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Genetic diversity and interrelationship among clusterbean (*Cyamopsis tetragonoloba*) genotypes for qualitative traits

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ABSTRACT

A study was conducted during 2006–07 to assess the extent of genetic variability and qualitative characters of clusterbean (*Cyamopsis tetragonoloba* L. Taub.). The range, genotypic and phenotypic coefficient of variation, heritability, genetic advance and correlation among 7 qualitative characters were estimated in 40 genotypes of cluster bean. The genotypes showed considerable amount of variability for all the traits. Irrespective of their place of collection the genotypes were grouped into 7 different clusters. Cluster analysis revealed that genotypes 'HGS 884', 'HGS 26–01' and 'HGS 02–20' will be useful for genetic resources. High magnitude of heritability and genetic advance for gum, fibre and protein contents suggested that the genotypic variation in the present material for these characters is due to high additive genetic effects. Carbohydrates were positively correlated with endosperm and gum contents. Endosperm exhibited significant positive association with gum content while the association of protein was negative with gum and endosperm contents.

Key words: *Cyamopsis tetragonoloba*, Correlation, Genetic divergence, Proximate analysis

Genetic variability is the basis of species' conservation (Banerjee *et al*. 2007, Zhao *et al*. 2006). Knowledge of genetic divergence among the varieties has immense importance for plant breeders. The use of diverse germplasm as a significant factor contributing to high yield and quality characteristics has been stressed by many workers using various crops (Gopala Krishnan and Dwivedi 2008, Medici *et al*. 2005). Large variability in the initial breeding material ensures better chances of producing new desired forms of a crop.

Clusterbean [*Cyamopsis tetragonoloba* (L) Taub.] belongs to the family leguminaceae and subfamily paplionaceae. It is an annual with long and deep root and well developed laterals, cultivated mainly as rainfed crop in arid and semi-arid regions during rainy (*kharif*) seasons for vegetable, forage and green manure. India is one of the main producers of cluster bean accounting 80% of the total production of the world, whereas Rajasthan occupies the largest area (82.1%) under guar cultivation in the country. In addition to its cultivation in India, the crop is also grown as a cash crop in other parts of the world (Pathak *et al*. 2010). The dicotyledonous seed of cluster bean from the outside to the interior consists of three major fractions, viz the husk or hull (14–17%), endosperm (35–42%) and germ (43–47%). The endosperm fraction of cluster bean seed is rich in galactomannan that ranges between 16.8 and 30.9%, while the germ and hull portion termed as guar meal obtained after the extraction of gum is rich in protein (approx. 28.9–46%) and used as animal and poultry feed (Lee *et al*. 2004, Rodge 2008). Seed of cluster bean has rather a large endosperm unlike most of other legumes and contains galactomannan type of gum, which forms a viscous gel even in cold water and has diversified industrial applications, viz. paper, food, cosmetics, mining, petroleum, well drilling, pharmaceuticals, etc. (Pathak *et al*. 2009, Senapati *et al*. 2006). Clusterbean gum has emerged as the most important agro-chemical, which is non-toxic, eco-friendly and Generally Recognized As Safe (GRAS) by FDA. Foreign exchange earned from its export has increased from 142 crores in 1994 to 1120 crores during 2007 in India (Henry and Mathur 2008).

Meager information is available for genetic variability in cluster bean addressing the qualitative traits. Studies were therefore, undertaken to assess the extent of genetic variability and association of qualitative characters, viz endosperm, gum, fibre, fat, protein, ash and carbohydrates

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contents among 40 promising genotypes of cluster bean.

MATERIALS AND METHODS

Forty genotypes of cluster bean including 3 released varieties were procured from different cluster bean growing states of India for present investigation and the experiments were conducted during rainy seasons of 2006 and 2007 at central research farm, Central Arid Zone Research Institute, Jodhpur (27°18'N latitude and 73°01'E longitude) in randomized block design with 3 replications. The plot size for each genotype in each block was 3 m × 0.9 m with row-to-row and plant-to-plant spacing of 30 and 10 cm, respectively. The crop was grown strictly under rainfed conditions and only basal dose of fertilizers was applied 20 kg N and 40 kg P_2O_5/ha. The soil was loamy sand in texture, low in organic carbon (0.12%) and available nitrogen (170 kg/ha) and medium in available phosphorus (21 kg P_2O_5/ha) and potassium (270 kg K_2O/ha) content with a pH of 8.3. The crop was harvested at seed maturity stage in October. A random sampling of five plants from each genotype was used for biochemical analysis. Harvested seeds were oven dried at 60°C for 1 week to eliminate the moisture content before analysis of proximate compositions. The seeds were grinded and flour of 32 mesh size was used to assess for protein, fat, ash and crude fibre using AOAC (1984) method. Carbohydrate content was analyzed as nitrogen free extractives while gum content was estimated using colorimetric method. Genetic analysis, correlation and cluster analysis on the basis of component traits were carried out using genetic model of INDOSTAT software. The relationship among 40 cluster bean genotypes was portrayed graphically in the form of a dendrogram.

RESULTS AND DISCUSSION

Chemical composition

The proximate compositions of clusterbean seed is illustrated in Table 1. Endosperm and gum content ranged from 30.4% ('CLBH 201') to 46.3% ('RGC 1030') and 23.5% ('HGS 880') to 33.5% ('GAUG 9808'), respectively. Crude fibre ranged from 4.1% ('HGS 02–1') to 8.0% ('AVKG 73') while fat content ranged from 1.8% ('VIKAS 35') to 5.2% ('GAUG 003') with the over all mean of 3.38%. The range for crude protein was recorded from 28.3 ('VIKAS 35') to 35.0% ('RGC 1038') with over all mean of 32.52%. Ash content ranged from 3.5 ('RGC 1059') to 6.0% ('GAUG 0101') while carbohydrates ranged from 38.8% ('HGS 26–01') to 59.1% ('VIKAS 35') with the overall mean of 53.0%. Such variations in the proximate compositions have also been reported by number of workers (Rodge 2008, Ahmed *et al.* 2006). Presently clusterbean is primarily used for extraction of gum but variations in protein and fat will also be of interest for the plant breeders as guar meal is an important source of animal feed (Rodge 2008). Fibre is an important constituent of any food and feed and there are adequate variations in fibre contents among the genotypes studied. Ash are primarily the minerals, silicates etc., even though detailed mineral analysis had been undertaken but the range indicates the existence of variability. The ash content of other legume grains ranged from 2.7 (gm) to 4.6% (soybean). Thus among pulses, clusterbean seeds appear to have the highest ash content and mineral concentrations. Carbohydrates are an important component of guar seed as guar gum is primarily a polymer of galactose and mannose. The variation in the proximal contents among the genotypes is of the great significance for industries.

Genetic variation

Except for carbohydrates contents, the analysis of variance showed wide range of genetic variability for all the characters studied suggesting that the present material of cluster bean was appropriate and hence suitable for further genetic analysis (Table 2). The phenotypic coefficient of variation (PCV) was invariably higher than their corresponding genotype

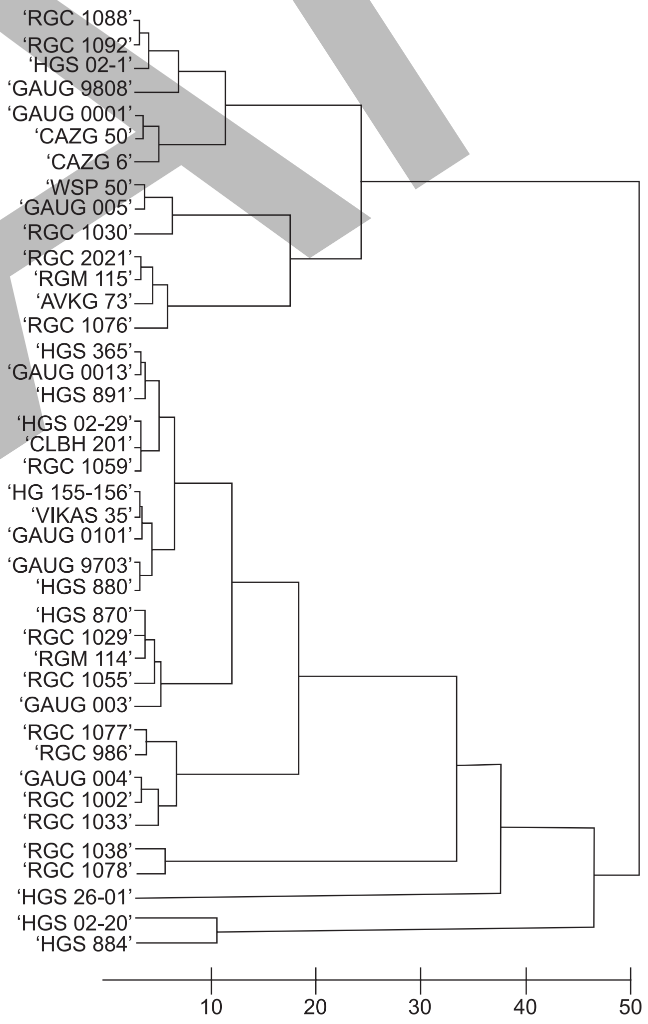

Fig 1 Dendrogram obtained by INDOSTAT for 40 cluster bean genotypes based on qualitative traits

Table 1 Mean value of different biochemical characters in guar seed during 2006, 2007

Genotype	Endosperm (%)	Gum (%)	Crude fibre (%)	Fat (%)	Crude Protein (%)	Ash (%)	Carbohydrate (%)
‘AVKG 73’	33.9	26.8	8.0	4.1	33.2	3.8	50.8
‘CAZG 50’	39.6	26.8	6.1	3.9	31.4	4.5	54.0
‘CAZG 6’	37.3	24.1	6.7	4.9	30.3	4.4	53.7
‘CLBH 201’	30.4	25.2	7.3	2.0	34.4	4.7	51.7
‘GAUG 001’	38.9	28.8	5.1	3.8	32.5	5.0	53.6
‘GAUG 0013’	36.1	27.3	6.1	3.4	34.8	4.4	51.0
‘GAUG 003’	42.6	30.2	5.7	5.2	34.9	4.6	49.7
‘GAUG 004’	40.9	33.1	7.7	4.2	33.5	3.9	50.6
‘GAUG 005’	38.8	29.2	5.9	4.6	33.2	4.3	52.0
‘GAUG 0101’	41.2	29.5	6.7	3.3	31.2	6.0	52.8
‘GAUG 9703’	35.5	26.2	6.7	2.9	32.3	3.9	54.3
‘GAUG 9808’	39.9	33.5	6.5	4.2	31.7	4.2	53.3
‘HG 155–156’	40.4	31.4	6.2	3.1	30.8	3.7	56.1
‘HGS 02–1’	42.5	29.7	4.1	4.0	34.6	4.6	52.7
‘HGS 02–20’	38.3	29.7	6.0	2.6	33.2	3.8	54.4
‘HGS 02–29’	43.6	30.9	6.3	3.3	32.8	3.9	53.8
‘HGS 26–01’	41.7	27.6	6.4	2.7	33.1	4.0	38.8
‘HGS 365’	40.6	30.2	5.4	2.3	33.3	4.6	54.3
‘HGS 870’	37.6	30.8	6.8	4.8	34.2	5.0	49.3
‘HGS 880’	35.4	23.9	6.5	2.4	33.8	5.6	51.7
‘HGS 884’	40.2	32.7	6.8	3.6	31.6	4.3	53.7
‘HGS 891’	41.9	31.1	6.4	2.0	33.6	4.0	53.9
‘RGC 1002’	43.2	34.2	5.3	2.8	31.7	4.6	55.6
‘RGC 1029’	41.9	31.9	6.4	3.8	31.8	4.6	53.4
‘RGC 1030’	46.3	28.0	5.7	4.3	28.7	4.0	57.4
‘RGC 1033’	42.4	26.9	6.1	2.9	34.7	4.9	51.4
‘RGC 1038’	40.8	25.0	6.4	2.7	35.0	4.3	51.7
‘RGC 1055’	36.5	30.3	6.8	4.8	33.9	4.0	50.4
‘RGC 1059’	39.4	33.2	6.6	4.0	32.1	3.5	53.8
‘RGC 1076’	36.8	29.6	6.6	1.8	33.7	3.9	54.0
‘RGC 1077’	40.0	27.4	6.4	2.0	31.9	4.6	55.2
‘RGC 1078’	43.8	28.3	6.3	2.4	33.1	3.7	54.6
‘RGC 1088’	39.5	30.3	5.6	2.9	31.9	4.0	55.6
‘RGC 1092’	36.9	30.6	6.5	2.3	30.7	4.7	55.7
‘RGC 2021’	40.5	25.9	7.4	3.9	33.6	4.5	50.7
‘RGC 986’	43.4	32.1	6.4	3.6	29.9	4.4	55.7
‘RGM 114’	41.6	30.1	5.7	2.4	30.7	4.7	56.5
‘RGM115’	37.8	31.6	6.5	5.1	31.2	5.8	51.5
‘VIKAS 35’	42.1	32.3	6.1	1.8	28.3	4.7	59.1
‘WSP 50’	35.0	28.2	6.1	4.4	33.3	5.1	51.1
Range (Min-Max)	30.4–46.3	23.9–34.2	4.1–8.0	1.8–5.2	28.3–35.0	3.5–6.0	38.8–59.1
Mean	39.6	29.4	6.3	3.4	32.5	4.4	53.0

Table 2 Genetic variation for qualitative traits and analysis of variance for different characters

Source of variation	Df	Endosperm (%)	Gum content (%)	Crude fibre (%)	Crude protein (%)	Fat (%)	Ash (%)	Carbohydrate (%)
Environments	1	105.8**	2.2	1501.8**	1258.4**	25.99**	15.7**	1591.4**
Varieties	39	29.6**	34.00**	0.90**	10.8**	3.92**	1.2**	40.3
Env ×Var	39	22.2**	23.3**	0.9**	11.1**	3.83**	1.2**	45.1**
Error	78	13.28	9.3	0.04	5.60	0.24	0.49	28.90
PCV		10.78	14.64	19.45	9.72	24.11	18.57	15.65
GCV		5.07	11.78	12.28	7.04	11.14	16.71	5.95
Heritability		22	65	40	52	21	81	15
GA as% of mean		4.92	19.51	15.96	10.50	10.60	30.98	4.66
Mean		39.6	29.4	6.31	32.52	3.38	4.43	53.0
Minimum		30.4	23.9	4.1	28.3	1.8	3.5	38.8
Maximum		46.3	34.2	8.0	35.0	5.2	6.0	59.1

** *P*=0.01 * *P*=0.05 GCV, genotypic coefficient of variation; PCV, phenotypic coefficient of variation; GA, genetic advance

Table 3 Correlation coefficient of phenotypic levels

Trait	Endosperm (%)	Gum content (%)	Crude fibre (%)	Fat (%)	Ash (%)	Carbohydrate (%)	Crude Protein (%)
Endosperm (%)	1.00	0.22 **	–0.15	0.02	–0.16 *	0.18 *	–0.18 *
Gum (%)		1.00	–0.06	0.01	–0.14	0.16 *	–0.17 *
Crude fibre (%)			1.00	0.10	0.03	–0.24 **	0.12
Fat (%)				1.00	–0.05	–0.1278	–0.14
Ash (%)					1.00	–0.27 **	0.18 *
Carbohydrates (%)						1.00	–0.65 **
Crude protein (%)							1.00

coefficient of variation (GCV) indicating that the apparent variability in these characters may not only be due to the genotypes but also environmental factors were influential in expressing these characters. Singh *et al.* (2005) also observed similar trends for GCV and PCV in cluster bean. The PCV was higher for fat (24.1%), followed by fibre content (19.5%). It was moderate for endosperm, gum and carbohydrates contents and low for crude protein. High magnitude of GCV was recorded for ash contents (16.7%), followed by crude fibre (12.3%). It was moderate for endosperm, gum and fat content and low for carbohydrates and crude protein content. It is clear indication of presence of genetic diversity among the genotypes.

The heritability in conjunction with genetic advance is more useful than heritability alone in the prediction of resultant effect of selecting the best individual (Singh *et al*. 2010). In the present investigation heritability ranged from 15% for carbohydrates to 81% in ash content. Similar observations were recorded by Chaudhary *et al.* (2003) in clusterbean. The high value of heritability for ash content demonstrated that this is least influenced by environmental changes, moderated values for gum, fibre and protein suggested that to some extent environment influenced the expression of these traits. Low values for endosperm, fat and carbohydrates indicated that these traits were highly influenced by the environmental changes. The high estimates of heritability coupled with higher genetic advance for ash, gum, protein and fibre content indicated the high contribution of additive gene effects, hence direct selection may be effective for these traits. High estimates of heritability and genetic advance have been observed for many traits by a number of workers (Pandiyan *et al*. 2006, Singh and Arora 2002). Genetic analysis revealed that both additive and non-additive gene effects were operated in expression of gum and protein content in cluster bean (Singh *et al.* 2005).

Correlation

Phenotypic correlation of different proximate components revealed that carbohydrate had positive correlation with endosperm and gum content, whereas it showed negative association with crude fibre, crude protein and ash content indicating that carbohydrate inhibits these biochemical parameters (Table 3). Endosperm showed significant positive association with gum content (0.22) and negative association with crude protein (–0.18) and ash (–0.16). Crude protein was significantly and negatively correlated with carbohydrate (–0.65), endosperm (–0.18) and gum content (–0.17), whereas it showed significantly positive association with ash content (0.18). Carbohydrate exhibited significantly positive correlation with endosperm and gum content whereas it was negatively but significantly associated with crude fibre, ash and crude protein.

The experiment showed that additive gene effects are important for gum, protein, ash and fibre content as indicated by variability components. Among these traits gum and protein had significant negative while protein and ash had significantly positive association. Whereas, other pairs of association were non-significant. Hence, selection of genotypes for gum and protein may not be carried out with similar genotypes of cluster bean.

Cluster analysis

A dendrogram was obtained by INDOSTAT using a total of 7 qualitative traits. Sixteen genotypes irrespective of their source were grouped in a single large cluster (Cluster III). 'HGS 26–01' was the most diverse genotype among the tested genotypes, further 'HGS 884' and 'HGS 02–20' were genetically diverse for the component traits and could be useful genetic resources. Genetic drift and selection in different environments have caused genetic diversity than the geographical distance as suggested by earlier studies in cluster bean (Singh *et al.* 2003; Henry and Mathur 2008).

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