JOURNAL OF AGRICULTURE AND APPLIED BIOLOGY
2022, Vol. 3, No. 2, 146 - 158
http://dx.doi.org/10.11594/jaab.03.02.08
E-ISSN: 2723-5106

Research Article

Evaluation of single cross maize hybrids during the spring season in Khairahani, Chitwan, Nepal

Khushubu Rai[1]*, Oshna Kulung[1], Sudha Bhandari[1], Himani Gautam Singh[1], Mahendra Tripathi[2]

[1]Institute of Agriculture and Animal Science, Tribhuwan University
[2]National Maize Research Program, Nepal

Article history:
Submitted 10 September 2022
Accepted 30 September 2022
Published 16 November 2022

Keywords:
Agro-morphological
Anthesis
Correlation
Heritability
Traits
Yield

*Corresponding author:
E-mail:
khushuburai38@gmail.com

Abstract

The experiment was conducted at Khairahani-5, Chitwan, Nepal from 28th February to 20th June 2021. Twenty single cross maize hybrids were evaluated for quantitative and qualitative traits. The experiment was conducted in a randomized complete block design (RCBD) with three replications. Data were recorded on flowering traits, physiological and disease traits, agro-morphological traits, and yield and yield contributing traits. Analysis of variance showed significant differences in all traits except for root lodging, the number of plants per hectare, leaf senescence, and plant aspect. The result indicated that HGABS2-15-2-1B/RL174 had the shortest days to anthesis and silking. The genotype RML138/RML140 was found to have double cob. The longest cob was found in RML76/RML146 (17.3 cm), while the highest cob diameter was found in the Shrestha (5.1cm). The maximum number of grains per row was obtained from RML57/RL174, while the highest thousand-grain weight was obtained in RAMPUR HYBRID-10. Shrestha variety produced highest grain yield (9.954tha^{-1}) followed by RML191/RML18 (9.41tha^{-1}), CAH1715 (9.356tha^{-1}) and RML4/RL111 (9.021tha^{-1}). The traits with the highest broad-sense heritability were the number of rows per ear (79%), days to fifty percent silking (75%), days to fifty percent anthesis (72%), thousand-grain weight (70%), and grain yield (68%). Correlation studies suggested that the number of ears per hectare, cob length, and thousand-grain weight showed a positive and significant correlation with grain yield. Therefore, RML191/RML18, CAH1715, and RML4/RL111 showed better performance in terms of grain yield.

Introduction

Maize (*Zea mays* L., 2n=2x=20), queen of cereals is the world's most versatile leading crop having wide adaptability, types, and uses. Maize is a monoecious, cross-pollinated, C4 plant that cycles CO_2 into 4-C sugar compounds to enter into the Calvin cycle. Thus, maize is very efficient in hot, dry climates and makes a

How to cite:
Rai, K., Kulung, O., Bhandari, S., Singh, H. G., & Tripathi, M. (2022). Evaluation of single cross maize hybrids during the spring season in Khairahani, Chitwan, Nepal. *Journal of Agriculture and Applied Biology, 3*(2): 146 - 158. doi: 10.11594/jaab.03.02.08

lot of energy. Global production of cereals in the year 2019 is 2.97 billion tonnes out of which production of maize account for 1.1 billion tonnes (38.55%). America is the leading country in the production of maize (49%) followed by China (22.7%) and Brazil (8.8%). Nepal contributes 0.23% (2.6 million tonnes) to global maize production. Maize is the second most-produced crop worldwide after the production grew three times faster than that of wheat and rice from the period of 2000-to 2019, and surpassed rice in 2001(FAOSTAT, 2021). In Nepal, maize is the second most important cereal crop in terms of area (979,776 hectares) and production (2,997,733 metric tons) and productivity (3.06 mtha $^{-1}$) after paddy (MoALD, 2021). About 31.7 % of the total cultivated land is covered by maize. Bagmati province contributes 13.05% of the national cereal production. It is also the second-highest producer of maize (691,437 metric tons) after province 1, which covers 23.07 % of the national maize production. In Chitwan, maize is cultivated on a total area of 26,019 ha with a total production of 98,644 metric tons and productivity of 3.79 mt ha^{-1} (MoALD, 2021).The contribution of the agricultural sector (agriculture, forest, and fisheries) to the total Gross Domestic Product is estimated to be 25.8% and its contribution to the economic growth is estimated to be 20.2% in the fiscal year 2020/21 (MoF, 2021).

Higher yield potential, increasing trend of poultry and livestock business along with rising population and assurance market of maize grains has increased the demand for hybrids (Tripathi et al., 2016). Due to very few options for released maize hybrids within the country, only 17% of farmers use hybrid maize varieties whereas 83% of them still cultivate open-pollinated varieties (OPVs) in Nepal also, the seed production of available hybrids is not satisfactory because of nicking problems in anthesis and silking of parents (Gairhe et al., 2021). The hybrid maize area, productivity, and seed replacement rate (15.3%) were below the targets set in Nepal's National Seed Vision, a policy document of the government (Gairhe et al., 2021). Thus, exploitation of heterosis can aid in doubling the current national average yield of maize (Kunwar & Shrestha, 2014) which can yield 25-30% more than better OPVs (Gairhe et al., 2021). Darwin and some naturalists recognized heterosis which can be defined as the superiority of the F1 hybrids over both the parents in terms of yield and some other characteristics (Kafle et al., 2020). As the primary step in the breeding program is selection, the performance of each genotype is determined by appropriate variety selection in line interacting with the existing environment. The strength and direction of the relationship between yield and its constituent parts determines how effectively the right variety is chosen. Estimates of genetic parameters, which are fundamental requirements in plant breeding because they help identify the action of genes involved in the control of quantitative traits and evaluate the effectiveness of various breeding strategies to obtain genetic gains, are used to determine the efficiency of selection (Vashistha et al., 2013).

Though the demand for hybrids is increasing over time, Nepal is still lagging in hybrid research and development (Thapa, 2013). In Nepal, hybrid seeds from multinational companies dominate the national seed market as the hybrid seed production is limited to National Maize Research Program only for research purposes. In order to speed up the development of hybrid maize, the NMRP is now examining and registering hybrid seeds from international corporations (Kandel & Shrestha, 2020). There is a crucial requirement to conserve and properly utilize the genetically varied open-pollinated genotypes of the local area through various plant breeding programs, as it helps in the selection of the most appropriate and compatible variations for the area. It also aids in the exchange of germplasm, which is required in the future for the improvement of new varieties (Magar et al., 2021). There is still a huge yield potential gap of maize in Nepal. Therefore, this study was conducted during the spring season of 2021 to identify high-performing single cross hybrids for the Terai region of Nepal.

Materials and methods

Description of the experimental site

A field experiment was conducted in Khairahani-5, Phasera of Chitwan district in Province number-3 of Nepal during the spring season, 2021. It was located at the altitude of 200.7masl, the latitude of 27.598809, and the longitude of 84.543720. The soil of the experimental field was slightly sandy.

The climatic condition of the experimental site

The experimental site was located in Nepal's subtropical climate region. The region experiences sub-humid weather with a cold winter, a warm summer, and a distinct rainy season. There are three distinct seasons namely the rainy season (June-October), cool winter (November-February), and hot spring season (March-May). The climatic condition of the research site during the research period is shown in the Figure 1 below.

Cropping history

The experimental field was previously cultivated with garden pea (*Pisum sativum*).

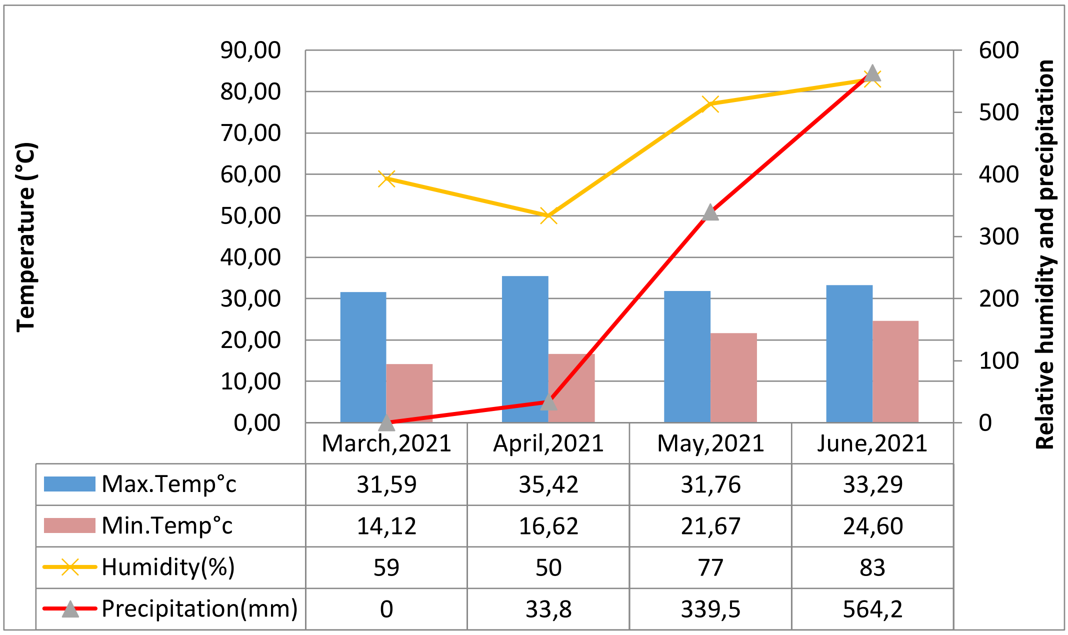

Figure 1. Climatic data of the research site during the research period

Experimental materials description

The experimental materials were obtained from National Maize Research Program (NMRP), Rampur, Chitwan. Twenty maize genotypes were evaluated at Khairahani-5, Chitwan from late February to June 2021.

Table 1. List of 20 single-cross hybrids used in the experiment at Khairahani-5, Chitwan during 2021

EN	Hybrids	Source
1	07SADVI-11-1-2BB/RL111	NMRP, Rampur, Chitwan
2	RML86/RML146	NMRP, Rampur, Chitwan
3	RML4/RL111	NMRP, Rampur, Chitwan
4	RML9/RML98	NMRP, Rampur, Chitwan
5	RML191/RML18	NMRP, Rampur, Chitwan
6	RL249/RML96	NMRP, Rampur, Chitwan
7	HGBS2-17-3-1/RML18	NMRP, Rampur, Chitwan
8	RL102/RML17	NMRP, Rampur, Chitwan
9	RML94/RL298	NMRP, Rampur, Chitwan
10	HGBS2-15-2-1B/RL174	NMRP, Rampur, Chitwan
11	RML57/RL174	NMRP, Rampur, Chitwan
12	RML138/RML140	NMRP, Rampur, Chitwan

Table 1. List of 20 single-cross hybrids used in the experiment at Khairahani-5, Chitwan during 2021 (continued)

EN	Hybrids	Source
13	RML153/RL105	NMRP, Rampur, Chitwan
14	RH-10 (Standard check)	NMRP, Rampur, Chitwan
15	CAH1715 (Pipeline check)	NMRP, Rampur, Chitwan
16	RML76/RML146	NMRP, Rampur, Chitwan
17	RL100/RML140	NMRP, Rampur, Chitwan
18	RML150/RML84	NMRP, Rampur, Chitwan
19	RL242/RL105	NMRP, Rampur, Chitwan
20	Shrestha (Commercial check)	Neejibeeni company

Experimental design and crop management

The experiment was conducted in Randomized Complete Block Design (RCBD) with three replications. The size of each experimental plot was 4.8m^2(4m × 1.2m) having two rows. The gross field size was 336m^2. The crop geometry was 60cm × 20cm and the inter-replication distance was 1m. The plant population per plot was 20. The Farm Yard Manure was applied at the rate of 6 ton per hectare. The applied dose of chemical fertilizer was 180:60:40 kg NPKha-^{1}. The half dose of N (90kgha-^{1}) and the full dose of P (60 kgha-^{1}) and K (40kgha-^{1}) was applied before the sowing. The remaining half dose of N was top-dressed in three equal split doses at 24DAS, 40DAS, and 60DAS. Pre-emergence herbicide, mixture of Atrazine @2.5 ml per litre + Pendimethyline @5ml per litre was applied 3 days after sowing. The irrigation was done thrice; at knee-high stage, tasseling stage, and milking stage. Different package of practices and applications of insecticides (i.e.Novaluron 10% EC @2ml litre^{-1}, Spinetoram 11.7% SC (w/w) @0.4mllitre^{-1}, and Lambda-cyhalothrin 55 EC @2mllitre^{-1} to control Fall Army Worm) were followed as per the recommendation of Nepal Agriculture Research Council (NARC).

Data collection and analysis

Data were recorded from five randomly selected plants for different morpho-physiological and yield-attributing traits like days to fifty percent anthesis, days to fifty percent silking, plant height (cm), ear height (cm), cob length (cm), cob diameter (cm), number of cobs plant^{-1}, number of rows cob^{-1}, number of kernels row^{-1}, thousand grain weight (g), grain yield (tha^{-1}). Other traits like root lodging, stalk lodging, husk cover, plant aspect, ear aspect, ear rot, leaf senescence, number of plants harvested, number of ears harvested, and field weight was taken plot-wise.

Grain yield (kgha^{-1}) at 12.5% moisture content was calculated using fresh ear weight with the help of the below formula:

Grain yield (kgha^{-1}) =

$$\frac{F.W.(kgplot-1)\times(100-HMP)\times S\times 10000}{(100-DMP)\times NPA}$$

Where, F.W. = Fresh weight of cob in kg per plot at harvest; HMP = Grain moisture percentage at harvest; DMP = Desired moisture percentage, i.e. 12.5%; NPA = Net harvest plot area, m^2; S = Shelling coefficient, i.e. 0.8

This formula was also adopted by Carangal et al. (1971) to adjust the grain yield (kgha^{-1}) at 12.5% moisture content, which was then converted into tonha^{-1}. The data collected were entered in Microsoft excel and analysis was done using RStudio (Version 1.4.1717).

Results and discussion

Table 2. Mean flowering traits of single-cross hybrids evaluated at Khairahani, Chitwan during spring season of 2021

Genotypes	Days to 50% anthesis	Days to 50% silking	Anthesis-Silking Interval
07SADVI-11-1-2BB/RL-111	71	73	1.7
CAH1715 (CHECK)	70	71	0.7
SHRESTHA	69	67	-2.0
HGABS2-15-2-1B/RL174	66	64	-1.3
HGBS2-17-3-1/RML18	71	74	2.3
RAMPUR HYBRID-10	70	70	0.0
RL100/RML140	69	71	2.0
RL102/RML17	69	69	0.0
RL242/RL105	70	71	1.3
RL249/RML96	66	70	3.7
RML138/RML140	69	69	0.3
RML150/RML84	67	68	0.3
RML153/RL105	69	71	2.3
RML191/RML18	70	71	0.7
RML4/RL111	72	73	1.3
RML57/RL174	69	69	0.3
RML76/RML146	71	71	-0.3
RML86/RML146	71	71	-0.7
RML9/RML98	69	69	0.0
RML94/RL298	73	71	-2.0
Grand Total	**70**	**70**	**0.5**
F-test	***	***	***
P-value	**0.0000000121**	**0.00000000107**	**0.0000199**
LSD, 0.05	**1.83264**	**1.987105**	**1.940887**
Heritability	**0.72**	**0.75**	**0.56**

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

Statistically, a highly significant difference was obtained for days to 50% anthesis, days to 50% silking, and anthesis-silking interval (Table 2). The mean days to anthesis and silking were 70 each. The days to anthesis ranged from 66-73 DAP, where genotypes RL249/RML96, HGABS2-15-2-1B/RL174, and RML150/RML84 showed early anthesis whereas genotypes RML4/RL111 and RML94/RL298 showed later anthesis. The days to silking ranged from 64-74 DAP. Early silking was observed in genotypes HGABS2-15-2-1B/RL174 and Shrestha whereas late silking was observed in genotypes HGBS2-17-3-1/RML18, 07SADVI-11-1-2BB/RL-111, and RML4/RL111. Similarly, the mean anthesis-silking interval was 0.5. The anthesis-silking interval of five genotypes was recorded as positive but 15 genotypes had a negative anthesis-silking interval. The broad-sense heritability of days to 50% anthesis, days to 50% silking and the anthesis-silking interval were 72%, 75%, and 56% respectively.

Table 3. Mean agro-morphological traits of single-cross hybrids evaluated at Khairahani, Chitwan during spring season of 2021

Genotypes	Plant Height	Ear Height	Ear Position	Shoot Lodging	Root Lodging
07SADVI-11-1-2BB/RL-111	260	142	0.54	64.17	1.67
CAH1715	273	138	0.51	59.17	1.67
Shrestha	223	107	0.48	13.33	0.83
HGABS2-15-2-1B/RL174	179	93	0.52	0.00	0.00
HGBS2-17-3-1/RML18	178	83	0.46	0.00	0.00
Rampur Hybrid-10	248	116	0.47	20.00	0.83
RL100/RML140	220	118	0.54	42.50	0.00
RL102/RML17	236	143	0.61	20.00	0.00
RL242/RL105	247	125	0.51	5.83	0.00
RL249/RML96	238	130	0.55	9.17	9.17
RML138/RML140	222	126	0.57	55.00	0.83
RML150/RML84	237	111	0.47	1.67	0.00
RML153/RL105	256	140	0.54	24.17	2.50
RML191/RML18	249	113	0.45	0.83	0.00
RML4/RL111	230	131	0.57	3.33	0.00
RML57/RL174	237	112	0.47	12.50	0.00
RML76/RML146	256	129	0.5	28.33	0.83
RML86/RML146	261	153	0.59	61.67	1.67
RML9/RML98	225	104	0.46	52.50	7.50
RML94/RL298	237	134	0.57	18.33	1.67
Grand Total	**236**	**122**	**0.52**	**24.63**	**1.46**
F-test	***	***	***	***	Ns
P-value	**0.000000825**	**0.00000054**	**0.000136**	**0.0000729**	**0.357**
LSD at 0.05	**27.763**	**19.88**	**0.602**	**32.82**	**6.65**
Heratibility	**0.63**	**0.64**	**0.49**	**0.52**	**0.04**

Note: *Significant at 5%level of significance, ** significant at 1%level of significance, and *** significant at 0.1% level of significance.

The highly significant difference in data was observed for plant height, ear height, ear position, and shoot lodging whereas, non-significant data was observed for root lodging (Table 3). The mean plant height was 236cm ranging from 178 cm to 273 cm. The longest plant height was found in genotype CAH1715 followed by RML86/RML146 and 07SADVI-11-1-2BB/RL-111.The shortest plant was found in genotype HGBS2-17-3-1/RML18 at par with HGABS2-15-2-1B/RL174. The mean ear height was 122cm ranging from 83 cm to 153 cm. The longest ear height was found in genotype RML86/RML146 followed by RL102/RML17 and 07SADVI-11-1-2BB/RL-111 whereas the shortest ear height was observed in HGBS2-17-3-1/RML18. The mean ear position was 0.52 which ranged from 0.45 to 0.61. The highest position of the ear was found in RL102/RML17, RML86/RML146, and RML138/RML140 at par with RML4/RL111 and RML94/RL298. The lowest position of the ear was found in RML191/RML18 and RML9/RML98 at par with HGBS2-17-3-1/RML18. The mean shoot lodging was found to be 24.63 which ranged from 0.0 to the highest value of 64.16. Highest rate of shoot lodging was found in genotype 07SADVI-11-1-2BB/RL-111 followed by RML86/RML146, CAH1715 (CHECK), and RML138/RML140 whereas no-shoot lodging in genotype HGABS2-15-2-1B/RL174 and HGBS2-17-3-1/RML18. The mean root lodging was found to be 1.46 which ranges from the minimum value of 0.0 to the highest value of9.17. The highest rate of root lodging was found in genotype RL249/RML96 followed by

RML9/RML98, RML153/RL105 whereas, the lowest rate of root lodging was found in genotype HGABS2-15-2-1B/RL174, HGBS2-17-3-1/RML18, RL100/RML140, RL102/RML17, RL242/RL105, RML150/RML84, RML191/RML18, RML4/RL111, RML57/RL174. The broad-sense heritability of plant height, ear height, ear position, shoot lodging, and root lodging was 63%, 64%, 49%, 52%, and 4% respectively.

Table 4. Mean yield and yield contributing traits of single-cross hybrids evaluated at Khairahani, Chitwan during the spring season of 2021(a)

Genotypes	NOPPha	NOEPha	NOEPP	CL	CD
07SADVI-11-1-2BB/RL-111	83333	83333	1.00	13.0	4.9
CAH1715	81944	88889	1.08	16.3	4.3
SHRESTHA	82639	89583	1.09	15.7	5.1
HGABS2-15-2-1B/RL174	83333	85416	1.03	12.0	4.8
HGBS2-17-3-1/RML18	83333	84722	1.02	14.0	4.7
Rampur Hybrid-10	81944	79861	0.97	16.7	4.6
RL100/RML140	83333	90278	1.09	15.7	4.6
RL102/RML17	81250	81945	1.01	15.0	4.8
RL242/RL105	81944	84722	1.03	15.3	4.5
RL249/RML96	82639	87500	1.06	11.7	4.7
RML138/RML140	83333	104861	1.26	15.7	4.1
RML150/RML84	83333	89584	1.08	16.0	4.3
RML153/RL105	83333	85417	1.03	15.3	4.3
RML191/RML18	83333	84028	1.01	16.0	4.4
RML4/RL111	83333	87500	1.05	14.3	4.9
RML57/RL174	80555	68750	0.86	16.0	4.8
RML76/RML146	83333	87500	1.05	17.3	4.8
RML86/RML146	80556	92361	1.15	14.3	4.7
RML9/RML98	80555	84028	1.04	15.7	4.6
RML94/RL298	83333	87500	1.05	14.7	4.2
Mean	**82534**	**86389**	**1.05**	**15.0**	**4.5**
F-test	**NS**	***	**	*	*
P-value	**0.0646**	**0.000361**	**0.00132**	**0.0222**	**0.048**
LSD,0.05	**2262.962**	**9944.229**	**0.122**	**3.09**	**0.502**
Heritability	**0.21**	**0.47**	**0.42**	**0.27**	**0.23**

Note: *Significant at 5% level of significance, ** significant at 1% level of significance, and *** significant at0.1% level of significance NOPPha**=** for number of plants per hectare, NOEPha= number of ears per hectare, NOEPP= number of ears per plant, CL= cob length, CD= cob diameter

A highly significant difference was observed for the number of ears per hectare and the number of ears per plant whereas significant difference was observed for cob length and cob diameter and a non-significant difference was observed for the number of plants per hectare among the genotypes (Table 4).The mean number of plants per hectare was 82534 which ranged from 80555 to 83333.Thirteen genotypes had higher and seven genotypes had a lower number of plants per hectare than the mean. The highest number of plants per hectare was found in genotypes 07SADVI-11-1-2BB/RL-111, RML4/RL111, RML191/RML18, and the lowest number of plants per hectare was found in genotypes RML57/RL174, RML9/RML98, and RML86/RML146. The mean number of ears per hectare was 86389 ranging from 68750 to 104861. The highest and the lowest number of ears per hectare were found in genotypes RML138/RML140 and RML57/RL174 respectively. The mean number of ears per plant was 1.05 which ranged from 0.86 to 1.2. The highest number of ears per plant was found in genotypes RML138/RML140, RML86/RML146, and the lowest number of ears per plant was found in genotypes RML57/RL174, RH-10(CHECK). The mean cob length was 15cm which ranged from 11.7 to 17.3. The longest cob was found in genotype RML76/RML146 followed by RAMPUR HYBRID-10 which was at par with CAH1715, RML150/RML84, and RML191/RML18. The shortest cob was found in genotype RL249/RML96 followed by HGABS2-15-2-1B/RL174 and 07SADVI-11-1-2BB/RL-111. The mean cob diameter was 4.5cm which ranged from 4.1cm to5.1cm.The highest cob diameter was found in genotype Shrestha followed by 07SADVI-11-1-2BB/RL-111 at par with RML4/RL111 and the lowest cob diameter was found in genotype RML138/RML140 followed by RML94/RL298.The broad-sense heritability for the number of ears per hectare, number of ears per plant, cob length, cob diameter, and number of plants per hectare was 21%, 47%, 42%, 27%, and 23% respectively.

Table 5. Mean yield and yield component traits of single-cross hybrids evaluated at Khairahani, Chitwan during the spring season of 2021(b)

Genotypes	**Grain Yield**	**Number of rows per ear**	**Number of grains per row**	**Thousand-Grain Weight**
07SADVI-11-1-2BB/RL-111	7.171	17	23	225.333
CAH1715	9.356	14	32	254.333
SHRESTHA	9.954	16	30	272.000
HGABS2-15-2-1B/RL174	6.728	14	22	292.333
HGBS2-17-3-1/RML18	5.600	16	18	300.333
RAMPUR HYBRID-10	7.679	14	26	340.333
RL100/RML140	7.572	13	27	268.000
RL102/RML17	7.262	14	23	268.000
RL242/RL105	8.408	14	29	255.333
RL249/RML96	6.729	15	17	286.333
RML138/RML140	6.487	15	30	226.333
RML150/RML84	8.355	14	26	304.000
RML153/RL105	7.996	14	32	237.667
RML191/RML18	9.410	14	24	331.667
RML4/RL111	9.020	15	26	273.333
RML57/RL174	3.803	16	35	217.000
RML76/RML146	7.881	14	30	258.000
RML86/RML146	6.847	14	28	218.000
RML9/RML98	7.061	15	29	222.000
RML94/RL298	6.239	11	27	279.333
Mean	**7.478**	**14**	**27**	**266.483**
F-test	***	***	***	***
P-value	**1.18E-07**	**9.39E-11**	**0.000000418**	**4.36E-08**
LSD, 0.05	**1.56421**	**1.086**	**5.708**	**40.718**
H’	**0.68**	**0.79**	**0.65**	**0.7**

Note: *Significant at 5% level of significance, ** significant at 1% level of significance, and *** significant at0.1% level of significance

Statistically, there was a highly significant difference in grain yield, number of rows per ear, number of grains per row, and thousand-grain weight between the genotypes (Table 5). The mean grain yield was 7.478tha^{-1}. The highest grain yield was obtained from Shrestha (9.954tha^{-1}) followed by RML191/RML18 (9.41tha^{-1}) which was at par with CAH1715 (9.356tha^{-1}) and RML4/RL111 (9.021tha^{-1}). The minimum grain yield was obtained from

RML57/RL174 (3.802tonha^{-1}). The mean number of rows per ear was 14 which ranged from 11 to 17. The maximum number of rows per ear was observed in 07SADVI-11-1-2BB/RL-111 which was at par withRML57/RL174, SHRESTHA, and HGBS2-17-3-1/RML18 whereas RML94/RL298 showed the minimum number of rows per ear. The mean number of grains per row was 27 which ranged from 17 to 35. The maximum number of grains per row was obtained from RML57/RL174 followed by RML153/RL105 and CAH1715. The minimum number of grains per row was found in RL249/RML96.The mean 1000- grain weight was 266g. Highest 1000-grain weight was obtained in genotypes Rampur Hybrid-10 (340g) followed by RML191/RML18 (331.667g), RML150/RML84 (304g) and HGBS2-17-3-1/RML18 (300g) while genotypes RML57/RL174 (217g) and RML86/RML146 (218g) showed the lowest 1000-grain weight. The broad-sense heritability of grain yield, number of rows per ear, number of grains per row, and thousand-grain weight were68%, 79%, 65%, and 70% respectively.

Table 6. Mean physiological and disease traits of single-cross hybrids evaluated at Khairahani, Chitwan during the spring season of 2021

Genotypes	Leaf Senescence	Ear Rot	Husk Cover	Plant Aspect	Ear Aspect
07SADVI-11-1-2BB/RL-111	16.67	27	1.3	2.0	1.7
CAH1715 (CHECK)	20.00	20	1.3	2.3	1.0
SHRESTHA	20.00	3	1.0	1.0	1.0
HGABS2-15-2-1B/RL174	23.33	18	1.3	1.0	1.7
HGBS2-17-3-1/RML18	20.00	3	1.7	2.0	2.3
RAMPUR HYBRID-10	16.67	9	1.7	1.7	1.7
RL100/RML140	23.33	15	1.3	2.0	1.7
RL102/RML17	23.33	0	1.0	2.3	1.7
RL242/RL105	26.67	8	1.3	2.0	1.3
RL249/RML96	20.00	1	1.0	2.0	2.0
RML138/RML140	23.33	12	1.3	2.3	1.7
RML150/RML84	16.67	9	3.0	1.7	1.3
RML153/RL105	23.33	1	1.3	1.7	1.3
RML191/RML18	16.67	1	1.0	1.7	1.0
RML4/RL111	20.00	1	1.3	1.7	2.0
RML57/RL174	16.67	1	1.0	2.7	1.0
RML76/RML146	16.67	5	1.0	2.0	1.3
RML86/RML146	16.67	18	1.3	2.3	1.7
RML9/RML98	16.67	8	1.0	2.3	1.3
RML94/RL298	23.33	2	1.0	1.7	1.7
Mean	**20.00**	**8**	**1.3**	**1.9**	**1.5**
F-test	**NS**	*	**	**NS**	**
P-value	**0.423**	**0.0202**	**0.00101**	**0.0751**	**0.07235**
LSD, 0.05	**9.038524**	**14.95383**	**0.7065739**	**0.9762722**	**0.878387**
Heritability	**0.02**	**0.28**	**0.43**	**0.19**	**0.2**

Note: *Significant at 5% level of significance, ** significant at 1% level of significance, and *** significant at 0.1% level of significance

Husk cover will be rated on a 1 to 3 scale, where 1=husk tightly arranged and extended, 2=medium, and 3=ear tips exposed

Plant aspect must be rated on a scale of 1 to 5, where 1= excellent in overall phenotypic appeal, 3=average, 5=poor in overall phenotypic appeal

Ear aspect must be rated on a scale of 1 to 5, where 1= clean, uniform large, and well-filled ears, 3=average, 5=rotten, variable,small, and partially filled ears

Statistically, there was a significant difference in ear rot, husk cover, and ear aspect between the genotypes whereas no significant difference was observed in the case of leaf senescence and plant aspect between the genotypes (Table 6). The mean leaf senescence percentage was 20 which ranged from 16.67 to 26.67. The highest leaf senescence was observed in genotype RL242/RL105. Seven genotypes showed a higher percentage and eight genotypes showed a lower percentage of leaf senescence than the mean. The mean ear rot percentage was 8 which ranged from 0 to 27. No ear rots were observed in genotype RL102/RML17.The highest ear rot was observed in the genotype 07SADVI-11-1-2BB/RL-111 followed by RML86/RML146 and HGABS2-15-2-1B/RL174 whereas the lowest ear rot was observed in RML4/RL111, RML191/RML18 and RL249/RML96. Husk cover with exposed ear tip was observed in genotype RML150/RML84 whereas tightly arranged and extended husk cover was observed in RML9/RML98, RML191/RML18, RL249/RML96, RL102/RML17, RML94/RL298, RML57/RL174, RML76/RML146, and Shrestha. The mean phenotypic appeal of the genotypes was excellent. The genotype RML57/RL174 was average in overall phenotypic appeal followed by RML86/RML146, RML9/RML98, RL102/RML17, RML138/RML140, and CAH1715 while genotype HGABS2-15-2-1B/RL174 and Shrestha variety were excellent in overall phenotypic appeal. Clean, uniform, large, and well-filled ears were obtained from genotype RML191/RML18, RML57/RL174, CAH1715, and Shrestha. Average ears were obtained from the genotype HGBS2-17-3-1/RML18.The broad-sense heritability for ear rot, husk cover, ear aspect, leaf senescence, and plant aspect was 28%, 43%, 20%, 2%, and 19% respectively.

Table 7. Pearson's correlation coefficient among different observed traits of maize

	AD	ASI	PH	EH	NOEPha	NOGPR	CL	CD	TGW	GY
AD	1									
ASI	-0.24	1								
PH	0.31*	0.02	1							
EH	0.34**	0.01	0.76***	1						
NOEPha	0.02	-0.01	-0.03	0.15	1					
NOGPR	0.05	-0.24	0.25	0.12	0.07	1				
CL	0.07	-0.2	0.1	-0.09	0.07	0.74***	1			
CD	-0.11	-0.08	-0.22	-0.10	-0.21	0.08	0.23	1		
TGW	-0.2	0.05	-0.24	-0.34**	0.01	-0.28*	0.17	0.08	1	
GY	-0.04	-0.1	0.23	0.13	0.28*	0.16	0.33**	0.16	0.35**	1

Note: AD= Days to 50% anthesis, ASI= Anthesis-Silking Interval, PH= Plant Height, EH= Ear Height, NOEPha= Number of Ear per hectare, NOGPR= Number of grains per row, CL= Cob Length, CD= Cob Diameter, TGW= Thousand grain weight, GY= Grain yield, *Significant at 5% level of significance, ** significant at 1% level of significance, and *** significant at0.1% level of significance

The result shows that the grain yield has a positive and significant correlation with the number of ears per hectare, cob length, and thousand-grain weight (Table 7). Other traits did not show a significant relationship with yield traits but showed positive and negative correlations (Table 7). Anthesis days and anthesis-silking interval indicated a negative correlation with Grain yield suggesting that the increase in value of these traits will decrease the yield of the maize while plant height, ear height, number of ears per hectare, number of grains per row, cob length, cob diameter, and thousand-grain weight indicated positive correlation with grain yield suggesting that yield of the maize will increase with the increase in the value of these traits.

Discussion

The presence of substantial variation among the hybrids under study is indicated by significant variances in attributes for single cross maize hybrids, which can be used to improve the genetics of the crop through selection and hybridization (Belay, 2018). Rai et al. (2021), Raut et al. (2017) obtained significant results for days to fifty percent anthesis and silking, ear height, number of rows per ear, number of grains per row, and grain yield. A similar result was reported for ear height, number of rows per ear, number of grains per row, and grain yield (Bartaula et al., 2019; Ghimire, 2017)and for days to fifty percent anthesis grain yield by Kafle et al. (2020). Days to fifty percent anthesis and silking are important characters that determine maturity period in maize and considered important for breeding (Ullah et al., 2017).

Bartaula et al. (2019) obtained significant results for the anthesis-silking interval, plant height, cob length, and thousand-grain weight. Genotypes HGABS2-15-2-1B/RL174, Shrestha, RML76/RML146, RML86/RML146, and RML94/RL298 showed negative anthesis-silking intervals, which indicates these genotypes are drought tolerant. Pollen grains dessicate and lose their viability if pollination does not occur within 1-2 days of anthesis as they remain viable for shorter period than silks. Pollen shedding at right time and its perfect synchronization with silking resulting high kernel filling and ultimately higher grain yield (Ullah et al., 2017). Ghimire (2017), Kafle et al. (2020), Raut et al. (2017) recorded significant results for cob diameter. Significant ear aspect and number of ear per plant (Wagle et al., 2020) and the number of ear per hectare (Dhakal et al., 2018) was recorded. The significant differences among the treatments for these traits show the presence of genetic variability among the experimental materials that supports crop improvement of those traits through selection (Bartaula et al., 2019).Tightly arranged and extended husk cover is preferred in maize as it avoids cob from pathogen and pest infestation along with climatic risk. Shoot lodging among the genotypes was found to be high; this might be due to the high nitrogen dose applied during the experiment and undesirable climatic conditions.

Heritability estimates provides information on the extent to which a particular trait can be inherited to subsequent generations (Belay, 2018). High heritability in broad sense estimate was recorded for days to fifty percent silking, days to fifty percent anthesis (Ullah et al., 2017) and grain yield (Neupane et al., 2020; Rai et al., 2021). Similarly, high heritability for thousand-grain weight, number of grains per row, anthesis-silking interval, plant height (Neupane et al., 2020), number of rows per ear, and ear height (Bartaula et al., 2019; Rai et al., 2021) was recorded, which shows the effect of the environment to the expression of these traits is low (Belay, 2018; Neupane et al., 2020; Sravanti et al., 2017) and improvement of the traits can be made based on phenotypic performance (Belay, 2018) and there might be a better correlation between breeding values and phenotypic traits (Sravanti et al., 2017). So, these traits have greater scope for genetic improvement through selection (Bartaula et al., 2019; Sravanti et al., 2017). These parameters are under the control of additive genetic effects (Sravanti et al., 2017).

Moderate sense heritability value was observed for antheis-silking interval which is supported by Ullah et al. (2017).This might be due to the environmental effects on the phenotypic nature of these traits (Neupane et al., 2020). So, breeders must be careful while breeding these complex traits. Low heritability was observed for cob length (Rai et al., 2021). This represents the greater effect of the environment on the expression of these traits (Rai et al., 2021).

The genotypic and phenotypic correlations among the traits studied pointed out the existence of several statistically significant relationships and are presented in Table 7. The study by Bartaula et al. (2019), Buso et al. (2019) found a positive and significant correlation between cob length and thousand-grain weight with grain yield. A similar result was obtained for cob length (Rai et al., 2021; Supraja et al., 2019) and thousand-grain weight (Kandel & Shrestha, 2020). The use of these traits to increase the grain production of the hybrid maize is suggested by the positive and significant correlation between grain yield to cob length and thousand-grain weight (Kandel & Shrestha, 2020).

Non-significant but positive correlation with grain yield was shown by plant height and the number of grains per row (Ghimire, 2017; Kandel & Shrestha, 2020; Supraja et al., 2019) and cob diameter (Wagle et al., 2020). Ear height is considered one of the important traits in maize. The ear position ranging from 40-50 is considered good. The mean ear position of different genotypes understudy was 52, which shows the position of the ear was appropriate and aids in higher grain yield. Positioning of the ear above the middle of the plants often leads to lodging (Kunwar & Shrestha, 2014). Plant breeders usually prefer genotypes with lower ear position as it minimizes the rate of root and shoot lodging that directly affects grain yield (Bello et al., 2012). The number of ears per plant has a direct relationship with grain yield. Genotypes having values more than 1.33 bear double cob. The value of genotypes understudy was less than 1.33, which manifests all of them bear single cob.

Similarly, a non-significant negative correlation with grain yield was observed for days to fifty percent anthesis and anthesis-silking interval (Kandel & Shrestha, 2020; Rai et al., 2021; Supraja et al., 2019) and a similar result was obtained by Bartaula et al. (2019) for the anthesis-silking interval. This negative correlation of traits with grain yield shows that with more days to 50% anthesis and anthesis-silking interval, there will be more vegetative growth and less time for reproductive growth resulting in decreased yield (Ghimire, 2017). So, breeders should prefer a hybrid with shorter days to anthesis and less anthesis-silking interval during selection.

Conclusion

The high-yielding hybrids under experiment were Shrestha (commercial check), RML191/RML18, and CAH171 (pipeline check). These hybrids were early flowering and had less anthesis-silking interval. The position of the ear in these hybrids was in the middle of the plant. The Shrestha had a greater number of rows per ear, CAH1715 had a greater number of grains per row, whereas RML191/RML18 had high thousand-grain weight. Moreover, the longer cob length and cob diameter was found in high yielding hybrids as compared to other genotypes. Therefore, this study recommends these single-cross hybrids for higher grain yield and commercial production at farmers' field in the context of Khairahani-5, Chitwan. Additionally, they can be evaluated across sites to determine their compatibility and adaptability.

Acknowledgment

The authors are very grateful to National Maize Research Program (NMRP), Chitwan, Nepal for providing the research materials and guidance. We are also thankful to Mr. Binod Chaudhary for providing research field. We equally appreciate Institute of Agriculture and Animal Science, Rampur Campus, Tribhuwan University, Nepal for additional support.

Author's declaration

The authors declare that there is no conflict of interest. All authors read and approved the final version of the manuscript.

References

Bahadur Kunwar, C., & Shrestha, J. (2014). Evaluating Performance of Maize hybrids in Terai Region of Nepal. *World Journal of Agricultural Research*, *2*(1), 22–25. CrossRef

Bartaula, S., Panthi, U., Timilsena, K., Acharya, S. S., & Shrestha, J. (2019). Variability, heritability and genetic advance of maize (*Zea mays* L.) genotypes. *Research in Agriculture Livestock and Fisheries*, *6*(2), 163–169. CrossRef

Belay, N. (2018). Genetic Variability, Heritability, Correlation and Path Coefficient Analysis for Grain Yield and Yield Component in Maize (*Zea mays* L.) Hybrids. *Advances in Crop Science and Technology*, *06*(05). CrossRef

Bello, O. B., Azeez, M. A., Mahmud, J., Afolabi, M. S., Ige, S. A., & Abdulmaliq, S. Y. (2012, April). Evaluation of grain yield and agronomic characteristics in drought-tolerant maize varieties belonging to two maturing groups. *Scholarly Journal of Agricultural Science*, *2*(4), 70–74.

Carangal, V. R., Ali, S. M., Koble, A. F., Rinke, E. H., & Sentz, J. C. (1971). Comparison of S_1 with Testcross Evaluation for Recurrent Selection in Maize [1]. *Crop Science*, *11*(5), 658–661. CrossRef

Dhakal, B., Shrestha, K. P., Joshi, B. P., & Shrestha, J. (2018). Evaluation of early maize genotypes for grain yield and agromorphological traits. *Journal of Maize Research and Development*, *3*(1), 67–76. CrossRef

DinizBuso, W. H., Lopes Gomes, L., Ballesta, P., & Mora, F. (2019). A phenotypic comparison of yield and related traits in elite commercial corn hybrids resistant to pests. *Idesia (Arica)*, *37*(2), 45–50. CrossRef

Gairhe, S., Timsina, K. P., Ghimire, Y. N., Lamichhane, J., Subedi, S., & Shrestha, J. (2021). Production and distribution system of maize seed in Nepal. *Heliyon*, *7*(4), e06775. CrossRef

Ghimire, B. (2017). Analysis of yield and yield attributing traits of maize genotypes in Chitwan, Nepal. *Journal of Food Processing & Technology*, *08*(01). CrossRef

Kafle, S., Adhikari, N., Sharma, S., & Shrestha, J. (2020). Evaluation of single-cross maize hybrids for flowering and grain yield traits. *Fundamental and Applied Agriculture*, *0*, 1. CrossRef

Kandel, B. P., & Shrestha, K. (2020). Performance evaluation of maize hybrids in inner-plains of Nepal. *Heliyon*, *6*(12), e05542. CrossRef

Magar, B. T., Acharya, S., Gyawali, B., Timilsena, K., Upadhayaya, J., & Shrestha, J. (2021). Corrigendum to "Genetic variability and traits association in maize (*Zea mays* L.) varieties for growth and yield traits." *Heliyon*, *7*(10), e08144. CrossRef

Ministry of Agriculture and Livestock Develepment. (2021). *Statistical Information on Nepalese Agriculture 2076/77(2019/200* [E-book].

Ministry of Finance, Singh Durbar, Kathmandu. (2021). *Economic Survey 2020/21* [E-book].

Neupane, B., Poudel, A., & Wagle, P. (2020). Varietal evaluation of promising maize genotypes in mid hills of Nepal. *Journal of Agriculture and Natural Resources*, *3*(2), 127–139. CrossRef

Organization, F. A. A. (2022). *World Food and Agriculture – Statistical Yearbook 2021 (English and French Edition)* (Bilingual ed.). Food & Agriculture Organization.

Rai, R., Khanal, P., Chaudhary, P., & Dhital, R. (2021). Genetic variability, heritability and genetic advance for growth, yield and yield related traits in maize genotypes. *Journal of Agriculture and Applied Biology*, *2*(2), 96–104. CrossRef

Raut, S., Ghimire, S. K., Kharel, R., Kunwar, C. B., Sapkota, M., Kunwar, U., & Kushwaha, U. K. S. (2017). Study of Yield and Yield Attributing Traits of Maize. *American Journal of Food Science and Health*, *3*(6), 123–129.

Sravanti, K., Devi, I. S., Sudarshan, M., & Supriya, K. (2017). Evaluation of Maize Genotypes (*Zea mays* L.) for Variability, Heritability and Genetic Advance. *International Journal of Current Microbiology and Applied Sciences*, *6*(10), 2227–2232. CrossRef

Supraja, V., Sowmya, H. C., Kuchanur, P. H., Arunkumar, B., & Kisan, B. (2019). Genetic Variability and Character Association Studies in Maize (*Zea mays* L.) Inbred Lines. *International Journal of Current Microbiology and Applied Sciences*, *8*(10), 646–656. CrossRef

Thapa, M. (2013). Regulatory framework of GMOs and hybrid seeds in Nepal. *Agronomy Journal of Nepal*, *3*, 128–137. CrossRef

Tripathi, M. P., Shrestha, J., & Gurung, D. B. (2016). Performance evaluation of commercial maize hybrids across diverse Terai environments during the winter season in Nepal. *Journal of Maize Research and Development*, *2*(1), 1–12. CrossRef

Ullah, Z., Rahman, H., & Muhammad, N. (2017). Evaluation of Maize Hybrids for Maturity and Related Traits. *Sarhad Journal of Agriculture*, *33*(4). CrossRef

Vashistha, A., Dixit, N. N., D., Sharma, S. K., & Marker, S. (2013). Studies on heritability and genetic advance estimates in Maize genotypes. *Bioscience Discovery*, *4*(2), 165–168. Direct Link.