

EVALUATION OF HYBRID MAIZE GENOTYPE FOR YIELD AND YIELD ATTRIBUTING TRAITS IN BIRENDRANAGAR, SURKHET

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ABSTRACT

Maize is the second most grown and staple food for most of the people in hilly region of Nepal. Also, it is used as source of feed and fodder. With changing consumer habit, increasing industrialization and urbanization, the demand of maize for food, fodder and feed is increasing day by day and the alternative to address increasing demand is hybrid maize which has higher yield potential as compared to traditional varieties. The main objective of this research is to study the performance and correlation between yield and yield attributing traits of different hybrid maize genotypes at Birendranagar-2, Hilekhali Surkhet. A field experiment was conducted during March to July of 2024 using alpha-lattice design. Among the genotypes evaluated RH16 (check variety) had the highest yield (5.47tha^{-1}) followed by NH2223 (4.88tha^{-1}), RML2141/RML2259 (4.82tha^{-1}) NH2226 (4.72tha^{-1}). As for correlation estimation observed traits showed positive correlation with yield traits. The phenotypic coefficient of variation ranged from 6.22 of plant height to 17.69 of yield and the genotypic coefficient of variation ranged from 4.81 of cob length to 14.23 of yield. The estimate of broad sense heritability was lowest (0.36) of cob length and moderate to high for plant height (0.93), cob diameter (0.85), number of rows per cob (0.81), ear height (0.72), number of grains per row (0.67) and yield (0.64). Higher heritability and high to moderate genetic advance as percentage of mean was observed for ear height, plant height, and numbers of row per cob, number of grains per row, thousand grain weight and yield. Based on yield performance, above genotypes could be promoted as high yielding genotype in Birendranagar, Surkhet.

Keywords: Performance, Correlation, Genetic Coefficient of Variation (GCV), Phenotypic Coefficient of Variance (PCV)

INTRODUCTION

Zea mays L., the scientific name of maize comprising of $2n= 20$ chromosome number is a cross-pollinated, monoecious crop belonging to Poaceae family (Hallauer et al., 2009). It is the second most significant crop in Nepal, right after paddy. One of the major foods in the country's mid-hill regions, maize is grown on roughly 78% of the total cultivated area in the hills and is primarily consumed by poorer families and marginalized groups (Sapkota et al., 2017). Ministry of Agriculture and Livestock Development, 2023 showed maize is cultivated in area of 985,565ha, with production and productivity of 3,106,397mt and 3.15mtha^{-1} . The changing consumer habit from starch to protein is increasing the poultry and livestock industry in Nepal. Hence, the demand of maize for food and feed is elevating on daily basis (Tripathi et al., 2016). Increasing the cultivation of hybrid maize can address the sky-rocketing demand of maize as hybrid yields more, have greater uniformity in maturity, plant height, ear height. Additionally, they have higher abiotic stress tolerance capacity as compared to open pollinated varieties (Tiwari et al., 2023).

Hybrid maize cultivation started since 1980s in Nepal. Around 7-10% of area was covered by hybrid maize in 2010 (Gurung et al., 2011; SQCC, 2013). National Maize Research Program (NMRP) conducts activities related to maize; it conducts research, evaluates and registers hybrids from multinational companies (Kandel & Shrestha, 2020). According to Kandel (2020), NMRP has developed and released 5 varieties, registered 2 and 52 registered varieties from multi-national companies.

Hybrid seed production is restricted to National Maize Research Program, i.e., solely for scientific uses. The lack of knowledge about hybrid maize research is a limiting factor in the poor adoption of hybrids (Kandel, 2014). Inadequate investment by public and private sectors, seed replacement every year, dependency on foreign maize genetic resources, etc. are some major problems resulting in low maize production (Kandel, 2020). Despite of increasing area under hybrids, the production remains low due to less research on hybrids development based on agro-ecological regime of the country.

Genetic evaluation is vital for selection, as selection is the fundamental step of breeding. Estimating genetic parameters gives insights to heritability, genetic advance, genetic variance, phenotypic and genotypic coefficient of variation and so on. Through which interdependence of traits with yield can be evaluated. As a complex characteristic, yield is determined by the number of polygenic traits that are inherited and are heavily influenced by external influence. The degree of progress that could be expected from selection, precise assessment on the trait of interest of the population, more accurate

information among variables can be achieved by evaluating genetic parameters (Shrestha et al., 2023). Therefore, major objective of this research is to identify high yielding promising genotype and their yield attributing traits and study the genetic parameters of hybrid genotype in Hilekhali, Birendranagar, Surkhet.

MATERIALS AND METHODS

Study area

The experiment was conducted in Hilekhali, Birendranagar, Surkhet located at longitude 81 35'30"E and latitude of 28°35'57"N from March to July of 2024 (Nepal Climate, 2014). The maximum temperature recorded during the research period was 33.17°C, minimum temperature of 19.01°C and, relative humidity ranging from 16 to 77% (National Aeronautics and Space Administration power, 2023).

Genotypes

Table 9.List of genotypes used in the research

S.N.	Entry name	S.N.	Entry name
1.	NH2213	10.	RML2141/RML2259
2.	CML161/CML165	11.	RML145/RML107
3.	NH2203	12.	RL252/RML18
4.	RML145/TZEIQR157	13.	RH16
5.	RH12	14.	CML582/TZEIOR157
6.	NH2223	15.	RML145/RL197
7.	RML150/RML98	16.	NH2227
8.	CML161/RL111	17.	NH2231
9.	NH2226	18.	NH2210

Design of experiment

The experiment was laid out in alpha lattice design consisting of two replications each with three blocks (six genotypes in each block). The length and breadth of the experimental field was 28m and 8.5m, total area of 238m². The plot size was 9m × 4m (36m²).

Fertilizer application

Recommended dose of chemical fertilizer = 120:60:40kgNPK/ha was applied in the form of urea, di-ammonium phosphate and muriate of potash. Full dose of potassium

and phosphorus and 1/4th dose of nitrogen were applied at the day of sowing. Remaining dose of nitrogen was applied at 45 and 60 days after sowing. Organic fertilizer was applied in the form of farm-yard manure at recommended dose 10t/ha before field preparation.

Data collection

Ten random plants were selected from each plot while 60 plants were selected from each block. Agronomic traits include plant height (PH), ear height (EH), ear aspects (EA), ear rot (ER) and, plant aspect (PA). Cob traits include cob diameter (CD), cob length (CL), number of rows per ear (NPRE) and number of grains per cob (NGPR). Field weight (FW) of harvested cob, economic yield (EY) and thousand grain weight (TGW) was measured as well.

Statistical analysis

Data collected from the trail was arranged in Microsoft Excel in accordance to the design used. Data analysis was done by using R-Studio. Packages like agricolae, metan, and variability were used for analyzing ANOVA, path analysis and correlation. The version 4.3.0 at 5% level of significance was used for analysis (Duncan's Multiple Range Test).

RESULT AND DISCUSSION

Agronomical characteristics of genotypes

Table 10. Mean performance of PH and EH of 18 different genotypes

Genotypes	EH (cm)	PH (cm)
RH12	96.2 ^{ab}	229.9 ^a
NH2213	104.3 ^{ab}	229 ^{ab}
CML161/CML165	88.1 ^{ab}	229 ^{ab}
NH2231	116.1 ^a	220.1 ^{abc}
RML2141/RML2259	80.7 ^{ab}	217.5 ^{abcd}
NH2203	98.3 ^{ab}	217.3 ^{abcd}
NH2226	84.7 ^{ab}	216.6 ^{abcd}
RL252/RML18	88.9 ^{ab}	213.3 ^{abcde}
NH2210	100.1 ^{ab}	212.7 ^{abcde}
CML161/RL111	91.8 ^{ab}	210.4 ^{bcd}
NH2227	98 ^{ab}	210.0 ^{cde}
RML145/RL197	76.5 ^{ab}	208.7 ^{cde}
RML150/RML98	79.6 ^{ab}	200.4 ^{def}
CML582/TZEIOR157	68.3 ^b	200.4 ^{def}
NH2223	75.3 ^{ab}	197.8 ^{ef}
RH16	89.7 ^{ab}	196.3 ^{ef}
RML145/RML107	89.7 ^{ab}	195.1 ^{ef}
Efficiency	0.80	0.80
F-test	***	***
CV %	7.32	1.36
Grand Mean	88.86	210.58

Note: PH: Plant Height including tassel, EH: Ear height, CV: Coefficient of Variation, means with same letters are non-significant at $p=0.05$ by DMRT, ns: non-significant, *: 5% level of significance, **: 1% level of significance, ***: 0.01% level of significance *Plant height and ear height*

Table 1 shows highly significant difference in plant height between the genotypes under study. The tallest plant was observed for check variety RH12 (229.9cm), followed by NH2213 (229 cm), while the shortest plant was observed for RML145/RML107 (195.1cm). There was a highly significant difference in ear height among the genotypes

under study. The ear height in the study ranged from 116 to 75.3 cm. The higher ear height was observed in genotype NH2231 (116.1cm), followed by NH2213, with value 104.3 cm, and the lower ear height was observed for RML145/TZEIQR157 (68.3 cm). Similar findings were reported by Kandel and Shrestha (2020) and Beulah (2018). According to Kandel and Shrestha (2020), the significant difference in plant height and cob height is due to the presence of inherent genetic differences of experimental materials as well as environmental factors. Light interception, carbon and nutrient capture, competitive environments, and weed competition all affect plant height. Similar, significant findings in ear height were reported by Nayaka et al. (2014).

Table 11. Mean performance of NGPR, NRPE, CD and CL of eighteen genotypes of hybrid maize

Genotypes	CL	CD	NGPR	NRPE
RH16	20.04	14.6 ^{ab}	36.8 ^{ab}	17.3 ^a
NH2223	19.25	13.4 ^{abcde}	37.5 ^{ab}	17.1 ^{ab}
RML2141/RML2259	18.38	14.7 ^a	29.5 ^b	16.6 ^{abc}
RML150/RML98	19.71	13.9 ^{abc}	29 ^b	15.8 ^{abcd}
NH2213	18.86	12.3 ^{cde}	30 ^{ab}	15.4 ^{abcd}
RH12	17.92	13 ^{abcde}	32.6 ^{ab}	15 ^{abcd}
NH2227	18.7	13.1 ^{abcde}	32.5 ^{ab}	14.9 ^{abcd}
RL252/RML18	16.1	12.2 ^{de}	29.6 ^b	14 ^{abcd}
NH2231	18.17	13.7 ^{abcd}	34.8 ^{ab}	14.5 ^{abcd}
NH2203	16.42	12.2 ^{de}	29.5 ^b	14.4 ^{abcd}
NH2226	18.65	13 ^{abcde}	32.2 ^{ab}	13.9 ^{bcd}
RML145/TZEIQR157	17.61	12.7 ^{cde}	32.8 ^{ab}	13.9 ^{bcd}
NH2210	17.79	12.3 ^{cde}	40.1 ^a	13.9 ^{bcd}
CML161/RL111	15.19	12.1 ^{de}	31.4 ^{ab}	13.7 ^{cd}
RML145/RL197	18.46	12.2 ^{de}	34.4 ^{ab}	13.7 ^{cd}
CML161/CML165	18.79	12.9 ^{bcde}	31.3 ^{ab}	13.7 ^{cd}
RML145/RML107	17.7	11.9 ^e	29.8 ^b	13.06 ^d
CML582/TZEIOR157	18.23	12.2 ^{de}	33.4 ^{ab}	13.04 ^d
Efficiency	0.80	0.80	0.80	0.80
F-test	ns	***	***	***
CV %	6.11	2.07	6.06	3.62
Grand Mean	18.10	12.97	32.67	14.73

Note: NRPE: Number of Rows Per Ear, NGPR: Number of Grains Per Row, CD: Cob Diameter, CL: Cob Length, CV: Coefficient of Variation, means with same letters are non-significant at $p=0.05$ by DMRT, ns: non-significant, *: 5% level of significance, **: 1% level of significance, ***: 0.01% level of significance, ns: non-significant

Yield and yield attributing traits

Number of rows per cob

In Table 2 there was a highly significant difference in the number of rows per cob of the genotypes under study. The maximum number of rows was observed for genotype RH16, which was 17.3, followed by NH2223, which was 17.1 and RML2141/RML2259, which was 16.6. The lowest value of number of rows per ear was observed for RML145/RML107, which was 13, CML161/CML165 and RML145/RL197, which were 13.7 (Table 3). A highly significant difference for NRPE was also reported by Khan and Mahmud (2021).

Number of grains per row

There was a highly significant difference in the number of grains per row of the genotypes under study. The maximum number of grains was observed for genotype NH2210, which is 40.1, followed by NH2223, which is 37.5, and RH16, which is 36.8. The lowest number of NGPR was observed for RML145/RML107 which is 29.8 followed by RL252/RML18 which is 29.6, RML2141/RML2259, which is 29.5, and NH2203, which is 29.5, and RL150/RML98, with 29. A significant result was obtained for the number of grains per row; similar results were also reported by Hepziba et al. (2013).

Cob diameter

There was a highly significant difference in cob diameter of the genotypes under study. The genotype with the highest diameter was RML2141/RML2259, with value 14.7cm, followed by RH16, with value 14.6cm, and lowest value was observed in CML161/RL111, with value 12.1cm, and RML145/RML107, with value 11.9cm (Table 3). Similar findings for CD were reported by Singh et al. (2017) and Pahadi and Sapkota, (2016).

Cob length

There was no significant difference in cob length of genotypes under study. The genotype observed with the longest cob was RH16, which is 20.04cm, followed by

RML150/RML98, which is 19.71cm, and the genotype having the shortest cob length was observed for RL252/RML18, which is 16.10cm and CML161/RL111 with the value of 15.19 cm. A significant result was obtained for the number of grains per row; similar results were also reported by Hepziba et al. (2013).

Table 12. Mean performance of TGW and TPH of different hybrid maize genotype

Genotypes	TGW (g)	TPH(t/ha)
RH16	398.8 ^a	5.4 ^a
NH2226	372.2 ^{ab}	4.7 ^{ab}
CML582/TZEIOR157	365.4 ^{ab}	4.6 ^{ab}
NH2210	365.4 ^{ab}	3.5 ^{ab}
NH2227	363.7 ^{ab}	3.9 ^{ab}
RML2141/RML2259	360.5 ^{ab}	4.6 ^{ab}
RML150/RML98	357.2 ^{ab}	4.3 ^{ab}
CML161/CML165	348.8 ^{ab}	3.4 ^{ab}
NH2231	343.7 ^{ab}	3.4 ^{ab}
NH2223	335.6 ^{ab}	4.8 ^{ab}
RL252/RML18	335.5 ^{ab}	3.4 ^{ab}
RML145/RL197	318.8 ^{ab}	3.8 ^{ab}
RML145/RML107	305.6 ^{ab}	3.4 ^{ab}
NH2213	298.9 ^{ab}	4.1 ^{ab}
CML161/RL111	297.2 ^{ab}	3.1 ^b
NH2203	293.9 ^b	3.2 ^{ab}
RH12	278.8 ^b	3.8 ^{ab}
RML145/TZEIQR157	263.9 ^b	3.6 ^{ab}
Efficiency	0.80	0.80
F-test	***	***
CV%	4.70	4.01
Grand Mean	333.61	11.1

Note: TGW: Thousand Grain Weight, TPH: yield in Ton Per Hectare, CV: Coefficient of Variation, means with same letters are non-significant at $p=0.05$ by DMRT, ns: non-significant, *: 5% level of significance, **: 1% level of significance, ***: 0.01% level of significance

Thousand grain weight

Table 3 showed there was a highly significant difference in the thousand grain weight of the genotypes under study. The genotype with the heaviest 1000 grain weight was observed for RH16, which is 398.8 g and the genotype with the lightest 1000 grain weight was observed for RML145/TZEIQR157, which is 263.9g. Similar, results for TGW were reported by Bharathiveeramani et al. (2012).

Yield in tons/ha

Similarly, in table 3 it showed highly significant difference in yield in tons per hectare for the genotypes under study. The top three yielders were genotype RH16 (5.4 t/ha), followed by NH2223 with a yield of 4.8t/ha, NH2226 with a yield 4.7t/ha. The lowest yielding genotypes were CML161/RL111 with a yield 3.1 t/ha, NH2203 with a yield 3.2 t/ha, RML145/RML107 and, RL252/RML18NH2231 with a yield of 3.4 t/ha (Table 4). According to Koirala et al. (2020) the reason behind variation in yield of different genotype is due to existence of variation in genetic makeup.

Significant differences among genotypes for yield and yield attributing traits are reported by Adhikari et al. (2018) which stated existence of genetic variability on yield potential on tested genotypes. Bhiusal et al. (2017) reported similar significantly different findings for yield and yield attributing traits. Also, the variation provides good opportunity for grain yield improvement in maize (Bhiusal et al., 2017). According to Koirala et al. (2020) genetic improvement can contribute at least 50-60% yield gain in maize. Production and productivity enhancement through improvement is effective (Koirala et al., 2020; Koirala et al. 2021).

Estimates of genetic parameter

Table 13. PCV, GCV, GA and GAM estimates for various characters of 18 genotypes

S.N.	Character	GCV (%)	PCV (%)	$h^2\%$	GA	GAM
1.	PH	6.03	6.22	0.93	25.37	12.04
2.	EH	12.63	14.80	0.72	19.74	22.21
3.	CL	4.81	8.01	0.36	1.06	5.95
4.	CD	5.41	5.86	0.85	1.31	10.29
5.	NRPE	7.64	8.45	0.81	2.06	14.23
6.	NGPR	8.13	9.89	0.67	4.49	13.76
7.	FW	4.82	19.16	0.06	0.12	2.50
8.	TGW	8.9	12.80	0.48	42.34	12.74
9.	TPH	14.23	17.69	0.64	0.56	23.5

Note: GCV: Genotypic Coefficient of Variation, PCV: Phenotypic Coefficient of Variation,

h^2 : heritability, GA: genetic advance, GAM: Genetic advance as percentage of mean

Deshmukh et al. (1986) classified PCV and GCV values into three categories: high (>20%), medium (10–20%), and low (<10%).

In Table 5 GCV ranged from 4.81(cob length) to 14.23 (yield in ton per hectare) and the PCV ranged from 5.86 (cob diameter) to 19.16 (field weight of harvested cob). The difference between GCV and PCV signifies the influence of environment on traits (Reddy et al., 2012). Slightly higher difference was seen in most of the traits except for CL and TGW which suggests the influence of environment on other remaining traits is low. These traits may be useful in the selection of promising genotypes, and their phenotypic expression would correspond with the genotypic potential. Moderate PCV and GCV were observed for the same traits which mean genotype could be reflected by phenotype. Selection of genotypes based on phenotypic performance of these traits will be effective (Bhiusal et al., 2017).

Heritability

As for broad sense heritability which is the estimate of total variance or ratio of genotypic and phenotypic variance. According to Burton (1952) heritability are estimated as high (greater than 70%), moderate (50-70%) and low (less 50%). Low heritability was observed on traits field weight of harvested cob, CL and TGW. High to moderate heritability was observed for PH, EH, NGPR, NRPC, CD and TPH.

All traits except CL and FW exhibited high to moderate heritability and GAM. These characters can be improved by selection as the respective traits are under control of additive gene action (Reddy et al., 2012). The high heritability values of the characteristics showed they were less affected by the environment, making it possible to successfully select traits based on phenotypic appearance using a straightforward selection strategy and suggesting the potential for genetic advancement (Reddy et al., 2022). Similar results were reported by Akbar et al. (2006), Bhiusal et al. (2017), and Reddy et al. (2012).

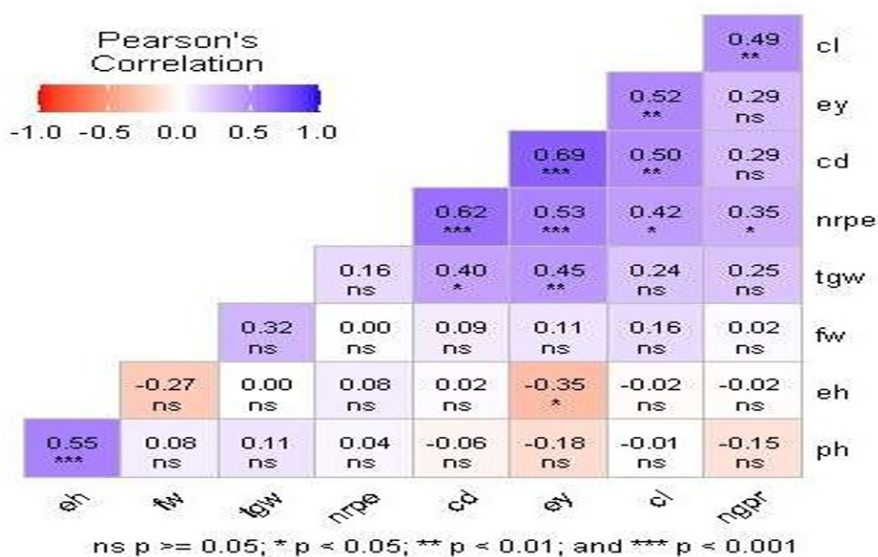


Figure 1. Pearson's correlation heat-map showing relation between yield and yield attributing traits

Correlation estimation

In fig1 traits like Cob Diameter (CD), Cob Length (CL), Number of Rows Per Ear (NRPE), and Thousand Grain Weight (TGW) were positive and significantly correlated with Economic Yield in kg (EY). According to Kandel and Shrestha, (2020) the positive correlation between yield and thousand grain weight suggests that the selection of these traits is important to increase yield. The reproductive stage is longer resulting in greater leaf area which provides the chance to accumulate and construct more photosynthetic material. Ultimately, yield increases (Valizadeh & Bahrampour, 2013).

However, for Ear Height (EH) and EY; negative and significant correlation was observed. Similarly, negative and non- significant correlation was observed between Number of Grains Per Row (NGPR) and Plant Height (PH); Economic Yield in kg (EY)

and PH; which shows direct selection of plant height is not suited to improve yield (Ali et al., 2022) Field Weight (FW) and Ear Height (EH).

Path analysis

In accordance to direct and indirect effect of various characters to the One of the most reliable statistical methods for assessing the degree of control of independent characters on seed production and the interdependence of features is path analysis (Reddy et al., 2022).

Traits like CD, NGPR, NRPE, CL and PH have direct and positive effects on yield whereas traits like ear height and numbers of ear harvested have direct and negative effects on yield. Linear row represents the cumulative effect of overall traits on yield. The residual value means the effect of other remaining factors on yield. The highest value of direct and positive effect on yield was found on CL and CD (Figure 2). Similar findings were mentioned by Eleweanya et al. (2005) and Reddy et al. (2022). Traits with high direct relation can be prioritized through hybrid development, parental line improvement.

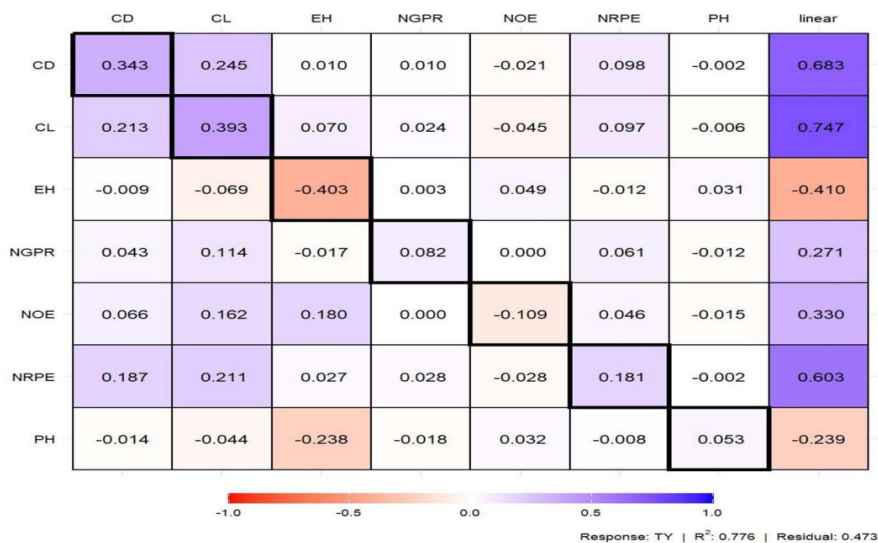


Figure 2. Path analysis representing the direct effect of other traits on yield

CONCLUSION

The research aimed at identifying high yielding promising genotypes and evaluating their yield attributing traits. The estimation of GCV and PCV showed influence of environment on traits was higher for CL and TGW whereas environmental influence was lower for other traits like; PH, EH, NRPE, NGPR, CD etc. As for correlation analysis, traits like CD, NRPE, CL and NGPR were positively and significantly correlated with yield.

Every examined trait exhibited high heritability except for CL. Such traits can be targeted for direct selection. Similarly, all observed traits showed highest GAM except CL and FW. High to moderate heritability and high GAM were observed for all traits except CL and FW. Highest yield in t/ha was observed for genotype RH16 which is 5.4 t/ha and lowest for CML161/RL111 with value 3.1 t/ha. From this experimental trial, genotypes with promising yield like RH16, CML161/RL111 are recommended for further improvement as they performed well in agro-ecological condition of Birendranagar, Hilekhali, Surkhet. Also, traits like PH, EH, NRPE, NGPR, CD can be considered for further breeding improvement.

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