J. Farm Sci., 37(2): (125-128) 2024

RESEARCH PAPER

Assessment of genetic variability for fodder yield and yield attributing traits in advanced breeding lines of fodder cowpea

*GOURAMMA SIDDAPUR, K. SRIDHAR, SUMANGALA BHAT AND N. S. KULKARNI

Department of Genetics and Plant Breeding, College of Agriculture, Dharwad
University of Agricultural Sciences, Dharwad - 580 005, India
[2]Department of Agricultural Entomology, ICAR-IGFRI Southern Regional Research Station, Dharwad - 580 005
*E-mail: gourisiddapur17@gmail.com

(Received: November, 2022 ; Accepted: April, 2024)

DOI: 10.61475/JFS.2024.v37i2.04

Abstract: An experiment was conducted to assess genetic variability in 57 advanced breeding lines (ABL's) of two crosses *viz*., MFC-09-12 x BL-2 and UPC-622 × EC-4216 in fodder cowpea. The ABL's along with their parents and two national check BL-1 and BL-2, one zonal check MFC-09-01 and IGFRI-DC-215 (state variety released for Karnataka) were evaluated in RCBD with two replications during *kharif* 2022 and *rabi* 2022-23. Environmental influence was minimum for the expression of all the traits which is evident from narrow difference between phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) estimates. In both the crosses, high heritability values were found for the all the traits in both the seasons. High heritability coupled with high genetic advance as per cent of mean has been observed for the traits *viz*., days to maturity, plant height, primary branches, L/S ratio, green fodder yield and dry matter yield in both the seasons for the two crosses indicating the preponderance of additive gene action for the above characters. Thus, the information on the genetic variability, heritability and genetic advance per cent mean for different yield related traits provides a basis for trait improvement for developing fodder cowpea genotypes with higher fodder yield potential.

Key words: Fodder Cowpea, Genetic advance as per cent mean, Genotypic coefficient of variation (GCV), Heritability, Phenotypic coefficient of variation (PCV)

Introduction

Cowpea [*Vigna unguiculata* (L.) Walp.] is a versatile leguminous plant belonging to the family Fabaceae. It is a diploid species with a somatic chromosome number of 2n=2x=22. Globally, cowpea is cultivated across an area of 23.40 million-hectare with total production of 18.29 million tonnes and an average productivity of 637 kg per hectare (Anon, 2021). In India, cowpea is grown over 4 million hectares, producing 2.70 million tonnes with an average productivity of 567 kg per hectare. Among the Indian states, Karnataka accounts for 12 per cent of the total pulse cultivation area in the country and ranks fourth in cowpea production. The average protein content of fodder cowpea is 21-35 per cent with 60-65 per cent dry-matter digestibility (Tarawali *et al*., 1997). Cowpea provides income for small farmers, improves soil fertility through nitrogen fixation and acts as a source of nutritious fodder for livestock (Sheidu *et al*., 2023).

Currently, the fodder cowpea varieties cultivated exhibit comparatively lower biomass yield coupled with lower L/S ratio, poor quality due to pubescence and challenging harvesting characteristics. Expanding the area under fodder cultivation faces limitations due to high population density and fragmented land holdings of small and marginal farmers. Given these challenges, the most viable approach to bridge the gap between fodder production and the year-round demand for green fodder is to prioritize the option for exploring on cultivation of high yielding fodder cowpea varieties. The development of such varieties largely depends on the magnitude of genetic variability present in the advanced breeding material. Keeping the above points in view, the present investigation was undertaken to assess the performance of advanced breeding lines for fodder yield and yield-related traits.

Material and methods

Fifty-seven ABL's (pooled F_6 & F_7 generations) of two crosses *viz*., MFC-09-12×BL-2 (30 ABL's) and UPC-622× EC-4216 (27 ABL's) were evaluated independently in Randomized Complete Block Design (RCBD) with two replications at ICAR-IGFRI, Dharwad during *kharif* 2022. Along with these lines, parents and two national checks, BL-1 and BL-2, as well as a zonal check MFC 09-01 and IGFRI-DC-215 (state variety released for Karnataka) were also included in the study. In both the replications, each line was sown in 3m row length with a spacing of 30 x 10 cm. All the recommended agronomic practices including appropriate plant protection measures were followed to raise the healthy crop. Observations such as days to first flowering, days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, L/S ratio, days to maturity, green fodder yield (g/plant), dry matter content (%) and dry matter yield (g/plant) were recorded onfive randomly selected plants for each breeding line in both the replications. The ABL's (pooled F_6 & F_7 generation) were further forwarded to next generation during *rabi* 2022-23. The same experimental set-up was followed during *rabi* 2022-23. The data collected from both the seasons were subjected to statistical analysis using the R Studio (R 4.2.2 version). Both genotypic and phenotypic variability were computed as per the method suggested by Burton and Devane (1953). Heritability in a broad sense was computed as suggested by Hanson *et al.* (1956) and genetic advance as per Johnson *et al.* (1955).

Results and discussion

The ANOVA showed significant differences among the genotypes for all the characters such as days to first flowering, days to 50% flowering, plant height (cm), number of primary branches per plant, number of secondary branches per plant, L/S ratio, days to maturity, green fodder yield (g/plant), dry matter content (%) and dry matter yield (g/plant) in both the crosses as well as in both the seasons (Table 1 and Table 2). It indicated the presence of substantial variability in the selected material for the above traits. Similar findings were reported by Malarvizhi *et al* (2005), Pandiyan *et al.* (2020) and Panchta *et al.* (2020) in cowpea.

The mean, range,genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance and genetic advance as per cent of the mean of cross MFC-09-12×BL-2 and UPC-622×EC-4216 are represented in Table 3 and Table 4, respectively. The variation for different traits revealed that PCV was slightly higher than GCV for all the characters indicating the influence of environment in the characters along with variation due to genetic changes. Moderate GCV and PCV (10-20%) was recorded for the traits such as plant height, primary branches, secondary branches, L/S ratio, days to maturity, green fodder yield per plant, dry matter yield per plant in both the crosses and both the seasons. Similar findings were also reported by Vamshi *et al.* (2022) for traits plant height, number of primary and secondary branches, green fodder yield, dry matter yield in fodder cowpea and Thapa *et al.* (2021) for plant height, number of branches and green forage yield in cowpea. Varanya *et al.* (2022) reported high phenotypic and genotypic coefficient of variation for leaf area index (LAI), green fodder yield per plant, stem dry weight per plant, leaf dry weight per plant, seed yield per plant etc. and minimum for days to maturity. Heritability and genetic advance was high for number of leaves per plant, LAI, green fodder yield per plant, stem dry weight per plant, leaf dry weight per plant, plant height and seed yield per plant. Malarvizhi *et al.* (2005) found that heritability and genetic advance was high for the characters number of branches per plant, number of leaves per plant, dry weight of leaves, dry weight of stem, dry matter yield and plant height indicating that these traits were controlled by additive genetic effects. Singh *et al.* (2010) reported high phenotypic and genotypic coefficient of variation coupled with high heritability and genetic advance as per cent of mean for plant height, stem weight, leaves weight, biological yield, dry matter yield and green fodder productivity indicating predominance of additive gene effects in controlling these characters. Kumar *et al.* (2017) also found that heritability in

Table 1. Analysis of variance for fodder yield and yield-attributing traits in advance breeding lines of cross MFC-09-12 × BL-2

Source of variation	d.f.	Mean sum of squares (*kharif*)									
		DF	DFF	DM	L/S ratio	PH	NPB	NSB	GFY	DMC	DMY
Genotypes	34	53.54**	57.12**	339.88**	0.11**	80.62**	0.78**	0.02**	183.16**	5.93**	19.75**
Replication	1	0.25	0.37	8.47	0.02	0.44	0.05	0.05	4.45	1.18	1.53
Error	34	4.11	3.08	18.11	0.01	3.82	0.04	0.02	6.18	0.51	0.80
Sources of variation	d.f.	Mean sum of squares (*rabi*)									
		DF	DFF	DM	L/S ratio	PH	NPB	NSB	GFY	DMC	DMY
Genotypes	30	46.27**	44.13**	392.35**	58.44**	17.41**	0.47**	2.66**	184.46**	6.70**	18.38**
Replication	1	0.31	0.41	3.65	0.54	0.01	0.04	0.01	4.09	0.14	0.26
Error	30	1.74	2.76	19.35	0.18	1.79	1.10	0.18	4.75	0.46	0.65

*Significant at 5% level; **Significant at 1% level

DF- Days to first flowering
PH- Plant height (cm)
L/S ratio - Leaf to stem ratio
DMY- Dry Matter Yield (g/plant)
DFF- Days to 50% flowering
NPB- Number of primary branches
GFY- Green Fodder Yield (g/plant)
DM- Days to maturity
NSB- Number of secondary branches
DMC-Dry matter content (%)

Table 2. Analysis of variance for fodder yield and yield-attributing traits in advance breeding lines of cross UPC-622 × EC-4216

Source of variation	d.f.	Mean sum of squares (*kharif*)									
		DF	DFF	DM	L/S ratio	PH	NPB	NSB	GFY	DMC	DMY
Genotypes	32	58.46**	56.24**	436.26**	56.95**	1.01**	1.02**	2.63**	154.67**	5.52**	15.29**
Replication	1	0.78	0.33	14.89	2.86	0.04	0.10	0.01	35.77	0.01	1.82
Error	32	4.18	3.59	18.06	4.57	0.07	0.05	0.08	8.47	0.38	0.54
Source of variation	d.f.	Mean sum of squares (*rabi*)									
		DF	DFF	DM	L/S ratio	PH	NPB	NSB	GFY	DMC	DMY
Genotypes	29	66.86**	57.13**	468.57**	36.95**	0.26**	1.16**	1.91**	117.47**	5.91**	10.12**
Replication	1	0.03	14.72	20.69	7.02	0.01	0.32	0.01	1.01	0.28	0.02
Error	29	3.27	3.83	21.77	1.84	0.01	0.09	0.08	4.52	0.24	0.33

*Significant at 5% level; **Significant at 1% level

DF- Days to first flowering
PH-Plant height (cm)
L/S ratio – Leaf to stem ratio
DMY- Dry Matter Yield (g/plant)
DFF- Days to 50% flowering
NPB- Number of primary branches
GFY- Green Fodder Yield(g/plant)
DM-Days to maturity
NSB- Number of secondary branches
DMC-Dry matter content (%)

Table 3. Genetic parameters for yield and yield attributing traits in cross MFC-09-12 × BL-2

Characters	Season	Mean	Range		GCV (%)	PCV (%)	h^2_{bs}	GAM (%)
			Minimum	Maximum				
Days to first flowering	*kharif*	50.08	31.19	55.98	10.61	11.36	87.28	20.43
	rabi	50.30	30.01	55.10	9.32	9.68	92.76	18.50
Days to 50% flowering	*kharif*	54.57	36.84	60.78	10.04	11.59	89.90	19.61
	rabi	55.00	37.04	60.62	8.20	8.72	88.47	15.90
Days to maturity	*kharif*	104.94	70.10	117.26	17.40	18.45	90.05	25.86
	rabi	102.59	70.10	118.75	13.29	13.96	90.59	26.07
Plant height (cm)	*kharif*	40.55	30.54	56.19	14.06	14.85	89.70	27.44
	rabi	40.26	32.85	54.49	13.14	13.70	91.8	25.95
Primary branches	*kharif*	4.52	3.40	5.60	13.30	14.08	89.72	26.05
	rabi	4.53	3.28	5.41	11.65	12.91	81.39	21.65
Secondary branches	*kharif*	3.26	2.02	3.98	10.15	11.24	83.48	18.12
	rabi	3.33	2.25	4.69	13.88	14.44	84.44	26.26
L/S ratio	*kharif*	1.33	0.88	1.85	16.72	17.36	92.73	34.29
	rabi	1.28	0.88	1.84	16.48	17.60	87.64	31.78
Green fodder yield (g/plant)	*kharif*	74.80	57.57	100.09	14.67	15.19	93.30	29.20
	rabi	65.80	52.19	98.75	11.80	11.47	94.40	22.96
Dry matter content(%)	*kharif*	22.73	16.02	27.40	7.45	9.88	83.32	14.02
	rabi	21.20	16.61	26.57	8.32	8.92	87.14	16.14
Dry matter yield (g/plant)	*kharif*	15.15	10.56	27.66	20.15	20.31	92.22	40.19
	rabi	15.88	11.43	26.59	17.46	18.09	93.16	34.72

Table 4. Genetic parameters for yield and yield attributing traits in cross UPC-622 × EC4216

Characters	Season	Mean	Range		GCV (%)	PCV (%)	h^2_{bs}	GAM (%)
			Minimum	Maximum				
Days to first flowering	*kharif*	47.64	33.65	57.24	14.45	15.72	86.64	20.53
	rabi	49.24	30.74	57.98	11.87	12.31	90.67	22.18
Days to 50% flowering	*kharif*	53.23	39.90	61.12	13.45	15.14	87.98	18.62
	rabi	54.22	36.94	61.57	9.55	10.18	87.44	18.34
Days to maturity	*kharif*	96.57	68.44	116.59	15.35	15.90	92.05	29.05
	rabi	97.09	6.42	115.52	14.90	15.57	91.55	29.37
Plant height (cm)	*kharif*	48.29	39.90	62.88	10.29	11.48	85.13	20.13
	rabi	42.59	36.47	52.68	11.34	11.89	90.52	19.28
Primary branches	*kharif*	3.99	3.15	5.73	17.21	18.40	87.12	33.10
	rabi	3.92	3.37	5.12	9.46	9.05	91.55	27.55
Secondary branches	*kharif*	4.0	2.90	5.24	17.31	18.15	90.98	34.02
	rabi	4.43	2.78	5.64	16.30	17.66	85.24	31.01
L/S ratio	*kharif*	1.15	0.74	1.68	17.69	18.45	91.91	34.94
	rabi	1.14	0.77	1.72	17.86	17.10	91.06	33.71
Green fodder yield (g/plant)	*kharif*	64.04	50.59	88.55	13.35	15.40	89.62	26.03
	rabi	61.00	50.88	87.09	12.31	12.80	92.59	24.41
Dry matter content(%)	*kharif*	23.25	19.91	26.99	7.39	8.50	86.98	13.24
	rabi	21.39	17.28	25.15	7.94	8.19	92.21	15.56
Dry matter yield (g/plant)	*kharif*	14.94	10.16	23.90	18.83	18.17	93.16	36.14
	rabi	13.36	9.89	19.24	16.11	16.55	93.59	33.01

broad sense was high for most of the traits coupled with high genetic advance as per cent over mean indicated presence of additive gene action for the characters in two population in fodder cowpea, Sogalad *et al.* (2022) reported high heritability coupled with high genetic advance for characters *viz*., number of clusters per plant, number of pods per cluster, number of pods per cluster, number of pods per plant, test weight and grain yield per plant indicated additive gene effects in cowpea.

Whereas the PCV and GCV were moderate for days to first flowering, days to 50% flowering in cross MFC-09-12× BL-2 during *kharif* while it was low during *rabi*. Both crosses showed low PCV and GCV for DMC (%) in both the seasons. This indicates less variation is present for the above among the ABL's studied. These results were in line with earlier findings of Vamshi *et al.* (2022) for days to first flowering and days to 50% flowering; Pandiyan *et al.* (2020) for traits days to first flowering, days to 50% flowering and dry matter content.

With the help of PCV and GCV alone, it is not possible to determine the extent of variation that is heritable. Hence, the knowledge of heritability and genetic advance for quantitative character aids in exercising the necessary selection procedure Johnson *et al.* (1955).

The study revealed that estimates of broad sense heritability were high (> 60%) for the all the characters under study in both the crosses and in both the seasons. Thus, the lesser magnitude of environmental variation indicates the flexibility of handling the above characters for further improvement. These findings were supported by Sogalad *et al.* (2022), Vinay *et al.* (2022) and Varanya *et al.* (2022).

The high heritability coupled with high GAM was observed for traits such as plant height, number of primary branches, L/S ratio, days to first flowering, days to maturity, green fodder yield, dry matter yield in both crosses as well as in both the seasons. This suggests the preponderance of additive gene action and selection pressure could profitably be applied to these characters for yield improvement. Vamshi *et al.* (2022) also reported high heritability with high GAM for traits plant height, number of primary branches, green fodder yield and dry matter yield; Varanya *et al.* (2022) for plant height, green fodder yield, dry fodder yield; Wagh *et al.* (2018) for leaf to stem ratio in fodder oat. The selection of these traits could be more effective for desired genetic improvement.

Conclusion

There was significant variation for all the traits among advanced breeding lines of fodder cowpea under study. Traits like plant height, number of primary branches, L/S ratio, days to first flowering, days to maturity, green fodder yield and dry matter yield could be taken for further improvement of fodder cowpea as the ABL's have reached the homozygous state and are stable. These lines can be evaluated in replicated yield trials and further contributed for national / state trials.

References

Anonymous, 2021, Food and Agriculture Organization. www. fao. org/statistics/en/

Burton G W and Devane E M, 1953, Estimating heritability in Tall Fescue (*Festuca arundinacea* L) from replicated clonal-materials. *Agronomy Journal*, 45: 478-481.

Hanson G H, Robinson H F and Comstock R E, 1956, Biometrical studies of yield in segregating population of Korean Lespedeza. *Agronomy Journal*, 48: 267-282.

Johnson H W, Robinson H F and Comstock R E, 1955, Genotypic and phenotypic correlations in soybean and their implications in selection. *Agronomy Journal*, 37: 477-483.

Kumar S, Sridhar K, Kumar V and Kulkarni N S (2017). Estimation of genetic variability for dual purpose in cowpea (*Vigna unguiculata* (L.) Walp). *Plant Archives*, 17: 887-891.

Malarvizhi D, Swaminathan C, Robin S and Kannan K, 2005, Genetic variability studies in fodder cowpea (*Vigna unguiculata* L. Walp). *Legume Research*, 28(1): 52-54.

Panchta R, Arya S, Singh D P, Satpal, Preeti and Rajender, 2020, Genetic variability and association studies in cowpea (*Vigna unguiculata* (L.) Walp) for seed yield and related traits. *Forage Research*, 46 (3): 232-235.

Pandiyan M, Vaithilingan M, Krishnaveni A, Sivakumar P, Sivakumar C, Jamuna E and Senthilkumar P, 2020, Genetic Variability Studies on Cowpea Genotypes. *International Journal of Current Microbiology and Applied Sciences*, 9(6):3794-3797.

Sheidu, A, Shammah A M and Jibrin I M, 2023, Genetic variability, heritability and genetic advance of improved cowpea genotypes (*Vigna unguiculata* L.Walp). *Fudma Journal of Sciences*, 7(3): 297-301.

Singh S B, Singh A K and Singh A P, 2010, Genetic variability, trait relationship and path analysis for green fodder yield and its components in Cowpea (*Vigna unguiculata*) under rainfed environment. *Progressive Agriculture*, 10(1): 42-46.

Sogalad M S, Deshpande S K and Kavyashree N M, 2022, Genetic variability, correlation and path analysis studies in grain cowpea (*Vigna unguiculata* (L.) Walp subsp. *unguiculata*). *Pharma Innovation*, 11(12): 3749-3754.

Tarawali S, Singh B B, Peters M and Blade S F, 1997, Cowpea haulms as fodder. *Advances in Cowpea Research,* p. 313-325.

Thapa B, Adhikari N R, Darai R and Kandel B P, 2021, Genetic variability of exotic cowpea genotypes for agro-morphological traits in midwestern region of Nepal. *Alinteri Journal of Agriculture Sciences*, 36(1): 47-54.

Vamshi S, Subramanian A, Ezhilarasi T, Gurusamy K and Ganesan K N, 2022, Analysis of genetic parameters, trait association and genetic diversity in fodder cowpea [*Vigna unguiculata* (L.) Walp.]. *Electronic Journal of Plant Breeding.* 13(2): 361-368.

Varanya A, Gayathri G, Arya K, Thomas U C, Gopinath P P and Hulsure P, 2022, Genetic variability and genetic parameters analysis of 143 fodder cowpea [*Vigna unguiculata* (L.) Walp] germplasm accessions for yield and yield attributing traits. *Pharma Innovation*, 11(2): 2595-2600.

Vinay K, Rao J M, Kishore N S and Hari Y, 2022, Genetic variability studies for seed yield and yield component traits in cowpea [*Vigna unguiculata* (L.) Walp]. *Electronic Journal of Plant Breeding*, 13(2): 544-548.

Wagh V, Sonone A and Damame S V, 2018, Assessment of genetic variability, correlations and path coefficient analysis in forage oat (*Avena sativa* L.). *Forage Research*, 44(3): 172-175.