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**Research Note**

# Genetic variability and association studies in guar [*Cyamopsis tetragonoloba* (L.) Taub.) for green fodder yield and quality traits

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**Abstract**

Seventy six clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.) genotypes were analysed for genetic variability, correlation and path coefficients. The genotypes were significantly different for all the characters, which indicated scope for further genetic studies. High heritability along with high genetic advance (GA) was recorded number of leaves per plant, number of branches, dry matter yield and green fodder yield indicating that selection would be rewarding for characters. The PCV estimates were invariably higher than their corresponding GCV values thereby suggesting the environmental influence. High estimates of GCV and PCV were observed for leaf weight, number of leaves per plant, number of branches per plant, stem girth, dry matter yield and green fodder yield suggesting that selection based on these characters would facilitate successful isolation of desirable types. Traits like plant height, leaf length, leaf weight, number of leaves per plant and dry matter yield had positive and significant correlation at genotypic as well as phenotypic level with green fodder yield. Hence the selection based on these traits will result in improving the green fodder yield GFY in guar. Most of the yield contributing traits like plant height, leaf length, leaf weight, number of leaves per plant and dry matter yield as well as the quality traits like acid detergent fibre, neutral detergent fibre and in vitro dry matter digestibility showed direct effect on green fodder yield.

**Key words:** *Cyamopsis tetragonoloba*, Variability, Genetic advance, heritability, Green fodder yield.

Cluster bean [*Cyamopsis tetragonoloba* (L.) Taub.], also known as guar, is arid legume crop that is cultivated mostly in the arid and semi arid areas as it is drought resistant. The long deep taproot system enables the plant to grasp all the water in the soil making it an ultimate drought resistant crop. Therefore, it is cultivated in rainy (*kharif*) season mainly as rainfed crop in the dry habitats. Its seed is mainly used to produce guar gum, which has wide range of applications in the food, pharmaceutical and cosmetics industry guar gum is used as an effective binder, stabilizer, disintegrator and thickener (Vaughan and Geissler, 1998). India is one of the major producers of clusterbean and large quantity of its gum is exported to other countries. India accounts for 80% of the total guar produced in the world. Rajasthan occupies the largest area under guar cultivation (82.1%), followed by Haryana (8.6%), Gujarat (8.3%) and Punjab (1%) which in turn produced 64, 22, 12 and 2% guar seeds, respectively (Pathak *et al.*, 2010). Besides its utility as a grain crop, it is a useful fodder crop and as a leguminous plant it also adds nitrogen to the soil, thereby enriching soil fertility. Crop residues (stubble and header trash) are a source of valuable, high protein animal feed. The crop can also be used to produce high quality hay. In many parts of the country including Punjab, it is an important legume fodder crop grown during *Kharif* to produce highly nutritious and palatable fodder for the cattle. Despite the importance of this crop, only limited breeding work has been done and very little attention has been given for its genetic improvement in the past, in order to enhance the productivity levels of *Kharif* cluster bean. Therefore, there is a great opportunity for forage breeders in identifying the genetic make-ups that are superior in green fodder yield.

To reach this goal, the basic requirements are to have adequate information on the extent of variability, heritability, expected genetic gain and degree of genetic association among the different characters. In view of this, the present investigation was carried out with the objective of assessing genetic variability and characters association amongst the various yield contributing traits and quality parameters.

The experiment was conducted during *Kharif* 2011 with 76 germplasm accessions available at Forage Research Farm, Punjab Agricultural University, Ludhiana. The material was grown in randomized complete block design (RBD), where each entry was accommodated in 4 sq. m. plot size containing 4 rows of 4 m length with inter row spacing of 25 cm with three replications. Recommended package of practices to raise a good crop were followed. Observations were recorded on five competitive and healthy plants selected randomly from each entry on nine quantitative variables viz; plant height - PH (cm), leaf length- LL (cm), leaf width - LW (cm), number of leaves/plant - NOL, number of branches/plant – NOB, stem girth – SG (cm), leaf stem ratio - LSR, green fodder yield – GFY (g/plot) and dry matter yield – DMY (g/plot) and four quality parameters viz; crude protein - CP (%), Neutral detergent fibre – NDF (%), Acid detergent fibre - ADF (%), and *In- vitro* dry matter digestibility – IVDMD (%). The data were analysed for variability, correlation and path coefficient analyses. Genotypic and phenotypic coefficients of correlation were calculated from genotypic and phenotypic co-variances and variances as described by Singh and Chaudhry (1977) and Johnson *et al*. (1955). Genotypic and phenotypic coefficients were calculated using the formulae as used by Burton and De Vane (1953) and Johnson *et al*. (1955). Heritability in broad sense was estimated as suggested by Burton (1952). The expected genetic advance at 5% selection intensity was calculated by the formula as used by Johnson *et al*. (1955). Direct and indirect effects were calculated by the path coefficient analysis as suggested by Dewey and Lu (1959) at both phenotypic and genotypic levels.

Estimates of genetic variability

It is evident from the range of mean values for different traits among the guar genotypes being evaluated (Table 1) that these had diverse genetic background. The traits like PH (56.3 – 129.3), LL (4.4 – 8.0), LW (2.1 – 4.6), NOL (41.0 – 290.0), NOB (1.0 – 15.3) and GFY (3117 – 12033) had wide range values.

Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability ($h^2$) and genetic advance as percent of mean (GA) are given in Table 2. Perusal of data revealed that GCV and PCV values were invariably higher for most of the traits except LL, LW and NOB, indicating primarily the genetic control for these traits rather the environment effect alone. Also high estimates of GCV and PCV were observed for LW, NOL, NOB, SG, DMY and GFY, suggesting that selection based on these characters would facilitate successful isolation of desirable types. However, the genetic variability together with heritability estimates would give a better idea on the amount of GA expected from selection (Burton, 1952). High values of GCV were reported for NOL, NOB, SG, DMY and GFY in accordance with the results of Shekhawat and Singhania (2005) and Vijay (1988). PH, LL and LSR along with all the four quality parameters evaluated had low GCV values indicating little scope of genotypes for improvement in these traits. Mahla and Kumar (2006) and Sidhu *et al*. (1982) also reported the low GCV values for traits like PH and LL, corroborating our results.

High $h^2$ along with high GA was recorded for NOL, NOB, DMY and GFY. Shekhawat and Singhania (2005) and Mahla and Kumar (2006) also reported similar results for many of these characters. Traits having high $h^2$ and high GA can be improved by selection based on phenotypic performance (Singh *et al.,* 2005a; Singh *et al.,* 2005b ). IVDMD had lowest $h^2$ (-15.92) followed by NDF (-5.71) thus are difficult to be improved by phenotype guided selection. Traits like PH, LW and LSR had high $h^2$ but low values of GA indicating poor response for selection.

Genotypic and phenotypic correlation coefficients

Fodder yield is a complex character controlled by several components which reflect positive and negative effects on this trait. Yield components of fodder yield in legumes like guar consist chiefly of traits like PH, LL, LW, NOL, NOB and SG (Arora and Lodhi, 1998; Henry *et al*., 1986; Shekhawat and Singhania, 2005). Thus, for achieving rational improvement in fodder yield and its components, knowledge of mechanism of association, cause and effect relationship provides a basis for formulating suitable selection methods for the yield components.

Results indicate that many yield contributing traits viz; PH, LL, LW, NOL and DMY had positive and significant correlation at genotypic as well as phenotypic level with GFY (Table 3)**.** On the contrary, LSR exhibited a negative and significant correlation with GFY and DMY. Hence selection based on these traits will result in improving the GFY in guar. Rest of the traits under study did not exhibit significant correlation with green GFY. Traits like PH, LL and LW showed positive and highly significant correlation amongst each other but exhibited negative and highly significant correlation with NOL and NOB which were also negatively correlated amongst each other. Highest value of positive and significant correlation was observed between GFY and DMY (0.98, 0.96) closely followed by LL and LW (0.97, 0.68) whereas PH and NOB (-0.51, -0.38) exhibited highest value of negative and significant correlation.

Amongst the four quality parameters under study viz; CP, ADF, NDF and IVDMD three traits except IVDMD exhibited positive and significant correlation with other yield contributing traits like CP with NOL and SG, ADF with PH, LL and LW, NDF with LW. IVDMD showed only negative and significant correlation with PH, LL, LW, ADF and NDF. There are no published reports on association study between forage quality traits and other fodder yield contributing traits, therefore, our study, for the first time, shed the light on association behaviour between forage quality and other fodder yield contributing traits.

Path coefficient analysis for direct and indirect effects on green fodder yield Partitioning of the total correlation coefficient into direct and indirect effects for GFY showed a positive and high direct effect DMY (Table 4). All other traits recorded negligible indirect and direct effects on green fodder yield. Sidhu *et al.* (1982) also reported positive indirect effect of LL, LW, NOL on GFY. Hence, selection for taller plants with more number of broader and longer leaves and less LSR will be significant for the improvement of green fodder yield in the material under study.

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Table **1. Estimates of genetic parameters for different traits in guar**

| Character | Range | $h^2$ (%) | GA (%) | PCV | GCV | GM |
|---|---|---|---|---|---|---|
| PH | 56.3 – 129.3 | 64.28 | 22.45 | 16.95 | 13.59 | 84.81 |
| LL | 4.4 – 8.0 | 35.81 | 13.22 | 17.92 | 10.73 | 5.98 |
| LW | 2.1 - 4.6 | 52.36 | 25.75 | 23.88 | 17.28 | 3.35 |
| NOL | 41.0 – 290.0 | 93.64 | 81.8 | 42.41 | 41.03 | 169.69 |
| NOB | 1.0 – 15.3 | 84.9 | 92.77 | 53.04 | 48.87 | 7.95 |
| SG | 0.5 – 1.7 | 48.25 | 29.69 | 29.87 | 20.75 | 0.78 |
| DMY | 262.0 – 1020 | 98.05 | 59.69 | 29.55 | 29.26 | 468.77 |
| LSR | 0.60 – 1.0 | 99.76 | 29.69 | 14.45 | 14.43 | 0.77 |
| CP | 17.6 – 20.8 | 38.52 | 3.96 | 4.99 | 3.1 | 19.62 |
| ADF | 31.9 – 36.6 | 11.81 | 1.00 | 4.11 | 1.41 | 32.85 |
| NDF | 43.0 – 47.8 | -5.71 | -0.44 | 3.76 | 0.01 | 45.12 |
| IVDMD | 59.0 – 63.6 | -15.92 | -1.07 | 3.27 | 0.01 | 62.35 |
| GFY | 3117-12033 | 98.97 | 52.79 | 25.89 | 25.76 | 6342 |

PH= plant height (cm), LL=leaf length (cm), LW= leaf width (cm), NOL= Number of leaves/plant, NOB= number of branches/plant, SG= stem girth (cm), DMY=Dry matter yield (g/plot), LSR= leaf stem ratio, CP=crude protein (%), ADF (%)= acid detergent fibre, NDF (%)= Neutral detergent fibre, IVDMD (%)= *In-vitro* dry matter digestibility, GFY= Green fodder yield (g/plot). $h^2$= heritability (broad sense); PCV= Phenotypic coefficient of variability; GCV= Genotypic coefficient of variability; GA (%)= Genetic advance as percentage of mean; GM= grand mean

**Table 2. Genotypic and phenotypic correlation coefficients among various traits of Guar**

| Characters | | PH | LL | LW | NOL | NOB | SG | DMY | LSR | CP | ADF | NDF | IVDMD |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **LL** | G | 0.50$^{**}$ | | | | | | | | | | | |
| | P | 0.30$^{**}$ | | | | | | | | | | | |
| **LW** | G | 0.66$^{**}$ | 0.97$^{**}$ | | | | | | | | | | |
| | P | 0.50$^{**}$ | 0.68$^{**}$ | | | | | | | | | | |
| **NOL** | G | -0.30$^{**}$ | -0.33$^{**}$ | -0.24$^{**}$ | | | | | | | | | |
| | P | -0.22$^{**}$ | -0.21$^{**}$ | -0.16$^{*}$ | | | | | | | | | |
| **NOB** | G | -0.51$^{**}$ | -0.38$^{**}$ | -0.40$^{**}$ | 0.67$^{**}$ | | | | | | | | |
| | P | -0.38$^{**}$ | -0.25$^{**}$ | -0.29$^{**}$ | 0.61$^{**}$ | | | | | | | | |
| **SG** | G | 0.11 | 0.10 | 0.09 | 0.17$^{*}$ | 0.08 | | | | | | | |
| | P | 0.15$^{*}$ | -0.05 | 0.05 | 0.16$^{*}$ | 0.15$^{**}$ | | | | | | | |
| **DMY** | G | 0.20$^{**}$ | -0.09 | 0.03 | 0.05 | -0.02 | 0.04 | | | | | | |
| | P | 0.17$^{*}$ | -0.06 | 0.01 | 0.04 | -0.02 | 0.03 | | | | | | |
| **LSR** | G | -0.08 | 0.30$^{**}$ | 0.19$^{**}$ | -0.11 | -0.12 | 0.20$^{**}$ | -0.20$^{**}$ | | | | | |
| | P | -0.06 | 0.18$^{**}$ | 0.14$^{*}$ | -0.10 | -0.10 | 0.14$^{*}$ | -0.20$^{**}$ | | | | | |
| **CP** | G | -0.30$^{**}$ | -0.50$^{**}$ | -0.42$^{**}$ | 0.14$^{*}$ | 0.20 | 0.29$^{**}$ | 0.04 | -0.05 | | | | |
| | P | -0.08 | -0.15$^{*}$ | -0.23$^{**}$ | 0.10 | 0.13 | 0.16$^{*}$ | 0.01 | -0.04 | | | | |
| **ADF** | G | 0.33$^{**}$ | 0.76$^{**}$ | 0.59$^{**}$ | -0.03 | -0.36$^{**}$ | -0.48$^{**}$ | -0.08 | 0.06 | -1.73 | | | |
| | P | 0.09 | 0.06 | 0.08 | -0.05 | -0.10 | -0.06 | -0.06 | 0.01 | -0.15 | | | |
| **NDF** | G | 0.01 | 0.02 | 0.01 | 0.01 | 0.01 | 0.02 | 0.01 | 0.01 | 0.01 | 0.01 | | |
| | P | -0.04 | 0.15$^{*}$ | 0.09 | -0.05 | -0.10 | -0.08 | 0.01 | 0.01 | -0.38$^{**}$ | -0.08 | | |
| **IVDMD** | G | 0.01 | 0.02 | 0.01 | 0.01 | 0.02 | 0.02 | 0.01 | 0.02 | 0.01 | 0.01 | 0.01 | |
| | P | -0.13$^{*}$ | -0.17$^{*}$ | -0.17$^{*}$ | -0.04 | 0.02 | 0.00 | 0.01 | -0.02 | -0.05 | -0.17$^{*}$ | -0.13$^{*}$ | |
| **GFY** | G | 0.24$^{**}$ | -0.18$^{**}$ | 0.13$^{*}$ | 0.14$^{*}$ | -0.03 | 0.05 | 0.98$^{**}$ | -0.24$^{**}$ | 0.02 | -0.11 | 0.01 | 0.01 |
| | P | 0.19$^{**}$ | -0.13$^{*}$ | 0.10 | 0.11 | -0.03 | 0.03 | 0.96$^{**}$ | -0.24$^{**}$ | -0.01 | -0.03 | 0.02 | 0.03 |

*,** significant at 5 and 1 % respectively; G= genotypic correlation coefficient; P= Phenotypic correlation coefficient

PH= plant height (cm), LL=leaf length (cm), LW= leaf width (cm), NOL= Number of leaves/plant, NOB= number of branches/plant, SG= stem girth (cm), DMY=Dry matter yield (g/plot), LSR= leaf stem ratio, CP=crude protein (%), ADF (%)= acid detergent fibre, NDF (%)= Neutral detergent fibre, IVDMD (%)= *In-vitro* dry matter digestibility, GFY= Green fodder yield (g/plot). $h^2$= heritability (broad sense); PCV= Phenotypic coefficient of variability; GCV= Genotypic coefficient of variability; GA (%)= Genetic advance as percentage of mean; GM= grand mean

**Table 3. Path coefficient analysis for direct (bold) and indirect effects on green fodder yield (g/plot) in Guar**

| Characters | PH | LL | LW | NOL | NOB | SG | DMY | LSR | CP | ADF | NDF | IVDMD |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **PH** | **0.0298** | 0.006 | 0.0051 | 0.0019 | 0.0003 | 0.0013 | 0.1571 | 0.0033 | 0.0001 | 0.0029 | -0.0007 | -0.0038 |
| **LL** | 0.0091 | **0.0194** | 0.0069 | 0.0019 | 0.0002 | -0.0004 | -0.057 | -0.0095 | 0.0001 | 0.0021 | 0.0027 | -0.0049 |
| **LW** | 0.0148 | 0.0131 | **0.0102** | 0.0014 | 0.0002 | 0.0005 | 0.0113 | -0.0073 | 0.0002 | 0.0027 | 0.0017 | -0.0047 |
| **NOL** | 0.0066 | 0.0041 | 0.0017 | **-0.0087** | -0.0005 | 0.0015 | 0.0422 | 0.0054 | 0.0001 | -0.0017 | -0.001 | -0.0012 |
| **NOB** | 0.0113 | 0.0049 | 0.003 | -0.0054 | **-0.0008** | 0.0013 | -0.0198 | 0.0056 | 0.0003 | -0.0032 | -0.0019 | 0.0005 |
| **SG** | 0.0043 | 0.0009 | 0.0005 | -0.0014 | -0.0001 | **0.009** | 0.0312 | -0.0074 | 0.0002 | -0.002 | -0.0014 | 0.0001 |
| **DMY** | 0.0049 | 0.0012 | 0.0001 | -0.0004 | 0.0001 | 0.0003 | **0.9524** | 0.0102 | 0.0001 | -0.002 | 0.0002 | 0.0003 |
| **LSR** | 0.0019 | 0.0035 | 0.0014 | 0.0009 | 0.0001 | 0.0013 | -0.186 | **-0.0521** | 0.0003 | 0.0004 | 0.0002 | -0.0008 |
| **CP** | -0.0023 | -0.0029 | 0.0024 | -0.0009 | -0.0001 | 0.0014 | 0.008 | 0.0023 | **0.0002** | -0.0049 | -0.0067 | -0.0013 |
| **ADF** | 0.0027 | 0.0013 | -0.0009 | 0.0005 | 0.0001 | -0.0006 | -0.0594 | -0.0006 | 0.0001 | **0.0321** | -0.0013 | -0.0049 |
| **NDF** | -0.0012 | 0.003 | -0.001 | 0.0005 | 0.0001 | -0.0007 | 0.0121 | -0.0006 | -0.0001 | -0.0024 | **0.0178** | -0.0037 |
| **IVDMD** | -0.004 | -0.0033 | 0.0017 | 0.0004 | 0.0001 | 0.0001 | 0.0114 | 0.0014 | 0.0001 | -0.0055 | -0.0023 | **0.0283** |

PH= plant height (cm), LL=leaf length (cm), LW= leaf width (cm), NOL= Number of leaves/plant, NOB= number of branches/plant, SG= stem girth (cm), DMY=Dry matter yield (g/plot), LSR= leaf stem ratio, CP=crude protein (%), ADF (%)= acid detergent fibre, NDF (%)= Neutral detergent fibre, IVDMD (%)= *In-vitro* dry matter digestibility, GFY= Green fodder yield (g/plot). $h^2$= heritability (broad sense); PCV= Phenotypic coefficient of variability; GCV= Genotypic coefficient of variability; GA (%)= Genetic advance as percentage of mean; GM= grand mean