Research Article

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

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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 midhills region of Nepal, where food and nutrition security are major challenges. Maize is also used in livestock and poultry rations [1].

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 midhills 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 agrometeorological 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 × 0.75 m = 3 m² 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), 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.

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:P₂O₅:K₂O, 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 weedicings 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:

\[ \text{NOEPH} = \frac{\text{Number of ears per plot} \times 10000 (\text{m}^2)}{\text{Plot size (m}^2)}. \]  

(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.
2.5.1. Morphological Traits

(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:

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

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].

\[ rp(xy) = \frac{\text{cov}(x,y)}{\sigma_1/2\sigma(x) \times \sigma_1/2\sigma(y)} \]

Where \( rp(xy) \) presents phenotypic correlation, \( \text{cov}(x,y) \) is covariance due to the phenotype of \( x \) and \( y \), and \( \sigma_1/2\sigma(x) \) and \( \sigma_1/2\sigma(y) \) 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.
\[ PCV = \frac{\sqrt{\delta^2_p} \cdot 100}{x} \]  
(4)

\[ GCV = \frac{\sqrt{\delta^2_g} \cdot 100}{x} \]  
(5)

Where, \( \delta^2_p \) is phenotypic variance and \( \delta^2_g \) is genotypic variance and \( x \) is the population mean.

\[ \text{Heritability}(h^2_p) = \frac{\delta^2_g}{\delta^2_p} \]  
(6)

\[ \text{Genetic advance} \ (GA) = K(\delta^2_p)(h^2_p) \]  
(7)

Where, \( K \) = selection differential that varies depending 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 photosynthesize 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 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), moderate (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...
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.

### Table 3: Estimation of genetic parameter of tested 13 traits.

<table>
<thead>
<tr>
<th>Traits</th>
<th>GCV</th>
<th>PCV</th>
<th>H²</th>
<th>GA</th>
<th>GAM (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>AD</td>
<td>3.02</td>
<td>3.49</td>
<td>0.74</td>
<td>2.67</td>
<td>5.39</td>
</tr>
<tr>
<td>SD</td>
<td>3.75</td>
<td>4.41</td>
<td>0.72</td>
<td>3.44</td>
<td>6.5</td>
</tr>
<tr>
<td>ASI</td>
<td>38.2</td>
<td>50.11</td>
<td>0.58</td>
<td>1.72</td>
<td>60</td>
</tr>
<tr>
<td>PHT</td>
<td>2.32</td>
<td>8.14</td>
<td>0.08</td>
<td>3.88</td>
<td>1.37</td>
</tr>
<tr>
<td>EHT</td>
<td>7.7</td>
<td>12.1</td>
<td>0.40</td>
<td>15.7</td>
<td>10.9</td>
</tr>
<tr>
<td>PLANT POPLN</td>
<td>2.6</td>
<td>12.7</td>
<td>0.04</td>
<td>0.39</td>
<td>1.39</td>
</tr>
<tr>
<td>Ear popln</td>
<td>14.5</td>
<td>20.4</td>
<td>0.51</td>
<td>6.63</td>
<td>21.49</td>
</tr>
<tr>
<td>Ear aspect</td>
<td>20.5</td>
<td>24.6</td>
<td>0.69</td>
<td>0.96</td>
<td>35.16</td>
</tr>
<tr>
<td>NORPC</td>
<td>9.78</td>
<td>10.6</td>
<td>0.84</td>
<td>2.72</td>
<td>18.5</td>
</tr>
<tr>
<td>NOGPR</td>
<td>10.9</td>
<td>13.9</td>
<td>0.61</td>
<td>4.7</td>
<td>17.6</td>
</tr>
<tr>
<td>CD</td>
<td>9.11</td>
<td>9.75</td>
<td>0.87</td>
<td>0.73</td>
<td>17.5</td>
</tr>
<tr>
<td>CL</td>
<td>9.9</td>
<td>10.6</td>
<td>0.86</td>
<td>3.5</td>
<td>19.05</td>
</tr>
<tr>
<td>GY</td>
<td>20.6</td>
<td>25.52</td>
<td>0.56</td>
<td>2.96</td>
<td>29.62</td>
</tr>
</tbody>
</table>

(* means significant at less than 0.01% 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).

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

<table>
<thead>
<tr>
<th></th>
<th>AD</th>
<th>SD</th>
<th>ASI</th>
<th>PHT</th>
<th>EHT</th>
<th>Plants popln</th>
<th>NORPC</th>
<th>NOGPR</th>
<th>CD</th>
<th>CL</th>
<th>Ear per hectare</th>
<th>GY</th>
</tr>
</thead>
<tbody>
<tr>
<td>AD</td>
<td>1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SD</td>
<td>0.787**</td>
<td>1</td>
<td></td>
<td></td>
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<td></td>
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<td></td>
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</tr>
<tr>
<td>ASI</td>
<td>0.070</td>
<td>0.670**</td>
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<td></td>
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</tr>
<tr>
<td>PHT</td>
<td>0.070</td>
<td>0.038</td>
<td>-0.023</td>
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<td></td>
<td></td>
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<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>EHT</td>
<td>0.194</td>
<td>0.067</td>
<td>-0.126</td>
<td>0.243</td>
<td>1</td>
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<tr>
<td>PLANTPOPLN</td>
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<td>0.054</td>
<td>0.094</td>
<td>-0.217</td>
<td>0.136</td>
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</tr>
<tr>
<td>NORPC</td>
<td>-0.057</td>
<td>0.203</td>
<td>0.397**</td>
<td>0.032</td>
<td>-0.131</td>
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<tr>
<td>NOGPR</td>
<td>0.064</td>
<td>0.078</td>
<td>0.049</td>
<td>0.221</td>
<td>-0.232</td>
<td>-0.244</td>
<td>1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CD</td>
<td>-0.113</td>
<td>0.021</td>
<td>0.170</td>
<td>0.102</td>
<td>-0.262</td>
<td>-0.098</td>
<td>-0.087</td>
<td>0.326*</td>
<td>1</td>
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</tr>
<tr>
<td>CL</td>
<td>-0.185</td>
<td>-0.243</td>
<td>-0.170</td>
<td>-0.218</td>
<td>-0.028</td>
<td>-0.013</td>
<td>-0.365**</td>
<td>0.303*</td>
<td>0.085</td>
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</tr>
<tr>
<td>EPH</td>
<td>-0.038</td>
<td>-0.096</td>
<td>-0.110</td>
<td>0.175</td>
<td>0.013</td>
<td>0.070</td>
<td>-0.022</td>
<td>0.002</td>
<td>0.022</td>
<td>0.341*</td>
<td>1</td>
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</tr>
<tr>
<td>GY</td>
<td>-0.275*</td>
<td>-0.453**</td>
<td>-0.401**</td>
<td>0.013</td>
<td>0.379**</td>
<td>0.147</td>
<td>-0.147</td>
<td>0.262</td>
<td>-0.131</td>
<td>0.221</td>
<td>0.174**</td>
<td>1</td>
</tr>
</tbody>
</table>

Figure 2: Dendrogram showing cluster analysis of 26 genotypes of maize.
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 Fapaw 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 evaluated 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 KH15846 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.

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