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Trait Specific Genetic Stocks for Clusterbean [*Cyamopsis tetragonoloba* (L.) *Taub.*] Improvement

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Abstract: Trait specific germplasm is important for altering plant architecture for maximization and stability of the yield. The traits like short duration (early flowering and maturing), branching pattern, pod length, plant height, internode length, peduncle length and determinacy have contributed substantially in the development of new varieties in legumes. However, in cluster bean (*Cyamopsis tetragonoloba* L. Taub.) most of the varieties embody a similar plant architecture and belong to same maturity group with comparable yield potential, limiting the scope for further improvement. The economically important traits like seed weight (test weight ≈3.5 g), pod length (≈6.0 cm), seeds per pod (≈6) and crop duration (≈95 d) have a very narrow range in seed type varieties of cluster bean. Realizing the paucity of diversity in traits for further yield improvement of yield and suitable plant type in guar efforts were made to identify trait specific genotypes to serve as donors. Genotypes possessing short life cycle, longer pods, high seed weight and longer seedling have been reported.

Key words: Guar, Cluster bean, Trait specific germplasm, Early maturing, Test weight.

Clusterbean or guar [*Cyamopsis tetragonoloba* (L.) Taub.] is an economically important annual legume cultivated in north western parts of Indian arid zone (Mahla *et al.,* 2018). It is being grown over an area of 4.0 to 5.0 million hectares in the States of Rajasthan, Haryana, and Gujarat and on some fringes of Punjab, Madhya Pradesh and Uttar Pradesh. More than 80 per cent areas fall under Rajasthan State receiving erratic and less rainfall during the crop growing period of kharif season in general. Traditionally, it serves the purpose of feed, fodder, food and soil enhancer in the regions that have limited choice of crops to grow; and is globally recognized for the industrially important seed borne gum having various applications. Enormous phenotypic plasticity regulating the growth pattern as per soil moisture availability guarantees crop survival during drought spells (Kumar *et al.*, 2017). Plant genetic improvement depends largely on extent of heritable variation available in the gene pool. Crop genetic improvement largely depends on combining of desirable traits from diverse germplasm considering traits contributing high to economic yield. Predominantly, understanding of quantitative inheritance pattern of yield and associated traits in clusterbean has been addressed in past following various biometrical approaches based on field experimentations techniques. However, the qualitatively inherited plant architectural genes are also influencing yield or agronomic traits significantly in the crop (Sharma *et al.*, 2021). In India, genetic improvement efforts are well are accounted by release of over 40 release varieties. However, most of the varieties embody a narrow genetic base depicting similar plant architecture and maturity group with comparable yield potential; limiting the scope for diversification under different growing environments and further yield improvement. The traits like short duration (early flowering and maturing), branching pattern, pod length, plant height, internode length, peduncle length and determinacy have contributed substantially in the development of new varieties in arid legumes (Dadheech *et al.*, 2020; Vishwanath *et al.* 2016). The economically important traits in cluster bean like seed weight (test weight ≈35 g), pod length (≈6.0 cm), seeds per pod (≈6) and crop duration (≈95 d) have very narrow range in seed type varieties (Dadheech *et al.*, 2019; Jukanti *et al.*, 2015; Boghara *et al.*, 2016) which depicts genetic limits for further genetic improvement. Realizing the paucity of

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Table 1. Mean grain yield and days to maturity assessed for promising entries of clusterbean over three locations consecutively for four years

Entry	Grain yield (kg ha^{-1})					Days to maturity				
	JOD		JS	BK	Mean	JOD		JS	BK	Mean
	SM	KF				SM	KF			
CAZG-17-4-1	1113	1108	956	989	1042	98.0	92.6	95.0	87.7	93.3
CAZG-17-4-5	1324	1003	719	850	974	96.0	91.9	95.0	87.7	92.7
CAZG-18-4	1244	800	872	788	926	94.0	92.7	93.0	91.0	92.7
CAZG-19-6	1197	951	718	904	942	99.0	93.9	95.0	88.7	94.2
CAZG-19-7	1226	983	947	787	986	97.0	95.3	94.7	91.3	94.6
CAZG-19-9	1215	1195	509	756	919	98.0	93.4	92.0	87.3	92.7
CAZG-19-10	1219	1241	546	1072	1020	95.0	93.5	94.3	88.3	92.8
CAZG-20-7	1142	612	1347	976	1019	96.0	93.6	95.0	86.7	92.8
CAZG-20-8	1022	845	1664	890	1106	96.0	91.7	91.7	90.3	92.4
CAZG-20-11	1168	510	1400	1018	1024	99.0	93.7	93.7	91.3	94.4
CAZG-20-13	1057	634	1419	802	978	98.3	92.4	93.3	88.7	93.2
CAZG-20-16	1000	616	697	1106	855	82.3	81.6	80.7	83.0	81.9
CAZG-20-17	1118	743	775	662	825	76.7	78.7	80.0	80.7	79.0
CAZG-20-20	1143	853	1197	856	1012	94.6	92.3	94.7	86.7	92.1
CAZG-20-25	1081	513	1505	1256	1089	97.7	92.7	94.3	86.7	92.9
CAZG-20-28	1110	681	734	1166	923	95.7	93.7	95.0	89.7	93.5
CAZG-20-29	1094	410	1183	1161	962	94.7	91.4	93.3	89.3	92.2
HG-2-20 (Ch.)	1086	678	928	802	873	101.3	94.9	90.3	91.3	94.5
RGC-1033 (Ch.)	992	639	789	699	780	98.9	93.7	89.9	91.6	93.5
RGC-1066 (Ch.)	931	571	770	667	735	102.7	95.3	90.4	92.9	95.3

Ch.: Check; SM: Summer; KF: Kharif; JOD: Jodhpur; JS: Jaisalmer; BK: Bikaner

diversity in clusterbean for yield contributing traits further improvement of yield may be achieved by breeding suitable plant types; efforts has been placed to develop trait specific genotypes to use as donors for breaking the yield plateau realized by narrow genetic base in clusterbean.

In year 2015, mutation was done in three morphologically distinct parents viz., HG-2-20 (Branched hispid cultivar), CAZG-15-6 (Branched glabrous dual purpose genotype) and CAZG 15-3 (Single stem hispid input responsive genotype) with graded doses of gamma rays (0-1600 Gy). In kharif 2015, 500 mutated seeds per treatment of each parent were sown in the field along with untreated parental seed as control; Fifty healthy plants were harvested from each treatment individually for raising M_2 population along with parents. In kharif 2016, over 2000 M_2 plants were phenotypically selected for further evaluation. Among the selection, few distinct mutants were identified for early maturity (short duration), high seed weight and elongated first three nodes (ground clearance) traits. To assess the performance of these trait specific genotypes, each were sown in 4 rows of 4 meter length spaced at 50 cm apart with plant to plant spacing of 10 cm in various field trials in Randomized Block Design with 3 replications along with test entering & check varieties consecutively for four years i.e., 2018 to 2021 at three locations ie., Jodhpur (summer and kharif season), Bikaner (kharif season), Jaisalmer (kharif season). In a set of 20 genotypes, two short duration genotypes were evaluated with 15 promising genotypes and 03 commercial cultivars varying for maturity duration. In another set one high seed weight and pod length genotype was tested with four cultivars and one promising genotype varying for seed weight and pod length. Moreover, inheritance study was conducted for a mutant with longer first three nodes; chi-square test was done to determine the goodness of fit.

The results for the each experiments showed high heritability of the specific traits for which the mutants were selected. The three mutants viz., CAZG-20-17 (Early maturing), CAZG-109

Fig. 1. *Field view of early maturing genetic stock CAZG-20-17 compared to Checks*

(High seed weight) and CAZG-110 (Slender with ground clearance) are potential donors for the identified traits. Description of each mutant and their comparison with other genotypes are presented below:

CAZG-20-17 (Short duration - Early maturing genotype): Mutant CAZG-20-17 is isolated from mutated population of the parent HG-2-20. It was compared with 19 entries in the trial; CAZG-20-17 showed earliest maturity duration of 79 days followed by CAZG-20-16 (81.9 days) (Table 1, Fig. 1). Days to maturity showed insignificant variation in the test entries over seasons and locations indicating predominance of genetic control. CAZG-20-17 and CAZG-20-16 showed more stability in expression for days to maturity while having comparable yields with commercial cultivars viz., HG-2-20, RGC 1033 and RGC 1066. Hence, they have potential as early cultivars or may serve as potent donors for breeding of early maturing high yielding varieties. Besides earliness, CAZG-20-17 shows basal branching behavior coupled with regular bearing and determinate growth habit, shorter internodes and rough surface (hairy). Early maturing genotypes have played a significant role in enhancing and stabilizing the yield in drought prone arid regions. Such genotypes are recognized for their effective completion of life cycle with fewer rain events which is a trend observed in last few decades (Vishwanath *et al.*, 2016). Genotypes/cultivars of different maturity duration are important for maximization of returns under different cropping systems.

Table 2. *Pooled performance of pod and seed characteristics observed in promising genetic stock*

Genetic stock	Pod length (cm)	Pod width (mm)	Seeds per pod	Test weight (g)
CAZG-102	6.3	7.6	8.6	28.8
RGC-936 (Ch)	5.9	7.9	7.4	32.1
HG-2-20 (Ch)	6.1	7.4	7.6	36.7
RGC-1066 (Ch)	6.1	8.3	8.0	33.8
Pusanavbahar (Ch.)	9.9	9.5	9.0	37.4
CAZG-109	12.3	10.9	9.6	46.8

Ch.: Check

CAZG-109 (High seed weight): Mutant CAZG-109 is isolated from mutated population of the parent CAZG-15-6. CAZG-109 have characteristics feature of long pod length (12.3 cm) and bold seed (test weight 46.8 g); CAZG-109. Five genotypes/cultivars were compared with the mutant; Pusanavbahar, a vegetable type variety showed maximum test weight (37.4 g) after CAZG-109, while CAZG-102 had minimum (28.8 g) (Table 2, Fig. 2). CAZG-109 expressed high values for pod length (12.3 cm), pod width (10.9 mm) and seeds per pod (9.6). Seed weight has been recognized as one of the important trait contributing to seed yield in most of the field crops. The test weight of released seed type varieties of clusterbean have been reported to be around 33 g (30-37 g). Interestingly, in clusterbean pod length and seed weight either lacked significant correlation or were negatively correlated to seed yield (Mittal *et al.*, 1971; Dadheech *et al.*, 2020; Jukanti *et al.*, 2015; Boghara *et al.*, 2016); nonetheless, if genetic source having large seed and longer pods are available it would be desirable for incorporating them in breeding program with a long term goal. Seed weight and pod length showed positive correlation with yield per plant among seed type varieties having pod length <6 cm and seed weight <3.6 g (Sharma

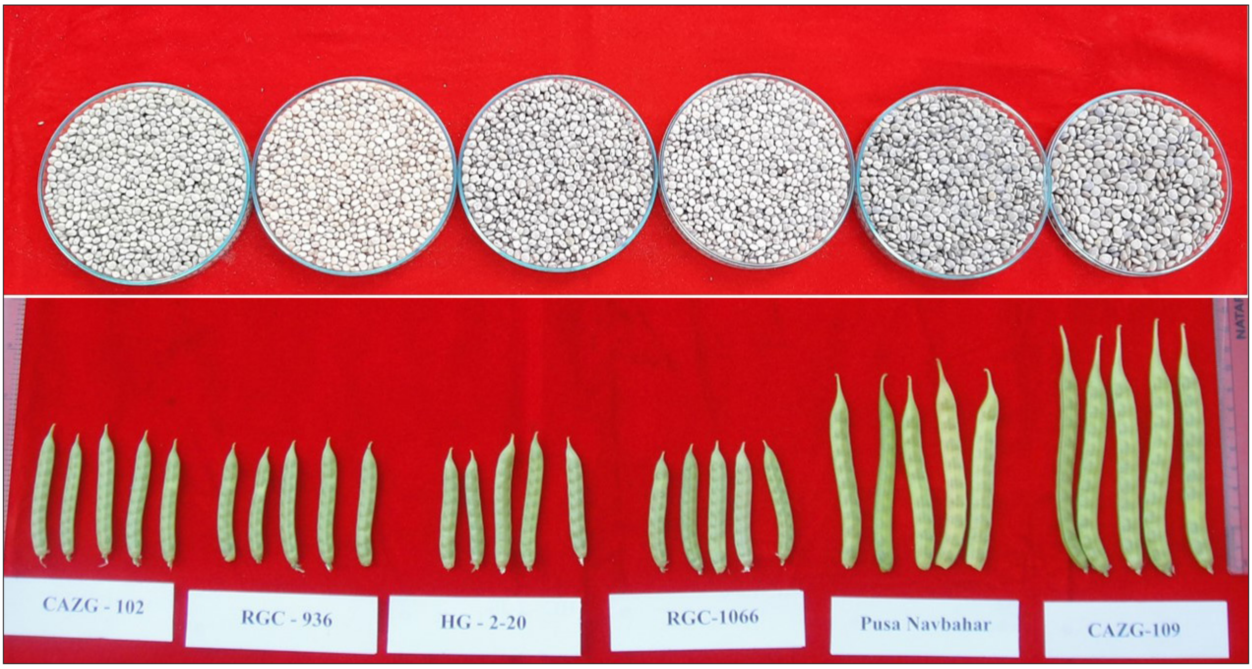

Fig. 2. Comparison of pods and seed of genetic stock CAZG-109 with checks.

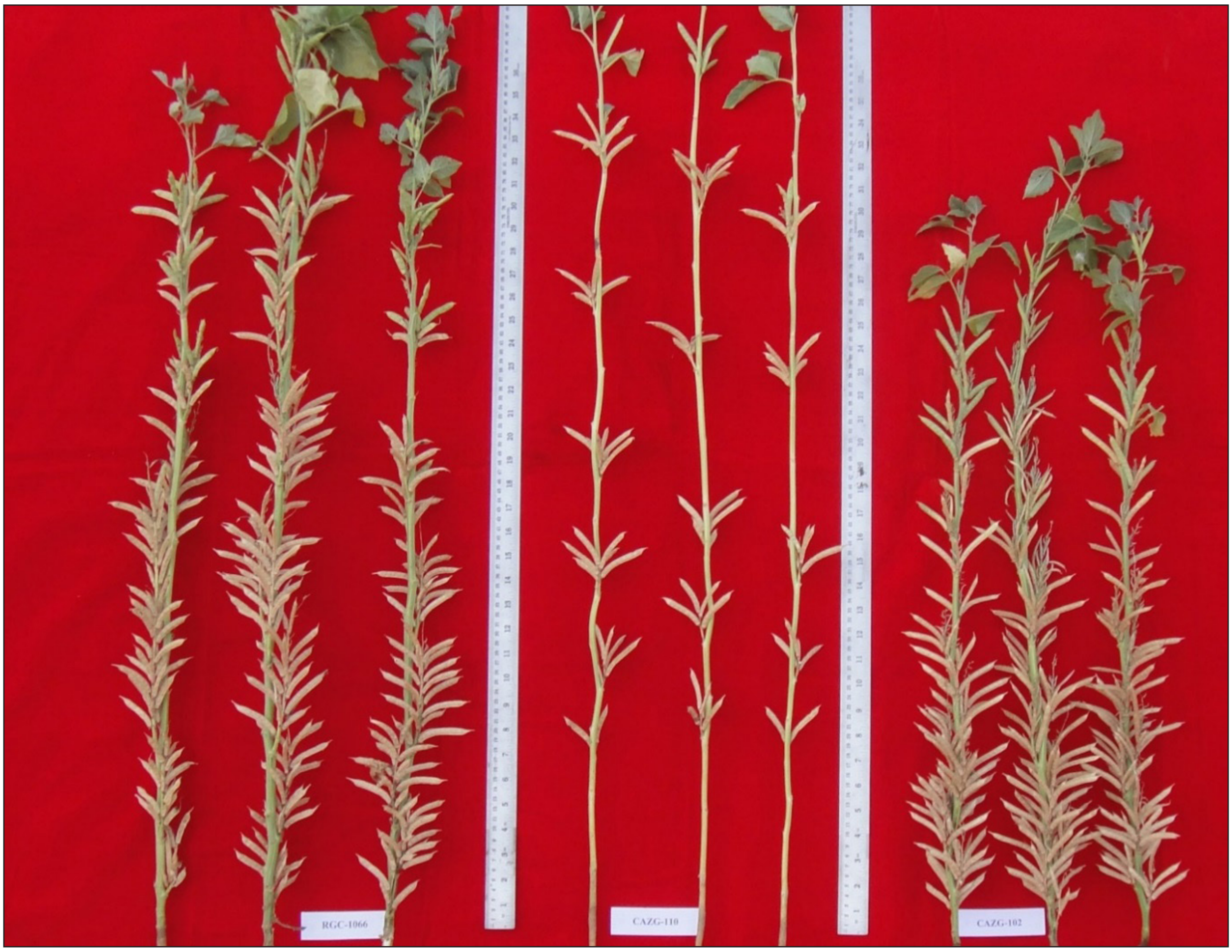

Fig. 3. Comparative view of ground clearance of genetic stock CAZG-110 (middle).

Table 3. Inheritance pattern of CAZG-110 trait (slender with ground clearance)

Phenotype	Observed plants (no.)	Expected plants (no.)	Observed – expected plants (no.)	$(Obs\text{-}Exp)^2$	$\chi 2$	P-value
Normal	111	114	3	9	0.0789	-
Slender	41	38	-3	9	0.2368	-
				Σ	0.3158	0.5742

et al., 2021). Thus there is possibility of altering linkages in favorable direction. Hence, CAZG-102 could be desirable donor for improving pod length, seeds per pod and seed weight depending upon linkages with other yield attributing traits especially pods per plant. Morphologically, CAZG-109 is branched, luxuriant, glabrous having long and thick pods that are suitable for vegetable type.

CAZG-110 (Slender with ground clearance): Mutant CAZG-110 is isolated from mutated population of the parent CAZG-15-3. CAZG-110 is a slender mutant having thin stem and longer seedlings. The first three nodes of this mutant were elongated to produce taller seedlings (Mahla *et al.*, 2018). The shoot of legumes is composed of a series of growth units called metamers. A metamer consists of an internode, leaf and axillary bud, in the mutant subsequent metamers had normal internode length but plants developed were thin and slender bearing normal pods but on alternative nodes. Clusterbean grows erect with branching appearing at varying angles taking up bush structure from combined elongation of main stem and branches. Internode length is crucial to develop a plant architecture influencing production potential of the genotype. Alike in legumes the initially produced 4 metamers of main shoot in clusterbean are separated by very short immeasurable internodes (Jim *et al.*, 2006). This gives the primary axis of vegetative growth a very pressed appearance and seedlings show stunted appearance. Later metamers appear with measurable internode size and bear trifoliate leaves showing abrupt seedling growth. Internode size varies along the length of stem appearing at different plant growth stages influencing the plant architecture. Each axillary bud has the capacity to develop into either axillary shoot or inflorescence. The slender types produced true to type progenies while normal types produced both segregating and true breeding progenies. A cross between parent CAZG-15-3 and true breeding mutant produced normal F_1 and F_2 plants segregated in a 3 normal: 1 slender ratio (Table 3). This confirmed the single gene inheritance with slender mutant being recessive. Having thin and weak stem and low yield this mutant may not have an obvious advantage. However, a greater ground clearance with early flowering may prove advantageous for mechanical harvesting. The mutant might be useful to understand evolutionary importance of shortening of first 4 nodes in legumes and its role in increased thickness and strength of stem.

The importance of trait specific germplasm may not be ignored in crop improvement practices. While such material has direct application in the improvement of desired trait for varietal release, it can be useful in basic genetic and molecular studies. The three trait specific genotypes identified in the present study viz., CAZG-20-17 (early maturing), CAZG-109 (high seed weight) and CAZG-110 (Slender with ground clearance) would be helpful in developing desired plant architecture in clusterbean for genetic improvement.

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