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## Appraisal of genetic parameters and character association for fodder yield and its related characteristics in fodder cowpea [*Vigna unguiculata* (L.) Walp.]

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### Abstract

Fodder cowpea (*Vigna unguiculata*) is a crucial leguminous fodder known for its high biomass yield, protein content, and rapid growth. A study on 40 genotypes at Anand Agricultural University revealed low environmental influence on traits. Plant height, dry matter yield, green forage yield, and number of leaves showed high genetic variability. Traits like plant height, green forage yield, dry matter yield, number of leaves per plant, leaf: stem ratio, leaf area index, and chlorophyll content exhibited high heritability and genetic advance, indicating additive gene action. Correlations and path coefficient analysis highlighted key traits i.e., plant height, leaf length, leaf: stem ratio, dry matter yield, leaf area index, and chlorophyll content, as major contributors to green forage yield, emphasizing their importance in selection for improvement.

**Keywords:** Fodder cowpea, variability, phenotypic and genotypic coefficient of variation, heritability, genetic advance, correlation coefficient, path analysis

### 1. Introduction

Cowpea [*Vigna unguiculata* (L.) Walp.] is an annual, self-pollinated legume belonging to the family Leguminosae with a diploid chromosome number of  $2n=2x=22$ . It is also called as southern pea and black-eyed pea, is well adapted to the tropics. Genome size of cowpea is 620 Mbp. Vavilov (1951) [30] recognized India and Africa as the centers of origin, while China is considered as secondary center of origin of cowpea. Cowpea is cultivated for both grain and fodder in all tropical and sub-tropical regions among fodder legumes (Nguyen *et al.*, 2017) [16]. It is a fast-growing, drought-resistant crop, which improves soil fertility by fixing atmospheric nitrogen (Ortiz, 1998) [17]. In crops like cowpea can also become a valuable component in cereal-based farming system as it restores soil fertility for succeeding crop. It fixes about 240 kg/ha atmospheric nitrogen and leaves about 60 to 70 kg/ha nitrogen for succeeding crop (Kumar, 2020) [12].

Cowpea has been referred to as "Poor man's meat" because of its high protein content (20-25%) [Sabale *et al.*, 2018] [22]. The average protein content of fodder cowpea stovers is 10-20% with 60% dry-matter digestibility and it differs greatly between leaves (60-75%) and stems (50-60%) [Savadojo *et al.*, 2000] [25]. This compares with 4.0 to 7.5% protein in cereal stovers with less than 50% digestibility (Powell, 1985) [19].

Area under cowpea is about 12.5 million hectares with an annual production of over 3 million tonnes worldwide. Cowpea is widely distributed throughout the tropics, but Central and West Africa amounts to 64% of the area with about 8 million hectares (Ngalamu *et al.*, 2015) [15]. India is accounting for one-third of the world's area under pulses and one-fourth of the world's production. Cowpea is grown in an area of 3.9 million hectares with a production of 2.21 million tonnes in India (Giridhar *et al.*, 2020) [8]. In Gujarat, a total pulse cultivated area is 5.16 lakh hectares and total production is 4.5 lakh tonnes with productivity is 873.08 kg per hectare.

In Gujarat, total cowpea cultivated area is 520 hectares and total production is 280 tonnes with a productivity is 550 kg per hectare (Anon., 2022)<sup>[3]</sup>.

Genetic variability is crucial for selecting heritable traits in breeding high-yielding varieties. In cowpea, with its easily manageable nature, wider adaptability, and abundant variability, studying genetic associations and path analysis is essential for simultaneous crop improvement by understanding the interrelationship among characters.

## 2. Materials and Methods

The present investigation was carried out at the experimental plots of Main Forage Research Station, Anand Agricultural University, Anand to generate information on genetic variability, heritability, character association and path coefficient analysis for green forage yield and its components traits in fodder cowpea [*Vigna unguiculata* (L.) Walp.]. The performance of 40 fodder cowpea genotypes were evaluated in a Randomized Complete Block Design with three replications during *Kharif* -2022.

Observations were recorded for 16 characters *viz.*, days to 50% flowering, number of branches per plant, number of leaves per plant, leaf length, internode length, plant height, green forage yield per plant, dry matter yield per plant, leaf: stem ratio, leaf area index, dry matter content, crude protein content, crude fiber content, acid detergent fiber, neutral detergent fiber and total chlorophyll content.

Mean values were then utilized for the purpose of statistical analysis, with each genotype being represented by observations from five competitive plants in each replication. Days to 50% flowering was recorded on plot basis.

The observed parameters were analyzed by R-Statistical Software (RStudio) v 2023.03. Further, for calculating the means of various parameters subsequently, an Analysis of Variance (ANOVA), following method was carried out by Johnson *et al.* (1955)<sup>[10]</sup>. The calculation of PCV and GCV was performed using the method introduced by Burton in 1952.

The estimation of heritability followed the approach outlined by Allard in 1960, while genetic advance was calculated utilizing the formula developed by Johnson *et al.* (1955)<sup>[10]</sup>. The analysis of correlation and path coefficient was conducted in accordance with the methodologies described by Dewey and Lu in 1959<sup>[6]</sup> and Falconer in 1960<sup>[7]</sup>.

## 3. Analysis of Variance

The examination of variance (ANOVA) indicated significant variations among the genotypes for all studied traits, affirming ample variability among them. The detailed ANOVA results for the 16 characters are outlined in Table 1.

These findings align closely with studies by Thorat and Gadewar (2013)<sup>[27]</sup>, Phogat *et al.* (2017)<sup>[18]</sup>, Sahu (2019)<sup>[23]</sup>, Vamshi *et al.* (2022)<sup>[28]</sup>, and Varanya *et al.* (2022)<sup>[29]</sup>.

### 3.1 Mean and Range

Mean, a straightforward measure in plant breeding, is employed to evaluate phenotypic variability and serves as a basis for identifying desirable genotypes. Table 1 provides the mean values of 40 fodder cowpea genotypes for all 16 characters, including standard error of mean (S.E.m.  $\pm$ ), critical difference (CD), and coefficient of variation (CV %).

The overall findings indicate significant variations among the studied genotypes for all characters. Regarding green forage yield, GFC 1 (358.40 g), GFC 3 (356.27 g), and Vijaya (308.13 g) exhibited high individual performance and are

considered promising for green forage yield (see Plate 4.1). GFC 3 (68.58 g), followed by EC 4216 (63.45 g) and VKP 4506, along with Vijaya (62.20 g), demonstrated higher dry matter yield per plant, making them promising for this trait. TNFC 1910 (53.33 days), EC 4216, and CL 367 (56.67 days) were identified as the earliest genotypes to reach 50% flowering.

From a quality perspective, Vijaya (14.38%) ranked first for crude protein content, followed by CO 9 (14.05%) and Kohinoor (13.86%). In contrast, VKP 4505 (11.17%) had the lowest crude protein content. Genotypes VKP 605 (40.47%), EC 4216 (44.20%), and VKP 4506 (60.63%) exhibited the lowest amounts of crude fiber, acid detergent fiber, and neutral detergent fiber, respectively. The highest chlorophyll content was recorded for CO 9 (25.80 mg/100 g), followed by EC 4216 (20.23 mg/100 g) and GFC 3 (19.63 mg/100 g).

### 3.2 Genetic variability, heritability, and genetic advance

Variability parameters, including genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense ( $h^2_b$ ), and genetic advance as a percentage of mean (GA % of mean), were calculated based on variance components and mean values. All these parameters are presented in Table 2.

For several traits such as number of leaves per plant, plant height, green forage yield per plant, and dry matter yield per plant, both GCV and PCV estimates were high. The elevated GCV values, coupled with slightly higher PCV values, indicate substantial variation among the genotypes. Therefore, straightforward selection methods would be effective for further enhancing this crop. Similar findings were reported by Gerrano *et al.* (2015)<sup>[9]</sup> and Ravi (2015)<sup>[21]</sup> for number of leaves per plant and plant height, as well as by Phogat *et al.* (2017)<sup>[18]</sup> and Vamshi *et al.* (2022)<sup>[28]</sup> for green forage yield per plant and dry matter yield per plant.

High heritability, along with a high genetic advance as a percentage of the mean, was noted for traits such as number of leaves per plant, plant height, green forage yield per plant, dry matter yield per plant, leaf: stem ratio, leaf area index, and total chlorophyll content. This suggests favourable potential for improvement through selection, as these traits are primarily influenced by additive genetic action. Therefore, a straightforward selection approach would be beneficial for enhancing these characteristics. These results are similar to the findings of Gerrano *et al.* (2015)<sup>[9]</sup>, Ravi (2015)<sup>[21]</sup> and Vamshi *et al.* (2022)<sup>[28]</sup> for number of leaves per plant, plant height, green forage yield per plant, dry matter yield per plant and leaf area index. Radhika (2002)<sup>[20]</sup>, Malarvizhi *et al.* (2005)<sup>[13]</sup> and Sanjeev *et al.* (2016)<sup>[24]</sup> for leaf: Stem ratio. Thorat and Gadewar (2013)<sup>[27]</sup> for total chlorophyll content.

### 3.3 Correlation coefficients analysis

The results of genotypic and phenotypic correlation for green forage yield and its 15 contributing traits among 40 genotypes of fodder cowpea are presented in Table 3.

In the present study of character association, it was observed that genotypic correlation coefficients were relatively higher than phenotypic correlation coefficients for majority trait, which indicated that there was a strong inherent association between characters studied and its phenotypic expression.

The traits *viz.*, number of branches per plant ( $r_g = 1.012$ ,  $r_p = 0.793$ ), number of leaves per plant ( $r_g = 0.583$ ,  $r_p = 0.514$ ), leaf length ( $r_g = 0.367$ ,  $r_p = 0.217$ ) internode length ( $r_g = 1.004$ ,  $r_p = 0.705$ ), plant height ( $r_g = 0.945$ ,  $r_p = 0.868$ ), dry matter yield per plant ( $r_g = 0.586$ ,  $r_p = 0.563$ ), leaf: stem ratio ( $r_g = 0.669$ ,  $r_p =$

0.511), leaf area index ( $r_g = 0.446$ ,  $r_p = 0.314$ ) and total chlorophyll content ( $r_g = 0.817$ ,  $r_p = 0.718$ ) recorded positive and significant correlation with green forage yield per plant at both phenotypic and genotypic levels, while dry matter content ( $r_g = 0.325$ ) showed significant and positive correlation with green forage yield at genotypic level only. The results indicating that these characters play an important role in selection for the improvement of green forage yield per plant.

The findings obtained were in confirmatory with the results reported by Radhika (2002) [20] and Navalselvakkumaran *et al.* (2019) [14] for leaf area index and crude protein content, Sheela and Gopalan (2006) [26] and Vamshi *et al.* (2022) [28] for number of branches per plant, number of leaves per plant, leaf length and dry matter yield per plant, Ravi (2015) [21] for internode length and dry matter content and Phogat *et al.* (2017) [18] for number of branches per plant, plant height, dry matter yield per plant and leaf: stem ratio.

### 3.4 Path coefficients analysis

The results obtained for direct and indirect effects of different characters on green forage yield are presented in Table 5 and graphical representation given in fig. 1.

The highest positive direct effect on green forage yield was registered by plant height (1.018) followed by leaf length (0.519), crude protein content (0.385), crude fiber content (0.297), total chlorophyll content (0.246), leaf: stem ratio (0.220), dry matter yield per plant (0.189), leaf area index (0.169) and acid detergent fiber (0.077).

The results are in accordance with those obtained by Navalselvakkumaran *et al.* (2019) [14] for days to 50%

flowering, plant height, dry matter yield per plant and leaf area index, Sheela and Gopalan (2006) [26] and Ravi (2015) [21] for leaf length, Bhandari and Verma (2007), Anamika and Tajane (2014) [2] and Phogat *et al.* (2017) [18] for leaf: stem ratio, Kaur *et al.* (2018) [11] for crude protein content, crude fiber content and acid detergent fiber (0.077).

### 4. Conclusion

From the present investigation, it can be concluded that due weightage should be given to plant height, number of branches per plant, number of leaves per plant, internode length, dry matter yield per plant, leaf: stem ratio and total chlorophyll content, while imposing selection for genetic improvement of green forage yield per plant in fodder cowpea.

### 5. Future Scope

This study presented information concerning variation within genotypic and phenotypic aspects, heritability, and the genetic advancement percentage relative to the mean. Going forward, the selection of genotypes based on these attributes is expected to be a productive approach for cultivating superior fodder cowpea strains with enhanced green forage yield. Emphasis will be placed on selecting for the specific traits highlighted in this study.

### 6. Acknowledgment

The authors thank their research supervisor for giving correct advice and the host institute (Anand Agricultural University, Gujarat, India) for providing the essential resources for the experiment.

**Table 1:** Analysis of variance (mean sum of squares) and mean performance of different characters in fodder cowpea genotypes

Sr. No.	Traits	Replications	Genotypes	Error	Mean	Range	S.Em.	CD at 5%	CV%
1.	Days to 50% flowering	3.23	77.11**	1.11	64.79	53.33-73.33	0.61	1.71	1.62
2.	Number of branches per plant	0.51	1.77**	0.24	7.31	5.73-8.93	0.29	0.81	7.83
3.	Number of leaves per plant	296.30	3295.00**	120.70	149.23	94.27-231.73	6.34	17.36	7.36
4.	Leaf length	0.94	1.41**	0.30	6.88	5.53-8.27	0.32	0.90	8.07
5.	Internode length	2.24	4.96**	1.02	14.87	10.69-17.37	0.59	1.65	6.82
6.	Plant height	85.89	2463.12**	56.75	104.36	65.00-167.33	4.35	12.25	8.01
7.	Green forage yield per plant	32.30	8890.20**	360.70	230.25	118.07-358.40	10.97	30.87	8.25
8.	Dry matter yield per plant	0.68	353.30**	15.07	44.40	26.97-68.58	2.24	6.31	8.70
9.	Leaf: stem ratio	0.028	0.073**	0.012	0.76	0.48-1.04	0.06	0.18	14.70
10.	Leaf area index	0.035	1.132**	0.178	4.62	3.42-6.44	0.24	0.69	9.15
11.	Dry matter content	4.660	9.867**	2.933	19.10	14.20-22.37	0.99	2.78	8.97
12.	Crude protein content	0.077	1.378*	0.256	12.96	11.17-14.38	0.29	0.77	3.64
13.	Crude fiber content	6.574	24.473**	4.308	47.50	40.47-53.08	1.20	3.37	4.37
14.	Acid detergent fiber	10.810	37.580**	4.003	51.15	44.20-57.53	1.16	3.25	3.91
15.	Neutral detergent fiber	0.860	32.834**	2.190	68.56	60.63-74.20	0.85	2.41	2.16
16.	Total chlorophyll content	0.800	25.946**	1.649	16.14	11.29-25.80	0.74	2.09	6.09

\*, \*\* Significant at 5% and 1% level of significance, respectively

**Table 2:** Genetic variability parameters for green forage yield and its contributing traits in fodder cowpea

Sr. No.	Characters	Variance		GCV (%)	PCV (%)	h <sup>2</sup> <sub>b</sub> (%)	GA (%) of Mean
		$\sigma^2_g$	$\sigma^2_p$				
1	Days to 50% flowering	25.33	26.44	7.77	7.94	95.82	15.66
2	Number of branches per plant	0.51	0.76	9.76	11.91	67.11	16.47
3	Number of leaves per plant	1058.11	1178.76	21.79	23.01	89.76	42.54
4	Leaf length	0.37	0.68	8.81	11.95	54.37	13.39
5	Internode length	1.31	2.34	7.70	10.29	56.08	11.88
6	Plant height	802.12	858.87	27.14	28.08	93.39	54.03
7	Green forage yield per plant	2843.18	3203.89	23.16	24.58	88.74	44.94
8	Dry matter yield per plant	112.75	127.81	23.81	25.35	90.00	46.06
9	Leaf: stem ratio	0.02	0.03	18.85	23.90	62.20	30.62
10	Leaf area index	0.32	0.50	12.22	15.26	64.09	20.15
11	Dry matter content	2.31	5.25	7.96	11.99	44.06	10.89

12	Crude protein content	0.41	0.63	4.93	6.13	64.69	8.17
13	Crude fiber content	4.31	6.72	5.46	6.99	60.94	8.78
14	Acid detergent fiber	11.19	15.20	6.54	7.62	73.66	11.56
15	Neutral detergent fiber	10.21	12.40	4.66	5.14	82.34	8.71
16	Total chlorophyll content	8.10	9.75	17.63	19.34	83.00	33.10

**Table 3:** Genotypic path coefficient analysis showing direct and indirect effects of different characters on green forage yield

Character	DFE	NBP	NLP	LL	IL	PH	DMY	LSR	LAI	DM%	CPC	CFC	ADF	NDF	TCC	GFY	
DFE	r <sub>g</sub>	1.000	-0.256	-0.207	-0.080	-0.295	-0.266	-0.239	-0.049	-0.021	-0.104	0.065	0.110	0.127	0.237	-0.429**	-0.194
	r <sub>p</sub>	1.000	-0.219*	-0.194*	-0.052	-0.195*	-0.250*	-0.222*	-0.061	0.008	-0.066	0.059	0.063	0.126	0.215*	-0.379**	-0.187*
NBP	r <sub>g</sub>		1.000	0.553 **	0.260	1.052 **	0.942 **	0.632 **	0.641 **	0.429 **	0.148	0.224	-0.001	-0.158	-0.095	0.861 **	1.012 **
	r <sub>p</sub>		1.000	0.423**	0.120	0.657**	0.764**	0.483**	0.372**	0.339**	0.071	0.114	0.074	-0.111	-0.088	0.578**	0.793**
NLP	r <sub>g</sub>			1.000	0.224	0.606 **	0.559 **	0.426 **	0.618 **	0.488 **	0.231	0.008	-0.004	-0.073	0.086	0.535 **	0.583 **
	r <sub>p</sub>			1.000	0.168	0.439**	0.486**	0.381**	0.452**	0.380**	0.131	0.004	-0.013	-0.017	0.075	0.461**	0.514**
LL	r <sub>g</sub>				1.000	0.399 *	0.208	0.150	0.271	-0.030	0.114	-0.230	-0.279	-0.119	0.131	0.120	0.367 *
	r <sub>p</sub>				1.000	0.222*	0.143	0.095	0.202*	-0.118	0.016	-0.201*	-0.200*	-0.083	0.005	0.079	0.217*
IL	r <sub>g</sub>					1.000	0.891 **	0.697 **	0.703 **	0.407 **	0.157	0.139	0.028	-0.347*	-0.143	0.765 **	1.004 **
	r <sub>p</sub>					1.000	0.662**	0.503**	0.407**	0.191*	0.055	0.042	-0.052	-0.150	-0.086	0.530**	0.705**
PH	r <sub>g</sub>						1.000	0.543 **	0.599 **	0.464 **	0.251	-0.125	0.144	-0.173	-0.024	0.779 **	0.945 **
	r <sub>p</sub>						1.000	0.500**	0.444**	0.354**	0.164	-0.076	0.115	-0.126	-0.010	0.697**	0.868**
DMY	r <sub>g</sub>							1.000	0.557 **	0.505 **	0.607 **	0.246	-0.112	-0.224	-0.082	0.363 *	0.586 **
	r <sub>p</sub>							1.000	0.432**	0.369**	0.367**	0.177	-0.086	-0.120*	-0.058	0.317**	0.563**
LSR	r <sub>g</sub>								1.000	0.535 **	0.364 *	0.081	-0.321*	-0.329*	0.053	0.632 **	0.669 **
	r <sub>p</sub>								1.000	0.302**	0.196*	0.029	-0.173	-0.221*	0.017	0.407**	0.511**
LAI	r <sub>g</sub>									1.000	0.525 **	-0.046	-0.089	0.074	0.119	0.353 *	0.446 **
	r <sub>p</sub>									1.000	0.256**	-0.028	-0.102	0.051	0.103	0.244**	0.314**
DM%	r <sub>g</sub>										1.000	-0.188	0.224	-0.203	-0.344*	0.026	0.325 *
	r <sub>p</sub>										1.000	-0.028	0.044	-0.130	-0.207*	0.006	0.144
CPC	r <sub>g</sub>											1.000	-0.295	-0.338*	-0.148	-0.064	0.044
	r <sub>p</sub>											1.000	-0.127	-0.229	-0.125	-0.061	0.039
CFC	r <sub>g</sub>												1.000	0.092	-0.054	0.145	0.081
	r <sub>p</sub>												1.000	0.089	-0.105	0.109	0.070
ADF	r <sub>g</sub>													1.000	-0.006	-0.143	-0.170
	r <sub>p</sub>													1.000	0.058	-0.082	-0.122
NDF	r <sub>g</sub>														1.000	-0.021	-0.102
	r <sub>p</sub>														1.000	0.012	-0.077
TCC	r <sub>g</sub>															1.000	0.817 **
	r <sub>p</sub>															1.000	0.718**
GFY	r <sub>g</sub>																1.000
	r <sub>p</sub>																1.000

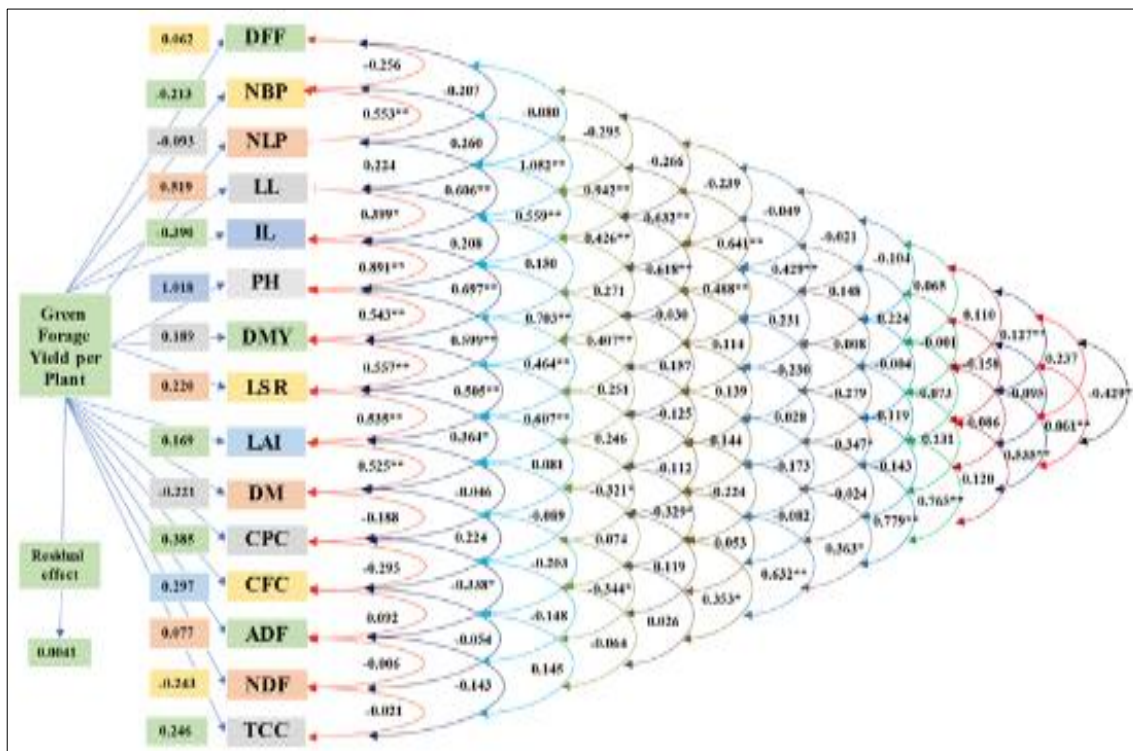
\* \*\* Significant at 5% and 1% level of significance, respectively

**DFE:** Days to 50% flowering, **NBP:** Number of branches per plant, **NLP:** Number of leaves per plant, **LL:** Leaf length, **IL:** Internode length, **PH:** Plant height, **DMY:** Dry matter yield per plant, **LSR:** Leaf: stem ratio, **LAI:** Leaf area index, **DM %:** Dry matter content, **CPC:** Crude protein content, **CFC:** Crude fiber content, **ADF:** Acid detergent fiber, **NDF:** Neutral detergent fiber, **TCC:** Total chlorophyll content and **GFY:** Green forage yield per plant.

**Table 4:** Genotypic path coefficient analysis showing direct and indirect effects of different characters on green forage yield

Cha.	DFE	NBP	NLP	LL	IL	PH	DMY	LSR	LAI	DM%	CPC	CFC	ADF	NDF	TCC	r <sub>g</sub> with 'GFY'
DFE	0.062	0.054	0.019	-0.041	0.115	-0.271	-0.045	-0.011	-0.003	0.023	0.025	0.033	0.010	-0.058	-0.106	-0.194
NBP	-0.016	-0.213	-0.051	0.135	-0.410	0.958	0.119	0.141	0.073	-0.033	0.086	0.000	-0.012	0.023	0.212	1.012 **
NLP	-0.013	-0.118	-0.093	0.116	-0.236	0.570	0.081	0.136	0.082	-0.051	0.003	0.000	-0.006	-0.021	0.132	0.583 **
LL	-0.005	-0.055	-0.021	0.519	-0.155	0.211	0.028	0.060	-0.005	-0.025	-0.089	-0.083	-0.009	-0.032	0.029	0.367 *
IL	-0.018	-0.224	-0.056	0.207	-0.390	0.907	0.132	0.155	0.069	-0.035	0.054	0.008	-0.027	0.035	0.188	1.004 **
PH	-0.017	-0.200	-0.052	0.108	-0.348	1.018	0.103	0.132	0.078	-0.055	-0.048	0.043	-0.013	0.006	0.192	0.945 **
DMY	-0.015	-0.134	-0.040	0.078	-0.272	0.553	0.189	0.123	0.085	-0.134	0.095	-0.033	-0.017	0.020	0.089	0.586 **
LSR	-0.003	-0.136	-0.058	0.140	-0.274	0.611	0.105	0.220	0.090	-0.080	0.031	-0.095	-0.025	-0.013	0.156	0.669 **
LAI	-0.001	-0.091	-0.045	-0.016	-0.159	0.473	0.095	0.118	0.169	-0.116	-0.018	-0.027	0.006	-0.029	0.087	0.446 **
DM%	-0.006	-0.032	-0.022	0.059	-0.061	0.256	0.115	0.080	0.089	-0.221	-0.072	0.066	-0.016	0.084	0.006	0.325 *
CPC	0.004	-0.048	-0.001	-0.119	-0.054	-0.128	0.046	0.018	-0.008	0.041	0.385	-0.087	-0.026	0.036	-0.016	0.044
CFC	0.007	0.000	0.000	-0.145	-0.011	0.147	-0.021	-0.071	-0.015	-0.049	-0.114	0.297	0.007	0.013	0.036	0.081
ADF	0.008	0.034	0.007	-0.062	0.136	-0.176	-0.042	-0.071	0.013	0.045	-0.130	0.027	0.077	0.002	-0.035	-0.170
NDF	0.015	0.020	-0.008	0.068	0.056	-0.025	-0.016	0.012	0.020	0.076	-0.057	-0.016	-0.001	-0.243	-0.005	-0.102
TCC	-0.027	-0.183	-0.050	0.062	-0.298	0.793	0.069	0.139	0.060	-0.006	-0.025	0.043	-0.011	0.005	0.246	0.817 **

**DFE:** Days to 50% flowering, **NBP:** Number of branches per plant, **NLP:** Number of leaves per plant, **LL:** Leaf length, **IL:** Internode length, **PH:** Plant height, **DMY:** Dry matter yield per plant, **LSR:** Leaf: stem ratio, **LAI:** Leaf area index, **DM %:** Dry matter content, **CPC:** Crude protein content, **CFC:** Crude fiber content, **ADF:** Acid detergent fiber, **NDF:** Neutral detergent fiber, **TCC:** Total chlorophyll content and **GFY:** Green forage yield per plant.



**Fig 1:** Path diagram showing direct and indirect of different characters on green forage yield

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