion for farming and

production has got the high attention of the farming community shown a steady increase since 2007 [3]. Maize contributes one-fourth of total edible cereal grain production in Nepal but the production of maize per hectare of land is below average as compared to other developed nations [3]. In order to attain self-sufficiency in maize for food, feed, and the hybrid seed inside the nation, the National Maize Research Program (NMRP) set out to pioneer a shift away from open-pollinated varieties (OPVs) toward hybrid maize [4]. As stated in National Seed Vision (NSV) and Agriculture Development Strategy, it is thought that the potential yield of maize cannot be realized alone by expanding farms, replacing them with modified ones, and popularizing OPVs (ADS) [5, 6]. The yield potential of OP cultivars was much higher than the national average yields in the previous year, but hybrid cultivars today often out-yield OP cultivars by more than half to double or more [7], having high yields of at least 15% above that of common OP cultivars and up to 90% of hybrid yields [7, 8]. According to the

study report of [9], open-pollinated and hybrid maize varieties in Dhading district found maize genotype Rampur hybrid-4 was high yielding and most beneficial as compared to others. Apart from this, there is no guarantee of getting a hybrid seed of adopted hybrid in the region because seed suppliers keep on changing such hybrids based on their availability from suppliers. Based on two years evaluation results of the study at Dukuchhap, Lalitpur by [10], recommended that maize hybrid Gaurav and OPV Deuti are comparable for grain yield and yield components in addition to their coping ability to stalk lodging problem. Accordingly, National Maize Research Program, Rampur has released 17 open-pollinated maize varieties for general cultivation for different agroecological zones. Among these, varieties Mankamana-1, Mankamana-3, and Deuti, all white-colored varieties are getting popularity among mid-hill farmers of eastern Nepal [11] and Rampur hybrid-10 is a recently released hybrid maize which is heat resilient and drought tolerant [12]. Hence, OPVs are widely cultivated and adopted at the farmer's level for seed and feed production but have low yields compared to hybrid maize out-yielded and OPVs. Thus, this study was conducted to identify high-yielding genotypes to the environment for domain-specific hybrid development, enhancing crop improvement programs and commercialization.

2. Materials and Methods

2.1. Study Area. The experiment was carried out at the Gokuleshwar Agriculture and Animal Science College's experimental farm in Dilasaini, Baitadi (Figure 1), located at 29.6880°N latitude and 80.5494°E longitude, at a height of 850 masl, from April 26 to August 22, 2021. Its average summer and winter temperatures are 21.1°C and 7.7°C, respectively, and it is located in the subtropical climate zones. The research region saw rainfall ranging from 44.61 mm to 254.18 mm, with the least amount occurring at the time of sowing in April and the highest amount occurring during the pretasseling/tasseling stage. In Figure 2, the specifics of the agroclimatic data are displayed. The experimental field's previous crops were rice, wheat, and maize (standing in the field).

2.2. Genetic Materials. The details of the genotype sources and varieties used in the study have been presented in

Table 1. The experiment consisted of twenty-six genotypes, among which twenty-three were heat stress tolerant maize hybrids developed by CIMMYT, Hyderabad, two are commercial maize hybrids of the world's leading company Bayer and Pioneer, and one internal check variety recently launched in Nepal i.e. RH-10 also known as Rampur hybrid-10 is used in the study.

2.3. Design of Experiment and Agronomic Practices. The experiment was laid out in an alpha-lattice design with two replications and four blocks (13 genotypes in each block). The plot size was 4-m × 0.75-m = 3-m² with row-to-row and plant-to-plant spacing of 75 and 20 cm, respectively. Every genotype was sown in two consecutive rows (Figure 3).

The field was prepared by deep tillage two times followed by leveling. Farm-yard manure was applied at the rate of 10 t/ha. Inorganic fertilizers were applied at the rate of 180 : 60 : 40 kg·ha⁻¹ of N : P₂O₅ : K₂O, respectively. Planting was done on the 26th of April, 2021 by line sowing in two consecutive rows, and the basal dose of Phosphorus and Potassium, and the half dose of Nitrogen were applied at the time of sowing. The remaining splits of Nitrogen were applied during the first and second weeding, respectively. Two weeding were carried out at 25 days after sowing (DAS) and 40 DAS. Earthing up was done as second weeding.

2.4. Data Collection. Five plants were tagged randomly from each block of two replication for agromorphometric measurements and genetic characteristics evaluations. All the data were taken 2 days before harvesting except for reproductive traits. Agronomic traits include plant height (PHT), ear height (EHT), ear aspect (EA), ear position (EP), and stem diameter (SG). Cob traits include cob length (CL), Cob diameter (CD), number of kernels per row (NOKPR), number of rows per cob (NORPC), and number of ears per plant (NEPP). Data were collected as per the methodology explained by [13, 14]. The recorded cob weight per plot, field weight (kg) was converted into grain yield (kg ha⁻¹) by multiplying the conversion factor 0.8 (shelling coefficient) with 12.5 percent moisture adjustment (equation (1)) [13]. The weight of the 1000-kernel weight of samples was recorded along with their moisture content by using a moisture meter and then it was converted to 12.5 percent moisture content (equation (2)).

$$\text{Grain yield} = \frac{\text{Field weight (kg)} \times 0.8 \times (100 - \text{Moisture content})}{\text{Plot size (m}^2\text{)} \times 87.5} \times 10, \quad (1)$$

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

2.5. Statistical Analysis. Data were analyzed using Microsoft Office Excel 2016 Analysis of variance, and cluster analysis was done using R Studio ver. 4.0.5 (Table 2), and the

estimation of genetic parameters was done according to the guidelines [15–19]. Pearson Correlation was computed using SPSS-26.

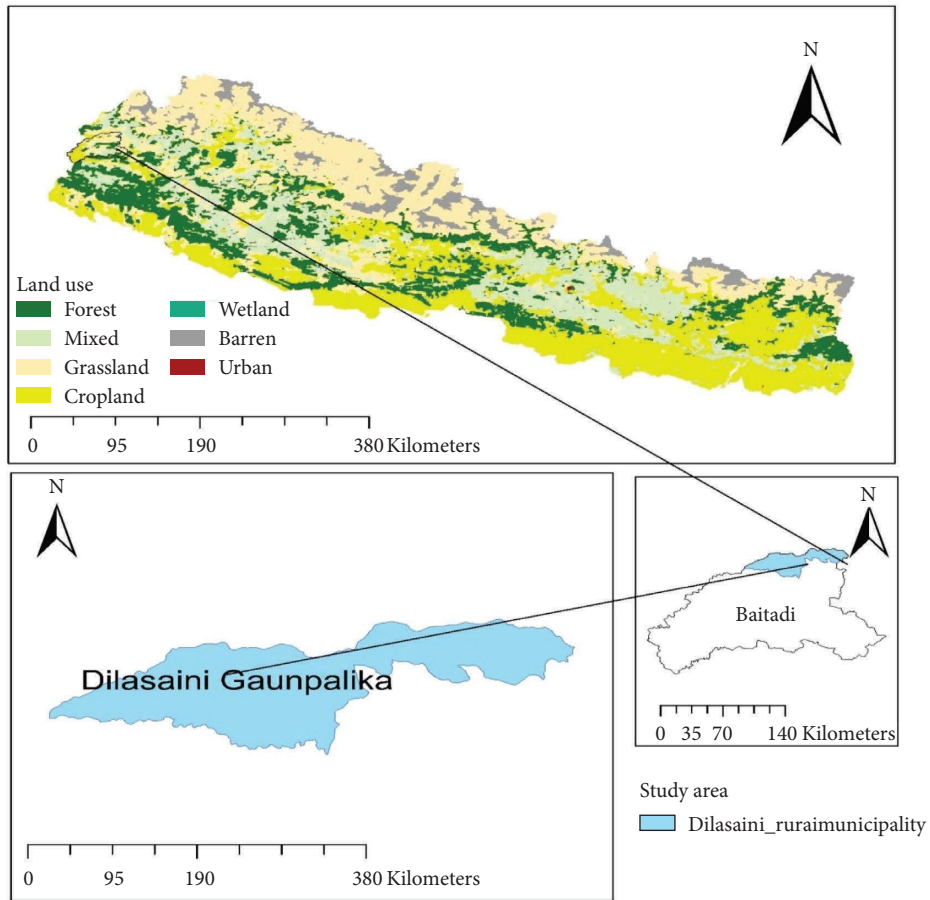


FIGURE 1: Map of the experimental area in Nepal.

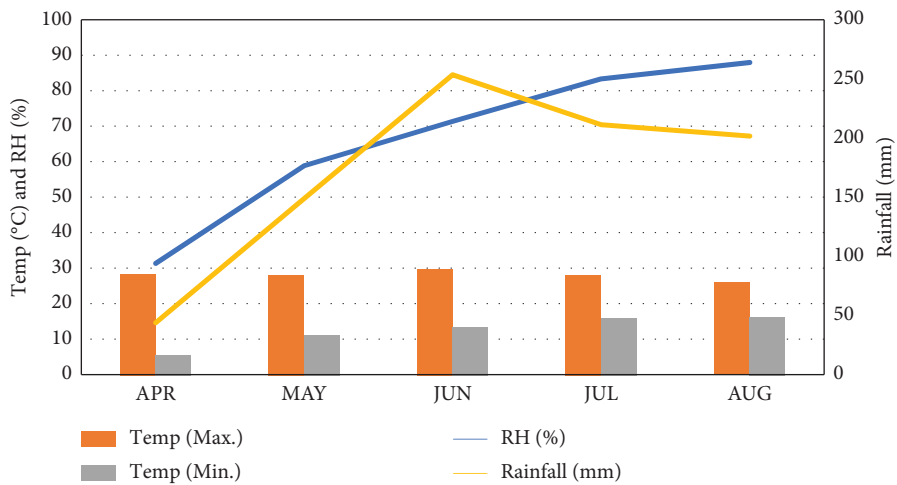


FIGURE 2: Agroclimatic characteristics of the experimental site.

TABLE 1: List of the genotype varieties used in for experimental study.

S.No.	Name of genotypes	Source
1	ZH191061	CIMMYT, Hyderabad
2	ZH191096	CIMMYT, Hyderabad
3	ZH192127	CIMMYT, Hyderabad
4	ZH192246	CIMMYT, Hyderabad
5	ZH19782	CIMMYT, Hyderabad
6	ZH19961	CIMMYT, Hyderabad
7	ZH192050	CIMMYT, Hyderabad
8	ZH192252	CIMMYT, Hyderabad
9	ZH191179	CIMMYT, Hyderabad
10	DKC9108	Bayer's crop science
11	ZH191063	CIMMYT, Hyderabad
12	ZH191100	CIMMYT, Hyderabad
13	ZH191037	CIMMYT, Hyderabad
14	ZH191965	CIMMYT, Hyderabad
15	ZH191158	CIMMYT, Hyderabad
16	ZH19814	CIMMYT, Hyderabad
17	ZH192201	CIMMYT, Hyderabad
18	ZH192010	CIMMYT, Hyderabad
19	ZH192030	CIMMYT, Hyderabad
20	ZH191155	CIMMYT, Hyderabad
21	CAH-153 (RH-10)	CIMMYT, Hyderabad
22	P1866	Pioneer seed company ltd.
23	ZH19940	CIMMYT, Hyderabad
24	ZH191953	CIMMYT, Hyderabad
25	ZH191065	CIMMYT, Hyderabad
26	ZH191046	CIMMYT, Hyderabad

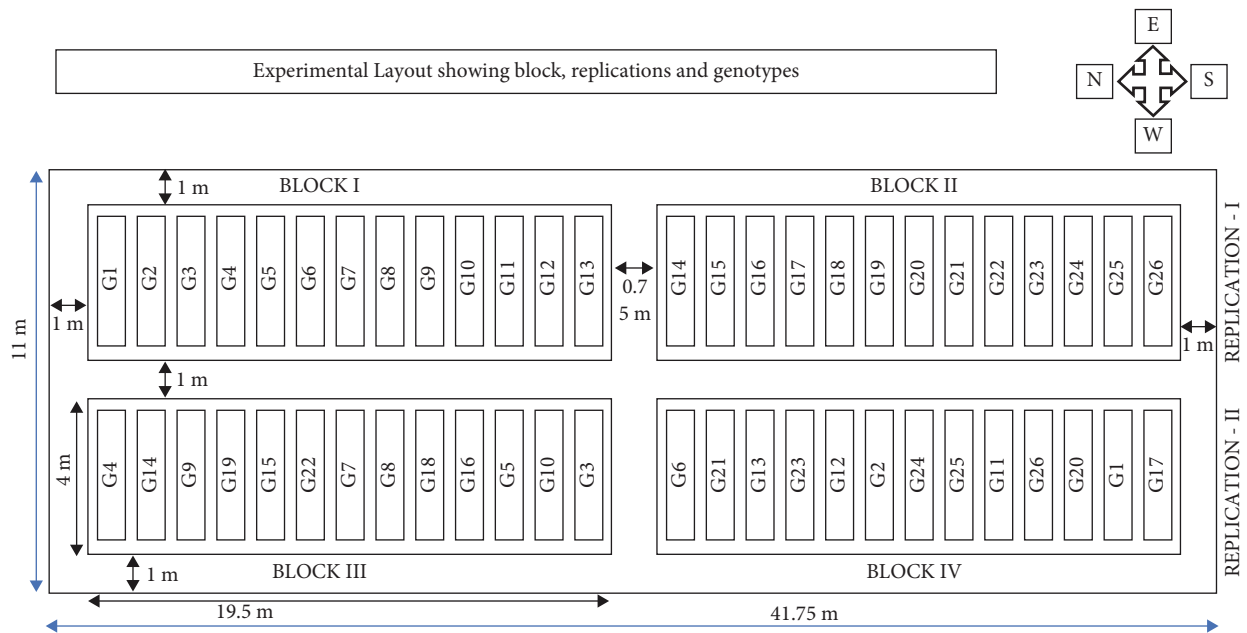


FIGURE 3: Experimental layout of alpha-lattice design for 26 genotypes.

3. Result and Discussion

3.1. Agromorphometric Characteristics of Genotypes

3.1.1. Plant Architectural Traits. Analysis of variance revealed that plant growth traits were nonsignificant ($p \geq 0.05$) except for ear aspect and stem diameter (Table 3). Tripathi et al. [16] reported that plant height was

nonsignificant in maize hybrids tested under the summer and winter season which supports our finding. Reference [20] reported that ear height in hybrid maize was similar among the genotypes which were accordingly reported in recent findings. In contrast to the recent findings, many authors (Patil et al. [21]; Tadesse et al. [22]; Bartaula et al. [23]; Kandel and Shrestha [12]; Koirala et al. [4]) reported that ear height varied among the genotypes. According to

TABLE 2: Analysis of variance for alpha-lattice design.

Source of variance	Degree of freedom (df)	Sum of square	Mean sum of square	F value	Pr (>f)
Replication (r)	(r - 1)	SSr	MSr	MSr/MSe	
Block within replication {b (r)}	r (b - 1)	SSb	MSb	MSb/MSe	
Genotypes (g)	g - 1	SSg	MSg	MSg/MSe	
Error	rg - rb - g + 1	SSE	MSe		
Total	n - 1	SSt			

TABLE 3: Average performance of plant architectural traits.

Genotypes	PHT	EHT	Ear position	Plant population per plot	Ear aspect	Stem diameter
DKC 9108	255.737	117.707	0.465	36.5	2.5	2.7
P1866	260.191	147.176	0.575	37.5	2.5	2.6
CAH-153	298.976	147.661	0.49	34	1.7	3.3
ZH191037	262.377	155.388	0.59	29	2.6	2.9
ZH191046	246.642	145.319	0.585	34	2.5	2.7
ZH191061	253.967	159.314	0.63	35	2.0	2.7
ZH191063	288.443	169.043	0.59	33	1.7	2.8
ZH191065	307.198	183.995	0.6	36	1.5	2.8
ZH191096	260.501	125.275	0.495	24	1.8	3.5
ZH191100	292.038	144.13	0.49	30.5	2.2	3.0
ZH191155	274.679	143.69	0.525	25	1.6	3.1
ZH191158	227.592	99.203	0.435	30.5	1.7	3.3
ZH191179	254.305	132.511	0.525	33	1.8	3.0
ZH191953	275.864	154.942	0.565	31	2.2	2.7
ZH191965	293.774	155.039	0.53	35	2.0	2.9
ZH192010	255.117	142.508	0.56	30.5	1.9	2.8
ZH192030	261.855	159.733	0.605	34.5	2.0	2.9
ZH192050	248.506	134.888	0.545	27.5	2.6	2.9
ZH192127	271.634	151.315	0.56	32	2.5	2.7
ZH192201	268.261	163.099	0.61	28.5	1.6	2.9
ZH192246	282.639	148.207	0.525	34	1.9	2.7
ZH192252	255.496	136.813	0.53	23.5	2.5	2.9
ZH19782	278.861	160.324	0.575	32	2.1	2.8
ZH19814	248.772	138.232	0.555	33.5	1.6	2.7
ZH19940	263.948	129.38	0.48	31.5	1.9	3.0
ZH19961	286.928	138.652	0.485	32	1.7	3.0
Mean	268.242	145.521	0.543	31.673	2.0	2.893
LSD (0.05)	15.679	19.308	0.093	7.9	0.5	0.64
CV	7.019	11.776	9.208	11.625	18.0	4.7
F-test	Ns	Ns	Ns	Ns	**	**
Min	227.592	99.203	0.435	23.5	1.5	2.6
Max	307.198	183.995	0.63	37.5	2.6	3.5

the study report plant height of most genotypes lies in the range of 250–260 cm. Comparably, the highest plant height and ear height of 307.2 cm and 184 cm was reported in ZH191065 and the lowest plant height and ear height of 227.6 cm and 99.2 cm were reported in ZH 191158, respectively. This stipulates that the genotypes were varied from parent lines, and usage of commercial and local checks [9] which are also from varied parental lines may have contributed to the variation in the plant height and ear height while statistically being at par.

A higher ear aspect was found in ZH191037 and ZH 192050 (2.6) and the lowest was found in ZH191065 (1.5) and shows variability among genotypes. The ear aspect ranges from one to five and resembles the cob characteristics from excellent to poor [14]. The variation observed in the ear

aspect shows an area for improvement in cob characteristics, and ranged from 1.5 to 2.6 which ranged from good to average cobs, none of the genotypes were reported with poor cob characteristics. The highest ear position was found in ZH191061 (0.63) and the lowest was found in ZH191158 (0.44) and were statistically nonsignificant. Several authors [4, 24] reported that ear position was statistically similar among the genotypes which were in line with our findings.

3.1.2. Reproductive Traits. The study revealed that anthesis days (AD), and anthesis-silking interval (ASI) show variations among the tested 26 genotypes while nonsignificant for silking days. The variability among the genotypes in AD and SD has been reported by [12, 22, 25] which supports our

finding. ZH 19814 showed earlier anthesis followed by P1866, DKC 9108, and ZH 19940 (Table 4), and genotype ZH 191155 showed higher days to anthesis. The silking days were shorter in P1866 and ZH 19814 and genotype ZH191155 showed higher days for silking. The least difference in the anthesis-silking interval was reported in ZH 19782, and the highest difference in the anthesis-silking interval has been reported in ZH 191179. The rate of pollination is directly influenced by duration of ASI: longer ASI have negative impact on grain yield [26, 27]. Reproductive traits viz. AD, SD, and ASI are widely dependent on daily mean temperature and genotype used i.e. optimum temperature reduces the length of AD and SD (as the growing degree days for tasseling and silking days reaches in a shorter period in spring) whereas lower temperature (winter) lengthens the duration for tasseling and silking; such that variation in days to anthesis has been reported in spring and winter season [4, 23, 28–30] and also influenced by genotype [20].

3.1.3. Grain Yield and Cob Characteristics. Cob characteristics include cob length, cob diameter, number of kernels per row, and number of rows per cob. Analysis of variance revealed high variability among genotypes for all of the cob characteristics and has a positive influence on grain yield and was further supported by the findings of [12, 23, 29]. Cob diameter ranged from 4.6 cm (ZH191965) to 5.8 cm (ZH 192252) with an average of 5.156 cm. Cob length ranged from 17.5 cm (ZH191061) to 26.4 cm (ZH19961), and the highest and lowest number of kernels in a row was reported in ZH 19961 and ZH 191065, respectively. Cob length assorted from 16–18 cm in provitamin A maize hybrids [31] which in comparison to our study has quite shorter cobs.

The study revealed that grain yield and thousand kernel weights were different among the genotypes. The genotype ZH 19782 showed higher grain yield followed by multinational hybrid DKC9108, ZH19961, ZH 19940, and ZH 191965; lower grain yield was reported in genotype ZH 192252 (Table 5). Grain yield is the primary economic trait for improvement in breeding programs as they are the one dependent to yield governing traits and cause direct influence on the productivity and profitability of farmers [32]. Several authors [16, 18, 24] reported that grain yield differed significantly in hybrid maize which provides an ample space for the selection of genotypes based on their performance. [30] reported that the grain yield of heat-resilient maize ranged from 2.2–9.25 t/ha. Similarly, [12] reported that grain yield ranged from 8.98–10.3 t/ha and [30] reported that grain yield ranged from 2.2–12.95 t/ha and was statistically significant. The above findings are in line with our study and provide ample information to support our findings.

3.2. Correlation Analysis. Grain yield showed a positive (medium) and highly significant correlation with the number of ears per plant (Table 6). The low levels of positive and nonsignificant correlation with grain yield were reported in plant height, ear height, number of grains per row,

TABLE 4: Reproductive trait performances of genotypes.

Genotypes	SD	AD	ASI
DKC 9108	60.59	58.59	2
P1866	58.40	57.54	1
CAH-153	65.40	64.36	1
ZH191037	64.09	63.46	1
ZH191046	62.40	61.44	1
ZH191061	64.85	62.72	1.5
ZH191063	64.09	62.13	2.5
ZH191065	65.640	62.66	3.5
ZH191096	68.85	65.78	2.5
ZH191100	67.35	64.17	3.5
ZH191155	69.40	68.14	1.5
ZH191158	67.64	65.20	1.5
ZH191179	66.35	61.59	4.5
ZH191953	64.64	63.15	2.5
ZH191965	62.40	60.07	2.5
ZH192010	65.64	62.15	3
ZH192030	66.14	61.04	3
ZH192050	67.35	66.27	2
ZH192127	62.09	60.46	1.5
ZH192201	67.40	65.16	2.5
ZH192246	66.35	65.26	1.5
ZH192252	65.59	64.44	1.5
ZH19782	64.5	63.65	0.5
ZH19814	59.14	57.43	1.5
ZH19940	60.14	58.6	1.5
ZH19961	64.85	63.39	2
Mean	64.67	62.65	2.01
LSD (0.05)	2.56	1.29	1.76
CV	1.9	4.36	46.7
F value	***	ns	*
Min	58.40	57.43	0.5
Max	69.40	68.145	4.5

and ear length. However, thousand kernel weight was weakly correlated with grain yield, yet there is a positive association between traits, and was supported by the finding of B. Ghimire and D. Timsina [33]. Reference [20] reported thousand kernel weight was the most yield-determining character followed by cob weight and the number of rows per cob. Reference [17] reported that plant height, ear height, ear length, ear weight, and number of kernels per row showed positive and significant correlations which contradict our finding.

Reproductive traits like anthesis day and silking day showed moderately negative and significant correlations with grain yield. However, the anthesis-silking interval showed a low level of negative and nonsignificant correlations with grain yield and was in line with the finding reported by [12, 17]. Anthesis days and silking days showed a moderately negative and significant correlation with the number of grains per row which suggests that higher chances of pollination are reported in genotypes with earliness to these traits. The most yield determinative traits were anthesis days, silking days, ear per plant, number of grains per row, ear height, and cob length, and hence, simultaneous selection for these traits might bring an improvement in grain yield. The details of the inter se correlation are presented in Table 6.

TABLE 5: Mean performance and analysis of variance of yield and cob characteristics.

Genotypes	Yield (T/ha)	Number of kernels per row	Number of rows per cob	Cob length	Cob diameter	Test weight
DKC 9108	12.72	40.5	16.3	26.2	5.4	304.6
P1866	10.00	42.3	17.2	23.3	5.2	268.1
CAH-153	8.17	36.4	14.2	22.4	5.1	366.7
ZH191037	6.78	32.5	17.2	20.0	5.3	308.4
ZH191046	8.89	42.4	13.8	22.8	4.8	257.1
ZH191061	8.94	35.1	17.2	17.5	4.9	310.1
ZH191063	10.55	36.7	12.2	21.8	5.1	359.7
ZH191065	9.60	31.5	16.6	19.3	5.4	308.5
ZH191096	5.82	37.7	15.0	25.0	5.0	307.4
ZH191100	4.26	34.7	14.4	24.0	5.0	350.4
ZH191155	5.15	32.6	13.6	20.7	4.7	280.3
ZH191158	7.76	34.8	15.2	22.7	5.4	336.6
ZH191179	8.91	33.7	17.0	20.9	5.4	323.9
ZH191953	9.30	38.7	13.6	23.0	5.0	365.2
ZH191965	10.57	36.2	15.8	22.1	4.6	325.3
ZH192010	8.21	40.4	16.8	20.6	5.1	261.1
ZH192030	10.21	42.2	16.6	21.1	5.1	277.7
ZH192050	6.21	36.2	14.2	22.5	5.5	335.0
ZH192127	9.37	41.0	12.4	20.2	4.9	314.3
ZH192201	4.20	36.2	15.6	22.9	4.9	329.9
ZH192246	8.00	38.1	18.0	24.3	5.7	315.7
ZH192252	3.85	36.3	19.8	21.4	5.8	332.9
ZH19782	13.75	36.0	15.8	23.4	5.0	298.7
ZH19814	7.69	41.1	15.2	23.9	5.0	347.8
ZH19940	10.84	44.2	17.6	23.9	5.2	277.5
ZH19961	11.94	50.9	14.6	26.4	5.5	334.7
Mean	8.53	38.015	15.612	22.400	5.156	315.290
LSD (0.05)	3.00	3.45	1.26	3.4	0.69	21.43
CV	30.21	5.1	3.5	5.6	3.9	16.0
F-test	**	***	***	***	***	*
Min	3.85	31.5	12.2	17.5	4.6	257.1
Max	13.75	50.9	19.8	26.4	5.8	366.7

3.3. *Cluster Analysis.* All the genotypes were clustered using phenological, plant architectural, quantitative, and yield and yield-attributing traits [32]. The dendrogram revealed that among 26 tested genotypes 25 were at about 50% similarity in clustering and genotype ZH192030 was found singular among the remaining 25 genotypes. The distance between the cluster centroid revealed that cluster 3 and cluster 5 were farthest (highest distance) and cluster 3 and cluster 4 are closest (lowest) (Tables 7 and 8) which concludes that similarity is higher in the cluster with the lowest average distance than that of higher. A similar finding was reported by [32].

There were two groups in the cluster as follows: groups A and B. Group B was characterized by the genotype ZH192030. The four clusters that made up group A were C-1, C-2, C-3, and C-4. Seven genotypes, or 26.9% of all genotypes, were found in cluster C-1 (Figure 4). This cluster of genotypes was characterized by the lowest yield, plant height, and ear height values (Table 9). Cluster C-2 which is characterized by the lowest SD, ASI consisted of 5 genotypes P1866, ZH 19046, ZH192010, ZH191155, and ZH19940 which consisted of 19.23%. Cluster 3 consisted of 6 genotypes, namely, RH-10, ZH191100, ZH191063, ZH191953,

ZH191965, and ZH19961 which accounts for 23% of genotypes, and is represented by the highest Plant height, and Cob length. Cluster 4 consisted of 7 genotypes, namely, ZH191037, ZH191061, ZH192201, ZH192127, ZH192246, ZH19782, and ZH191065. Cluster 4 is distinguished by the highest ear height, ear per plant. Cluster 5 consisted of only one genotype, namely, ZH192030, and is individualized by the highest grain yield, ear position, Plant population, number of kernels per row, and number of rows per cob. The main reason for clustering genotypes is to classify the genotype based on its complexity to traits such that selection is more effective [32].

3.4. Estimation of Genetic Parameters

3.4.1. *Heritability (h^2).* Among quantitative characters, high heritability (>0.60) has been observed for silking days (0.8), anthesis days (0.78), plant height (0.86), ear height (0.7) cob diameter (0.63), cob length (0.66), number of row per cob (0.91), and number of kernels per row (0.79) (Table 10). These estimates suggest the possibility of indirect selection for yield through traits with high

TABLE 7: Distance between clusters of 26 genotypes.

	Number of observations	Within cluster sum of squares	Average distance from the centroid	Maximum distance from the centroid
Cluster 1	7	3848.39	21.7911	36.9005
Cluster 2	5	1399.99	15.9370	23.5468
Cluster 3	6	2605.26	20.2770	26.3060
Cluster 4	7	3394.96	20.1428	40.6888
Cluster 5	1	0.00	0.0000	0.0000

TABLE 8: Distances between cluster centroids.

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	0.000	61.031	52.353	44.655	216.652
Cluster 2		0.000	87.253	49.829	156.681
Cluster 3			0.000	41.874	238.865
Cluster 4				0.000	199.530
Cluster 5					0.000

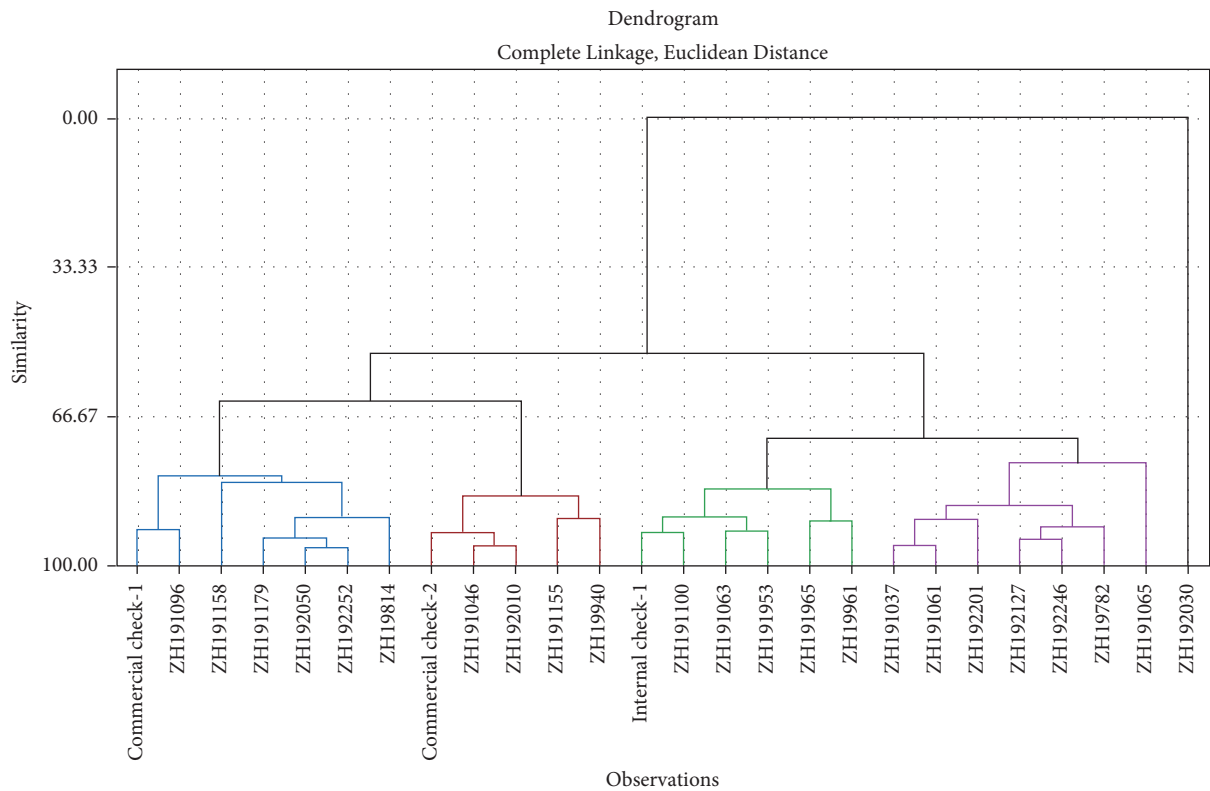


FIGURE 4: Cluster analysis of 26 genotypes.

heritability. Moderate heritability (0.30 to 0.60) has been found for the number of ears per plant (0.48), anthesis-silking interval (0.4), stem diameter (0.47), and grain yield hectare⁻¹ (0.46). Low heritability (<0.3) has been found for the ear aspect (0.18), and thousand kernel weight (0.26). Reference [17] reported that ear length, number of kernels per row, plant height, ear height, days to tasseling, and days to silking are the highly heritable traits that were in line with our findings. A similar finding was also reported by [31] but plant height and ear height were low and moderately heritable. High heritability for yield and yield-

attributing traits viz. days to tasseling and silking, plant height, ear height, cob length, number of kernels per row, and ear weight has been reported by [34].

3.4.2. Genetic Advance as Percentage of Mean (GAM). High disparities for many quantitative traits were seen in GAM at 5% selection intensity (Table 3). ASI, NEPP, NORPC, and yield were assessed to have high GAM values (greater than 20 percent). Plant height, ear height, cob length, number of kernels per row, and thousand kernel

TABLE 9: Distance between clusters of yield traits.

Variable	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Grand centroid
Yield (T/ha)	7.565	8.616	9.132	8.661	10.206	8.526
SD	65.079	63.199	64.794	65.007	66.141	64.673
AD	62.762	61.586	62.883	63.343	61.045	62.654
ASI	2.214	1.600	2.333	1.714	3.000	2.019
PHT	250.130	260.115	289.337	274.991	261.855	268.242
EHT	126.376	141.615	151.578	160.235	159.733	145.521
Ears per plant	1.197	1.159	1.173	1.428	1.377	1.253
Number of kernels per row	37.177	40.403	38.928	35.762	42.242	38.015
Number of rows per cob	16.100	15.800	14.133	16.114	16.600	15.612
Cob length	23.246	22.239	23.290	21.099	21.060	22.400
Cob diameter	5.364	5.002	5.070	5.135	5.135	5.156
Test weight	326.874	268.813	350.348	312.230	113.278	308.968

TABLE 10: Estimation of the genetic parameter of yield and yield-attributing traits of maize.

Traits	GCV	PCV	h^2	GA	GAM
SD	4.2	4.7	0.8	5.04	7.79
AD	4.07	4.5	0.78	4.6	7.4
ASI	36.3	55.1	0.4	0.9	49.3
PHT	7.26	7.78	0.86	37.17	13.95
EHT	10.7	12.8	0.7	27.1	18.6
CL	8.39	10.32	0.66	3.14	14
CD	4.9	6.2	0.63	0.42	8.1
NEPP	14.8	21.2	0.48	2.67	21.3
NORPC	11.2	11.7	0.91	3.4	22.26
NOKPR	10.5	11.9	0.79	7.3	19.3
Stem diameter	5.8	8.4	0.47	0.23	8.26
Yield	15.9	23.4	0.46	2	22.03
Test weight	10.8	20.9	0.26	44.3	11.5
Ear aspect	8.8	20.5	0.18	0.15	7.86

weight have all shown GAM between 10 and 20% (Table 10). For the cob diameter, silking days, anthesis days, and stem diameter, lower values were predicted. GAM values over a certain threshold suggest that traits with greater GAM are strictly governed by additive genes. According to [31], GAM revealed that highly heritable traits are governed by additive genes and traits with high heritability and low GAM suggest the influence of nonadditive genes.

(1) *Phenotypic and Genotypic Coefficient of Variation (PCV and GCV)*. A considerable difference in PCV and GCV values for different traits was observed (Table 4). For all the traits, the PCV value was higher than the GCV value i.e. environment has a significant impact on the expression of traits. The traits evaluated in this study had low (less than 10% phenotypic and genotypic coefficients of variation), moderate (10–20% phenotypic and genotypic coefficients of variation), and high (more than 20% phenotypic and genotypic coefficients of variation).

Among the studied quantitative traits, high PCV and GCV values (>20) were estimated for anthesis-silking intervals whereas NEPP, yield, and test weight had moderate GCV (10 to 20) and high PCV (>20) values. Ear height, NORPC, and NOKPR had moderate GCV and PCV values. Plant height, silking days, anthesis days cob diameter, and stem diameter had lower PCV and GCV values (>10)

(Table 10). Also, low GCV and high PCV values were reported in the ear aspect. The difference between GCV and PCV ranged from 0.43 to 18.8. This showed the presence of higher genetic effects in these parameters for variation. A larger portion of variations is heritable to offspring when broad sense heritability was higher. The reliability of a parameter to be selected for the breeding program among other factors is dependent on the magnitude of its coefficient of variations (CV), especially the GCV. However, the differences between the genotypic and phenotypic coefficient of variability explain the influence of the environment over the traits. While a lower value of CV generally depicts low variability among the tested sample; a high proportion of GCV to the PCV is advantageous in breeding works [34]. The higher the PCV and GCV values higher will be the efficacy of the selection of traits from the population or genotype for further excellence in the breeding program. From our study traits with high GCV in the anthesis-silking interval and tassel branch number; these two reproductive traits can be further considered for improvement in the population. Reference [17, 34] reported the highest GCV values for yield and yield-attributing traits for further improvement, but reproductive trait has been reported in our study.

4. Conclusion

Any breeding effort aims to improve yield while maximizing traits that have a positive impact on economic traits. The findings of the study showed that reproductive factors and cob characteristics differ significantly and directly affect yield. Also, genetic parameter estimation showed that a trait with high heritability and genetic progress is caused by the action of additive genes and has a direct influence on genotype selection. The generated genotypes are pipelines that are still in the earliest stages, therefore genotypes ZH 19782, ZH 19961, and DKC 9108 should be further assessed in local conditions to ensure that they are adaptable in the selected area.

Data Availability

Data associated with the manuscript will be made available from the corresponding author upon request.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

Authors' Contributions

Sara Rawaland and Sandesh Thapa contributed equally to this work.

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