Research Article

Agro-Morphological Characterization and Estimation of Genetic Parameters of Spring Maize Hybrids in the Inner Plains of Far-West Nepal

Prachi Bista,[1] Sandesh Thapa [ID],[1] Sara Rawal [ID],[1] Deependra Dhakal,[2] and Darbin Joshi[3]

[1]*Gokuleshwor Agriculture and Animal Science College, Baitadi, Nepal*
[2]*Regional Seed Testing Laboratory, Gandaki, Nepal*
[3]*International Maize and Wheat Improvement Center (CIMMYT), Kathmandu, Nepal*

Correspondence should be addressed to Sandesh Thapa; sand.thapa.2056@gmail.com

Heat resilient maize hybrids are an important input in maize cultivated area coupled with high temperature during the flowering period, with a specific focus on the Terai region of Nepal. The research was conducted in the Dhangadhi district from April 2020 to August 2020 in an alpha-lattice design with 26 genotypes and two replications. Analysis of variance suggests that genotypes were significantly different for all traits except plant height and plant population. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all traits. High PCV and GCV values were found in the anthesis silking interval, ear aspect and grain yield and low values in the anthesis days and silking days. Highly heritable traits were days to 50% tasseling (0.74), days to 50% silking (0.74), ear aspect (0.69), number of rows per cob (0.84), number of grains per row (0.61), cob diameter (0.87), and cob length (0.86). Genetic advance ranged from the lowest in plant height to the highest in anthesis silking interval. Correlation studies revealed that grain yield showed a negative and significant correlation with reproductive traits, while a positive and significant correlation between ear height and number of ears per hectare was observed. Cluster analysis grouped 26 genotypes into 5 major clusters, and the intracluster distance ranged from 4034.3 to 34960.3. Thus, traits having high variation can be used as selection indices for indirect selection for the improvement of maize productivity and suggest genotype like ZH182079, ZH1767, and KH15486 with high yield for commercialization and distribution to farmers.

1. Introduction

Maize (*Zea mays* L.) is an important cereal crop worldwide, serving as a major staple for both human consumption and animal feed. In Nepal, maize is an important staple food, both in terms of production and consumption. It is produced and consumed as a major food in the midhill region of Nepal, where food and nutrition security are major challenges. Maize is also used in livestock and poultry rations [1].

The maize area in Nepal is dominated by the spring season; however, the cultivation can also be seen in the winter season. Timsina et al. [1] reported that 56% of the total area was under maize in the midhills and of this, 56% was covered by hybrid maize. The average production and productivity trend of maize suggests that annual production of maize is increasing in Nepal but globally declining due to climate change and heat stress; especially in tropical and subtropical environments [2]. Among the various biotic stressors arising due to climate change, heat stress is one of them. To address heat stress tolerance in maize, CIMMYT initiated a project, "Heat Tolerant Maize for Asia (HTMA)" in September 2012 and it is still in progress in India, Nepal, Pakistan, Bangladesh, and Bhutan.

Climate change has an adverse effect on the environment and leads to various ecological imbalances. Among them, an increase in temperature causes stress on plant physiology, and a wide range of plants are being adversely affected. Among them, maize is one that, when subjected to a temperature of about 30°C during flowering, causes a significant yield loss [3, 4]. Heat stress increases the length of the

anthesis silking interval which is positively correlated with yield loss [5]. The sources of kernel loss, i.e., yield loss due to heat stress, are decreased floret differentiation, pollination failure, and kernel abortion [6].

In Nepal, the Terai and Inner Terai have a tropical environment which is also known as the granary basket of Nepal have experienced an elevation in temperature, which has a negative impact on yield. To address the heat stress on maize, HTMA was launched in 2013 in Nepal and is effective till date. With the increment in yield and for adopting the stress due to heat, heat resilient maize hybrids are of great importance in the south east. Asia Zaidi et al. [4] in India suggested that ZH16878 (5.69 t/ha) and ZH16930 (4.58 t/ha) were identified as promising for grain yield under heat stress and could be promoted for extensive testing and commercialization. To address heat stress and for adaptability of hybrids, location-specific trials are needed [7] which need to be performed over a wide range of locations and one suitable for each corresponding area should be further processed for commercialization and distribution. Developing and deploying climate resilient maize germplasm has become one of the top most priorities in the tropical and sub-tropical maize growing regions [8] especially in rainfall regions and during the spring season. Thus, the objective of this paper was to evaluate the variability of agro-morphological traits, yield and yield-attributing traits, and the correlation between these traits with their cluster analysis.

2. Materials and Methods

2.1. Study Area. The study was carried out in the Agronomy field of Unique Seed Company Limited, Dhangadhi. The research site lies (28.6852° N, 80.6216° E) at an altitude of 109 masl and is in inner plains characterized by hot and humid weather in summer and cold winter. Soil in the field was slightly acidic (pH = 5.95) and sandy loam soil. The agro-meteorological data was taken from the agro-meteorological station of the seed company and presented in (Figure 1).

2.2. Experimental Details. The experiment was laid out in an alpha-lattice design with two replications. There were two blocks within two replications and thirteen genotypes within each block. The genotypes were allotted randomly to the 26 plots in each replication. The plot size was $4\,m \times 0.75\,m = 3$-m^2 with inter and intra row spacing of 75 cm and 20 cm, respectively [9]. Every genotype was shown in two consecutive rows, with 21 plants in each row.

2.3. Genetic Materials. The genetic materials used in the study were provided by the National seed and fertilizer project, Kathmandu, Nepal, of CIMMYT. A total of 23 heat resilient genotypes were provided (heat resilient hybrid developed by CIMMYT, Hyderabad as a part of project HTMA[1]), one commercial check (CP 666), and two popular local varieties as an internal check was used. The details of the genetic materials used in the study are presented in Table 1.
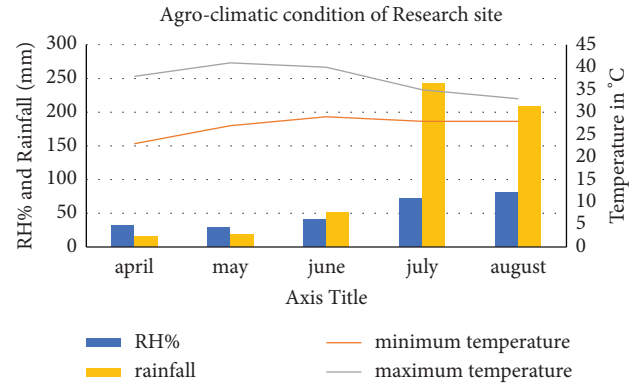

FIGURE 1: Agro-climatic conditions during the research period.

2.4. Crop Management Practices. Adequate crop management, including timely application of recommended inputs and agronomic operations, is a prerequisite for quality phenotyping [10]. Land preparation was performed by ploughing twice followed by leveling. Farm yard manure was applied at the rates of $15\,t\,ha^{-1}$. Chemical fertilizers were applied at the rates of $180:60:40\,kg\,ha^{-1}$ of $N:P_2O_5:K_2O$, respectively. Planting was done on April 26, 2020 by a manually operated sowing machine. A full dose of phosphorus and potassium and a half dose of nitrogen were applied at the time of sowing. The remaining half dose of nitrogen was applied in two split doses during the first and second weeding. Two weedings were carried out at 25 DAS and 40 DAS. Thinning was done during the first weeding. Earthing up was done as a second weeding. And harvesting was done between August 24 and 28.

2.5. Data Collection. Five plants were tagged randomly for recording observations for each entry for all the quantitative traits except for days to 50 percent anthesis and silking and average values were taken for analysis [11]. The details of the data collection technique and method have been followed as suggested by [11, 12] and are as follows.

2.5.1. Yield Attributing Traits

(1) No of Ears per hectare (NOEPH). Number of ear per hectare was calculated by counting the entire ears number in the row within the plot and converting it into hectares by using the following formula:

$$\text{NOEPH} = \frac{\text{Number of ears per plot} \times 10000\left(m^2\right)}{\text{Plot.size}\left(m^2\right)}. \quad (1)$$

(2) Number of rows per cob (NORPC). Number of kernel rows from a randomly selected ear from each of five randomly selected cobs was counted and average value was taken.

(3) Cob length (CL), cm. Length of the ear was measured and recorded in centimeters at the time of harvest as its total length (from the base to the tip of the ear) for five selected ear and average values was taken.

TABLE 1: Details of the genetic materials used.

S.N.	Name of genotypes	Source	S.N.	Name of genotypes	Source
1	ZH1798	CIMMYT, Mexico	14	KH15486	CIMMYT, Mexico
2	ZH191079	CIMMYT, Mexico	15	ZH1799	CIMMYT, Mexico
3	VH18567	CIMMYT, Mexico	16	VH18568	CIMMYT, Mexico
4	VH151703	CIMMYT, Mexico	17	VH16995	CIMMYT, Mexico
5	ZH191081	CIMMYT, Mexico	18	CAH1519	CIMMYT, Mexico
6	ZH17118	CIMMYT, Mexico	19	VH153258	CIMMYT, Mexico
7	RH-10	CIMMYT, Mexico	20	VH153492	CIMMYT, Mexico
8	ZH191077	CIMMYT, Mexico	21	VH153252	CIMMYT, Mexico
9	ZH1767	CIMMYT, Mexico	22	VH16223	CIMMYT, Mexico
10	ZH17119	CIMMYT, Mexico	23	ZH182079	CIMMYT, Mexico
11	VH171295	CIMMYT, Mexico	24	ZH191078	CIMMYT, Mexico
12	VH171006	CIMMYT, Mexico	25	InternalCheck-2**	Farmers variety
13	CP-666*	Charoen popkhand seed pvt. Ltd.	26	InternalCheck-1**	Farmers variety

*indicates commercial check and ** indicates local check.

(4) Cob diameter (CD), cm). From five randomly selected plants, ear (cob) diameter was recorded using a Vernier calliper and an average value was taken.

2.5.2. Reproductive Traits

(1) Days to 50% Anthesis (AD). The number of days taken from the days of sowing to the day on which 50% of the plants in a treatment plot showed full-tassel emergence with shedding of pollen was recorded as days to 50% tasseling.

(2) Days to 50% silking (SD). The number of days taken from the days of sowing to the day on which 50% of the plants in a treatment plot showed complete emergence of silk was recorded as days to 50% silking.

(3) Anthesis Silking Interval (ASI). This is a very important parameter to be determined for the appropriate pollination of maize. The interval between days to 50% tasseling and days to 50% silking is recorded as the anthesis silking interval (ASI).

2.5.3. Growth Traits

(1) Plant Height (PHT). Plant height was expressed in centimeters by measuring the plant stalk from the ground level to the base of the tassel branch of the matured plant. The plant height was observed from the representative five tagged plants.

(2) Ear Height (EHT). The height of the plant from ground level up to the base of the uppermost bearing internode from where cobs emerge (major cob) was recorded as ear height in centimeters.

2.5.4. Grain Yield (ton Ha^{-1}). The recorded per plot field weight (kg) was converted into grain yield (kg ha^{-1}) by multiplying the conversion factor (shelling coefficient) 0.8 with 12.5 percent moisture adjustment by using following formula:

Grain yield

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

The formula has also been adopted by [7, 9, 13–16] in estimating grain yield.

2.6. Statistical Analysis. Data was entered in Microsoft Excel (Ms-excel) 2016 and was analyzed using R-Studio 4.0.5 and SPSS v.20. Analysis of variance was done by using the R-Studio package "Agricolae" and genetic parameters were estimated via the package "Variability". The correlation coefficient was estimated using SPSS v.20 and cluster analysis was done via Minitab 19.1.

The correlation coefficient was computed by the formula Equation (1) given by Webster and Moorty and also used by [9, 14, 17–22].

$$rp(xy) = \frac{\text{cov}\, p(xy)}{\sigma 1/2g(x) * \sigma 1/2p(y)} (1). \quad (3)$$

Where rp (xy) presents phenotypic correlation, cov p (xy) is covariance due to the phenotype of xy, and $\sigma 1/2g(x)$, and $\sigma 1/2p(y)$ are the genotypic and phenotypic standard deviation of x and y, respectively. The phenotypic coefficient of variation (PCV) is presented in Equation (2). and the genotypic coefficient of variation (GCV) equation (3). has been calculated as suggested by Singh and Chaudary [23]. Followingly, similar formula was adopted by [9, 14, 24–27] in estimation of PCV and GCV in maize. Heritability in the broad sense (4) was estimated using the formula suggested by [28] and genetic advance (5), and genetic advance as a percentage of the mean using the formula suggested by [29]. Similarly, the abovementioned procedure has been adopted by [9, 13, 14, 24, 30–34] in the estimation of genetic parameters in maize.

$$PCV = \frac{\sqrt{\delta^2 p} * 100}{x}, \qquad (4)$$

$$GCV = \frac{\sqrt{\delta^2 g} * 100}{x}. \qquad (5)$$

Where, $\delta^2 p$ IS phenotypic variance and $\delta^2 g$ is genotypic variance and x is the population mean

$$\text{Heritability}\left(h^2 bs\right) = \frac{\delta^2 g}{\delta^2 p}, \qquad (6)$$

$$\text{Genetic advance}\,(GA) = K\left(\delta^2 p\right)\left(h^2 bs\right). \qquad (7)$$

Where, K = selection differential that varies depending up on the selection intensity and stands at 2.056 for selecting 5% of the genotypes.

3. Result and Discussion

3.1. Mean Performance and Analysis of Variance. The analyses of variance for the different traits recorded are presented in Table 2.

In the table, a significant difference was observed in all traits except for plant height and plant population per plot. Similar to our finding, Neupane et al. [35] reported significant differences in all the traits under study. The details of the analysis of variance and performance of genotypes are presented in the following text:

3.1.1. Reproductive Trait. The analysis of variance of reproductive traits suggests that anthesis day, silking day, and anthesis silking interval showed a highly significant difference. The duration of anthesis day ranged from 46.3 (ZH1767) to 54.2 days (ZH191081) and silking days ranged from 47.57 (ZH1767) to 57.19 days (VH151703). The anthesis silking interval of the tested genotypes ranged from 0.99 (VH153252) to 5.51 days (VH151703).

The mean day to 50% tasseling of 54 days with the range of 52–55 days in summer maize has been reported by Bello et al. [36]. The anthesis and silking days of spring maize are comparatively shorter than those of winter maize [7], where the average length varies from 100 to 111 days in anthesis and 102–11 days in silking. The ASI of heat resilient hybrids in the range of 2–4 days has been reported in chitwan and dang condition [16]. When maize is subjected to stress during flowering due to light, nutrients, drought, or long photoperiods, the duration of the ASI increases, which appears to be a general response by the plant to a reduction in photosynthate formed during this growth stage [5]. The following, yield and its components show dependence on the ASI [5].

3.1.2. Growth Traits. Analysis of variance revealed that plant height was not significantly different but ear height was significantly different ($P \leq 0.01$). The mean plant height was 283.4 cm and the tallest genotype was ZH191081 (312.5 cm) and the shortest plant genotype was ZH182079 (240 cm).

The average ear height was 156.33 cm and ranged from 119.84 cm to 185.28 cm in genotypes VH16223 and ZH191081, respectively. The differences in the plant height, though being nonsignificant, might be because of the fact that the hybrids were from diversified parent lines [7] and checks were also used in the study, which were of high importance in the study area. Similar to our finding, Tripathi et al. [37] and Koirala et al. [15] reported that plant height was not significantly different in three-way cross yellow maize hybrids and single-cross hybrids, respectively.

3.1.3. Yield and Yield Component Trait. A significant difference was observed in yield and yield-attributing traits of maize (number of ears per hectare, number of grains per row, number of rows per cob, cob length, and cob diameter). Analysis of variance revealed that grain yield was significantly different with a mean grain yield of 10.01 t/ha. The grain yield ranged from 5.08 to 13.94 t/ha making VH151703 the lowest yielder and ZH182079 the highest grain yielder. The popular local variety used as checks had a grain yield of 11.59 and 11.98 t/ha. A significant difference in grain yield has been reported by many authors [9, 35, 38, 39]. Yield-attributing traits are correlated positively in increasing yield and contribute for enhancing grain yield [38]. The ear aspect was significantly different, ranging from 1.97 to 3.97 with a mean of 2.75. The ears with aspect 1 were considered with good appeal and with aspect 5 with poor appeal [11].

The average number of ears per hectare was 51474 and was highest in ZH182079 (71190 ears) and the lowest count in genotype ZH191081. The number of grains per row was highest in KH15486 and the highest number of rows per cob was reported in ZH17118. VH18568 had the highest cob diameter, and the longest cob was ZH1767. Similar to our finding, a highly significant difference in grain yield and the yield-attributing trait has been recorded by Kumar and Bhati (2014) [38].

3.2. Estimation of Genetic Parameter

3.2.1. Heritability. Heritability has been classified as high (>0.6), moderated (0.3–0.6) and low heritable trait (<0.3) [28]. Considerable differences in the heritability among traits have been observed (Table 3). Highly heritable traits with heritability >0.6 are days to 50% tasseling (0.74), days to 50% silking (0.74), ear aspect (0.69), number of rows per cob (0.84), number of grains per row (0.61), cob diameter (0.87), and cob length (0.86). Moderate heritability between 0.3 and 0.6 has been observed in anthesis silking interval (0.58), ear height (0.4), ear population (0.51), grain yield (0.56), and low heritability (<0.3) has been found in plant height and plant population. Similar to our finding, high heritability in reproductive traits has been reported by many authors [35, 36, 40]. High heritable traits have genotypic variance far larger than environmental variance and being equal to phenotypic variance when the traits are fully governed by genotypes; in seedling germination [36]. The number of grains per ear and ear weight along with grain yield have high heritability as

TABLE 2: Mean performance and analysis of the variance of the 26 genotypes.

Genotypes	AD	SD	ASI	PHT	EHT	Plant population	EA	NOGPR	NORPC	CD	CL	NOEPH	GY (ton ha^{-1})
CAH1519	51.30	51.57	0.99	281.00	153.22	33.37	2.28	27.86	12.17	4.46	19.38	52857	11.48
CP-666	46.89	48.19	1.01	290.00	137.66	32.05	3.52	26.38	15.51	4.22	17.17	45139	7.85
InternalCheck-1	49.39	52.69	3.01	289.00	161.16	38.05	2.52	25.54	14.84	4.34	18.32	57639	11.59
InternalCheck-2	48.20	53.43	4.51	305.00	147.78	31.13	2.22	33.81	15.83	4.68	20.57	48810	11.98
KH15486	49.11	51.31	2.49	260.00	162.34	35.45	1.98	34.79	12.16	4.20	20.08	55694	12.06
RH-10	50.70	52.43	1.01	292.50	163.28	31.13	2.47	24.81	13.83	4.10	18.31	46310	10.62
VH151703	51.39	57.19	5.51	291.00	137.16	35.55	3.77	25.04	15.51	4.18	17.19	31806	5.08
VH153252	47.61	48.31	0.99	277.50	131.84	34.95	3.48	22.12	15.83	4.33	18.56	52361	9.15
VH153258	49.80	53.07	3.99	275.00	133.72	32.87	3.53	20.19	13.84	4.16	16.63	34524	5.16
VH153492	50.80	52.57	2.49	272.50	144.72	37.87	2.28	28.69	14.84	4.52	18.44	56190	10.98
VH16223	50.11	52.81	2.99	241.00	119.84	36.95	3.73	23.12	15.49	4.31	21.38	47361	8.95
VH16995	50.61	53.31	2.99	277.00	151.34	33.45	2.98	27.96	14.16	4.05	16.40	51528	10.99
VH171006	48.89	52.69	3.51	289.00	160.16	37.05	3.27	24.21	14.17	4.21	16.87	51806	7.86
VH171295	47.70	52.43	4.01	302.00	163.28	33.63	1.97	30.47	13.83	4.43	19.46	50476	9.83
VH18567	48.70	51.93	2.51	291.00	161.28	30.13	2.22	27.47	13.83	4.09	18.46	53810	11.49
VH18568	50.30	51.57	1.99	275.00	155.72	33.87	2.53	29.53	14.84	4.68	20.11	54524	11.31
ZH17118	48.70	54.43	5.01	286.50	149.78	32.13	1.97	24.47	18.83	4.35	14.31	57143	9.81
ZH17119	50.20	55.93	5.01	283.50	151.78	34.63	3.22	29.14	16.16	4.23	19.02	42143	6.51
ZH1767	46.30	47.57	1.99	287.00	159.22	40.87	2.53	24.69	12.84	4.59	22.53	66190	11.42
ZH1798	48.39	51.19	2.51	292.50	165.66	39.55	2.52	24.38	15.51	4.39	14.40	64306	12.22
ZH1799	50.11	53.81	3.99	278.50	171.34	41.95	2.73	27.12	15.83	4.42	17.51	53194	10.26
ZH182079	49.30	51.07	2.49	240.00	167.72	43.37	2.28	24.19	15.84	3.04	19.03	71190	13.94
ZH191077	50.11	51.81	1.99	304.50	183.84	32.95	2.48	24.12	16.16	3.01	18.90	54028	11.63
ZH191078	49.80	51.57	2.49	282.00	164.22	35.87	2.03	28.53	11.50	4.23	18.31	55357	11.29
ZH191079	49.39	52.69	3.01	293.00	181.16	31.55	3.02	27.54	14.51	4.39	19.37	53472	10.10
ZH191081	54.20	56.93	2.01	312.50	185.28	36.63	3.97	26.81	14.50	3.93	17.02	30476	6.73
Grand mean	49.54	52.40	2.87	283.40	156.33	35.27	2.75	26.65	14.71	4.21	18.37	51474	10.01
CV%	1.60	2.4	32.3	8.1	9.4	12.7	13.9	8.5	4.3	3.2	4	14.6	17.4
LSD (at 0.05)	1.78	2.5	1.9	69.8	30.06	9.02	0.77	4.72	1.27	0.3	1.49	138.6	3.47
F-test	***	***	***	*	*	ns	***	***	***	***	***	**	**

(*** means significant at less than 0.1% LOS; ** significant at less than 1% LOS and * means significant at less than 5% LOS; AD = days to 50% anthesis, SD = days to 50% silking, ASI = Anthesis silking interval, PHT = plant height, EHT = Ear height, EA = ear aspect, NOGPR = number of grain per row, NORPC = number of row per cob, CD = cob diameter, CL = cob length, NOEPH = number of ear per hectare, GY = Grain yield).

TABLE 3: Estimation of genetic parameter of tested 13 traits.

Traits	GCV	PCV	H^2	GA	GAM (%)
AD	3.02	3.49	0.74	2.67	5.39
SD	3.75	4.41	0.72	3.44	6.5
ASI	38.2	50.11	0.58	1.72	60
PHT	2.32	8.14	0.08	3.88	1.37
EHT	7.7	12.1	0.40	15.7	10.9
PLANT POPLN	2.6	12.7	0.04	0.39	1.39
Ear popln	14.5	20.4	0.51	6.63	21.49
Ear aspect	20.5	24.6	0.69	0.96	35.16
NORPC	9.78	10.6	0.84	2.72	18.5
NOGPR	10.9	13.9	0.61	4.7	17.6
CD	9.11	9.75	0.87	0.73	17.5
CL	9.9	10.6	0.86	3.5	19.05
GY	20.6	25.52	0.56	2.96	29.62

reported by Bello et al. [36]. Neupane et al. [35] also reported high heritability in grain yield, number of grains per row, number of rows per cob, cob length, and cob diameter. The synthesis silking interval was moderately heritable [35]. High heritability in grain yield and plant height has been reported by Neupane et al. [35, 36] which contradicted our findings, which are moderately and low heritable traits respectively, but was in line with the findings of Tripathi et al.

[37]. The expression of a trait is highly influenced by environmental effects and effects on the degree of expression but not on the degree of inheritance [41]. Thus, optimum environmental conditions are necessary for expressing the potential of genotypes such that environmental variation is kept to a minimum.

3.2.2. Genetic Advance as Percentage of Mean. Higher heritability is coupled with the higher genetic advance in the next generation coupled with additive gene action for the expression of these traits which is fixable in subsequent generations. This also provides evidence that a larger proportion of phenotypic variance has been attributed to genotypic variance, and that reliable selection could be made for these traits on the basis of phenotypic expression. Higher genetic advances of more than 20% were estimated for anthesis silking interval, ear population, ear aspect, and grain yield (Table 3). A similar finding was reported by Bello et al. [36]. Genetic advance between 10–20% was observed for ear height, number of grains per row and number of rows per cob, cob length, and cob diameter. And lower values were estimated for anthesis day, silking day, plant height, and plant population per plot. Neupane et al. [35] reported a moderate

TABLE 4: Phenotypic correlation among yield and yield-attributing traits.

|	AD	SD	ASI	PHT	EHT	Plants popln	NORPC	NOGPR	CD	CL	Ear per hectare	GY
AD	1											
SD	0.787**	1										
ASI	0.070	0.670**	1									
PHT	0.070	0.038	−0.023	1								
EHT	0.194	0.067	−0.126	0.243	1							
PLANTPOPLN	−0.006	0.054	0.094	−0.217	0.136	1						
NORPC	−0.057	0.203	0.397**	0.032	-0.131	0.068	1					
NOGPR	0.064	0.078	0.049	0.029	0.221	−0.232	−0.244	1				
CD	−0.113	0.021	0.170	0.102	−0.262	−0.098	−0.087	0.326*	1			
CL	−0.185	−0.243	−0.170	-0.218	−0.028	−0.013	−0.365**	0.303*	0.085	1		
EPH	−0.038	−0.096	−0.110	0.175	0.013	0.070	−0.022	0.002	0.022	0.341*	1	
GY	−0.275*	−.453**	−.401**	0.013	0.379**	0.147	−0.147	0.262	−0.131	0.221	0.174**	1
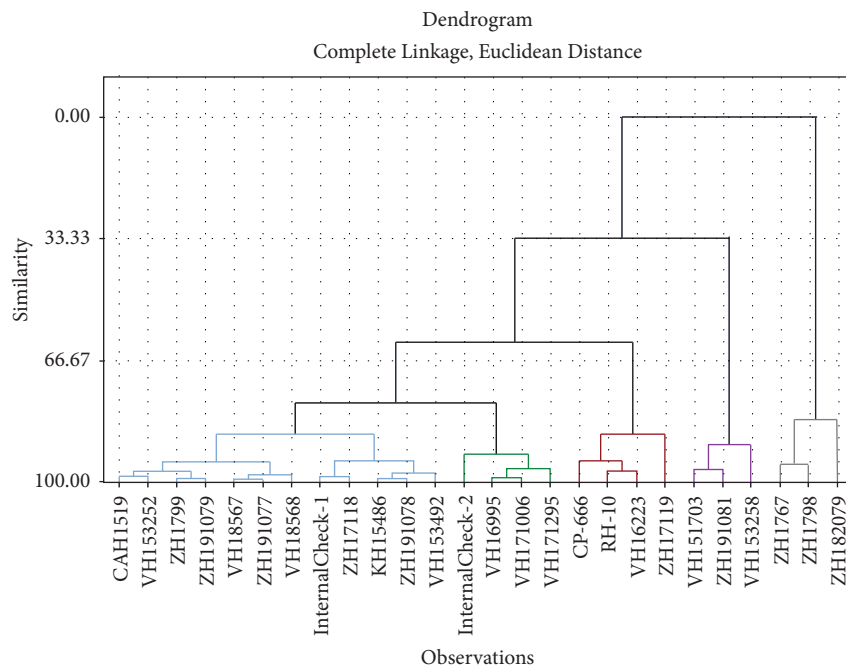
FIGURE 2: Dendrogram showing cluster analysis of 26 genotypes of maize.

genetic advance in ear length, ear diameter, and ear height and low genetic advance in plant height; however, [9] reported lower genetic advance of all 4 aforementioned traits.

High heritability and low genetic advance are due to the presence of nonadditive effects governing this trait [36]. Since high heritability does not always indicate a high genetic gain, heritability is recommended to be considered in association with genetic advancement to predict the effect of selecting superior crop varieties [34],

3.2.3. Genotypic Coefficient of Variation and Phenotypic Coefficient of Variation. The genotypic coefficient of variation (GCV) was less than its corresponding estimates of the phenotypic coefficient of variation (PCV) for all the traits which indicated a significant role of the environment in the expression of these traits [42]. Higher GCV and PCV values were reported in anthesis silking interval, ear aspect, and grain yield. Highest estimate of GCV and PCV was found in grain yield, ear height, anthesis silking interval, and ear aspect [27]. Moderate GCV and highest PCV were reported in ear population and ear height. Similarly, moderate GCV and PCV were reported in a number of row per cob and the number of grain per rows and remaining traits have lowest GCV and PCV values (Table 3).

3.3. Correlation Coefficient. The phenotypic correlation coefficient of yield and yield-attributing characters are shown in Table 4.

Both positive and negative correlations have been reported. Yield was found negatively and significantly correlated with reproductive traits such as anthesis days

TABLE 5: Distance between cluster centroids.

	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5
Cluster1	0.0				
Cluster2	9451.0	0.0			
Cluster3	4034.3	5416.7	0.0		
Cluster4	22420.6	12969.6	18386.3	0.0	
Cluster5	12539.7	21990.7	16574.0	34960.3	0.0

TABLE 6: Centroid of clustering of 26 genotypes evaluated for agro-morphological traits.

Variable	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Grand centroid
AD	49.6	49.5	48.8	51.8	48.0	49.5
SD	52.0	52.3	53.0	55.7	49.9	52.4
ASI	2.6	2.5	3.8	3.8	2.3	2.9
PHT	282.5	276.8	293.3	292.8	273.2	283.4
EHT	160.1	143.1	155.6	152.1	164.2	156.3
PLANTPOPLN	34.8	33.7	33.8	35.0	41.3	35.3
EA	2.5	3.2	2.6	3.8	2.4	2.8
NOGPR	27.3	25.9	29.1	24.0	24.4	26.7
NORPC	14.6	15.2	14.5	14.6	14.7	14.7
CD	4.3	4.2	4.3	4.1	4.0	4.2
CL	18.5	19.0	18.3	16.9	18.7	18.4
NOEPH	54689.1	45238.1	50654.8	32268.5	67228.8	51474.4
GY	10.9	8.5	10.2	5.7	12.5	10.0

(-0.275^*), silking days (-0.453^{**}), and anthesis silking interval (-0.401^{**}). A negative correlation has been reported by [7, 9, 43] in reproductive traits; i.e., short days to tasseling and silking has influenced grain yield. Ear height and the number of ears per hectare were positively and significantly correlated with yield. Similarly, plant height, plant population, number of grains per row, and cob length were positively correlated with grain yield. Similar findings were reported by Thapa wt et al. [9] that ear height was positively correlated, and Maize et al. [13] reported a positive correlation of ear length with grain yield.

Similarly, the interset correlation between the yield governing traits has been reported and found to have a positive and significant correlation between anthesis day and silking days, anthesis silking interval and silking days, number of rows per cob and anthesis silking interval, number of grains per row with both cob diameter and cob length, and cob length with ear per hectare. And, only cob length was negatively and significantly correlated with the number of rows per cob. Kandel and Shrestha [7] reported that interset correlation was positively and significantly correlated with anthesis day and silking day, ear height and plant height, and the number of grain rows per ear with ear height, respectively.

Cluster analysis has significant aptitude to recognize the homogenous variables at different degrees of similarities in the form of dendrogram [44]. Twenty-six maize genotypes used in the present study were grouped into five clusters based on their performance for twelve plant traits (Figure 2). The dendrogram revealed that among the tested 26 genotypes 23 genotypes were similar at 33.33% level of similarity and rest 3 genotypes were dissimilar with other 23

genotypes. The distance between the cluster centroid was found highest between cluster IV and cluster V and lowest distance was found between cluster III and cluster I. The distance between two cluster centroids is presented in Table 5. High levels of intra- and intercluster distances indicate the presence of broad genetic variation between and within a cluster [38].

Cluster I consist of CAH1519, VH153252, ZH1799, ZH191079, VH18567, ZH191077, VH18568, Internal check 1, ZH17118, KH15846, ZH191078, and VH153492 and is characterized by highest cob diameter (Table 6). Cluster II consists of Internal check 2, VH16995, VH171006, and VH171295 and characterized by highest number of row per cob and cob length. Cluster III consists of CP666, RH10, VH16223, and ZH17119 and is characterized by plant height, number of grain per row, and cob diameter. Cluster IV consists of VH151703, ZH191081, and VH153258 and is characterized by highest ear aspect and cluster- V consists of ZH1767, ZH1798, and ZH182079 and is characterized by lowest AD, SD, and ASI and highest ear height, plant population, number of row per cob, number of ear per hectare and grain yield. The favorable yield-attributing traits can be observed in cluster- V where fewer days for flowering with high grain yield has been observed.

4. Conclusion

The essence of location-specific trails is of great importance in the maize hybrid development program. Since the resulting genotypes are the pipelines, and their promising performance and high yield could contribute for commercialization and distribution of genotypes at farmer level which is the main aim of the crop development program.

Thus, in the trail, all the agro-morphological traits except plant population and plant height showed variation and differed significantly. Results indicate that higher yield is correlated with reproductive traits, number of ears per hectare, and ear aspect. Thus, with high yield genotype ZH182079, ZH1767, and KH15846 are suggested for further evaluation and release as a new heat-resilient variety in the inner plains of Nepal.

Data Availability

Data will be made available on request.

Additional Points

Correlation between yield and yield-attributing traits revealed that reproductive trait, ear height, and ear number had a positive effect on yield. Cob length, cob diameter, and number of row per cob were highly heritable trait. Genotype ZH182079, ZH1767, and KH15486 with high yield can be further recommended for seed multiplication and commercial distribution.

Conflicts of Interest

The authors declare that there are no conflicts of interest.

Acknowledgments

References

[1] K. P. Timsina, Y. N. Ghimire, and J. Lamichhane, "Maize production in mid hills of Nepal: from food to feed security," *Journal of Maize Research and Development*, vol. 2, pp. 20–29, 2016.

[2] P. Ranum, J. P. Peña-Rosas, and M. N. Garcia-Casal, "Global maize production, utilization, and consumption," *Annals of the New York Academy of Sciences*, vol. 1312, pp. 105–112, 2014.

[3] A. Dinesh, A. Patil, P. H. Zaidi et al., "Dissection of heat tolerance mechanism in tropical maize," *Research on Crops*, vol. 17, no. 3, pp. 462–467, 2016.

[4] P. Hanamappa Kuchanur, M. Dhanoji, P. H. Kuchanur et al., "Heat Tolerant Maize for Asia:Stability of Maize (Zea mays L.) Hybrids across Heat Stress Environments," 2019, https://www.researchgate.net/publication/341343262.

[5] G. O. Edmeades, J. Bolanos, A. Elings, J. M. Ribaut, M. Banziger, and M. E. Westgate, "The role and regulation of the anthesis-silking interval in maize," *Physiology and Modeling Kernel Set in Maize*, vol. 29, pp. 43–73, 2015.

[6] J. I. Rattalino Edreira, E. Budakli Carpici, D. Sammarro, and M. E. Otegui, "Heat stress effects around flowering on kernel set of temperate and tropical maize hybrids," *Field Crops Research*, vol. 123, no. 2, pp. 62–73, 2011.

[7] B. P. Kandel and K. Shrestha, "Performance evaluation of maize hybrids in inner-plains of Nepal," *Heliyon*, vol. 6, no. 12, Article ID e05542, 2020.

[8] J. E. Cairns and B. M. Prasanna, "Developing and deploying climate-resilient maize varieties in the developing world," *Current Opinion in Plant Biology*, vol. 45, pp. 226–230, 2018.

[9] B. T. Magar, S. Acharya, B. Gyawali, K. Timilsena, J. Upadhayaya, and J Shrestha, "Genetic variability and trait association in maize (Zea mays L.) varieties for growth and yield traits," *Heliyon*, vol. 7, no. 9, Article ID e07939, 2021.

[10] P. H. Zaidi1, M. Zaman-Allah, S. Trachsel, K. Seetharam, J. E. Cairns, and M. T. Vinayan, "Phenotyping for Abiotic Stress Tolerance in Maize," *CIMMYT*, pp. 238–249, 2016.

[11] B. Badu-Apraku, M. A. B. Fakorede, A. Menkir, and D. Sanogo, "Conduct and Management of Maize Field Trials," 2012, https://www.researchgate.net/publication/281106351_Conduct_and_Management_of_Maize_Field_Trials.

[12] M. Abdou Zaman-Allah, "Phenotyping for abiotic stress tolerance maize-Heat stress Projet FONIO-UAM: De la connaissance à la valorisation du fonio au Niger View project Technologies for African Agricultural Transformation (TAAT) Fall Armyworm Project View project," 2016, https://www.researchgate.net/publication/308500365_PHENOTYPING_FOR_ABIOTIC_STRESS_TOLERANCE_IN_MAIZE_DROUGHT_STRESS.

[13] T. Maize, C. O. Alake, D. K. Ojo, O. a Oduwaye, and M. a Adekoya, "Genetic variability and correlation studies in yield and yield related characters of," *Plant Breeding*, vol. 8, pp. 14–27, 2008.

[14] S. Bartaula, U. Panthi, K. Timilsena, S. S. Acharya, and J. Shrestha, "Variability, heritability and genetic advance of maize (Zea mays L.). Research in Agriculture Livestock and," *Research in Agriculture, Livestock and Fisheries*, vol. 6, no. 2, pp. 163–169, 2019.

[15] K. Babu Koirala, S. Subedi, and M. Prasad Tripathi, "Performance of single cross maize (Zea mays L.) hybrids under rainfed middle hill environments of Nepal," *Azarian Journal of Agriculture*, vol. 7, no. 4, pp. 102–111, 2020.

[16] K. Koirala, M. Tripathi, K. Seetharam, M. Vinayan, and P. Zaidi, "Field evaluation of heat stress-resilient maize hybrids for improved and stable maize production in Nepal," *SAARC Journal of Agriculture*, vol. 19, no. 1, pp. 27–43, 2021.

[17] P. K. Reshmika, V. D. Gasti, S. Evoor, J. Jayappa, and R. Mulge, "Genetic variability studies for growth, earliness, yield and quality parameters in brinjal (Solanum melongena L.)," *Environment and Ecology*, vol. 33, pp. 761–766, 2015.

[18] S. S. Singh and D. Singh, "Study of genetic variability for yield and its contributing characters in tomato (Solanum lycopersicum L.) under polyhouse condition," *Journal of Pharmacognosy and Phytochemistry*, vol. 8, pp. 2694–2697, 2019.

[19] R. Goudar, V. Srinivasa, and D. Lakshmana, "Genetic variability and divergence studies in cluster bean [Cyamopsis tetragonoloba (L.) Taub] under hill zone of Karnataka, India," *Legume Research - An International Journal*, vol. 40, pp. 237–240, 2017.

[20] S. Kumar Roy, L. Hijam, M. Chakraborty et al., "Cause and effect relationship in yield and its attributing traits in early segregating generations of mustard crosses under terai agro-climatic zone of West Bengal, India," *International Journal of Current Microbiology and Applied Sciences*, vol. 7, no. 3, pp. 198–211, 2018.

[21] A. Panchbhaiya, D. K. Singh, P. Verma, and S. Mallesh, "Estimation of genetic variability for yield and yield related traits in tomato (Solanum lycopersicum L.) under polyhouse condition," *International journal of current microbiology and applied sciences*, vol. 7, no. 9, pp. 1553–1559, 2018.

[22] C. M. Rafiq, M. Rafique, A. Hussain, and M. Altaf, "Correlation and path analysis in maize," *Journal of Agricultural Research*, vol. 48, pp. 35–38, 2010.

[23] R. K. Singh and B. D. Chaudhary, *Biometrical Methods in Quantitative Genetic Analysis*, Kalyani Publishers, New Delhi, india, 1977.

[24] P. S. Setimela, C. Magorokosho, R. Lunduka et al., "On-farm Yield Gains with Stress-Tolerant Maize in Eastern and Southern Africa," *Agronomy journal*, vol. 109, 2017.

[25] M. A. Murtadha, O. J. Ariyo, and S. S. Alghamdi, "Analysis of combining ability over environments in diallel crosses of maize (*Zea mays*)," *Journal of the Saudi Society of Agricultural Sciences*, vol. 17, no. 1, pp. 69–78, 2018.

[26] F. Nzuve, S. Githiri, D. M. Mukunya, and J. Gethi, "Genetic Variability and Correlation Studies of Grain Yield and Related Agronomic Traits in Maize," 2014, https://www.ccsenet.org/journal/index.php/jas/article/view/39260.

[27] J. Tadesse, T. Leta, B. Techale, and B. Lemi, "Genetic variability, heritability and genetic advance of maize (*Zea mays* L.) inbred lines for yield and yield related traits in southwestern Ethiopia," *Journal of Plant Breeding and Crop Science*, vol. 10, pp. 281–289, 2018.

[28] H. W. Johnson, H. F. Robinson, and R. E. Comstock, "Estimates of genetic and environmental variability in Soybeans1," *Agronomy Journal*, vol. 47, no. 7, pp. 314–318, 1955.

[29] H. F. Robinson and R. E. Comstock, *Genotypic and Phenotypic Correlations in Corn and Their Implications in Selection*, NC State Department of Statistics, USA, 1949.

[30] S. M. Patil, K. Kumar, D. S. Jakhar, A. Rai, U. M. Borle, and P. Singh, "Studies on variability, heritability, genetic advance and correlation in maize (*Zea mays* L.)," *International Journal of Agriculture Environment & Biotechnology*, vol. 9, no. 6, pp. 1103–1108, 2016.

[31] G. B. Saleh, D. Abdullah, and A. R. Anuar, "Performance, heterosis and heritability in selected tropical maize single, double and three-way cross hybrids," *Journal of Agricultural Sciences*, vol. 138, no. 1, pp. 21–28, 2002.

[32] D. Tesfaye, D. Abakemal, and E. Habte, "Genetic variability, heritability and genetic advance estimation of highland adapted maize (*Zea mays* L) genotypes in Ethiopia," *Journal of Current Opinion in Crop Science*, vol. 2, pp. 184–191, 2021.

[33] S. Sujiprihati, G. Bin Saleh, and E. S. Ali, "Heritability, performance and correlation studies on single cross hybrids of tropical maize," *Asian Journal of Plant Sciences*, vol. 2, 2003.

[34] D. J. Ogunniyan and S. A. Olakojo, "Genetic variation, heritability, genetic advance and agronomic character association of yellow elite inbred lines of maize (*Zea mays* L.)," *Nigerian Journal of Genetics*, vol. 28, no. 2, pp. 24–28, 2014.

[35] B. Neupane, A. Poudel, and P. Wagle, "Varietal evaluation of promising maize genotypes in mid hills of Nepal," *Journal of Agriculture and Natural Resources*, vol. 3, no. 2, pp. 127–139, 2020.

[36] O. B. Bello, S. A. Ige, M. A. Azeez, M. S. Afolabi, S. Y. Abdulmaliq, and J. Mahamood, "Heritability and genetic advance for grain yield and its component characters in maize (*zea mays* L)," *International Journal of Plant Research*, vol. 2, no. 5, pp. 138–145, 2012.

[37] M. P. Tripathi, K. B. Koirala, D. Gautam et al., "Field performance of three-way cross yellow and white maize hybrids in Nepal," *Asian Journal of Advances in Agricultural Research*, vol. 15, pp. 24–33, 2021.

[38] V. Kumar and P. Bhati, "Correlation, Path and Genetic Diversity Analysis in Maize (Zea mays L) Correlation, Path and Genetic Diversity Analysis," *Envrionment and ecology*, 2014.

[39] M. S. Yahaya, I. Bello, and A. Y. Unguwanrimi, "Correlation and path-coefficient analysis for grain yield and agronomic traits of maize (*zea mays* L)," *Agronomy*, vol. 16, pp. 10–13, 2021.

[40] S. Kumar, M. P. Chauhan, A. Tomar, and R. K. Kasana, "Coefficient of variation (GCV & PCV), heritability and genetic advance analysis for yield contributing characters in rice (*Oryza Sativa* L)," *Journal of Pharmacognosy and Phytochemistry*, vol. 7, pp. 2161–2164, 2018.

[41] B. Badu-Apraku and M. A. B. Fakorede, *Improvement of early and extra-early maize for combined tolerance to drought and heat stress in sub-saharan africa Advances in Genetic Enhancement of Early and Extra-Early Maize for Sub-Saharan Africa*, pp. 311–358, Springer International Publishing, Berlin, Germany, 2017.

[42] R. Reddy and M. Sudarshan, "ICRISAT-HarvestPlus Project on Sorghum Biofortification View Project Biofortification View Project," 2018, https://www.icrisat.org/biofortification-icrisat/.

[43] M. A. Alam, K. Seetharam, P. H. Zaidi, A. Dinesh, M. T. Vinayan, and U. K. Nath, "Dissecting heat stress tolerance in tropical maize (Zea mays L.)," *Field Crops Research*, vol. 204, pp. 110–119, 2017.

[44] S. D. Wahi and A. R. Rao, "Clustering Techniques for Classification of Crop Genotypes," 2003, http://bioinformatics.iasri.res.in/BAMAST/Lectures/Clustering%20Techniques%20for%20Classification%20of%20Crop%20Genotypes.pdf.