RESEARCH ARTICLE

DIVERGENCE STUDIES IN INDIAN CLUSTER BEAN (*CYAMOPSIS TETRAGONOLOBA* L. TAUB.) FOR DEVELOPING VARIETY FOR VEGETABLE PURPOSE

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Received-06.04.2019, Revised-27.04.2019

Abstract: In a quest for developing improved vegetable type guar, the available germplasm at ICAR- Indian Institute of Horticultural Research, Bangalore collected from different parts of the country were evaluated. Narrow genetic base of the crop due to its self-pollinated nature is a hindrance in getting variability in natural pollination. But, hybridization based on genetic distance is a potential tool to get transgressive segregants. Therefore, this study was formulated to estimate the divergence present in the population and based on their genetic distance the genotypes were classified into 4 different clusters. Inter cluster distance was found maximum between cluster II and IV followed by between cluster I and III and cluster I and II. As the objective is to develop vegetable guar, hybridization between genotypes of cluster I (vegetable guar) and distant genotypes with the desirable trait from different cluster will be advantageous. Direct selection for traits like yield per plant and plant height in cluster I was done to identify the potential parents due to their maximum contribution toward divergence. Based on their genetic distance with desirable genotypes of other clusters which have the supplementary traits missing in cluster I, 11 crosses has been identified which has the potential to bring worthwhile improvement in vegetable guar.

Keywords: Cluster bean, Divergence, Diversity, SAS, Vegetable guar

INTRODUCTION

In India, cluster bean/ guar (*Cyamopsis tetragonoloba* L. Taub.) is considered as a highly nutritious vegetable of family *Leguminosae.* Apart from its tender nutritious pods, it also acts as an excellent green manure crop for its nitrogen fixing ability. Being a hardy crop, it requires a low input and amenable to high density planting. Therefore, suitable for small and marginal farmers. In recent past, this crop has got visibility for its galactomannan gum content which has a high export value and many new varieties have been developed in India with high gum recovery. Mainly, north Indian arid and semi-arid states are cultivating guar for gum purpose. India shares 80% of total world production (Boghara *et al.*, 2010). However, its use as a vegetable is still under-exploited. In South Indian states, it is grown as a vegetable unlimited scale and in north Karnataka districts it is grown year round. But breeding for gum type and vegetable type varieties are entirely different hence, varieties developed for gum cannot be best fitted as vegetable. In India, cultivars (vegetable type) available in public domain are developed long time ago and do not match the productivity level of commercial varieties. Therefore, an intensive breeding programme for vegetable type guarwas initiated which can improve the genetic gain under low input conditions.

In self-pollinated crops like guar, germplasm is available in the form of an array of homozygous lines which can be directly released as genetically improved cultivars after selection but creation of variation is not possible this way. However, for a long-term crop improvement programme, diversity is the pre-requisite which can be achieved through hybridization and subsequent selection for quantitatively inherited traits (Singh *et al.*, 2005). For broadening the genetic base of cultivars, the genetic diversity present in cultivated and wild relatives must be explored (Mishra *et al.*, 2010). Therefore, a study was under taken to determine the variation present in the germplasm and then grouping the genotypes into different clusters based on their genetic distance. Based on which choice of parents for bi-parental mating can be done particularly for getting transgressive segregants for quantitative traits (Arunachalam *et al.*, 1984).

MATERIALS AND METHODS

The study was conducted during Kharif, 2018 at ICAR- Indian Institute of Horticultural Research, Bangalore, Karnataka, India (Latitude: 13^0 $7^{'}$ N and Longitude: 77^0 $29^{'}$E ; altitude 890 MSL). A total of 38 genotypes of guar collected from different regions of India were evaluated in Randomized Block Design (RBD) with three replications. Bunds of size 2 x 1 m. were made and the row to plant spacing was maintained at 60 x 20 cm. The crop was raised as per the recommended package of practices for guar in Karnataka, India. Observations were recorded on 5 randomly selected plants per replication for each genotype for various characters namelydays to 1st flowering (DF), number of pods per plant (NPP), yield per plant (YP), pod length (PL), pod breadth

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(PB), single pod weight (PW), number of clusters per plant (NCP), number of pods per cluster (PC), plant height (PH) and number of seeds per pod (SP).PROC GLM sub routine of Statistical Analysis System (SAS V 9.3, 2012) was utilized to build up programming codes to evaluate the significant difference ($p<0.05$) among the genotypes individually for all the traits. Least significant Difference (LSD) was computed as a Post-hoc test (Cochran and Cox, 1957). Using quantitative traits the genetic distance among the populations is calculated using D^2 statistics (Rencher, 1995) on the basis of multiple characters. PROC CLUSTER sub routine of Statistical Analysis System (SAS V 9.3, 2012) was utilized to build up programming codes to study the genetic divergence based on Euclidean distance following Ward's method for clustering (Ward,1963). Ward's minimum variance method was used to generate a dendrogram. Contribution of traits for divergence was also estimated and presented graphically for ease of understanding.

RESULTS

The result of analysis of variance (ANOVA) (Online Supplementary Table S1) in the present investigation revealed significant differences (at $p<0.05$) among the genotypes for all the traits.The dendrogram generated by Ward's minimum variance method classified the genotypes into 2 broad groups (Fig. 1). First group includes the slower seed development types with longer pods and 2nd group includes the faster seed development types. 2nd group was further classified into 3 sub group *viz.*, i.) bold seeded with more parchment tissues and small pods, ii.) bold seeded but fleshy, small to medium pods and iii.) bold seeded, fleshy medium long pods. All together it was grouped into 4 clusters,as justified by the screen plot presented beneath the dendrogram. Cluster II got maximum (19) genotypes followed by cluster I (11), cluster III (7) and cluster IV got minimum (1) genotype (Table 1). Cluster wise mean performance for each trait was estimated (Table 2). It is observed that Cluster I is superior in terms of DF (29.57), YP (153.22), PL (11.92), PB (1.00), PW (2.83), PH (130.89), SP (7.58) and it includes all the vegetable podded type non branchedgenotypes. Cluster II showed maximum NPP (137.85) and PC (12.24). But it was of medium height plant with branching and late flowering type with smaller and shorter pods. It includes mostly the genotypes suitable for dual purpose (both for pod and seeds). Cluster III includes dwarf plants (33.34) with medium to small pods (7.07) and more NPP (102.54), hairy pods with bold seeds (Table 2). These are the varieties grown for seeds. Whereas, Cluster IV has only one genotype IIHRCB 30which is a private variety developed by Sarpan Hybrid seeds company and it is an improved dual purpose variety developed having more NCP(26.9)(Table 2).Intra cluster distance is maximum in cluster III (3.4114). Minimum inter cluster distance was observed between cluster II and III (3.3262) and maximum inter cluster distance was observed between cluster II and IV (6.5112) followed by between cluster I and III (5.7682); I and II (5.7081); cluster III and IV (5.5378) and cluster I and IV (5.407) (Table 3).Out of 10 characters, as elucidated by the pie-chart (Fig. 2) YP contributed to maximum diversity of 15% followed by PH (12%). Based on that, IIHRCB 01, IIHRCB 04, IIHRCB 05 and IIHRCB 23 were selected from cluster I to be used as first parent in hybridization programme. To identify the source for the traits like NPP, NPC and NCP, the genotype showing higher mean values were identified. For NPP plant genotypes identified are IIHRCB 31(170.1), IIHRCB 38 (169.0) and IIHRCB 11 (155.0); for NCP genotypes identified are IIHRCB 30 (26.9) and IIHRCB 27 (26.3); for PC, IIHRCB 31 (18.6), IIHRCB 34 (16.35), IIHRCB 18 (15.55) and IIHRCB 38 (15.45) respectively (Table 4). Based on their genetic distance with identified genotypes from cluster I, crosses were identified (Online supplementary Table S2). It was noted that genetic distance is higher between the genotypes compared to their inter cluster distance except in case of IIHRCB 23 x IIHRCB 30, IIHRCB 01x IIHRCB 27, IIHRCB 04 x IIHRCB 27, IIHRCB 05 x IIHRCB 27 and IIHRCB 23 x IIHRCB 27. Total 23 crosses (IIHRCB 01 x IIHRCB 31, IIHRCB 01 x IIHRCB 38, IIHRCB 01 x IIHRCB 11, IIHRCB 01x IIHRCB 30, IIHRCB 01 x IIHRCB 34 and IIHRCB 01 x IIHRCB 18, IIHRCB 04 x IIHRCB 31, IIHRCB 04 x IIHRCB 38, IIHRCB 04 x IIHRCB 11, IIHRCB 04 x IIHRCB 30, IIHRCB 04 x IIHRCB 34,IIHRCB 04 x IIHRCB 18, IIHRCB 05 x IIHRCB 31, , IIHRCB 05 x IIHRCB 38, IIHRCB 05 x IIHRCB 11, , IIHRCB 05 x IIHRCB 30,, IIHRCB 05 x IIHRCB 34, , IIHRCB 05 x IIHRCB 18, IIHRCB 23 x IIHRCB 31, IIHRCB 23 x IIHRCB 38, IIHRCB 23 x IIHRCB 11, IIHRCB 23 x IIHRCB 34 and IIHRCB 23 x IIHRCB 18) were identified to give improvement in vegetable type guar in terms of NPP, NPC and NCP. As the genotypes IIHRCB 31 and IIHRCB 38 have the potential for simultaneous improvement of NPP and PC, The number of crosses were narrowed down to 11 (Table 4) namely, IIHRCB 01 x IIHRCB 31, IIHRCB 01 x IIHRCB 38, IIHRCB 04 x IIHRCB 31, IIHRCB 04 x IIHRCB 38, IIHRCB 05 x IIHR 31, IIHRCB 05 x IIHRCB 38, IIHRCB 23 x IIHRCB 31 and IIHRCB 23 x IIHRCB 38, IIHRCB 01 x IIHRCB 30, IIHRCB 04 x IIHRCB 30 and IIHRCB 05 X IIHRCB 30.

DISCUSSION

Above study on genetic divergence, classified the genotypes into different clusters based on their domestication since introduction. History suggests that, it is a crop of African origin and was introduced to India as a fodder crop between 9th to 13th century AD during Arab-Indian trade. Domestication happened around 1000 years ago in dry region of North-West Indo-Pakistan subcontinent (Hymowitz,1972). Gopal Krishnan *et al.* (2011) confirmed the presence of a linking species between the wild and cultivated one known as Adak guar in the arid region of north-west India where it is grown mainly for the gum content and fodder purpose. Important traits of domestication syndrome observed in cultivated guar includes compact growth habit, indehiscence of pods, loss of seed dormancy, edible pods, large seed size and cylindrical seed shape (Gopal Krishnan *et al.*, 2011). Currently, India has the maximum diversity in cluster bean owing to its different uses such as gum, fodder, vegetable and green manure etc. In the present investigation, we found inter cluster distances are always higher than intra cluster distance but, higher intra cluster distance in cluster IIIindicateda lot of scope for exchange of genetic materials among genotypes within these cluster.Minimum inter cluster distance between cluster II and III indicated that one group has little improvement over the other for few traits only.The objective here is to develop vegetable type varieties and all of them are included in Cluster Iwith few defects namely, less NPP, less NCPand PC. Hybridization with distant parent is an alternative to improve them. Further, the characters contributing the most towards divergence is responsive towards effective selection and the choice of parentsfor hybridization.So, direct selection for tall plants with more YP will be useful in improvement of vegetable guar. Choudhury and Kumhar (2010) also had similar observations while studying diversity in cluster bean. Based on that,genotypesfrom cluster I were selected to be used as first parent in hybridization programme. To supplement the traits like NPP, PC and NCP in them second parents were also identified from other clusters based on their higher mean performance.Genetic distance between the parents were referred to identify the crosses with potential of giving desirable recombinants. Because higher the genetic distance, more is the chance of getting transgressive segreggants. Here genotypes showing more genetic distance then their corresponding inter cluster distance were selected as second parents. Based on which 8 potential crosses were identified.

Table 1. Analysis of variance (mean sum of squares) for 10 characters in cluster bean

	DF	**NPP**	**YP**	**PL**	**PD**	**PW**	**PH**	**NCP**	**PC**	**SP**
Replication **(df=1)**	2.22	525.74	517.55	0.16	0.01	0.02	63.41	0.05	0.26	0.01
Genotype (df=37)	27.79*	3499.46*	2069.08*	14.1*	0.5*	1.73*	3220.13*	60.4*	57.51*	2.82*
Error (df=37)	0.65	130.32	206.57	0.16	0.01	0.02	62.5	4.24	5.05	0.07

*significant at $p<0.05$ level, DF: Days to flowering, NPP: Number of pods per plant, YP: Yield per plant (g), PL: Pod length (cm), PD: Pod breadth (cm), PW: single pod weight (g), PH: Plant height (cm), NCP: Number of clusters per plant, PC: Pods per cluster, SP: seeds per pod

Table 2. Clustering pattern of 38 genotypes of cluster bean based on Euclidean distance following Ward's method and the member present in each respective cluster

Cluster	**Number of genotypes**	**Genotype**
I	11	IIHRCB 01 , IIHRCB 05, IIHRCB 33, IIHRCB 02, IIHRCB 04, IIHRCB 23, IIHRCB 22, IIHRCB 32, IIHRCB 37, IIHRCB 03, IIHRCB 06
II	19	IIHRCB 07, IIHRCB 29, IIHRCB 11, IIHRCB 31, IIHRCB 36, IIHRCB 09, IIHRCB 12, IIHRCB 34, IIHRCB 20, IIHRCB 38, IIHRCB 13, IIHRCB 16, IIHRCB 17, IIHRCB 08, IIHRCB 14, IIHRCB 25, IIHRCB 24, IIHRCB 15, IIHRCB 35
III	7	IIHRCB 10, IIHRCB 27, IIHRCB 18, IIHRCB 28, IIHRCB 19, IIHRCB 21, IIHRCB 26
IV	1	IIHRCB 30

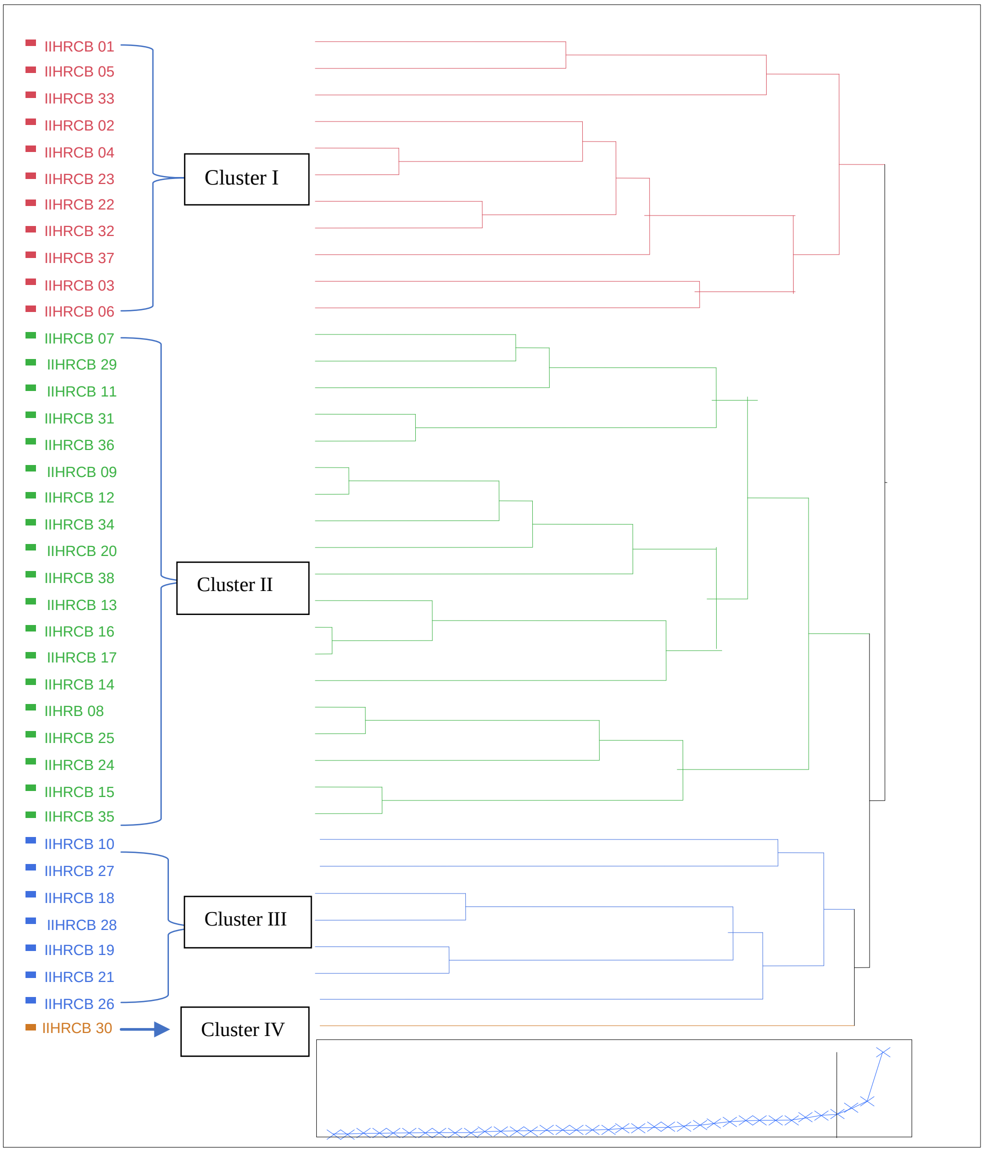

Figure 1: Dendrogram showing cluster bean genotypes in different clusters

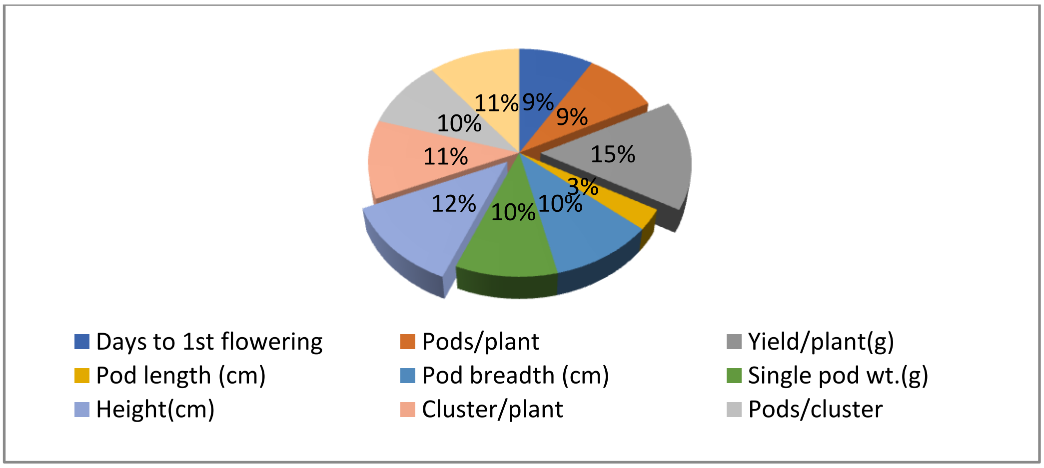

Figure 2: Contribution of various traits for cluster bean diversity

Table 3. Cluster wise mean performance for 10 different quantitative traits

	DF	**NPP**	**YP**	**PL**	**PD**	**PW**	**PH**	**NCP**	**PC**	**SP**
Cluster I	29.57	55.26	153.22	11.92	1.00	2.83	130.89	19.61	2.99	7.58
Cluster II	36.28	137.85	138.47	6.38	0.70	1.01	70.88	11.94	12.24	6.88
Cluster III	33.63	102.54	113.21	7.07	0.75	1.16	33.34	12.57	10.04	5.50
Cluster IV	35.80	31.30	71.60	11.30	0.90	2.30	102.50	26.90	1.20	3.20

DF: Days to flowering, NPP: Number of pods per plant, YP: Yield per plant, PL: Pod length, PD: Pod breadth, PW: single pod wt., PH: Plant height, NCP: Number of clusters per plant, PC: Pods per cluster, SP: seeds per pod

Table 4. Average inter and intra cluster distance among the four clusters of cluster bean

Average intra and inter cluster D^2 values				
Cluster	**I**	**II**	**III**	**IV**
I	**2.6671**	5.7081	5.7682	5.4047
II		**2.1256**	3.3262	6.5112
III			**3.4114**	5.5378
IV				**0.0000**

*****Values in bold fonts indicate intra cluster distance

Table 5. Best genotypes identified for traits like number of pods per plant, number of clusters per plant and pods per cluster along with their values

Trait	**Genotype**	**Cluster**
Number of pods per plant	IIHRCB 31(170.1) IIHRCB 38 (169.0) IIHRCB 11 (155.0)	II II II
Number of clusters per plant	IIHRCB 30 (26.9) IIHRCB 27 (26.3)	IV III
Pods per cluster	IIHRCB 31 (18.6) IIHRCB 34 (16.35) IIHRCB 18 (15.55) IIHRCB 38 (15.45)	II II III II

Table 6. Genetic distance between genotypes of cluster I and the best genotypes identified to be used as parent

	IIHRCB 31	**IIHRCB 38**	**IIHRCB 11**	**IIHRCB 30**	**IIHRCB 27**	**IIHRCB 34**	**IIHRCB 18**
IIHRCB 01	7.09*	6.02*	5.75*	6.73*	5.00	6.27*	7.41*
IIHRCB 04	7.51*	6.55*	6.12*	6.10*	5.29	6.56*	7.33*
IIHRCB 05	7.70*	6.60*	6.45*	6.66*	5.33	6.90*	7.89*
IIHRCB 23	7.15*	6.34*	5.70*	5.19	4.79	6.42*	6.95*

*****indicates genotypes having higher genetic distance than their respective inter cluster distance

Table 7. Parents predicted to give desirable recombinants

P1	**P2**	**Trait to be improved**
IIHRCB 01 x	IIHRCB 31 IIHRCB 38 IIHRCB 30	NPP, PC NPP, PC NCP

IIHRCB 04 x	IIHRCB 31	NPP, PC
	IIHRCB 38	NPP, PC
	IIHRCB 30	NCP
IIHRCB 05 x	IIHRCB 31	NPP, PC
	IIHRCB 38	NPP, PC
	IIHRCB 30	NCP
IIHRCB 23 x	IIHRCB 31	NPP, PC
	IIHRCB 38	NPP, PC

NPC: Number of pods per plant, NCP: number of clusters per plant and PC: pods per cluster

CONCLUSION

Production and productivity level of vegetable guar has reached a plateau because of continuous selection within the same vegetable type germplasm. To create variation and to get transgressive segreggants, hybridization between divergent parents from different cluster is a potential option. From the above investigations, we identified 3 genotypes (IIHR 31, IIHR 38 and IIHR 30) with the potential to bring improvement in terms of NPP, PC and NCP.Using them,11 crosseshave been identified to give worthwhile improvement. Further evaluation of the hybrids and their subsequent generations is required to identify the improved vegetable type and to prove the robustness of genetic divergence study in crop improvement.

ACKNOWLEDGEMENTS

The authors express their gratitude to Director,ICAR-IIHR for extending all necessary facilities by granting permission to carry out the research work and SSCNARS, IASRI for providing SAS V 9.2 software to the nodal centre ICAR-IIHR under NAIP project.

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