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Genetic Dissection of Advance Maize Lines for Yield and Protein Content

Aditi Roy[1], Ruan Binte Haque[2], Nazifa Tasnia[1,3], Raiyyan Abdur Rahim[1], Md. Ashraful Haque[1*]

[1]Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh, Bangladesh
[2]Department of Biochemistry and Molecular Biology, Jahangirnagar University, Dhaka, Bangladesh
[3]Department of Biological Science, University of Southern Mississippi, Hattiesburg, USA
Email: *ashraf_gpb2000@bau.edu.bd

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Abstract

Maize, an expanding grain crop in Bangladesh, faces high food and feed demand. However, domestic output is insufficient to meet demand, necessitating exports from other countries. Developing high-yielding cultivars is critical to meeting the national need for maize, and nutritional value should also be considered. This study aims to assess the protein content and yield of twenty maize lines by estimating the mean performance of twenty lines with fifteen quantitative characters and protein content, as well as measuring genetic variability factors, correlation coefficients, and path coefficients. The experiment was conducted at Bangladesh Agricultural University, Genetics and Plant Breeding Farm. The results of the analysis showed a significant difference at 0.1% level for most of the characters except cob length, cob diameter, and leaf number per plant in the analysis of variance. Finally, L3 (489.33 g), L10 (468.39 g), L13 (458.66 g), L9 (452 g), L4 (439 g) were evaluated as high yielding and L4 (12.51%), L18 (12.37%), L10 (12.57%), L7 (12.24%), L20 (12.23%), L3 (11.83%) were rich with protein content. In genetic variance analysis, plant height, cob weight, 1000 kernel weight, and protein content showed moderate GCV and PCV values, and cob weight per plant showed high GCV and PCV. Additive genetic advance deciding on plant height, cob weight, yield per plant, and protein content as high heritability along with GAM was observed for these traits. Correlation coefficient and path analysis showed that cob weight, diameter, and 1000 kernel weight positively contributed to yield per plant. Therefore, these parameters should be considered for further improvement of the lines.

Keywords

Maize, Yield, Protein, Nutritional Value, Genetic Variability, Genotypic Variance, Phenotypic Variance, Correlation Coefficient, Heritability,

Path Coefficient

1. Introduction

Maize (*Zea mays* L., 2n = 20) is one of the world's most significant grains, as well as in Bangladesh, behind rice and wheat. Maize is grown in Bangladesh throughout both the Rabi (winter) and kharif (summer) seasons because to its high genetic flexibility. Maize, a staple crop for many people, is used as both food (flour and starch) and feed in the poultry, dairy, and fishery sectors. It provides people and animals with a significant amount of protein and other nutrients. A maize grain includes around 73% carbohydrate, 8% - 12% protein, 4% oils, and 14% other components, including dietary fiber [1].

In FY 22-23, Bangladesh produced around 4.55 million tonnes of maize with an average productivity of 10.19 tonnes per hectare, while 2.46 million tonnes were imported [2]. According to DAE (Department of Agriculture Extension), 5.81 million tonnes of domestic maize output are planned for FY 23-24, with an annual need of approximately 7 million tonnes [3]. In Bangladesh, the feed industry is the primary consumer of produced maize grain due to its higher protein content compared to other cereals. USDA Foreign Agricultural Service report for 2024, forecasts that the feed industry will require approximately 2.1 million metric tons of maize in the marketing year 2024-25 [4]. There is a significant disparity between maize demand and output, providing an excellent potential to enhance maize production. If the maize cultivar has a higher protein quality, it will have a greater impact. Normally, Lysine and Tryptophan are two key amino acids that are missing in maize endosperm, resulting in low protein quality [5]. A lack of these amino acids can lead to a variety of health issues and decreased animal feed quality [6]. Maize with high protein content will yield nutritionally dense food products and this can address malnutrition issues in regions like the char areas of Brahmaputra and Jamuna basins and can provide higher market price to the farmers [7].

Maize grain yield is a complicated polygenic trait influenced by a number of morphological yield-contributing factors, including plant height, cob length, cob diameter, cob weight, and 1000 gain weight [8]. For an effective breeding program to select genotypes for certain qualities, the nature of performance, level of genetic variability, heritability, and correlation among yield components must all be taken into account. The purpose of this study was to evaluate ten inbred and ten hybrid lines for higher yield and protein content by estimating mean performance, genetic parameters such as phenotypic and genotypic variance, coefficient of phenotypic and genotypic variance, heritability, genetic advance, correlation at the phenotypic and genotypic levels, and path analysis of morphological and biochemical traits.

2. Materials and Methods

A total of 20 advanced maize lines were selected for this experiment, including 10 inbreds (L1 to L10) and 10 hybrids (L11 to L20), which were collected from the Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh. The experiment was conducted following Randomized Complete Block Design (RCBD) with three replications in Genetics and Plant Breeding Farm, Bangladesh Agricultural University, Mymensingh during *Robi* season, 2023. To maintain optimum plant growth, intercultural operations such as irrigation, fertilization, earthing up, and pesticide application were done as needed. Fifteen quantitative traits and one biochemical parameter were studied in the experiment by recording five randomly selected plants from each plot at different growth stages and maturity of the plant. Plant height (cm) was measured after anthesis and silkingfrom ground level to tip of the plant. Average leaf length (cm) was calculated by averaging the length of flag leaf, ground leaf and the leaf surrounding the cob. The number of days from seed sowing to tassel and silk emergence of 50% plants in a plot was recorded as days to 50% tasseling and 50% silking respectively. The tassel color and silk color recorded by giving yellow color—1, bright purple color—2, purple color—3. The tassel and silk color that more than 80% of the plants had in a plot was recorded. The rest of the morphological parameters measured at the time of harvest. Statistical analysis *viz* analysis of variance, mean comparison using Tukey test, analysis of variability, path coefficient analysis, and correlation coefficient analysis was performed using R programming language in RStudio 4.3.0 software [9]. The package doebioresearch [10], variability [11], RColorBrewer [12], Performance Analytics [13] and corrplot [14] were used to estimate analysis of variability, path coefficient analysis, correlation coefficient analysis, path analysis respectively. The total protein estimated through Kjeldahl method following procedure described by [15].

3. Results

3.1. Analysis of Variance (ANOVA) and Mean Comparison

Analysis of variance showed highly significant differences among the treatments (lines) at a 5% level of significance for cob length (cm), at a 1% level of significance for leaf number per plant and cob diameter (cm), and the rest of the traits (plant height, average leaf length, days to 50% tasseling, days to 50% silking, tassel color, silk color, cob weight, number of cobs per plant, number of rows per cob, number of kernel per cob, 1000 kernel weight, cob yield per plant and protein content) showed significant difference at 0.1% level of significance (**Table 1**).

Identification of the best line is essential for a breeding program; for this purpose, a mean comparison test was done. The mean comparison test for 16 traits of 20 lines presented significant variation among the lines under the experimental study (**Table 2**). Lines with the same letter for each trait were statistically similar. Among the 20 lines that were evaluated, L3 (489.33), L10 (468.39), L13 (458.66), L9 (452), L4 (439) were evaluated as high yielding and L4 (12.51), L18 (12.37), L10 (12.57), L7 (12.24), L20 (12.23), L3 (11.83) were rich with protein content.

Table 1. Analysis of Variance (ANOVA) of quantitative characteristics.

SV	df	Plant height (cm)	Leaf no./ Plant	Avg. Leaf length (cm)	Days to 50% tasseling	Days to 50% silking	Tassel colour	Silk colour	Cob length (cm)	Cob diameter (cm)	Cob weight (g)	Cob no./ Plant	Row no/ Cob	No. of kernel/ row	1000 kernel weight	Cob yield/ Plant (g)	Protein content (%)
Replication	2	0.03	1.40	1.06	16.46	13.22	0.11	0.35	0.44	0.93	22.49	0.01	1.34	1.66	1454.2	230.5	0.058
Treatment	19	1518.14***	1.30**	105.01***	12.54***	107.32***	1.86***	1.57***	8.08*	2.72**	2830.18***	0.15***	7.64***	25.26***	12384.5***	13567.1***	10.47***
Error	38	1.12	0.49	0.865	3.78	3.54	0.32	0.35	0.96	0.85	46.87	0.03	1.71	6.58	2307.5	491.4	0.07

Where, *** and ** indicate 0.1% and 1% level of significance respectively.

Table 2. Mean performance of 20 maize lines for different quantitative characteristics.

SL	Lines	Plant height (cm)	Leaf no./ Plant	Avg. Leaf length (cm)	Days to 50% tasseling	Days to 50% silking	Tassel color	Silk color	Cob length (cm)	Cob diameter (cm)	Cob weight (g)	Cob no./ Plant	Row no/ Cob	No. of kernel/ row	1000 kernel weight	yield/ Plant (g)	Protein content (%)
1	L1	208.38 ± 0.34 l	12.83 ± 0.76 ab	81.22 ± 1.07 ij	208.38 ± 0.34 bc	83.33 ± 1.52 ab	3 ± 0 a	3 ± 0 a	18.56 ± 2.3 a-c	13.66 ± 1.05 d	157.66 ± 2.51 fg	2 ± 0 b	12.66 ± 0.57 cd	33.66 ± 1.52 a-d	371.59 ± 39.92 d-f	322 ± 7.21 f	9.67 ± 0.42 g
2	L2	264.5 ± 0.5 a	12 ± 1 bc	85.11 ± 0.84 e-g	264.5 ± 0.5 a	81.33 ± 1.52 b-e	1.66 ± 0.57 bc	1.66 ± 0.57 c-e	18.58 ± 0.87 a-c	14.33 ± 1.04 b-d	203 ± 7 bc	2 ± 0 b	15.66 ± 0.57 b	32.33 ± 2.08 b-d	401.63 ± 19.08 b-f	412.66 ± 7.02 cd	10.95 ± 0.26 e
3	L3	180.48 ± 0.83 o	11.11 ± 1.01 cd	73.27 ± 1.11 l	180.48 ± 0.83 c	79.66 ± 1.52 c-f	1 ± 0 c	1 ± 0 e	16.58 ± 1.01 de	14.1 ± 0.52 b-d	180 ± 7 e	2.33 ± 0.57 a	13.5 ± 0.5 cd	30.33 ± 0.57 d	440.00 ± 23.55 a-d	489.33 ± 64.69 a	11.83 ± 0.24 bc
4	L4	234.16 ± 1.0 f	11.83 ± 0.28 b-d	83.83 ± 0.76 gh	234.16 ± 1.04 a	85 ± 1 a	1 ±0 c	1 ± 0 e	16.41 ± 0.94 ef	15.55 ± 0.92 ab	222.83 ± 11.79 a	1.16 ± 0.28 d	13.5 ± 0.86 cd	32 ± 2 cd	519.31 ± 63.17 a	439 ± 34.59 bc	12.51 ± 0.27 a
5	L5	228.29 ± 1.12 g	10.72 ± 0.75 d	80.11 ± 0.51 jk	228.29 ± 1.12 a	61.83 ± 1.60 i	2.33 ± 1.15 ab	2.66 ± 0.57 ab	18.33 ± 0.76 a-c	14.66 ± 0.76 b-d	192.66 ± 4.93 cd	2 ± 0 b	12.66 ± 0.76 cd	33.66 ± 1.52 a-d	452.43 ± 6.86 a-c	385.33 ± 9.86 de	10.2 ± 0.33 f
6	L6	255.59 ± 1.42 c	12.78 ± 0.25 ab	86.51 ± 0.50 de	255.59 ± 1.4 a	73.33 ± 3.51 g	3 ± 0 a	2 ± 0 b-d	18.16 ± 0.87 b-d	14.66 ± 0.76 b-d	161.5 ± 3.7 f	2 ± 0 b	19.33 ± 0.57 a	31.66 ± 2.88 cd	265.43 ± 26.61 g	323 ± 7.54 f	11.54 ± 0.34 cd
7	L7	260.95 ± 0.935 b	12.5 ± 0.5 ab	85.85 ± 0.79 gh	260.95 ± 0.93 a	82 ± 1 a-d	1.33 ± 0.57 c	1.33 ± 0.57 de	17.16 ± 1.15 c-e	13.66 ± 0.76 d	157.25 ± 5.00 fg	2 ± 0 b	13.33 ± 1.15 cd	35.66 ± 2.08 a-c	332.16 ± 19.23 fg	314.5 ± 10.01 f	12.24 ± 0.26 ab
8	L8	200.14 ± 1.67 n	12 ± 0.5 bc	74.37 ± 1.36 l	200.14 ± 1.67 c	79 ± 2.64 d-f	2.66 ± 0.57a	2 ± 0 b-d	19.86 ± 1.48 a	14.33 ± 0.76 b-d	192.5 ± 9.36 cd	1.5 ± 0.5 c	13.83 ± 1.25 b-d	34.5 ± 0.86 a-d	404.59 ± 20.48 b-f	227.83 ± 17.75 g-i	10.33 ± 0.17 f
9	L9	200.75 ± 0.75 n	12.5 ± 0.5 ab	81.37 ± 1.51 ij	200.75 ± 0.75	84 ± 1 ab	2.66 ± 0.57 a	2.33 ± 1.15 a-c	19 ± 0.5 ab	14.83 ± 0.57 b-d	226 ± 10.39 a	2 ± 0 b	13.66 ± 0.57 b-d	37 ± 1 a	447.08 ± 10.43 a-d	452 ± 20.78 b	6.35 ± 0.13 k
10	L10	215.29 ± 0.60 j	12.66 ± 0.28 a-c	82.5 ± 0.5 hi	215.29 ± 0.60 ab	78.66 ± 3.21 ef	3 ± 0 a	**3 ± 0 a**	15.66 ± 0.57 e-g	15.5 ± 1 a-c	190 ± 5.40 de	2 ± 0 b	12.83 ± 0.76 cd	31.66 ± 1.52 cd	468.39 ± 9.30 ab	380 ± 10.81 de	12.57 ± 0.33 a
11	L11	204.52 ± 0.50 m	12.16 ± 0.28 a-c	74.33 ± 1.04 l	204.52 ± 0.50 c	79.33 ± 1.52 c-f	1 ± 0 c	1 ± 0 a	19.63 ± 0.67 ab	133.27 ± 4.5 ij	13.93 ± 0.95 d	2 ± 0 b	12.27 ± 0.85 d	25.88 ± 3.36 e	425.75 ± 61.40 b-e	266.55 ± 9.06 hi	11.13 ± 0.12 de
12	L12	203.29 ± 0.61 m	11.83 ± 0.28 a-c	87.05 ± 0.42 cd	203.29 ± 0.61 c	79 ± 2.64 d-f	2.66 ± 0.57 a	2 ± 0 b-d	14.66 ± 0.76 g	150.11 ± 7.57 gh	14 ± 0.5 cd	2 ± 0 b	13 ± 0 cd	32.33 ± 2.51 b-d	358.83 ± 38.12 ef	300.22 ± 15.14 f-h	9.44 ± 0.30 g
13	L13	228.66 ± 1.52 g	11.05 ± 0.57 b-d	78.88 ± 0.83 k	228.66 ± 1.52 a	65 ± 2 h	2.33 ± 1.15 ab	2.66 ± 0.57 ab	19.16 ± 0.76 ab	229.33 ± 5.85 a	14.16 ± 1.25 b-d	2 ± 0 b	12.83 ± 1.04 cd	34.66 ± 2.51 a-c	517.44 ± 8.23 a	458.66 ± 11.71 ab	7.69 ± 0.19 j
14	L14	215.92 ± 0.89 j	11.33 ± 1.15 cd	74.18 ± 1.28 l	215.92 ± 0.89 ab	81.66 ± 1.52 b-e	3 ± 0 a	3 ± 0 a	14.79 ± 0.82 fg	185.66 ± 1.7 de	16.63 ± 0.22 a	2 ± 0 b	12.33 ± 0.57 d	32.66 ± 6.80 b-d	478.18 ± 121.09 ab	371.33 ± 3.51 e	8.18 ± 0.15 i
15	L15	224.5 ± 0.5 h	12.5 ± 1 ab	84.94 ± 1.35 fg	224.5 ± 0.5 a	81.66 ± 3.05 b-e	1.66 ± 0.57 bc	1.33 ± 0.57 de	16.16 ± 0.76 e-g	185.33 ± 3.81 de	13.73 ± 0.75 d	2 ± 0 b	14.5 ± 4.7 bc	33.33 ± 1.52 a-d	408.40 ± 113.49 b-f	370.66 ± 7.63 e	7.78 ± 0.29 ij
16	L16	217.77 ± 2.03 i	12.16 ± 0.28 a-c	90.61 ± 0.78 b	217.77 ± 2.03 ab	78.66 ± 1.52 ef	1 ± 0 c	1.33 ± 0.57 de	15.91 ± 0.62 e-g	127.33 ± 3.25 j	13.94 ± 2.20 d	2 ± 0 b	12.33 ± 0.57 d	25.66 ± 2.51 e	404.452 ± 29.13 b-f	254.66 ± 6.50 i	11.55 ± 0.33 cd
17	L17	235.05 ± 0.41 f	12.16 ± 0.28 a-c	90.55 ± 0.50 b	235.05 ± 0.41 a	83 ± 2 ab	2.66 ± 0.57 a	2.33 ± 1.15 a-c	16.06 ± 0.59 e-g	149.16 ± 5.34 gh	13.46 ± 0.37 d	2 ± 0 b	13.66 ± 1.15 b-d	32 ± 3 cd	342.98 ± 15.97 fg	305 ± 14.17 fg	9.29 ± 0.23 g
18	L18	244.35 ± 1.06 e	13.16 ± 1.04 a	82.15 ± 1.23 i	244.35 ± 1.06 a	77.66 ± 0.57 f	3 ± 0 a	2 ± 1 b-d	17.01 ± 0.29 c-e	141.16 ± 7.78 hi	13.63 ± 1.05 d	2 ± 0 b	12.83 ± 0.76 cd	32.66 ± 0.57 b-d	337.71 ± 30.12 fg	362.33 ± 36.53 e	**12.37 ± 0.39 a**
19	L19	211.90 ± 0.09 k	12.83 ± 0.76 ab	88.5 ± 0.5 c	211.90 ± 0.09 bc	83.33 ± 1.52 ab	3 ± 0 a	3 ± 0 a	19.48 ± 1.06 ab	205.66 ± 11.59 b	16.83 ± 0.85 a	2 ± 0 b	13 ± 0 cd	36.33 ± 2.30 ab	437.13 ± 45.44 b-e	411.33 ± 23.18 cd	8.71 ± 0.19 h
20	L20	247.44 ± 1.34 d	11.87 ± 0.58 b-d	93.96 ± 0.39 a	247.44 ± 1.34 a	82.33 ± 2.08 a-c	2.33 ± 1.15 ab	1.33 ± 0.57 de	18.61 ± 0.34 a-c	194.77 ± 4.29 b-d	14.65 ± 0.08 b-d	2 ± 0 b	14.66 ± 0.57 bc	35 ± 1 a-c	379.79 ± 11.88 c-f	376.22 ± 17.97 de	12.23 ± 0.33 ab

3.2. Variability, Heritability & GMA

Crop breeding strategies depend heavily on genetic heterogeneity. Table 3 shows the estimated variability for sixteen parameters of 20 lines, including phenotypic variance, genotypic variance, environmental variance, heritability in a broad sense, genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), environmental coefficient of variance (ECV), genetic advance (GA), and genetic advance over mean. The phenotypic variance and coefficients of the examined characteristics were slightly bigger than the genotypic variance and coefficient. Leaf number per plant, days to tasseling, tassel color, silk color, cob diameter, cob number per plant, number of kernels per row, and number of rows in cob all showed greater differences in phenotypic and genotypic variance. Lower GCV and PCV for leaf number per plant, average leaf length, days to tasseling, days to silking, cob length, and cob diameter were estimated. Plant height, cob weight, thousand kernel weight, and protein content showed moderate GCV and PCV values, whereas yield per plant showed high GPV and PCV.

Table 3. Genetic variability parameters for different quantitative characteristics of maize.

Parameter	Genotypic Variance	Environmental Variance	Phenotypic Variance	Heritability (Broad Sense)	Coefficient of Variance (%)			GA	Genetic Advance as percentage of mean
					GCV	ECV	PCV		
Plant height (cm)	505.67	1.12	506.79	99.78	10.03	0.47	10.04	46.27	20.64
Leaf no./Plant	0.27	0.49	0.76	35.43	4.29	5.80	7.22	0.63	5.27
Avg. Leaf length(cm)	34.71	0.86	35.58	97.57	7.10	1.12	7.18	11.98	14.45
Days to tasseling	2.92	3.78	4.40	43.57	2.24	2.55	3.40	2.32	3.05
Days to silking	34.59	3.54	38.13	90.70	7.44	2.38	7.81	11.53	14.60
Tassel colour	0.51	0.32	0.84	61.10	32.34	25.80	41.37	1.15	52.08
Silk colour	0.40	0.35	0.75	53.92	32.00	29.58	43.57	0.96	48.40
Cob length (cm)	2.37	0.96	3.33	71.07	8.80	5.61	10.44	2.67	15.29
Cob diameter (cm)	0.62	0.85	1.48	42.13	5.43	6.37	8.38	1.05	7.27
Cob weight (g)	927.76	46.87	974.63	95.19	16.99	3.81	17.41	61.21	34.15
Cob no./Plant	0.04	0.03	0.07	54.62	10.43	9.51	14.11	0.30	15.88
Row no/Cob	1.97	1.71	3.69	53.58	10.32	9.60	14.10	2.12	15.56
No. of kernel/row	6.85	17.05	23.90	28.67	7.64	7.85	10.96	3.58	10.97
1000 kernel weight (g)	3359.00	2307.50	5666.51	59.28	14.14	11.72	18.37	91.92	22.43
Yield/Plant (g)	5106.09	1440.64	6546.73	77.99	20.06	10.65	22.71	130.00	36.50
Protein Content (%)	3.46	0.07	3.54	97.76	18.02	2.73	18.22	3.79	36.70

Estimation of heritability and genetic advance is necessary to estimate the amount of heritable variation. Heritability, in a broad sense, is estimated as the proportion of genetic variance to phenotypic variance with additive and non-additive portions. High heritability was calculated for plant height (99.78), average leaf length (97.57), days to silking (90.70), cob weight (95.19), yield per plant (77.99), protein content (97.76), whereas only numbers of kernel per row showed low heritability (28.67) and rest of the characters showed moderate heritability. High GAM (Genetic Advance over Mean), along with high heritability, was found for plant height, cob weight, yield per plant, and protein content, indicating the presence of additive genetic variance. For average leaf length, and days to silking, high heritability and low GAM were observed. Among all the traits that were studied in the experiment, both low heritability and genetic advance were estimated by the number of kernels per row, as presented in Table 3.

3.3. Correlation Coefficient Analysis

Table 4 and Table 5 show the genotypic and phenotypic correlation coefficients between yield and yield contributing characteristics respectively. 1000 kernel weight showed a strong positive correlation with cow weight (0.74**, 0.56**), cob diameters (0.63**, 0.36**), a negative correlation with average leaf length (−0.47**, −0.37**), number of rows per cob (−0.52**, −0.54**), and a strong negative correlation with leaf number per plant (−0.33**) and average leaf length (−0.37**) at the phenotypic level. Cob weight per plant had a substantial positive connection with cob weight (0.79**, 0.77**), cob diameter (0.45**, 0.28**), number of kernels per row (0.51**, 0.34**), and 1000 kernel weight (0.51**, 0.48**) at both the genotypic and phenotypic levels. However, yield per plant had a significant negative correlation with average leaf length at the phenotypic level, a non-significant positive association with days to tasseling, silk color, cob length, cob number per plant, number of rows per cob, and a non-significant negative correlation with protein content at both the genotypic and phenotypic levels, respectively.

On the other hand, at phenotypic level protein content found to have significant positive correlation with plant height (0.33**) and significant negative correlation with silk color (−0.37**), cob weight (−0.35**) and number of kernels per row (−0.33**), while at genotypic level significant negative only with number of kernels per plant was found.

3.4. Path Coefficient Analysis

The correlation coefficient merely shows the relationship between yield and yield-contributing qualities, whereas path analysis breaks out the overall direct and indirect effect on yield of other yield-contributing traits. Table 6 and Table 7 provide path analyses at the genotypic and phenotypic levels, with direct and indirect effects on yield per plant.

The path analysis at the genotypic level revealed that cob weight (0.883) had the greatest positive direct effect, followed by cob number per plant (0.567), 1000 kernel weight (0.430), leaf number per plant (0.401), protein content (0.277), number of kernels per row (0.239), and days to tasseling (0.190). The direct negative effect of plant height (−0.114), average leaf length (−0.181), days to silking (−0.250), tassel color (−0.347), silk color (−0.008), cob length (−0.301), and cob diameter (−0.133).

At the phenotypic level, cob weight (1.379), cob number per plant (0.372), days to tasseling (0.353), leaf number per plant (0.125), and protein content (0.190) had a direct positive effect on cob yield per plant, whereas 1000 kernels weight (−0.508), number of kernels per row (−0.265), number of rows per cob (−0.293), cob weight (−0.012), cob length (−0.269), silk color (−0.115), tassel color (−0.069), days to silking (−0.209), average leaf length (−0.190), and plant height had direct negative effect.

Table 4. Correlation coefficient at genotypic level among yield and yield contributing components of maize.

	PH	LNP	LL	DT	DS	TC	SC	CL	CW	CD	CNP	NRC	NKR	TKW	YP	PC
PH	1															
LNP	0.26	1														
LL	0.53*	0.45*	1													
DT	0.34	0.67**	0.42	1												
DS	−0.09	0.68**	0.23	0.43	1											
TC	0.001	0.41	0.06	0.20	−0.11	1										
SC	−0.14	0.14	−0.09	0.12	−0.30	1.14**	1									
CL	0.03	−0.01	−0.18	0.02	−0.22	0.07	0.04	1								
CW	−0.01	−0.41	−0.14	0.38	−0.09	0.11	0.25	0.32	1							
CD	−0.14	−0.11	−0.08	0.33	0.13	0.37	0.45	0.02	0.62**	1						
CNP	−0.12	0.11	0.02	−0.26	−0.22	0.17	0.19	−0.05	−0.38	−0.28	1					
NRC	0.56	0.28	0.32	0.22	−0.007	0.12	−0.24	0.18	0.09	−0.16	0.005	1				
NKR	0.19	0.17	0.13	0.55	0.04	0.68**	0.59**	0.29	0.74**	0.50*	−0.15	0.19	1			
TKW	−0.44	−0.76	−0.47*	0.04	−0.16	−0.26	0.16	0.07	0.71**	0.63**	−0.36	−0.52*	0.22	1		
YP	−0.06	−0.38	−0.19	0.44	−0.08	−0.04	0.09	0.10	0.79**	0.45*	0.04	0.03	0.51*	0.51*	1	
PC	0.33	0.17	0.15	−0.15	0.04	−0.36	−0.53	0.13	−0.36	−0.19	−0.17	0.15	−0.47*	−0.47	−0.28	1

Where, *** and ** indicate 0.1% and 1% level of significance respectively; PH = Plant height (cm), LNP = Leaf number per plant, LL = Leaf number, DT = Days to Tasseling, DS = Days to Silking, TC = Tassel color, SC = Silk color, CL = Cob length (cm), CW = Cob weight (g), CD = Cob diameter (cm), CNP = Cob number per plant, NRC = Number of rows per cob, NKR = Number of kernels per row, TKW = 1000 kernel weight (g), YP = Yield per plant (g), PC = Protein content (%).

Table 5. Correlation coefficient at Phenotypic level among yield and yield contributing components of maize.

	PH	LNP	LL	DT	DS	TC	SC	CL	CW	CD	CNP	NRC	NKR	TKW	YP	PC
PH	1															
LNP	0.14	1														
LL	0.52**	0.28*	1													
DT	0.23	0.16	0.29*	1												
DS	−0.09	0.34**	0.21	0.40**	1											
TC	0.003	0.19	0.06	0.10	−0.10	1										
SC	−0.10	−0.005	−0.07	0.18	−0.16	0.48**	1									
CL	0.03	0.16	−0.12	0.11	−0.15	0.03	0.05	1								
CW	−0.01	−0.25	−0.13	0.26	−0.08	0.10	0.19	0.28*	1							
CD	−0.10	−0.06	−0.08	0.17	0.10	0.22	0.39	−0.06	0.41**	1						
CNP	−0.09	−0.14	−0.004	−0.13	−0.13	0.03	0.11	−0.12	−0.23	−0.15	1					
NRC	0.41**	0.17	0.24	0.04	−0.05	0.11	−0.12	0.16	0.08	0.06	−0.01	1				
NKR	0.13	−0.001	0.09	0.24	0.02	0.33	0.26*	0.29*	0.49**	0.02	−0.02	0.02	1			
TKW	−0.34**	−0.33**	−0.37**	0.06	−0.09	−0.16	0.12	−0.04	0.56**	0.36**	−0.18	−0.54**	−0.17	1		
YP	−0.063	−0.28*	−0.191	0.32	−0.08	−0.01	0.10	0.06	0.77**	0.28*	0.12	0.02	0.34**	0.48**	1	
PC	0.33**	0.08	0.14	−0.12	0.04	−0.29	−0.37**	−0.11	−0.35**	−0.09	−0.14	0.12	−0.33**	−0.22	−0.19	1

Where, *** and ** indicate 0.1% and 1% level of significance respectively; PH = Plant height (cm), LNP = Leaf number per plant, LL = Leaf number, DT = Days to Tasseling, DS = Days to Silking, TC = Tassel color, SC = Silk color, CL = Cob length (cm), CW = Cob weight (g), CD = Cob diameter (cm), CNP = Cob number per plant, NRC = Number of rows per cob, NKR = Number of kernels per row, TKW = 1000 kernel weight (g), YP = Yield per plant (g), PC = Protein content (%).

Table 6. Path coefficient analysis at genotypic level among yield and yield contributing components of maize.

	PH	LNP	LL	DT	DS	TC	SC	CL	CW	CD	CNP	NRC	NKR	TKW	PC
PH	**−0.114**	0.105	−0.096	0.065	0.024	−0.0005	0.001	−0.011	−0.010	0.019	−0.0701	0.068	0.046	−0.190	0.093
LNP	−0.030	**0.401**	−0.082	0.128	−0.172	−0.145	−0.0012	0.005	−0.367	0.015	0.06797	0.0346	0.041	−0.331	0.049
LL	−0.060	0.182	**−0.181**	0.080	−0.058	−0.024	0.0008	0.055	−0.125	0.011	0.01479	0.039	0.031	−0.204	0.041
DT	−0.039	0.271	−0.077	**0.190**	−0.108	−0.070	−0.0010	−0.006	0.340	−0.044	−0.149	0.026	0.133	0.0179	−0.041
DS	0.011	0.276	−0.042	0.082	**−0.250**	0.038	0.002	0.066	−0.082	−0.017	−0.125	−0.0009	0.011	−0.069	0.013
TC	−0.0001	0.168	−0.012	0.038	0.027	**−0.347**	−0.009	−0.021	0.104	−0.049	0.098	0.015	0.164	−0.115	−0.102
SC	0.016	0.059	0.017	0.023	0.077	−0.397	**−0.008**	−0.014	0.229	−0.060	0.110	−0.029	0.143	0.071	−0.149
CL	−0.004	−0.006	0.033	0.004	0.055	−0.024	−0.0004	**−0.301**	0.289	−0.002	−0.029	0.022	0.069	0.031	−0.036

Continued

CW	0.001	−0.167	0.025	0.073	0.023	−0.041	−0.002	−0.098	**0.883**	−0.083	−0.217	0.011	0.177	0.307	−0.102
CD	0.017	−0.046	0.015	0.063	−0.033	−0.128	−0.003	−0.006	0.553	**−0.133**	−0.1641	−0.0201	0.120	0.272	−0.054
CNP	0.0141	0.048	−0.004	−0.050	0.055	−0.060	−0.001	0.015	−0.338	0.038	**0.567**	0.0006	−0.037	−0.157	−0.049
NRC	−0.064	0.114	−0.059	0.042	0.0019	−0.043	0.002	−0.056	0.083	0.022	0.003	**0.121**	0.047	−0.225	0.0425
NKR	−0.0224	0.069	−0.024	0.106	−0.0116	−0.239	−0.005	−0.087	0.655	−0.067	−0.0899	0.02411	**0.239**	0.096	−0.132
TKW	0.050	−0.309	0.086	0.007	0.0403	0.093	−0.001	−0.022	0.630	−0.084	−0.207	−0.063	0.0536	**0.430**	−0.080
PC	−0.038	0.071	−0.027	−0.028	−0.012	0.128	0.004	0.039	−0.326	0.026	−0.100	0.018	−0.114	−0.124	**0.277**

Where, PH = Plant height (cm), LNP = Leaf number per plant, LL = Leaf number, DT = Days to Tasseling, DS = Days to Silking, TC = Tassel color, SC = Silk color, CL = Cob length (cm), CW = Cob weight (g), CD = Cob diameter (cm), CNP = Cob number per plant, NRC = Number of rows per cob, NKR = Number of kernels per row, TKW = 1000 kernel weight (g), PC = Protein content (%).

Table 7. Path coefficient analysis at phenotypic level among yield and yield contributing components of maize.

	PH	LNP	LL	DT	DS	TC	SC	CL	CW	CD	CNP	NRC	NKR	TSW	PC
PH	**−0.114**	0.018	−0.100	0.082	0.018	−0.0002	0.012	−0.008	−0.016	0.001	−0.035	−0.121	−0.035	0.173	0.063
LNP	−0.016	**0.125**	−0.054	0.059	−0.072	−0.013	0.0006	−0.045	−0.345	0.0008	−0.052	−0.052	0.0002	0.168	0.016
LL	−0.060	0.0362	**−0.190**	0.104	−0.043	−0.004	0.008	0.032	−0.191	0.0009	−0.001	−0.073	−0.024	0.188	0.027
DT	−0.026	0.021	−0.056	**0.353**	−0.085	−0.007	−0.021	−0.031	0.37	−0.002	−0.049	−0.012	−0.064	−0.034	−0.024
DS	0.010	0.043	−0.039	0.144	**−0.209**	0.007	0.019	0.042	−0.111	−0.001	−0.049	0.014	−0.007	0.046	0.007
TC	−0.0003	0.023	−0.013	0.038	0.021	**−0.069**	−0.056	−0.010	0.140	−0.002	0.014	−0.034	−0.089	0.082	−0.056
SC	0.012	−0.0006	0.013	0.066	0.034	−0.033	**−0.115**	−0.013	0.275	−0.004	0.043	0.037	−0.071	−0.063	−0.072
CL	−0.003	0.021	0.023	0.041	0.033	−0.002	−0.005	**−0.269**	0.397	0.0007	−0.044	−0.047	−0.076	0.024	−0.022
CW	0.001	−0.031	0.026	0.094	0.016	−0.007	−0.0230	−0.077	**1.379**	−0.004	−0.085	−0.026	−0.130	−0.289	−0.067
CD	0.011	−0.008	0.015	0.062	−0.022	−0.015	−0.046	0.016	0.572	**−0.012**	−0.056	−0.017	−0.007	−0.184	−0.017
CNP	0.011	−0.017	0.0009	−0.047	0.027	−0.002	−0.0134	0.032	−0.317	0.0018	**0.372**	0.005	0.005	0.092	−0.027
NRC	−0.047	0.022	−0.047	0.015	0.010	−0.008	0.014	−0.043	0.1224	−0.0007	−0.007	**−0.293**	−0.007	0.276	0.022
NKR	−0.015	−0.0001	−0.017	0.086	−0.005	−0.023	−0.031	−0.078	0.680	−0.0003	−0.007	−0.008	**−0.265**	0.091	−0.063
TSW	0.039	−0.041	0.070	0.024	0.019	0.011	−0.014	0.013	0.784	−0.0043	−0.068	0.159	0.047	**−0.508**	−0.042
PC	−0.037	0.0108	−0.027	−0.044	−0.008	0.020	0.0436	0.031	−0.490	0.001	−0.053	−0.035	0.088	0.113	**0.190**

Where, PH = Plant height (cm), LNP = Leaf number per plant, LL = Leaf number, DT = Days to Tasseling, DS = Days to Silking, TC = Tassel color, SC = Silk color, CL = Cob length (cm), CW = Cob weight (g), CD = Cob diameter (cm), CNP = Cob number per plant, NRC = Number of rows per cob, NKR = Number of kernels per row, TKW = 1000 kernel weight (g), PC = Protein content (%).

4. Discussion

4.1. Analysis of Variance (ANOVA) and Mean Comparison

Significant difference was observed in analysis of variance (ANOVA) which indicates high genetic variability among the studied materials which is a must for successful plant breeding program and desirable lines cab be selected from them on the basis of yield component traits. [16] and [17] have observed similar experimental results. Among the 20 lines that were studied L3, L10, L13, L9, L4 were evaluated as high yielding and L4, L18, L10, L7, L20, L3 were rich with protein content. These lines should be considered for further improvement.

4.2. Variability, Heritability & GMA

The phenotypic, genotypic variance and coefficient demonstrated substantial variation among the lines. The phenotypic variance and coefficients of the examined characteristics such as leaf number per plant, days to tasseling, tassel color, silk color, cob diameter, cob number per plant, number of kernels per row, and number of rows in cob had slightly bigger than the genotypic variance and coefficient, indicating that the environment had an impact on trait expression. For the other qualities, higher phenotypic variance was detected alongside their genotypic equivalents, indicating that the environment had a minimal to low effect on the traits and that there was enough diversity in the materials for selection for these traits. [18] [19], and [20] all reported the same findings. Corresponding results had been presented [16] and [21] for plant height, days to tasseling, days to silking, cob diameter, number of kernels per row, number of rows in cob and for yield per plant by [22]. These results suggested the exitance of significant genetic diversity, and for a successful breeding program, a high proportion of GCV to PCV is desired.

The high broad sense heritability values and GAM were recorded for plant height, cob weight, protein content in the current study reveal that selection of lines on the basis of these traits is possible. A non-additive genetic variance may be present in average leaf length, and days to silking, as high heritability and low GAM were observed for these traits. Among all the traits that were studied in the experiment, both low heritability and genetic advance were estimated by the number of kernels per row, as presented. These were in agreement with [23] [24].

4.3. Correlation Coefficient Analysis

For the maximal traits, genotypic correlation was greater than phenotypic correlation, indicating a strong intrinsic link between the qualities tested. At both genotypic and phenotypic level cob yield per plant showed considerable positive correlation with cob weight, cob diameter, number of kernels per row, and 1000 kernel weight suggests that these variables can be considered when indirectly selecting for cob weight per plant. These estimates were found to agree with the findings of [17] [25], and [26]-[28], and [24] all found that increasing cob weight, cob diameter, number of kernels per row, and 1000 kernel weight increased cob yield per plant. The considerable positive correlation between cob yield per plant and cob weight, cob diameter, number of kernels per row, and 1000 kernel weight suggests that these variables can be considered when indirectly selecting for cob yield. Yield per plant had a significant negative correlation with average leaf length at the phenotypic level, a non-significant positive association with days to tasseling, silk color, cob length, cob number per plant, number of rows per cob, and a non-significant negative correlation with protein content at both the genotypic and phenotypic levels, respectively.

However, protein content found to have significant positive correlation with plant height and significant negative correlation with silk color, cob weight only at phenotypic level suggesting that these traits appear to be correlated based on observable characteristics, this correlation does not stem from their genetic makeup may be due to environmental influence or lack of pleiotropy and linkage. Significant negative association between protein content and number of kernels per row, at both phenotypic and genotypic level implying that these traits could not be selected together and [29] and [30] observed similar association in maize genotypes.

4.4. Path Coefficient Analysis

The path analysis was carried out to ascertain how the agronomic and quality traits are related to cob yield. Cob weight, cob number per plant, days to tasseling, leaf number per plant, and protein content showed a direct positive effect on cob yield per plant at the phenotypic level, and 1000 kernels weight, number of kernels per row, number of rows per cob, cob weight, cob length, silk color, tassel color, days to silking, average leaf length, and plant height found to have direct negative effect. [31] reported similar findings. Whereas positive direct contribution of cob weight, cob number per plant, 1000 kernel weight, leaf number per plant, protein content, number of kernels per row, and days to tasseling to cob yield per plant and direct negative effect of plant height, average leaf length, days to silking, tassel color, silk color, cob length, and cob diameter was identified at genotypic level . These findings identified cob weight as major contributor to cob yield per plant while acting as a route for indirect contribution of many secondary characteristics to cob yield per plant. This study is consistent with the results of [32].

From correlation and path analysis cob weight, cob diameter, and 1000 kernel weight were identified as essential features that positively contribute yield per plant and should be considered for yield improvement in the maize lines under study. For protein content and cob yield separated selection should be done. The features that directly impacted cob yield per plant should be modified through management practices before being used as selection criteria.

5. Conclusion

In conclusion, based on mean performance L3 (489.33 g), L10 (468.39 g), L13 (458.66 g), L9 (452 g), L4 (439 g) were best for yield and L10 (12.57), L4 (12.51), L18 (12.37), L7 (12.24), L20 (12.23), L3 (11.83) were best for protein content. For both yield and protein content L10 and L3, two inbred lines showed the best performance. For higher yield selection based on cob weight, cob diameter, and number of kernels per cob, 1000 kernel weight could bring out the expected improvement for high yielding from the selected line. Protein content showed a non-significant negative correlation with yield per plant, so a separate selection of protein content may be done. For simultaneous selection for yield and protein content, it is possible to improve L10 and L3 for protein content and yield based on cob diameter, cob weight, 1000 kernel weight, and protein content.

Limitations and Future Scope

The study was conducted in one season due to limited resource and time. Further experiment in another season would have present better insights to the study. For successful improvement of the selected inbred and hybrid lines, proper management of the selected traits is needed.

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Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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