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Genetic variation studies among physiological characters in *Cyamopsis tetragonoloba* (L.) under rainfed condition of Jaisalmer district Rajasthan, India

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ABSTRACT

The multiple plant traits associated with drought were assessed in 21 genotypes of cluster bean including check RGC-936 for their contribution to rainfed adaptation of the genotypes. All the assessed traits showed significantly different genotypic responses under rainfed conditions. Clusterbean genotypes showed wide range of variability for most of the characters and all the traits exhibited broad spectrum of ranges during both years. Total sugar content, specific leaf area at 30 and 45 DAS, number of branches plant^{-1}, number of clusters plant^{-1}, number of pods cluster^{-1} and seed yield plant^{-1} showed high genotypic (Vg) and phenotypic (Vp) variances. The high estimates of heritability coupled with high values of genetic advance over mean (GAM) were observed for the characters such as total sugar content, specific leaf area at 45 DAS, clusters plant^{-1} and seed yield plant^{-1} indicates predominance of additive component for these traits and hence direct selection would be more effective in improving these traits. Correlation study revealed that number of clusters plant^{-1} (0.81**, 0.84**), number of pods cluster^{-1} (0.69**, 0.86**), pod dry weight (0.99**, 0.67**) showed positive significant correlation with seed yield plant^{-1} during both the years which indicates strong association of these characters with seed yield plant^{-1}. On the basis of above findings, it can be concluded that the characters like, number of clusters plant^{-1}, number of pods cluster^{-1}, showed positive significant correlation with seed yield plant^{-1}. Thus, these traits may be considered as effective parameters of selection to increase seed yield of clusterbean under rainfed situation of Jaisalmer.

Key words: Clusterbean, Correlation, Genetic advance, Genotypic variance, Heritability, Phenol and sugar content, Phenotypic variance, Seed yield.

INTRODUCTION

Clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.], a summer growing annual legume of dry land agriculture is having drought tolerant characteristics with deep rooted system. It grows well in soils with low fertility in the arid and semi-arid areas of the tropics and subtropics where the rainfall is scanty. India is one of the main producers of clusterbean accounting for 80 per cent of the total production of the world, whereas Rajasthan occupies the largest area (82.1%) under clusterbean cultivation in the country. Total production of guar in India is 2.7 million tons from an area of 5.6 mha with productivity being 485 kgha^{-1} (Bhatt *et al.,* 2017). Rajasthan covered an area of 3.09 mha with the production of 1.47 mt and productivity is 471 kgha^{-1} (Anonymous, 2019). The area, production and yield of the crop are inconsistent due to its overdependence on weather, and production confined to limited geographical area largely arid regions.

Clusterbean is the main *kharif* crop of Jaisalmer district with an area of 2,96,000 ha out of which 2,78,000 ha comes under rainfed. The average productivity of clusterbean in Jaisalmer is just only 83 kgha^{-1} against the India's total average productivity of 478 kgha^{-1}. This is mainly because of very poor rainfall and its variability. The average rainfall of Jaisalmer is just 168mm only. The use of diverse germplasm in crop improvement is one of the most sustainable method to conserve valuable genetic resources and simultaneously to increase agricultural production and food security (Ogwu *et al.,* 2014). The genetic variability provides the basis in selecting the suitable genotypes in any breeding programme. Thus, the present investigation was undertaken to study the genetic variability for physiological, biochemical, growth, yield attributing and seed yield parameters.

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MATERIALS AND METHODS

The present study was carried out at ICAR- Central Arid Zone Research Institute, Regional Research Station, Jaisalmer (Rajasthan), India. The experimental material used in the present investigation consisted of 21 germplasm of clusterbean including check RGC-936. The experiment was laid out in randomized block design with three replications during *kharif* season of 2015 and 2016. Each plot comprised of three rows of 4-meter length, the spacing between row to row and plant to plant was 45 cm and 15 cm, respectively. All agronomic practices were kept same for all the replications and treatments. The observations were recorded on the basis of five randomly selected plants from each replication for different characters *viz*. plant height, number of branches plant^{-1}, number of clusters plant^{-1}, number of pods plant^{-1}, number of seeds pod^{-1}, pod length, canopy temperature depression, specific leaf area, relative water content, 100-seed weight, biological yield plant^{-1}, harvest index and seed yield plant^{-1} while days to flowering and days to maturity were recorded on plot basis.

The total phenolic content of the extract was determined by the Folin-Ciocalteu method of Kaur and Kapoor (2002). The total phenol content was calculated from the calibration curve, and the results were expressed as mg of gallic acid equivalent per g dry weight. Total sugar content was estimated by colorimetric method using anthrone reagent (Dubois *et al.,* 1951). The data were subjected for analysis of variance (Steel *et al.,* 1997). The genotypic and phenotypic correlations were calculated by Kwon and Torrie (1964) technique. The genetic advance in percentage of mean was calculated by using Falconer (1989) formula.

Genetic variance (Vg) =

$$\frac{\text{Genotype mean square (GMS) - Error mean square (EMS)}}{\text{Number of replications (r)}}$$

Environmental Variance = Error Mean Square (EMS)

Phenotypic Variance (Vp) = Vg + Ve / r

Genotypic (GCV), Phenotypic (PCV) and Environmental coefficient of Variation (ECV) was calculated as

$$\text{GCV (\%)} = \frac{\sqrt{V_g}}{\bar{x}} \times 100, \qquad \text{PCV \%} = \frac{\sqrt{V_p}}{\bar{x}} \times 100,$$

$$\text{ECV \%} = \frac{\sqrt{V_e}}{\bar{x}} \times 100,$$

Where,

GCV(%) = Genotypic Coefficient of variation; Vg = Genotypic Variance; PCV (%) = Phenotypic Coefficient of variation; Vp = Phenotypic Variance; ECV (%) = Environmental Coefficient of variation; Ve =Environmental Variance, $\bar{x}$ = germplasm mean.

Heritability (H^2) on Entry Mean Basis was calculated as

$$H^2 = \frac{V_g}{V_p}$$

The expected Genetic Advance for each trait was calculated as

$$\overline{GA} = K\sqrt{V_p H^2}$$

Where,

K = 1.40 at 20% selection intensity for trait; Vp = Phenotypic variance for trait; H^2 = Broad Sense Heritability of the trait. Genetic Advance as percentage of mean is calculated as,

$$GA(\%) = \frac{GA}{\bar{x}} \times 100$$

RESULTS AND DISCUSSION

Soil moisture content

Soil moisture content (%) of field varied from 3.1 to 7.8 in 2015 and 3.8 to 9.5 in 2016 during the cropping season. Further, it was 7.8 and 8.0 at the time of sowing and 3.1 and 3.8 at time of harvest in the year 2015 and 2016, respectively (Fig 1).

Range of variation

The descriptive statistics including the extreme mean values of genotype and the means together with their standard errors obtained on the basis of average data for both the year are summarized in Table 1. In general, clusterbean genotypes showed wide range of variability for most of the characters and the traits exhibited broad spectrum of ranges between maximum and minimum mean values during both years. For instance, the days to 50% flowering ranged from 26.4 to 33.0 during 2015-16 and 24.3 to 34.0 during 2016-17 with mean value of 26.4 and 28.6 respectively. The wide range of variability was also observed for different yield attributing characters. The number of clusters plant^{-1} varied from 5.8 to 14.9 (2015-16) and 8.0 to 30.7 (2016-17) with the mean value of 10.8 and 16.1 respectively. Similarly, the number of pods cluster^{-1} and number of seeds pod^{-1} also ranged from 2.3 to 4.7 and 5.3 to 7.4 during 2015-16 and 3.7 to 7.0 and 7.0 to 8.7 during 2016-17 with mean value of 3.1 (2015-16) and 4.8 (2016-17) for number pods cluster^{-1} and 6.7 (2015-16) and 8.0 (2016-17) for number of seeds pod^{-1}. The seed yield (g plant^{-1}) ranged from 4.0 to 9.7 with a mean of 6.1 during 2015-16 and 7.2 to 18.9 g/plant with a mean value of 13.5 during 2016-17. Thus, it is possible to succeed in improving grain yield by direct selection. The

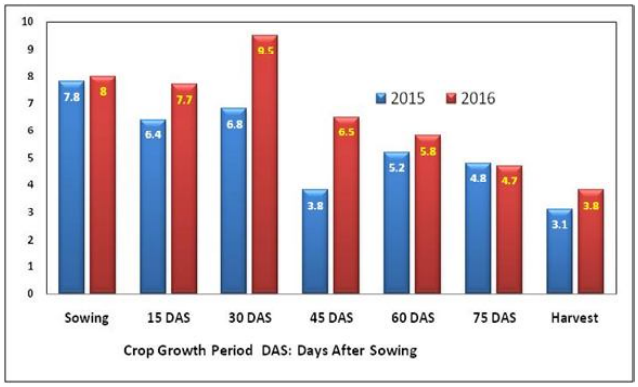


Fig 1: Soil moisture content (%) of Cluster bean field during *Kharif* season of the years 2015 and 2016.

Table 1: Range, mean, standard deviation and critical value of different characters.

Characters/ parameters	Year	Range	Mean ± S.Em	CD	C.V
Phenological					
Days to flowering	2015-16	26.4-33.0	26.4 ± 0.74	2.13	4.88
	2016-17	24.3-34.0	28.6 ± 0.79	2.26	4.79
Physiological					
SLA at 30 DAS (cm^2g^{-1})	2015-16	166.5-435.9	270.4 ± 27.37	78.22	17.53
	2016-17	185.87-358.14	242.9 ± 18.65	53.3	13.3
SLA at 45 DAS (cm^2g^{-1})	2015-16	76.47-289.2	162.5 ± 21.6	61.8	26.3
	2016-17	116.4-260.75	191.0 ± 9.20	23	8.34
RWC at 30 DAS (%)	2015-16	55.97-88.72	74.60 ± 0.53	1.52	5.86
	2016-17	67.94-81.07	75.6 ± 2.05	1.23	4.7
RWC at 45 DAS (%)	2015-16	70.5-96.36	81.29 ± 0.69	1.97	1.47
	2016-17	80.3-91.7	85.73 ± 1.4	4.1	2.9
Biochemical					
Total phenol (mgg^{-1})	2015-16	15.47-26.71	20.21 ± 0.81	2.33	2.12
	2016-17	15.10-22.07	18.38 ± 0.74	6.98	6.29
Total sugar (mgg^{-1})	2015-16	58.76-112.91	82.0 ± 8.9	25.6	9.58
	2016-17	73.97-144.47	100.58 ± 3.35	18.9	5.77
Morphological / yield attributing characters					
Plant height (cm)	2015-16	35.8-62.1	48.6 ± 1.86	5.32	6.63
	2016-17	23.3-40.3	31.05 ± 1.44	4.12	8.05
Number of branches $plant^{-1}$	2015-16	0.7-5.3	3.8 ± 0.30	0.87	13.73
	2016-17	0.7-5.3	3.6 ± 0.52	1.47	24.61
Number of cluster $plant^{-1}$	2015-16	5.8-14.9	10.8 ± 0.77	2.21	3.05
	2016-17	8.0-30.7	16.1 ± 1.07	12.45	11.48
Number of pods $cluster^{-1}$	2015-16	2.3-4.7	3.1 ± 0.26	0.57	1.63
	2016-17	3.7-7.0	4.8 ± 0.57	11.28	20.7
Number of seeds pod^{-1}	2015-16	5.3-7.4	6.7 ± 0.41	1.18	1.47
	2016-17	7.0-8.7	8.0 ± 0.51	10.6	11.07
Total plant dry weight $plant^{-1}$	2015-16	15.7-28.7	21.6 ± 1.23	3.5	9.85
	2016-17	5.0-16.1	10.4 ± 0.87	2.47	14.36
Seed yield (g $plant^{-1}$)	2015-16	4.0-9.7	6.1 ± 0.23	0.67	1.67
	2016-17	7.2-18.9	13.5 ± 0.58	6.58	7.48

results obtained under study for the traits such as the number of pods $plant^{-1}$ at harvest and seed yield $plant^{-1}$ were corresponds well with the works of Kumhar *et al.,* (2012) as they obtained (31.1) and (10.12 g), respectively for the traits under one among different INM treatment (application of 100% RDN through Urea + Rhizobium + PSB). The works of Om Vir and Singh (2015), Singh *et al*., (2017), Pathak *et al.,* (2009), Saini *et al.,* (2010) and Shabarish *et al.,* (2012) also confirm the above findings. The total biomass yield (g $plant^{-1}$) ranged from 15.7 to 28.7 with a mean value of 21.6 during 2015-16 and 5.0 to 16.1 with mean value of 10.4 during 2016-17. As far as physiological and biochemical characters are concerned, specific leaf area, relative water content, total sugar and phenol content also showed vide variability among the different genotypes as shown in Table 1. Thus, significant variation was present between the accessions for all the recorded traits. This variation is very important for the plant breeders and selection is effective when magnitude of variability in the breeding population is too enough.

Estimation of genotypic and phenotypic coefficient of variation

The analysis of variance showed highly significant differences among the genotypes for all the 13 characters studied and the phenotypic variance was higher than genotypic variance for all the characters. The physiological and biochemical characters also showed wide genetic variability among the genotypes. High genotypic (Vg) and phenotypic (Vp) variances observed for the characters such as specific leaf area and total sugar content, whereas, the characters like number of seeds pod^{-1}, number of pods $cluster^{-1}$, number of branches $plant^{-1}$ and seed yield $plant^{-1}$ showed low.

The coefficient of phenotypic and genotypic variance was also calculated for all the traits under study. The phenotypic coefficient of variance (PCV) was higher than the genotypic coefficient of variance (GCV). The GCV values ranged up to 26.6 during 2015 and 31.79 during 2016 while the PCV value ranged up to 31.8 during 2015 and 40.2 during 2016.

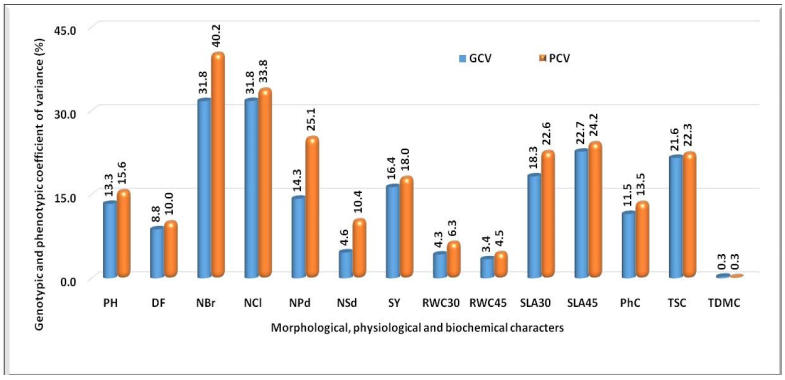


Fig 2: Genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) of different characters (PH- Plant height; DF- Days to 50% flowering; NBr- Number of branches per plant; NCl- Number of cluster per plant; NPd- Number of Pods per Cluster; NSd- Number of seeds per pod; SYd- Seed yield; RWC30- Relative water content at 30 DAS; RWC45- Relative water content at 45 DAS; SLA30- Specific leaf area at 30 DAS; SLA45- Specific leaf area at 45 DAS; PhC- Phenol content; TSC- Total sugar content; TDMC- Total dry matter content).

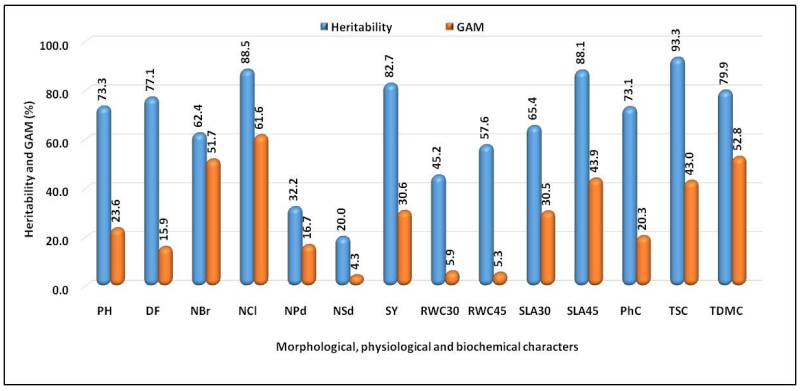


Fig 3: Heritability and genetic advance over the mean of different characters (PH- Plant height; DF- Days to 50% flowering; NBr- Number of branches per plant; NCl- Number of cluster per plant; NPd- Number of Pods per Cluster; NSd- Number of seeds per pod; SYd- Seed yield; RWC30- Relative water content at 30 DAS; RWC45- Relative water content at 45 DAS; SLA30- Specific leaf area at 30 DAS; SLA45- Specific leaf area at 45 DAS; PhC- Phenol content; TSC- Total sugar content; TDMC- Total dry matter content).

This higher PCV than GCV indicating that the little influence of environment on the expression of the characters and these findings are in accordance with the results of Shabarish *et al.* (2012), Malaghan *et al.* (2013), Kumar *et al.* (2015), Santhosha *et al.,* (2017) and Preeti and Prasad, (2018) who also observed greater value of phenotypic coefficient of variation than genotypic coefficient of variation. High GCV and PCV were observed for total sugar content, specific leaf area at 30 and 45 DAS, number of branches plant^{-1}, number of clusters plant^{-1}, number of pods cluster^{-1} and seed yield plant^{-1}. It indicates existence of broad genetic base, which would be amenable for further selection. Similar results were also observed by Hanchinamani (2004), Malaghan (2012), Rai *et al.,* (2012) and Santhosha *et al.,* (2017) for number of branches plant^{-1} and number of clusters plant^{-1}; Prakash *et al*. (2008), Dwivedi (2009) and Santhosha *et al.,* (2017) for number of pods cluster^{-1}.

The difference between PCV and GCV values was high for number of branches plant^{-1}, number of pods cluster^{-1} and number of seeds pod^{-1} indicating the influence of environment on these characters. However, this difference was low for days required for flowering, specific leaf area, plant height, number of clusters plant^{-1}, phenol and sugar content and seed yield plant^{-1} suggesting minimal influence of environment on the expression of the characters, thereby having the highest estimates of heritability. Similar result was found by Yucel *et al.,* (2006) for days to flowering, plant height and harvest index. Low GCV and PCV were observed for relative water content, number of seeds pod^{-1} and days to 50% flowering. These results are in conformity with results of Saini *et al.,* (2010), Singh *et al.,* (2010) and Manivannan and Anandakumar (2013) for the number of seeds pod^{-1}. This low GCV and PCV obtained under study for the above traits indicating the narrow genetic base and hence, variability has to be generated in these characters either through introduction or hybridizing divergent genotypes to recover transgressive segregates or by mutation breeding. Since the variation depends upon the magnitude of the measuring units of the traits, coefficient of variation is independent of the measuring units so it is more useful in

Table 2: Correlation studies among different biochemical and yield attributing characters with seed yield.

Characters	PDWt	SY	NBr	NCl	NPd	NSd	PdDwt	PhC
				2015				
Plant dry weight (PDWt)								
Seed yield (SY)	0.87**							
Number of branches plant^{-1} (NBr)	0.36	0.38						
Number of clusters plant^{-1} (NCl)	0.86**	0.81**	0.36					
Number of pods cluster^{-1} (NPd)	0.68**	0.69**	-0.02	0.50				
Number of seeds pod-$^{-1}$ (NSd)	0.29	0.31	0.25	0.50	0.12			
Pod dry weight (PdDWt)	0.88**	0.99**	0.37	0.81**	0.88**	0.35		
Total phenol (PhC)	0.57*	0.62*	0.09	0.42	0.66	0.20	0.62	
Total sugar	0.55*	0.66*	0.06	0.48	0.53	0.18	0.63	0.50
				2016				
Plant dry weight (PDWt)	-							
Seed yield (SY)	0.98**	-						
Number of branches plant-1 (NBr)	0.01	0.03	-					
Number of clusters plant-1 (NCl)	0.81**	0.84**	0.06	-				
Number of pods cluster-1 (NPd)	0.84**	0.86**	0.07	0.82**	-			
Number of seeds pod-1 (NSd)	0.88**	0.85**	-0.13	0.73**	0.77**	-		
Pod dry weight (PdDWt)	0.68*	0.67*	0.05	0.57*	0.6*	0.62*	-	
Total phenol (PhC)	0.32	0.35	0.10	0.41	0.31	0.40	0.49	
Total sugar	0.09	0.10	0.06	-0.03	0.04	0.04	-0.04	-
Plant dry weight (PDWt)	-0.34	-0.38	-0.05	-0.45	-0.34	-0.27	-0.05	0.30

At 5% - 0.404; at 1%- 0.515.

comparing the population. The highest genotypic and phenotypic coefficient of variation indicates that selection can be applied on the traits to isolate more promising line.

Estimation of heritability in broad sense and genetic advance

Estimates of heritability in broad sense ranged from 25.61% for number of seeds pod^{-1} to 98.6 % for relative water content during 2015-16 and 20.0% for number of seeds pod^{-1} to 93.3% for sugar content during 2016-17 (Fig 3). According to Singh (2001), if heritability of a character is very high, say 80% or more, selection for such characters could be fairly easy. This is because there would be a close correspondence between the genotype and the phenotype due to the relative small contribution of the environment to the phenotype. On the other hand, for characters with low heritability, say 40% or less, selection may be considerably difficult or virtually impractical due to the masking effect of environment. Considering this bench-mark, heritability estimate was high (>80%) for total sugar and phenol content, relative water content, number of branches plant^{-1}, number of clusters plant^{-1} and seed yield plant^{-1}. Similar results were also obtained by Hanchinamani (2004), Anandhi and Oommen (2007), Malaghan (2012), Rai *et al.,* (2012) and Santhosha *et al.,* (2017) for the number of clusters plant^{-1}.

Genetic advance under selection (GA) refers to the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at a given selection intensity (Singh *et al.,* 2001). The characters those exhibit maximum heritability and high genetic advance as percentage of mean could be used as powerful tool in selection process such characters are controlled by the additive genes and less influenced by the environment (Panse and Sukhatme, 1995). For efficient selection, we cannot solely believe on heritability and the combination of high heritability with high genetic advance will provide a clear base on the reliability of that particular trait in the selection of variable entries. The genetic advance as percentage of mean ranged from 6.49 to 69.5% during 2015-16 and 4.28 to 61.6 % during 2016-17. The high estimates of heritability coupled with high values of genetic advance over mean (GAM) were observed for the characters, total sugar content, specific leaf area at 45 DAS, number of clusters plant^{-1} and seed yield plant^{-1}. This indicates predominance of additive component for these traits and hence direct selection would be more effective in improving these traits. These traits are highly reliable during selection process of the accessions.

Correlation studies

Correlation study revealed that number of clusters plant^{-1} (0.81**, 0.84**), number of pods cluster^{-1} (0.69**, 0.86**), pod dry weight (0.99**, 0.67**) showed positive significant correlation with seed yield plant^{-1} during both the years which indicates strong association of these characters with seed yield plant^{-1} (Table 2a and 2b). Therefore, by increasing the value of these component traits, yield may easily push up suggesting that selection for these characters will be useful in improving seed yield plant^{-1}. These results are in agreement with the earlier findings in clusterbean by

Preeti and Prasad (2018), Rai and Dharmatti (2014), Girish *et al.,* (2012), for number of clusters plant^{-1}, number of pods cluster^{-1} and hundred seed weight. The positive significant correlation was also measured between number of clusters plant^{-1} and number of pods cluster^{-1} (0.50*, 0.82**). Similar findings were also observed by Saini *et al.,* (2010).

CONCLUSION

Thus, the present study revealed that selection can be applied on the traits having high genotypic and phenotypic coefficient of variation to isolate more promising germplasm. The total sugar content, specific leaf area at 30 and 45 DAS, number of branches plant^{-1}, number of clusters plant^{-1}, number of pods cluster^{-1} and seed yield plant^{-1} showed high GCV and PCV in present study. The high estimates of heritability coupled with high values of genetic advance over mean (GAM) were observed for the characters *i.e*., total sugar content, specific leaf area at 45DAS, number of clusters plant^{-1} and seed yield plant^{-1} indicates predominance of additive component for these traits and hence direct selection would be more effective in improving these traits. The characters like, number of clusters plant^{-1}, number of pods cluster^{-1} and pod dry weight showed positive significant correlation with seed yield plant^{-1} (g) during both the years which indicates strong association of these characters with seed yield plant^{-1}. Therefore, by increasing the value of these component traits, yield can be increased suggesting that selection for these characters will be useful in improving seed yield plant^{-1}. A few of the most promising germplasm for seed yield and other yield attributing characters were GST-15-101, GST-15-202, GST-15-204 and GST-15-205 as they showed higher seed yield, number of clusters plant^{-1}, number pods cluster^{-1}, number of seeds pod^{-1} and harvest index.

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