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RESEARCH ARTICLE

Magnitude and impact of genetic heterogeneity on nutritional and fodder quality traits in segregating population of fodder maize (*Zea mays* L.)

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Abstract

Green fodder, a vital and cost-effective source of animal nutrition, plays a crucial role in sustaining livestock productivity. However, the limited availability of nutritionally rich green fodder poses a major constraint in India, underscoring the need for genetic improvement in forage crops, such as maize. To address this, the present investigation focused on evaluating genetic variability in F_3 progenies segregating for biomass yield and nutritional quality traits in fodder maize. The study revealed that several progenies exhibited significantly higher mean values for key traits compared to the better parent, African Tall. High heritability and genetic advance were recorded for plant height (PH), leaf length (LL), leaf breadth (LB), internode length (INL), crude protein (CP), acid detergent fiber (ADF), dry matter yield (DMY) and green fodder yield (GFY), indicating the predominance of additive gene action and the effectiveness of selection based on these traits. Correlation analysis revealed that all biomass yield components were positively correlated with GFY, except for leaf stem ratio (LSR), which showed a significant negative correlation. Nutritional traits, such as CP and ADF showed no significant association with GFY, while crude fiber (CF) and neutral detergent fiber (NDF) exhibited significant negative correlation. Notably, CF, ADF and NDF were positively correlated with each other but negatively associated with CP. DMY, PH and stem girth (SG), demonstrated significant positive correlation, as well as a high positive direct effect on GFY, indicating a true relationship that could be taken as a component trait for GFY improvement. Therefore, a selection index comprising traits such as PH, LL, LB, SG, INL, CP and DMY would be effective in improving both biomass yield and nutritional quality in fodder maize.

Keywords: correlation; crude protein; fodder quality; green fodder yield; heritability

Introduction

Globally, India has the largest and most diverse livestock population. The livelihoods of almost 70 % of households rely on livestock and agricultural sector (1). Livestock rearing provides essential resources such as milk, meat, manure, fuel, draught power and rural transportation, significantly contributing to the income of subsistence farmers and offering insurance against crop failure. Despite being the top milk producer globally, India's animal productivity is low at 1538 kg per lactation, compared to the global average of 2238 kg per lactation. Lower animal productivity is due to malnutrition. It is caused by a major gap in the supply chain resulting in an insufficient amount of animal feed. To mitigate this concern, concentrates are fed to the livestock, although it increases milk production, it also has a higher impact on animal health by causing rumen acidosis and damage to the liver (2). With animal feed and fodder accounting for 60-70 % of milk production costs, green fodder emerges as a cost-effective nutritional supplement (3). Annually, the livestock population increases at the rate of 0.66 % and there is a current deficit of 35.6 % of green fodder. With the current rate of green fodder supply, there will be a shortage of 18.4 % green fodder by 2050 (4).

Maize is a nutritious non-legume green fodder used as livestock feed due to its quick growth, high biomass, protein content, energy, digestibility, palatability and absence of anti-nutritional factors (5). As a C4 crop, maize's high photosynthetic efficiency offers resilience to global climate change, ensuring food and nutritional security (6). Maize, being a naturally cross-pollinated crop, presents the opportunity for hybrid vigour, where the offspring of crosses between diverse inbred parents are superior to the parents (7).

While most of the hybrids developed in the market are bred with the objective of grain productivity, there are only a few studies that focused on the development of superior fodder maize genotypes with enhanced biomass and quality (8-14). These studies showcased the considerable genetic variability present within maize genetic resources and have provided insights into the associations among various fodder-related traits. However, these investigations have largely been confined to genotypes and established inbred lines. There is a noticeable lack of research focusing on segregating populations, which are crucial for understanding the inheritance patterns and trait variability during early selection stages. To the best of our knowledge, the present study is among the first to report on the extent of genetic variability and trait associations in a segregating generation of fodder maize, thereby addressing this critical research gap.

The availability of adequate variability and selection efficiency leads to progress in the genetic improvement of a crop (14). For effective selection, the selected traits should contribute to crop productivity and should have heritable variation (15). It is important to consider the secondary traits that contribute to both biomass yield and quality for efficient selection (16). Considering the potential of maize as a forage crop, the current study was undertaken to 1) estimate the genetic variability and heritability for fodder yield, along with its contributing traits and quality traits and 2) determine the relationship between fodder yield and various traits.

Materials and Methods

Field experiment and laboratory analysis

Seventy $F_{2:3}$ progenies derived from the cross DM94 × African Tall were studied for forage quality and biomass yield. DM94 has higher CP content with lower CF, ADF and NDF. In contrast, African Tall has low CP content and higher fiber content. In the previous study, the contrasting performance of parents for quality characteristics over different seasons has been reported (17). The $F_{2:3}$ progenies and their parents were grown in an experimental field during *Rabi* 2024 in a non-replicated trial under irrigated conditions at New Area Farm, Department of Forage Crops, Tamil Nadu Agricultural University, Coimbatore. Each progeny line was raised in two rows of 4 m length with a 30 × 15 cm spacing. Standard agronomic practices were followed. Field observation of metric traits related to GFY was recorded from five randomly selected plants from each progeny row at the 50 % flowering stage (around 60-65 days after sowing (DAS)). The harvested plant samples were shade-dried for two weeks to remove moisture and fine-powdered by Wiley Miller for fodder quality analysis. Metric traits viz., PH, cob height (CH), LL, LB, number of leaves (NOL) and nodes (NON), internode length (INL), stem girth (SG), leaf stem ratio (LSR), drymatter yield (DMY) and GFY were recorded. Fodder quality traits such as CP, CF, ADF and NDF were analysed by using the Near Infrared Spectrophotometer (NIR) (Model: SpectraAlyser; Make: ZEUTECH, Germany).

Statistical analysis

To estimate variability parameters, the variance of each $F_{2:3}$ progeny is considered as phenotypic variance. The average parental variance was estimated and used as the environmental variance. The statistical methods suggested by different scientists for estimating variability parameters such as phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), broad sense heritability (h^2) and genetic advance as a percent of the mean were employed (18-20). Additionally, the estimates were characterized based on the scales set by previous researchers for variability (< 10 % low, 10-20 % moderate, > 20 % high), for heritability (< 30 % low, 30-60 % moderate, > 60 % high) and genetic advance as a percent of the mean (< 10 % low, 10-20 % moderate, > 20 % high) (20, 21). Skewness and kurtosis were estimated using the statistical method provided by earlier researchers (22). For trait association studies, Karl Pearson's coefficient of correlation by an online software tool grapes, regression by R package ggpubr version 0.6.0 and path analysis by TNAUSTAT were used (23, 24).

Results and Discussion

Mean performance

The population has a wide variation as indicated by the results of the range values (Table 1) for different fodder traits under study. The occurrence of higher and lower values in the progenies compared to their parents for all characters suggested the presence of transgressive segregants in the population. The mean performance indicated that 68 progenies for GFY and 21 progenies for CP had significant differences from the better parent, African Tall. Notably, 18 progenies had a superior mean for both GFY and CP. These lines are considered promising lines. These findings suggest that these 18 progenies could be advanced to later generations to evolve a promising genotype with yield and nutritional traits in fodder maize.

Assessment of variability

For a successful crop improvement program, understanding the different sources of variation is highly essential. Among these, the variation arising due to genetic components holds more significance because they are the ones that can be inherited by the subsequent generations. For all the studied traits, the values of the PCV were higher than the GCV, indicating the influence of the environment (Table 1 and Fig. 1). All traits showed high or moderate GCV values except for the NOL, CF, ADF and NDF. High/moderate GCV values indicate that the character is predominantly under genetic control with minimal environmental influence. Characters such as LB, LSR, DMY and GFY showed higher values of GCV, whereas PH, CH, LL, NOL, NON, INL and SG showed moderate values of GCV. A wide difference of more than 10 % is seen between PCV and GCV values of fodder yield, indicating the character is adversely affected by the environment, which is similar to the study conducted by previous researchers in the F_2 populations of tropically adapted maize (14). Among the quality traits, only CP showed moderate estimates of GCV. Therefore, the selection of progenies based on these traits will be highly rewarding. Traits such as NOL, CF, ADF and NDF have lower GCV values, suggesting that there is a limited scope for further improvement in these traits under the material studied. Few researchers reported similar results for CP and NDF in forage maize (8, 14).

Heritability and genetic advance

The heritable portion of phenotypic variance is known as heritability. The estimates of heritability, along with genetic advances, are more useful in predicting the genetic gain under selection (20). The high/moderate heritability and genetic advance as percent of mean observed for PH, CH, LL, LB, NOL and NON, INL, SG, LSR, GFY, DMY and quality traits such as CP content and ADF. It indicated the prevalence of additive gene action in the inheritance of these traits (Table 1 and Fig. 1). This

Table 1. Estimates of genetic variability parameters for different fodder traits in F_3 segregants of DM94 × African Tall

Characters	P1	P2	Progeny Mean	Range	PCV (%)	GCV (%)	h^2 (%)	GA (%)
PH	105.17	242.20	157.94	77.50-223.50	16.24	14.34	78.02	26.10
CH	52.56	108.20	74.52	32.00-121.00	19.97	12.49	39.08	16.64
LL	68.83	101.65	82.68	41.50-107.00	13.90	11.69	70.75	18.57
LB	7.87	7.61	8.33	4.00-11.50	47.28	46.40	96.31	27.57
NOL	11.89	12.70	12.02	9.00-15.00	10.56	7.99	57.30	12.47
NON	9.22	12.10	11.16	7.00-14.00	12.93	11.11	73.93	19.69
INL	9.11	14.74	10.74	4.00-16.50	18.83	14.68	60.80	23.59
SG	5.24	8.99	6.83	4.20-10.80	17.78	13.65	58.92	21.58
LSR	0.32	0.18	0.28	0.10-0.51	22.28	14.47	42.19	19.36
CP	12.96	10.11	10.09	6.46-15.02	15.19	11.59	58.16	18.20
CF	24.00	25.00	26.51	16.61-35.05	9.52	6.79	50.89	9.98
ADF	31.64	34.66	32.85	21.64-52.27	9.52	8.51	80.03	15.69
NDF	54.73	55.74	57.23	44.83-65.57	5.64	4.21	55.63	6.47
DMY	61.00	139.63	100.32	35.00-210.00	30.53	24.13	62.49	39.30
GFY	230.86	762.25	344.17	80.00-860.00	37.01	25.38	47.04	35.86

PH- Plant height (cm), CH- Cob placement height (cm) , LL- Leaf length (cm), LB- Leaf breadth (cm), NOL- Number of leaves, NON- Number of nodes, INL- Internode length (cm), SG- Stem girth (cm), LSR- Leaf-stem ratio, CP- Crude protein (%), CF- Crude fiber (%), ADF- Acid detergent fiber (%), NDF- Neutral detergent fiber (%), DMY- Dry matter yield (g/plant), GFY- Green fodder yield (g/plant), PCV- Phenotypic coefficient of variation, GCV- Genotypic coefficient of variation, h^2 (%)- Heritability (broad sense), GA (%)- Genetic advance as percentage of mean.

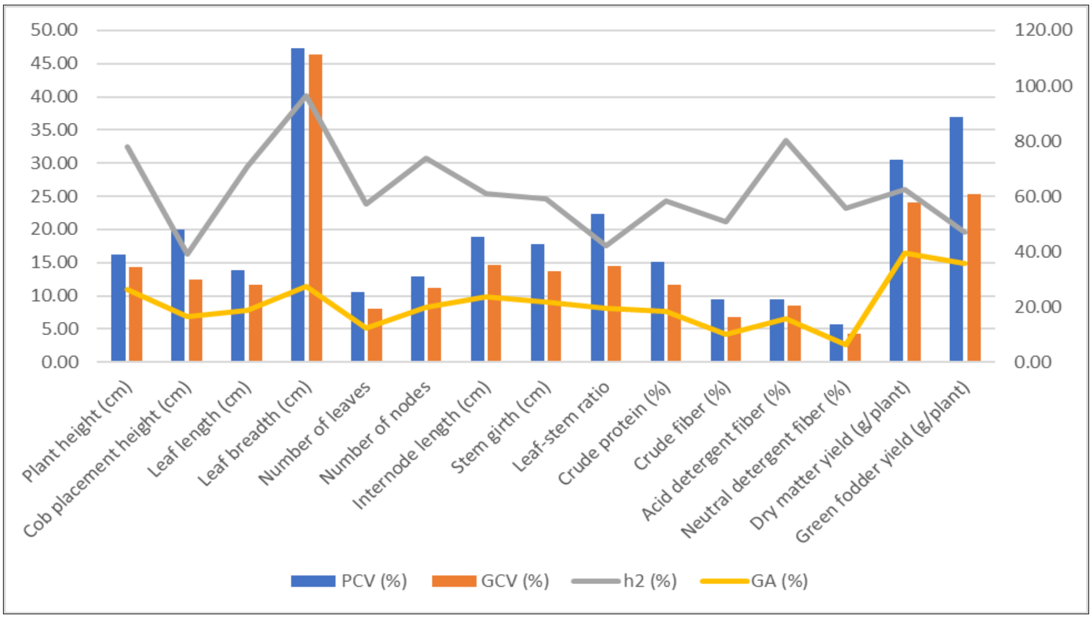


Fig. 1. Graph depicting the genetic variability, heritability and genetic advance of different fodder traits. PCV- Phenotypic coefficient of variation (%), GCV- Genotypic coefficient of variation (%), h^2 (%)- Heritability (broad sense), GA (%)- Genetic advance as percentage of mean.

suggests that phenotypic-guided selection for these traits is highly effective. Moderate heritability accompanied by low genetic advance percentage observed for CF and NDF reveals that the character is controlled by non-additive gene action. Hence, it is difficult to improve these characters by phenotypic selection. The current experiment showcased that GFY and CP content of forage maize progenies expressed high GCV along with higher genetic advance percentage. These traits also had moderate heritability, which is attributed to additive gene action (25). Hence, selection will be effective for these traits. These findings are in accordance with previous studies for both biomass and protein content and for biomass in fodder maize (14, 26).

Skewness and kurtosis

Skewness and kurtosis are important statistical measures that help to identify the distribution. Skewness indicates the asymmetry of a normal distribution, whether the data leans more to the left or right-sided. A distribution with a skewness of zero is perfectly symmetrical. On the other hand, kurtosis indicates the tailness, reflecting the presence of outliers in a distribution. A kurtosis value of zero indicates normal distribution, is said to be mesokurtic. Higher kurtosis, i.e., values greater than 1, is leptokurtic. This indicates taller peaks with heavier tails, suggesting that while most values are close to the mean. Lower kurtosis, i.e., values less than 1, is platykurtic. This is indicated by a flatter peak with lighter tails, suggesting that the values are evenly spread out around the mean, with fewer outliers.

Non-significant skewness was observed for traits like CH, NOL and INL indicating the curve has no skewness, i.e., the data has normal/symmetric distribution (Table 2). Significant positive skewness was recorded for SG, LSR, DMY and GFY which indicates the presence of lesser proportion of plants with an ability of high yielding, thicker stem diameter and increased LSR. Similar findings for SG, LSR, DFY and GFY has been reported by earlier researchers in forage sorghum (27). Significant negative skewness was recorded for PH, LL, LB and NON suggesting the presence of higher proportion of taller plants, more number of nodes with longer and wider leaves in the studied population. Non-significant skewness for all the former traits has been previously reported in forage oats, while negative skewness for PH and LL has also been observed (27, 28). With respect to the quality traits, significant positive skewness was observed for CP and significant negative

Table 2. Distribution characteristics (Skewness and Kurtosis) for different fodder traits in F_3 progenies of DM94 × African Tall

Characters	Skewness	Kurtosis
PH	-0.21**	-0.05
CH	-0.09	-0.28
LL	-0.41*	0.25
LB	-0.29*	0.47*
NOL	0.07	-0.50*
NON	-0.27*	-0.33**
INL	-0.07	-0.02
SG	0.40*	-0.07
LSR	0.64*	1.00*
CP	0.40*	0.13
CF	-0.27*	0.96*
ADF	-0.21**	4.48*
NDF	-0.45*	0.90*
DMY	0.36*	-0.01
GFY	0.48*	0.57*

skewness for CF, ADF and NDF. It reveals the presence of lesser number of plants with higher CP content and a greater number of plants with higher fiber content. Overall, it indicates that there is a lesser proportion of segregants with higher yield and CP content in the studied material, hence intensive selection should be done to enhance the GFY with improved quality. Positive skewness for CP, ADF and NDF has been previously reported in forage sorghum (29).

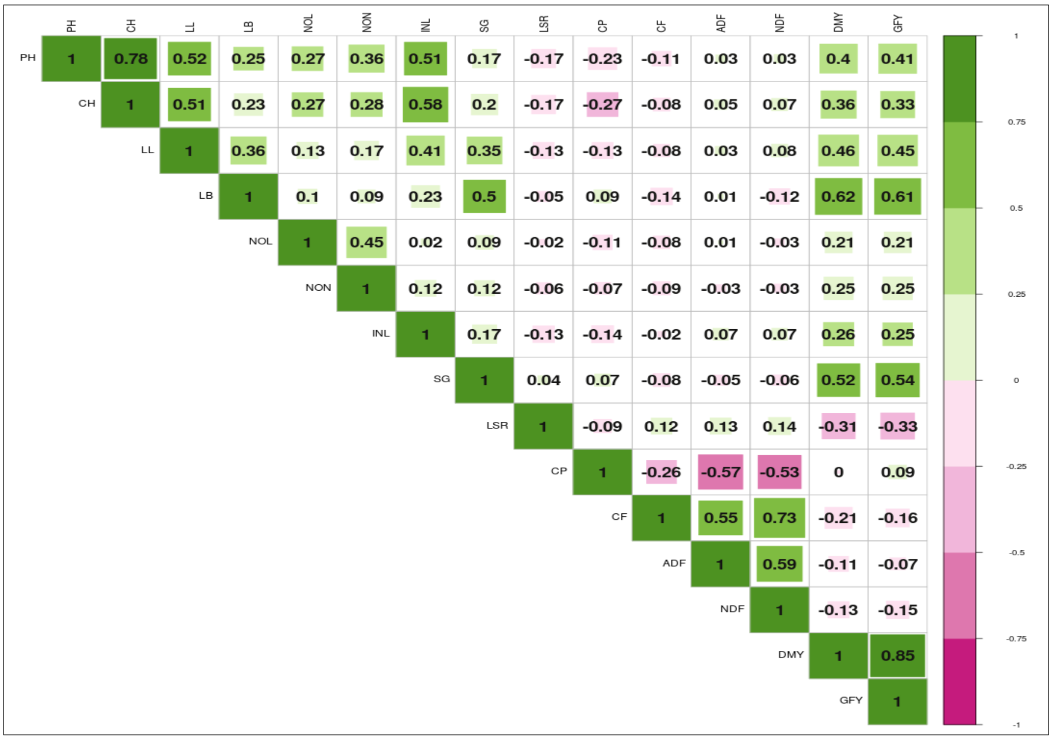
Non-significant kurtosis for the traits like PH, CH, LL, INL, SG and DMY indicated the mesokurtic distribution of the curve and the data for these traits has a normal distribution (Table 2). Similar results for PH, LL, SG, DMY and GFY has been previously reported in forage oats (28). Number of leaves and nodes showed platykurtic distribution of curve, indicating wider variation for these traits. Hence, there is more scope for the selection of these traits. In terms of quality traits CP showed mesokurtic distribution whereas, ADF showed leptokurtic distribution suggesting a narrow level of variability and limited scope for selection. CF and NDF showed platykurtic distribution, indicating wider variation for these traits. Earlier study in forage sorghum has reported leptokurtic distribution for NDF and platykurtic distribution for CP and ADF (29).

Correlation analysis

Correlation coefficients are statistical measures that estimate the strength of the linear relationship between two traits. These coefficients range from -1 to +1. Values closer to +1 indicate a strong positive relationship, while values closer to -1 indicate a strong negative relationship. A value of zero shows that there is no linear relationship between the traits being studied.

Enhanced GFY is the foremost breeding objective in any forage improvement programme. It is a complex character influenced by several component traits both in positive and negative directions and indirect selection of yield through these contributing traits such as PH, LL, LB, NOL, NON, INL and SG are desirable (12). A positive significant correlation was observed between DMY (0.847), LB (0.612), SG (0.541), LL (0.451), PH (0.413), CH (0.334), INL (0.252), NON (0.249) and NOL (0.207) with GFY (Fig. 2). This is in corroboration with earlier studies for all the former traits in forage maize (9, 10, 12); for DMY in Napier grass and fodder pearl millet (30, 31). PH correlated positively with CH (0.776), LL (0.519), INL (0.514), DMY/plant (0.404), NOL (0.275) and NON (0.358), LB (0.253) and SG (0.166) suggesting the selection of these traits is desirable for fodder yield improvement. On the contrary, LSR (-0.328), NDF (-0.147) and CF (-0.157) had a significant negative association with GFY, suggesting the increase in these variables will adversely decrease the GFY. However, CP and ADF fiber did not show any relationship with fodder yield. Earlier study also reported the same for CP and ADF in fodder maize (14).

Considering forage quality, the neutral detergent treatment leaves behind the residues of cellulose, hemicellulose



	PH	CH	LL	LB	NOL	NON	INL	SG	LSR	CP	CF	ADF	NDF	DMY	GFY
PH	1	0.78	0.52	0.25	0.27	0.36	0.51	0.17	-0.17	-0.23	-0.11	0.03	0.03	0.4	0.41
CH		1	0.51	0.23	0.27	0.28	0.58	0.2	-0.17	-0.27	-0.08	0.05	0.07	0.36	0.33
LL			1	0.36	0.13	0.17	0.41	0.35	-0.13	-0.13	-0.08	0.03	0.08	0.46	0.45
LB				1	0.1	0.09	0.23	0.5	-0.05	0.09	-0.14	0.01	-0.12	0.62	0.61
NOL					1	0.45	0.02	0.09	-0.02	-0.11	-0.08	0.01	-0.03	0.21	0.21
NON						1	0.12	0.12	-0.06	-0.07	-0.09	-0.03	-0.03	0.25	0.25
INL							1	0.17	-0.13	-0.14	-0.02	0.07	0.07	0.26	0.25
SG								1	0.04	0.07	-0.08	-0.05	-0.06	0.52	0.54
LSR									1	-0.09	0.12	0.13	0.14	-0.31	-0.33
CP										1	-0.26	-0.57	-0.53	0	0.09
CF											1	0.55	0.73	-0.21	-0.16
ADF												1	0.59	-0.11	-0.07
NDF													1	-0.13	-0.15
DMY														1	0.85
GFY															1

Fig. 2. Correlogram depicting the correlation coefficients among 15 fodder traits of forage maize. The green cells represent positive correlations and the pink cells represent negative ones, with color intensity reflecting the correlation strength. PH- Plant height (cm), CH- Cob placement height (cm), LL- Leaf length (cm), LB- Leaf breadth (cm), NOL- Number of leaves, NON- Number of nodes, INL- Internode length (cm), SG- Stem girth (cm), LSR- Leaf-stem ratio, CP- Crude protein (%), CF- Crude fiber (%), ADF- Acid detergent fiber (%), NDF- Neutral detergent fiber (%), DMY- Dry matter yield (g/plant), GFY- Green fodder yield (g/plant).

and lignin called NDF, whereas the acid detergent treatment leaves the residues containing cellulose and lignin called ADF. These cell wall components such as higher lignin and fiber concentrations reduce the cell wall digestibility and are negatively correlated with CP content (7, 32–34). In our study, the CP content is negatively associated with the cell wall components viz., CF (-0.255), ADF (-0.566) and NDF (-0.532) (Fig. 2) and these cell wall components had positive associations with each other. This relationship is further supported by the regression plot (Fig. 3), where the regression line illustrates the declining trend of CP with increasing CF, ADF and NDF. The findings were in accordance with earlier studies for NDF and for ADF (8, 12, 14, 35). Therefore, while practicing selection, plants possessing lower proportion of CF, ADF and NDF should be considered in order to increase the dry matter digestibility and better intake.

Regression analysis

Linear regression analysis revealed that DMY, with an R^2 of 0.72 (p < 0.01), explains the largest proportion of variance in GFY. This indicates that DMY is the most significant predictor of GFY. Following DMY, LB (R^2= 0.37: p < 0.01), SG (R^2 = 0.29: p < 0.01) and LL (R^2= 0.20: p < 0.01) also have notable impacts on GFY, though their contributions are less pronounced. These traits should be considered as secondary important variables in the optimization of GFY. Traits such as PH (R^2 = 0.17: p < 0.01) and CH (R^2 = 0.11: p < 0.01), also contribute positively, but to a lesser extent compared to the aforementioned traits.

In contrast to the above traits, the traits with negative significance, such as LSR (R^2= 0.11: p< 0.01), CF (R^2= 0.02: p < 0.01) and NDF (R^2=0.02: p < 0.01) showed minimal impact on GFY. Their low R^2 values indicate that they contribute minimally to the variability in GFY. The independent traits that showed R^2 of less than 20 % had a negligible contribution to yield.

Path coefficient analysis

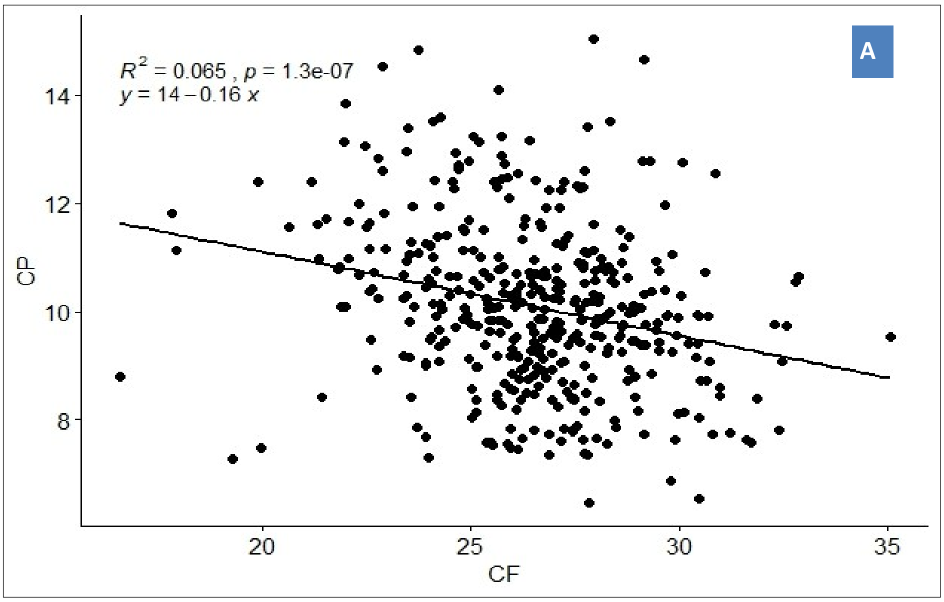
Due to the quantitative nature of GFY, selecting superior genotypes based only on correlation can be misleading, therefore, it is necessary to identify the other pathways through which the fodder yield is inherited. Therefore, path coefficient analysis serves as a valuable breeding tool by elucidating the relationships and breaking down correlations into direct and indirect effects (12). In our context, it is used to estimate the contribution of direct and indirect effects of the independent variables on the dependent variable (GFY). The direct and indirect effect of 14 independent traits over the GFY per plant is depicted in Table 3.

The residual effect was found to be 0.474 and the total variability contributed by both dependent and independent traits in the F_3 population was 52.6 %. Most metric traits such as PH, LL, LB, NON, NOL, INL, SG and DMY/plant had a positive correlation with fodder yield, but they had negligible direct effect on GFY except DMY, PH and SG. DMY (0.64) had the highest positive direct effect, whereas PH (0.15) and SG (0.14) had lowest positive direct effect on GFY. Previous studies for DMY and for PH reported high direct effect on GFY, whereas for SG reported low direct effect on GFY (8-10, 13, 36). Hence, these traits exhibit a true relationship with GFY and could be taken as component traits for fodder yield improvement. Incase of indirect effect, LB (0.40) had the highest positive indirect effect on GFY via DMY followed by SG (0.33) and LL (0.29). Similar results has been reported earlier for LL and for SG (8, 13). Hence, traits viz., PH, SG, LL, LB and DMY may be considered as selection indices for higher GFY.

Overall, the integrated analysis of phenotypic correlations, regression coefficients and path analysis provides a comprehensive understanding of the trait interrelationships influencing GFY. The use of a large sample size further strengthens the reliability and robustness of the findings. However, it is important to acknowledge certain limitations. The study was conducted under non-replicated conditions and was limited to a single location and season. These factors may restrict the extrapolation of results across varied agro-climatic conditions. Therefore, multi-location and replicated trials are recommended in future studies to validate these trait relationships under broader environmental contexts.

Conclusion

The study revealed that the most vital trait GFY and the most important nutritional trait CP content had higher estimates of



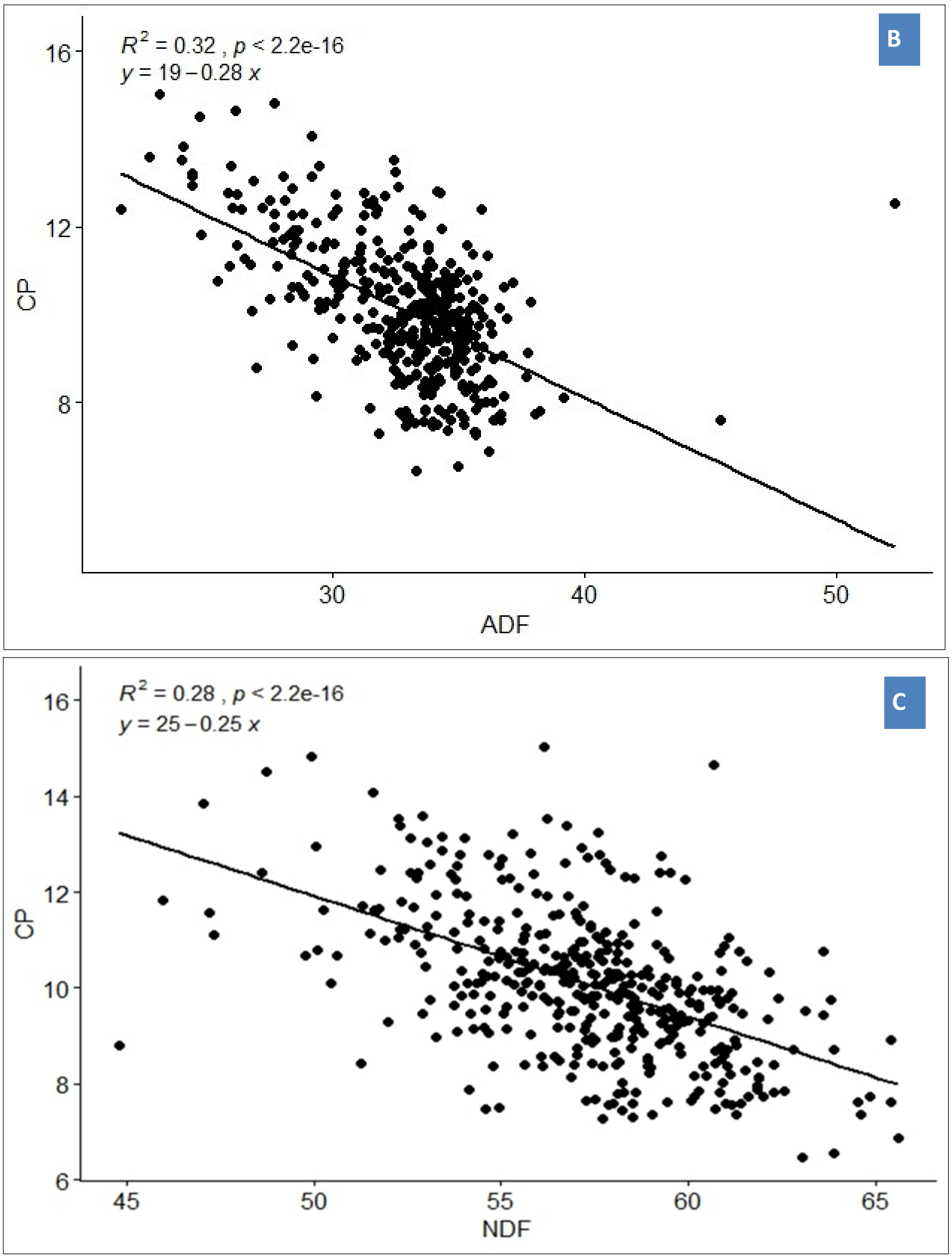


Fig. 3. Linear regression curve illustrating the relationship between CP- Crude protein (%) and fiber-related traits, namely CF- Crude fiber (%) (A), ADF- Acid detergent fiber (%) (B) and NDF- Neutral detergent fiber (%) (C).

Table 3. Direct (bold) and indirect effect of yield components on green fodder yield per plant in F_3 segregants

	PH	CH	LL	LB	NOL	NON	INL	SG	LSR	CP	CF	ADF	NDF	DMY	Genotypic Correlation with GFY
PH	0.15	-0.04	0.02	0.02	0.01	0.01	-0.01	0.02	0.02	-0.03	-0.01	0.00	0.00	0.26	0.4135***
CH	0.11	-0.06	0.02	0.02	0.01	0.01	-0.01	0.03	0.02	-0.03	-0.01	0.00	0.00	0.23	0.3337***
LL	0.08	-0.03	0.04	0.03	0.00	0.00	-0.01	0.05	0.01	-0.02	0.00	0.00	-0.01	0.29	0.4513***
LB	0.04	-0.01	0.01	0.09	0.00	0.00	0.00	0.07	0.01	0.01	-0.01	0.00	0.01	0.40	0.6116***
NOL	0.04	-0.02	0.01	0.01	0.03	0.01	0.00	0.01	0.00	-0.01	0.00	0.00	0.00	0.13	0.2075***
NON	0.05	-0.02	0.01	0.01	0.01	0.02	0.00	0.02	0.01	-0.01	-0.01	0.00	0.00	0.16	0.2490***
INL	0.07	-0.03	0.02	0.02	0.00	0.00	-0.02	0.02	0.01	-0.02	0.00	0.01	0.00	0.17	0.2516***
SG	0.02	-0.01	0.01	0.04	0.00	0.00	0.00	0.14	0.00	0.01	-0.01	-0.01	0.00	0.33	0.5412***
LSR	-0.02	0.01	-0.01	0.00	0.00	0.00	0.00	0.01	-0.11	-0.01	0.01	0.01	-0.01	-0.20	-0.3281***
CP	-0.03	0.02	0.00	0.01	0.00	0.00	0.00	0.01	0.01	0.13	-0.02	-0.05	0.03	0.00	0.0907
CF	-0.02	0.00	0.00	-0.01	0.00	0.00	0.00	-0.01	-0.01	-0.03	0.06	0.05	-0.05	-0.14	-0.1575**
ADF	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.01	-0.01	-0.07	0.03	0.09	-0.04	-0.07	-0.0714
NDF	0.01	0.00	0.00	-0.01	0.00	0.00	0.00	-0.01	-0.02	-0.07	0.04	0.06	-0.06	-0.08	-0.1465**
DMY	0.06	-0.02	0.02	0.05	0.01	0.01	-0.01	0.07	0.03	0.00	-0.01	-0.01	0.01	0.64	0.8466***

, * significant at 1 % and 0.1% levels, respectively.

PH- Plant height (cm), CH- Cob placement height (cm), LL- Leaf length (cm), LB- Leaf breadth (cm), NOL- Number of leaves, NON- Number of nodes, INL- Internode length (cm), SG- Stem girth (cm), LSR- Leaf-stem ratio, CP- Crude protein (%), CF- Crude fiber (%), ADF- Acid detergent fiber (%), NDF- Neutral detergent fiber (%), DMY- Dry matter yield (g/plant), GFY- Green fodder yield (g/plant).

RESIDUAL= 0.47

variability along with substantial genetic advance as a percent of mean with moderate heritability. Therefore, selection will accumulate the favorable additive alleles and genetic improvement would be effective for the above traits. DMY/plant, PH and SG had a positive correlation and direct effect on fodder yield, therefore it could be used as selection indices for increasing the GFY per plant. The traits such as LSR and NDF may adversely affect the enhancement of fodder yield due to its significant negative correlation and negative indirect effect on GFY. Therefore, the selection of taller plants with thicker stem diameters and a greater number of wider and longer leaves possessing a higher proportion of CP would improve the biomass yield as well as fodder quality in the studied population. Evaluating the selected genotypes across multiple environments will also be essential to confirm trait stability and adaptability, ensuring the development of resilient, high-performing fodder crops suited for sustainable animal husbandry systems. Studies focusing on the digestibility and nutritional impact of selected genotypes on livestock performance would also support the practical relevance of the breeding program.

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Authors' contributions

PKD collected the literature, conducted research, performed statistical data analysis and prepared the manuscript. KNG provided research guidance, edited, revised and organized the overall manuscript. MN offered guidance on quantitative and biometrical techniques. SVK provided research guidance in the protocols for quality traits measurement. NS provided guidance for enhancing the manuscript scientifically. PM assisted in recording biometric observations and offered laboratory support. All authors read and approved the final manuscript.

Compliance with ethical standards

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