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Research Article

Varietal evaluation of promising maize genotypes in mid hills of Nepal

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ABSTRACT

The varietal evaluation of hybrid maize (*Zea mays* L.) genotypes with desired performance is one of the main objectives of maize breeding program. Fourteen hybrid maize genotypes were evaluated for 17 quantitative and nine qualitative traits in randomized complete block design with three replications at Sundarbazar, Lamjung, Nepal during May to September, 2019. The major objective was to identify superior genotypes based on genotypic and phenotypic variability, heritability, genetic advance, and correlation between grain yield and yield associated traits. We observed significant differences for 17 quantitative traits among the tested genotypes. Large variation was observed for grain yield among genotypes. Genotype RL-24-0/ RL-111 had the lowest yield (5.53 mt/ha) and Pioneer had the highest yield (11.98 mt/ha) whereas check variety Rampur Hybrid-10 yielded of 8.23 mt/ha. Grain yield showed highly significant positive correlations with stem girth (r= 0.67) and number of ears (r=0.6), but significant negative correlation with anthesis-silking interval (r= -0.55). The dendrogram grouped 14 genotypes into four clusters. Cluster I incorporated the highest number (five) of genotypes, which also had highest cluster mean (average yield of ~10 mt/ha) for grain yield. Traits namely test weight, ear aspect, anthesis-silking interval, number of ears, and tassel branching had high genotypic and phenotypic coefficient of variations, and heritability along with high genetic advances, indicating that these traits can be considered for maize breeding program.

Keywords: Cluster, GCV, Genetic advance, Heritability, Hybrid, PCV

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INTRODUCTION

Maize *(Zea mays L.*) is one of the World's leading crops cultivated in tropics, sub-tropics, and temperate regions. It was domesticated around 7000 years ago in Central Mexico. Maize belongs to family Poaceae and tribe Maydae with the chromosome number 2n=20. It has the highest yield potential over other cereals and is therefore known as 'the queen of cereals' (Singh, 2002). It is the only crop adaptable to different agro-ecological zones due to its large diversity (Ferdu *et al.*, 2002). In Nepal, maize is the second most important cereal crops in terms of area and production after paddy rice (*Oryza sativa L.*) (Adhikari, 2007; MoALD, 2020). It is grown in an area of 956,

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447 ha with a total production of 2,713,635 metric ton (mt) and productivity of 2.84 mt/ha (MoALD, 2020). In Lamjung district, maize is cultivated in an area of 9,935 ha producing up to 23,943 mt with the productivity of 2.41 mt/ha (MoALD, 2020).

The hybrid maize of multinational seed companies is progressively being popular among farmers in Nepal (Tripathi *et al.*, 2016). Although few hybrids are developed from national research system of Nepal, they are not competitive with hybrids of multinational seed companies (Tripathi *et al.*, 2016). Large numbers of multinational companies' hybrids have been registered in National Seed Board of Nepal. The commercial seed companies are the main source of seed as the acreage of hybrid maize has expanded extensively in Terai (i.e., plain area) and partly in mid hill of Nepal. Farmers and breeders need to select suitable maize hybrids with high yield and other essential agronomic characteristics. Most of the released maize varieties in Nepal are trialed at research stations only, lacking field evaluations most likely due to lack of proper extension service. Even some released varieties are not accepted by farmers due to lower than expected levels of production at the farmer's fields (Gurung *et al.*, 2011). Consequently, there is dominance of the multinational varieties over locally released varieties on the market (Gurung *et al.*, 2011).

Hybrid maize seed marketing is flourishing every year. However limited commercial hybrids are suitable for cultivation due to the country's diverse agro ecological regions. Therefore, it is necessary to identify superior maize hybrids that are suitable for different agro-ecological regions. A previous study assessed 117 maize hybrids of 20 seed companies for grain yield and other traits at three sites (eastern, central, and inner Terai of Nepal) in winter season of 2011 and 2012 to identify superior maize hybrids suitable for winter time planting in those regions (Tripathi *et al.*, 2016). To our knowledge, extensive evaluation of several maize varieties from different seed companies is lacking for mid hills of Nepal. Thus, this study was undertaken to compare germplasms of locally released and multinational maize varieties under field conditions in mid hill of Nepal. Such type of evaluation of germplasms is useful to produce improved maize varieties.

MATERIALS AND METHODS

Experimental site

This experiment was carried out at Sundarbazar, Lamjung, Nepal during a growing season from May to September, 2019. The experiment site was located at latitude of 28.1448° N, longitude of 84.4120° E, and altitude of 610 m. It was situated in the sub-tropical climatic zone of Nepal with an annual average rainfall of 203 mm. Total rainfall of 1040 mm was recorded during the growing season (May to September, 2019). The P^H of experimental site was slightly acidic and the texture of the soil was silt loam.

Experimental materials

Fourteen hybrid maize genotypes namely Rampur Hybrid-4, Rampur Hybrid-6, Rampur Hybrid-10 (Standard check), Pariposa 4525, Ganga Kaberi, Pioneer, Rashi 3022, RL-24-8/RML-25, RL-213/RML-17, RL-24-0/RL-111, RML-95/RML-96, RML-86/RML-96, RML-11-2/RML-18 and RL-35-1/RL-105 were used in the experiment. Four multinational varieties (Pariposa 4525, Ganga Kaberi, Pioneer, and Rashi 3022) were received from local market. Except multinational varieties, all ten genotypes were received from National Maize Research Program, Rampur, Chitwan, Nepal.

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Experimental design and crop management

The experiment was conducted in randomized complete block design (RCBD) with three replications. Each experiment plots were of size $10m^2$ (5m × 2m). The seeds were sown using crop geometry of 75cm × 25cm (row to row × plant to plant). Fertilizer was applied at the rate of 120:60:40 NPK kg/ha. Nitrogen was applied in two splits (half/half) at knee-high and pre-tasseling/silking stages. Earthing up was done at knee high stage.

Data collection

Observations on yield and yield components included plant height (cm), number of ears per plant, ear height (cm), ear length (cm), ear girth (cm), number of kernels row per ear, number of kernels per row, days to 50% tasseling, days to 50% silking, anthesis-silking interval, stem girth (cm), tassel branching, ear aspect, germination percentage (%), 1000 grain weight (gm) and grain yield (mt/ha). Grain yield was calculated using equation 1 as adopted by Carangal *et al.*, (1971) and Shrestha *et al.*, (2018) by adjusting the grain moisture at 15% and converted to the grain yield per hectare basis. Qualitative observations included tassel-glume base color, silk color at emergence, pubescence, leaf color, leaf orientation, leaf width, kernel row arrangement, husk cover and grain texture. Data were obtained on randomly selected 10 plants from each experimental plot for all the traits under consideration except for 50% tasseling, 50% silking and anthesis-silking interval. Standard staging system was used during the test period to identify the development stages of maize varieties, and a stage was characterized when 50% of plant population reached the corresponding stage.

$$\text{Grain yield}\left(\frac{\text{kg}}{\text{ha}}\right) = \frac{\text{FWT}\left(\frac{\text{kg}}{\text{plot}}\right)\times(100-\text{HMP})\times\text{SCF}\times 10000}{(100-\text{DMP})\times\text{NPA}} \qquad (1)$$

Where,

FWT = Fresh weight of ear in kg per plot at harvest
HMP = Grain moisture percentage at harvest
DMP = Desired moisture percentage, i.e. 15%
NPA = Net harvest plot area, m^2
SCF = Shelling coefficient, i.e. 0.8

Statistical analysis

The R Studio, SPSS version 25 and Minitab were used for statistical analyses. Data were assigned to analysis of variance (ANOVA) considering genotypes as fixed effects and replications as random effects. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were estimated according to the procedure outlined by Chaudhary and Prasad (1968). The GCV and PCV were categorized as low if less than 10%, moderate if 10-20%, and high if ≥ 20% as presented by Sivasubramanian and Menon, (1973). Heritability percentage was categorized as low if less than 20%, medium if 20%-40%, and high if ≥40% as indicated by Adhikari et al. (2018). Genetic advance (GA) and genetic advance as percent of mean (GAM) were determined by using equations 2 and 3, as in Johnson et al. (1955) and Falconer (1996). Correlation coefficient between two characters was calculated by using components of variance and covariance as in Weber & Moorthy, (1952). Cluster analysis among genotypes was performed by complete linkage (farthest-neighbor) method under Euclidean distance. Qualitative observations were evaluated following the guidelines provided by CIMMYT, Mexico.

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Genetic Advances (GA) = k.σp.H (2)
Where,
k = selection differential constant (k = 2.056 at 5% selection intensity)
σp = phenotypic standard deviation
H = broad sense heritability

Genetic advances as per mean (GAM) = $\frac{GA}{X} \times 100$ (3)
Where,
GA = genetic advances under selection
X = population mean in which selection will be employed

RESULTS AND DISCUSSION

Comparison of maize genotypes for traits

The analysis of variance revealed the existence of significant differences among genotypes for all the traits, indicating the presence of considerable genetic variability among tested genotypes (Table 1). Large differences among genotypes indicate the potential for improving different quantitative and qualitative characters via selection. Similar to our current findings, (Ogunniyan & Olakojo, 2014) reported significant genotypic differences for plant height, ear height, days to 50% tasseling and silking, anthesis-silking interval (ASI), number of leaves per plant, number of ears per plant, 1000 grain weight and so on in inbred lines of maize in Nigeria.

Table 1. Analysis of variance for 17 traits in hybrid maize.

SN	Traits	Mean sum of squares		
		Replications (D.F. =2)	Treatments (D.F. =13)	Error (D.F. =26)
1.	Days to 50% Tasseling	0.67	21.97***	1.58
2.	Days to 50% Silking	1.50	23.69***	1.96
3.	Anthesis-Silking Interval	0.30	2.44*	0.92
4.	Plant Height (cm)	7.55	774.60***	3.67
5.	Number of Ears Per Plant	0.46	0.44***	0.07
6.	Ear Height (cm)	176.32	493.96***	91.13
7.	Ear Length (cm)	4.71	9.04***	0.90
8.	Ear Girth (cm)	0.35	2.15***	0.27
9.	Number of Kernels Row Per Ear	0.14	6.11***	0.31
10.	Number of Kernels Per Row	2.78	23.97***	4.24
11.	Number of leaves	1.64	2.19**	0.73
12.	Stem Girth (cm)	0.59	0.64**	0.17
13.	Tassel Branching	7.88	35.46***	3.10
14.	Ear Aspect	0.51	1.37*	0.49
15.	Germination Percentage (%)	85.71	64.45*	27.42
16.	1000 Grain Weight (gm)	182.2	6994.1***	212.00
17.	Grain Yield (t/ha)	6.14	9.01***	0.42

Significant at 5 percent level, ** significant at 1 percent level and * significant at 0.1 percent level.*

Genotypic and phenotypic coefficient of variations

The estimation of GCV was high for ear aspect (21.25), ASI (20.60) and tassel branching (20.03). This result was in agreement with previous studies for tassel branching in hybrid maize in Iran (Majid, 2011) and for ASI in inbred maize lines in India (Arunkumar *et al.*, 2015). The estimation

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of PCV was high for ear aspect (34.79), ASI (34.64), number of ears per plant (25.02), tassel branching (22.73) and grain yield (20.26). Several previous studies had also recorded similar results for grain yields in maize (Ghimire and Timsina, 2014; Taye, 2014 and Abirami et al., 2005). Similar result were recorded for ASI (Arunkumar *et al., 2015)* and tassel branching in inbred maize line in Ethiopia (Taye, 2014). High PCV and GCV shows that there is a probability of improving traits through selection process. Likewise, PCV values were higher than their counterpart GCV values for all the characters considered (Table 2). The results were consistent with those obtained by single cross hybrid protein maize in Nigeria (Yusuf, 2010).

The differences between GCV and PCV were small for days to 50% tasseling, days to 50% silking, and plant height, indicating that the environmental effect on the expression of those traits is lower and selection based on these traits will be effective for considerable genetic improvement. Large differences between GCV and PCV for ear aspect, ASI, and number of ears per plant indicates selection based on phenotypic performance will be ineffective for considerable genetic improvement. Similar results were reported for days to 50% silking, days to 50% tasseling and ear aspect in hybrid maize in India (Manjunatha *et al.,* 2018).

Heritability

The heritability in broad sense estimate varied from 0.31 for germination percentage to 0.98 for plant height (Table 2). Plant height (0.98), 1000 grain weight (0.91), grain yield (0.87), number of kernel rows (0.85), days to 50% tasseling (0.81), days to 50% silking (0.78), tassel branching (0.77), ear length (0.74), ear girth (0.69), number of ear per plant (0.61), number of kernels per row (0.60), ear height (0.59) and stem girth (0.46) were high heritable traits. This indicates that the traits under study are less affected in their expression by the environment. Similar results were reported for grain yield and ear length in inbred maize in India (Nadagoud, 2008). Similar results were reported for ear height and plant height (Vashistha, 2013; Nadagoud, 2008 and Taye, 2014), and for days to 50% tasseling, days to 50% silking and number of kernels per row in maize (Nadagoud, 2008 and Taye, 2014). Similar results were also reported for tassel branch and number of kernel row per ear (Taye, 2014), 1000 grain weight (Bartaula *et al.,* 2019), and ear girth in monsoon season in Telengana, India (Sridhar, 2017), and stem girth in maize in Ludhiana, India (Kapoor and Batra, 2015). Number of leaves (0.39), ear aspect (0.37), ASI (0.35), and germination percentage (0.31) were moderately heritable traits, while there were no any low heritable traits. Similar result for ASI was recorded in maize genotypes in Allahabad, India (Vashistha, 2013). The influence of environment on the phenotypic nature of traits can be lead to moderate heritability estimates.

Genetic advance and genetic advance as percent of mean

The GAM was the highest for grain yield (36.38) followed by tassel branching (36.37), 1000 grain weight (34.55), number of ears per plant (31.97), ear aspect (26.75), and ASI (25.21). The GAM was moderate for number of kernel rows (17.79), ear height (17.12), ear length (14.06), plant height (11.84), and number of kernels per row (11.50). Low magnitude of GAM was observed for ear girth (8.85), days to 50% tasseling (8.11), days to 50% silking (7.80), stem girth (7.33), number of leaves (6.57) and germination percentage (4.58) (Table 2). The results indicate control of non-additive gene action on these traits, suggesting that heterosis breeding will be useful (i.e. the pure lines with these traits can be used for crop improvement). Similar results were presented for maize

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inbred lines in Ethiopia for tassel branching, grain yield and 1000 grain weight (Taye, 2014) and days to 50% silking (Tadesse *et al.*, 2018). Number of leaves, ear length, and ASI have also shown similar results in maize during summer season in Dang, Nepal (Bartaula et al., 2019).

Heritability estimates alone is not suitable as high heritability along with high GAM would be more effective. High heritability coupled with high GAM was observed for grain yield, tassel branching, 1000 grain weight, and number of ears per plant, indicating the control of additive gene of action and a greater scope for selection of these traits. Similar findings were recorded for grain yield in India (Freeman et al., 2019) and 1000 grain weight for maize in Bangladesh (Rahman *et al.*, 2018).

Table 2. Estimation of genetic parameters for 17 traits in hybrid maize.

SN	Traits	PCV %	GCV %	Heritability (h^2_{bs})	GA	GAM
1.	Days to 50% Tasseling	4.86	4.37	0.81	4.83	8.11
2.	Days to 50% Silking	4.81	4.27	0.78	4.91	7.80
3.	Anthesis-Silking Interval	34.64	20.59	0.35	0.87	25.21
4.	Plant Height (cm)	5.83	5.78	0.98	32.78	11.84
5.	Number of Ear Per Plant	25.05	19.71	0.61	0.56	31.97
6.	Ear Height (cm)	13.95	10.77	0.59	18.42	17.79
7.	Ear Length (cm)	9.11	7.88	0.74	2.93	14.06
8.	Ear Girth (cm)	6.14	5.14	0.69	1.36	8.85
9.	Number of Kernels Row Per Ear	10.05	9.32	0.85	2.65	17.79
10.	Number of Kernels Per Row	9.19	7.16	0.60	4.11	11.50
11.	Number of leaves	8.07	5.07	0.39	0.90	6.57
12.	Stem Girth (cm)	7.60	5.20	0.46	0.55	7.33
13.	Tassel Branching	22.73	20.03	0.77	5.96	36.37
14.	Ear Aspect	34.79	21.25	0.37	0.68	26.75
15.	Germination Percentage (%)	7.16	3.99	0.31	4.03	4.58
16.	1000 Grain Weight (gm)	18.34	17.54	0.91	93.65	34.55
17.	Grain Yield (t/ha)	20.26	18.91	0.87	3.25	36.38

PCV = Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, GA= Genetic advancement and GAM= Genetic advance as percent of mean.

Correlation

Correlation studies showed that stem circumference (r=0.67) and number of ears per plant (r=0.59) had positive and significant relationship with grain yield. This result signifies that selection of these traits would directly affect the expression of grain yield facilitating the selection and progress on breeding program. The ASI showed highly significant negative correlation (r=-0.58) with grain yield. Correlations of grain yield with other traits were not significant (Table 3). Similar results were reported earlier in maize by several studies for different characters *viz.*, for number of ear per plant (Taye, 2014) and ASI (Bartaula *et al.*, 2019)

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Table 3. Correlation of 17 traits in hybrid maize.

	EL	EA	EH	EPP	NKPR	NL	NKR	PH	SG	TB	TGW	DTT	DTS	ASI	GP	GY
EG	0.38*	0.01	0.11	-0.27	0.19	0.01	0.04	0.12	-0.04	-0.05	0.19	-0.22	-0.17	0.08	0.01	0.09
EL		0.07	0.20	-0.17	0.67**	0.44**	0.35*	0.01	-0.04	0.14	-0.27	-0.05	0.05	0.27	-0.02	-0.11
EA			-0.19	0.13	-0.06	0.01	0.39*	0.18	0.16	-0.07	-0.23	0.11	-0.02	-0.35*	-0.26	0.15
EH				-0.09	-0.08	0.40**	-0.04	0.42**	-0.13	-0.15	-0.05	0.10	0.21	0.31*	-0.19	-0.07
EPP					0.01	0.12	-0.05	0.25	0.54**	0.07	-0.23	-0.38*	-0.50**	-0.33*	-0.25	0.6**
NKPR						0.31*	0.38*	-0.13	0.21	0.06	-0.36*	-0.23	-0.15	0.17	0.08	0.08
NL							0.35 *	0.18	0.16	0.00	-0.18	-0.01	0.07	0.21	-0.19	0.03
NKR								-0.28	0.18	0.17	-0.46**	0.35*	0.32*	-0.04	-0.05	0.07
PH									0.08	-0.12	-0.13	-0.33*	-0.26	0.13	-0.29	0.03
SG										0.05	0.03	-0.05	-0.19	-0.34*	-0.13	0.67**
TB											-0.21	-0.13	-0.17	-0.10	-0.09	-0.07
TSW												0.32*	0.25	-0.13	-0.04	0.17
DTT													0.92**	-0.08	-0.10	-0.04
DTS														0.31*	0.03	-0.25
ASI															0.30	-0.55**
GP																-0.29

EG= Ear Girth, EL=Ear Length, EA= Ear Aspect, EH= Ear Height, EPP= Ears per plant, NKPR= Number of kernels per row, NL= Number of leaves, NKR= Number of Kernel rows, PH= Plant Height, SG= Stem Girth, TB= Tassel Branching, TGW= Thousand Grain Weight, DTT= Days to Tasseling, DTS= Days to Silking, ASI= Anthesis-Silking Interval, GP= Germination Percentage, GY= Grain Yield., ** significant at 5 percent and 1 percent respectively.*

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Cluster analysis

Among 14 hybrid maize genotypes, cluster analysis grouped into four clusters following complete linkage method. Maximum genotypes (five) were aggregated in cluster I, while minimum genotypes (two) were aggregated in cluster IV. Cluster II and III comprised three and four genotypes, respectively (Table 4). In consideration in improvement of various traits, mean value of 17 different traits were calculated. Mean performance for these traits showed that cluster I had maximum grain yield and, number of ears, and minimum days to tasseling and silking. The cluster II was characterized with maximum ear circumference and ear height. The cluster III was grouped with maximum 1000 grain weight and, stem circumference, and minimum ASI. Similarly, the cluster IV was characterized with maximum germination percentage, tassel branching, no of kernels per row, no of kernel rows, ear length, and, ear aspect, number of leaves and minimum plant height (Table 5).

Table 4. Grouping of 14 hybrid maize genotypes into four clusters.

Cluster	Number of genotypes	Name of genotypes
I	5	Pariposa 4525, Ganga Kaberi, Pioneer, RL-24-8/RML-25, RL-213/RML-17
II	4	RML-95/RML-96, Rampur Hybrid-4, Rampur Hybrid-6, RML-86/RML-96
III	3	RL-24-0/RL-111, Rampur Hybrid-10, Rashi 3022
IV	2	RML-11-2/RML-18, RL-35-1/RL-105

Table 5. Cluster mean for 17 traits in hybrid maize.

SN	Traits	Cluster Means			
		Cluster-I	Cluster-II	Cluster-III	Cluster-IV
1.	Days to 50% Tasseling	56.80	62.33	59.00	61.67
2.	Days to 50% Silking	59.73	65.25	63.67	65.67
3.	Anthesis-Silking Interval	2.93	2.91	4.67	4.00
4.	Plant Height (cm)	282.98	274.16	282.44	258.73
5.	Number of Ear Per Plant	2.13	1.82	1.37	1.38
6.	Ear Height (cm)	105.34	108.29	116.63	98.00
7.	Ear Length (cm)	20.93	19.20	21.61	22.95
8.	Ear Girth (cm)	15.55	15.04	16.17	14.63
9.	Number of Kernels Row Per Ear	14.48	15.15	14.16	16.68
10.	Number of Kernels Per Row	36.86	33.13	35.06	39.41
11.	Number of leaves	13.57	13.50	14.01	14.01
12.	Stem Girth (cm)	7.81	7.87	7.13	7.30
13.	Tassel Branching	17.14	16.22	14.87	17.15
14.	Ear Aspect	2.67	2.70	1.93	2.86
15.	Germination Percentage (%)	87.14	86.45	89.08	91.96
16.	1000 Grain Weight (gm)	248.93	301.05	297.43	226.67
17.	Grain Yield (t/ha)	10.01	9.72	7.24	7.24

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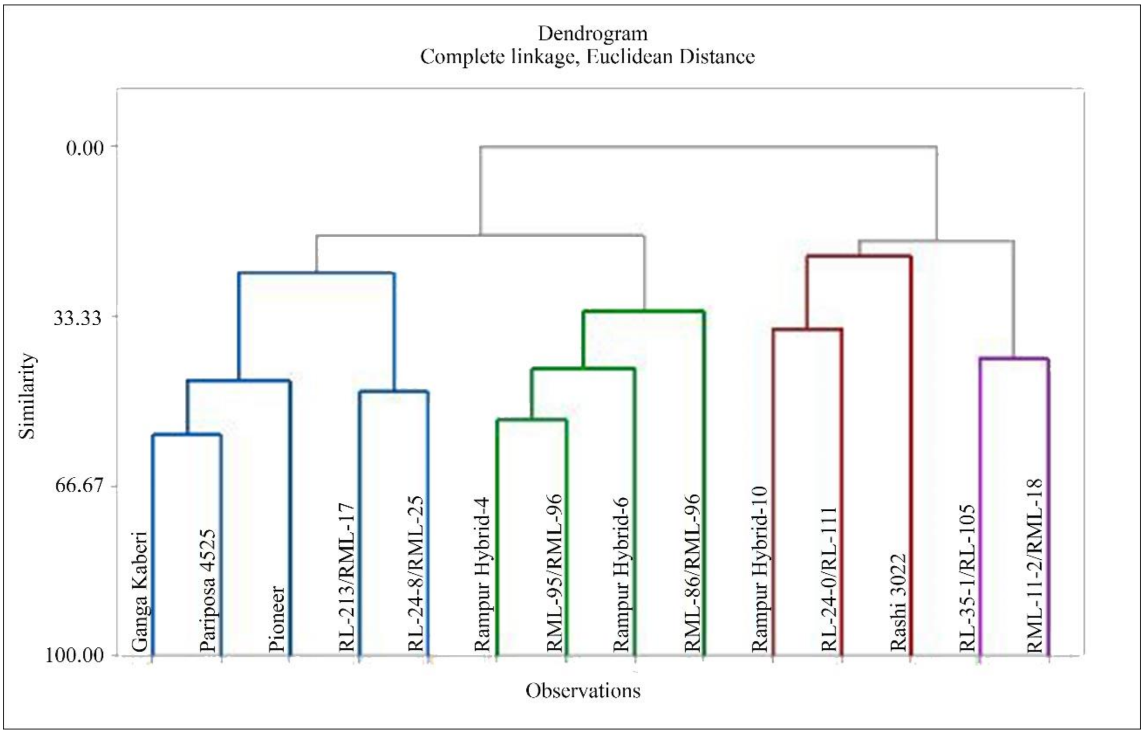

Figure 1: Dendrogram of 14 hybrid maize genotypes for quantitative traits.

Qualitative traits

Graphical representation showing the frequencies of the qualitative traits for maize genotypes studied are presented in Table 6.

Tassel-glume base color- Out of fourteen maize genotypes studied, ten genotypes (71%) had glume base color, indicating glume base color at tassel might be linked to high yielding or yield attributing traits.

Silk color at emergence- Thirteen genotypes (93%) out of fourteen had pink silk color whereas only one genotype (7%) had green silk color at emergence. It indicates that the pink silk color determining gene might be linked to high grain yielding genes.

Pubescence- All fourteen genotypes (100%) had pubescence in their leaf suggesting that presence of pubescence might have some effect in the yield improvement.

Leaf color- Light green color was expressed in two genotypes (14%), green in nine genotypes (64%), and dark green in three genotypes (22%). The results indicate that suggesting medium green leaf color might be favorable with respect to grain yield improvement.

Leaf orientation- Nine genotypes (64%) had erect leaf orientation whereas five genotypes (36%) had drooping leaf orientation. It shows that erect leaf orientation may be the primary interest of breeders for selection to maximize photosynthesis and yield.

Leaf width- Two genotypes (14%) had narrow, five genotypes (36%) had medium, and seven genotypes (50%) had broad leaf width. The results indicate that leaf width may have some roles in yield.

Kernel row arrangement- All fourteen genotypes (100%) were having regular kernel row arrangement, indicating common interest of breeders.

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Husk cover- Ten out of fourteen genotypes (71%) had good husk cover whereas four genotypes (29%) had poor husk cover. Breeders might have selected genotypes which were high yielding.

Grain texture- Round grain texture was expressed in eight genotypes (57%) and flat texture in six genotypes (43%), indicating a mixed results of grain texture to grain yield.

Table 6: Observation of the qualitative traits in maize genotypes.

Maize Genotypes	TGBC	SCE	LP	LC	LO	LW	KRA	HC	GT
Rampur Hybrid-4	Pink	Pink	Present	Green	Erect	Medium	Regular	Good	Round
Rampur Hybrid-6	Green	Pink	Present	Green	Erect	Medium	Regular	Good	Flat
Rampur Hybrid-10	Pink	Pink	Present	Dark Green	Erect	Medium	Regular	Good	Round
RML-86/ RML-96	Green	Pink	Present	Light Green	Droop	Broad	Regular	Bad	Round
RML-95/ RML-96	Pink	Pink	Present	Green	Droop	Broad	Regular	Good	Round
RML-11-2/ RML-18	Pink	Pink	Present	Light Green	Erect	Broad	Regular	Bad	Flat
RL-24-0/RL-111	Green	Pink	Present	Green	Erect	Medium	Regular	Good	Round
RL-213/RML-17	Pink	Pink	Present	Green	Droop	Broad	Regular	Good	Round
RL-24-8/RML-25	Pink	Pink	Present	Dark Green	Droop	Broad	Regular	Good	Flat
RL-35-1/RL-105	Pink	Pink	Present	Green	Droop	Narrow	Regular	Good	Flat
Ganga Kaberi	Pink	Pink	Present	Green	Erect	Medium	Regular	Good	Flat
Pioneer	Green	Green	Present	Green	Erect	Broad	Regular	Bad	Flat
Pariposa 4525	Pink	Pink	Present	Dark Green	Erect	Broad	Regular	Bad	Flat
Rashi 3022	Pink	Pink	Present	Green	Erect	Narrow	Regular	Good	Flat

TGBC = Tassel glume base color, SCE =Silk color at emergence, LP = Leaf pubescence, LC = Leaf color, LO = Leaf orientation, LW= Leaf width, KRA= Kernel row arrangement, HC= Husk cover, and GT= Grain texture.

CONCLUSION

The present study revealed presence of considerable amount of genetic variability among tested 14 maize genotypes. Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) in all traits, indicating low influence of the environment. Traits having high GCV, PCV, heritability along with high genetic advance as percentage of mean (GAM) suggested prevalence of sufficient variability that offered scope of selection. Correlation studies showed that selection of traits (number of ears per plant and stem girth) would directly affect the expression of grain yield facilitating the selection and progress on breeding program. The dendrogram grouped 14 genotypes into four clusters. Cluster I incorporated the highest number (five) of genotypes, which also had highest cluster mean (average yield of ~10mt/ha) for grain yield. Considering grain yield to be the most important trait for evaluating maize hybrids, genotypes under cluster I (Pariposa 4525, Ganga Kaberi, Pioneer, RL-24-8/RML-25 and RL-213/RML-17) looked more promising for mid-hills of

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Nepal. In general, the results indicate that multinational varieties have greater adaptability than locally released hybrid varieties. The existence of large genetic variability among maize genotypes offer tremendous opportunity for future maize breeding program.

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Authors' contributions

B. Neupane: Designed & conducted experiment, data collection & analysis, and manuscript writing
A. Poudel: Designed experiment, and data analysis
P. Wagle: Data analysis, and manuscript writing

Conflict of interests

The author declares that there are no conflicts of interests regarding the publication of this paper.

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