

Floral Abscission in Pigeonpea (*Cajanus cajan* (L.) Millsp.): Genotypic Disparity in Land Races, Hybrids and Advanced Breeding Lines

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ABSTRACT

Abscission of flower/s and fruit/pod/s is one of the momentous bottlenecks in pulses in general and pigeonpea in particular, resulting in poor reproductive efficiency. Abscission occurs both before and after fertilization. Knowledge on nature and extent of genetic variation available in the genotypes help breeders for planning breeding programmes to identify genotypes that retain maximum flowers hence increase pod set. A total of 51 genotypes were studied; 37 advanced stabilized breeding lines, six hybrids and eight landraces. The results exhibited a wide genotypic variation in flower production and abscission. Seven advanced genotypes including Maruti, BSMR-736 and GRG-152; hybrids ICPH-2751 and ICPH-3762; landraces Raichur pink, Bennur local and Katti beeja showed good number of pods set per plant. Hence, the trait can be used in identifying the genes governing it and developing mapping population, also can be used in further breeding and crop improvement programmes.

Key words: floral abscission, pigeonpea, land races, variability, hybrids.

INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millsp.]; one of the major pulse crops of the tropics and sub-tropics. It ranks sixth in global grain legume production and worldwide it is cultivated in about more than 5.50 m ha area. India is the largest producer and also consumer of pigeonpea with an area of 5.13 m ha, annual production of 4.23 m t and productivity of 824 kg/ha [Project Coordinator's report, (2016-17) AICRP on Pigeonpea].

Pigeonpea flowers profusely during September-October (short day), a higher per

cent of them abscise (70-96%) without setting into pods. Grain yield depends upon percentage of flowers transforming into pods. Mineral nutrients are known to develop economic source-sink relationship in plants that ultimately increase the flower, fruit set and seed filling, thereby increasing the yield³. Pre-mature abscission of flowers and fruits lead to reduced realization of sink potential. Thus, flower or fruit dropping is considered as a bottleneck in productivity.

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Floral abscission studies are more often difficult, laborious and time consuming. Hence, it is believed that it has not been attempted in pigeonpea on a large scale by involving several number of genotypes. Probably, this could be a serious attempt in this direction where genotypic differences has been quantified using three set of pigeonpea genotypes; land races – genotypes more often maintained by farmers without much selection and improvement, hybrids – uniform genetically and advanced breeding lines – which are developed through hybridization and also stabilized for uniformity. Hence, it is very necessary to have a reliable data on the extent of abscission, its impact on yield and the ways to compensate the high degree of floral abscission by decrease in floral abscission or increase in pod set. In the present study, investigation was carried out to analyse genotypic differences for floral abscission.

MATERIAL AND METHODS

Investigation was carried out during *Kharif* 2016 at Agriculture Research Station, Kalaburagi which belongs to the agro-climatic zone-2 (North Eastern Dry Zone) of Karnataka state, India. The experimental material consisted of 51 pigeonpea genotypes which include 37 advanced breeding genotypes, six hybrids and eight land races. Experiment was laid out in Randomized Block Design (RBD) with 2 replications. Each genotype was sown in a single row with wider spacing of 150 cm between the rows and 75cm between the plants. This spacing would help differentiate the flowers from adjacent lines and would make the collection of dropped flower/s and/or pod/s convenient. Dropped buds, flowers and pods were collected from each line of every genotype as represented in Figure 1.



Fig. 1: Dropped buds, flowers and pods in pigeonpea

Pod set per cent was calculated using the following equation

$$\text{Pod set (\%)} = \frac{\text{No. of mature pods per plant}}{\text{Total no. of flowers produced per plant}} \times 100$$

Per cent flower drop was calculated using the following equation

$$\text{Flower drop (\%)} = \frac{\text{No. of flowers dropped per plant}}{\text{Total no. of flowers produced per plant}} \times 100$$

In order to identify and ascertain the genetic variability among the genotypes and also to confirm the presence of environmental effect on various characteristics of genotypes, different genetic parameters were estimated by adopting standard formulae. Multivariate analysis was carried out using WINDOSTAT ver 8.5 software developed by Indostat services, Hyderabad.

RESULTS AND DISCUSSION

All the genotypes investigated for floral abscission displayed considerable amounts of differences in their mean performance with respect to all the characters studied. The details of analysis of variance (ANOVA) are presented in Table 1.

Genetic variability

Genetic variability parameters 12 characters is presented in the Table 2. Variability parameters of yield and floral abscission are discussed here under.

Seed yield per plant. There was high genotypic (44.4) and phenotypic (44.86) coefficients of variation observed for the trait with a moderate difference between phenotypic (871.39) and genotypic (853.54) variation. High heritability (97.95%) coupled

with high GAM (90.51) is suggestive of high response to appropriate selection procedures and thus selection for this trait will result in high genetic gain (Table 2).

Similar results were reported by Mahantesh⁴ and Shunyu *et al.*¹¹ who obtained high GCV, PCV heritability and GAM. High heritability and high GAM was reported by Saroj *et al.*⁹, Pandey *et al.*⁵, Birhan *et al.*² and Abid *et al.*¹ whereas, Yogendra *et al.*¹⁶ obtained high GAM and low heritability for the trait.

Table 1: Analysis of variance for yield and yield attributing traits of 51 pigeonpea genotypes

Source of variation	d.f.	DFP	PH	PB	SB	PBL	SPP	DM	PPY	SW	FP	FD	PPP
Replications	1	0.35**	67.82**	3.34**	0.42**	7.89**	0.01**	7.15**	16.92**	0.10**	3931948.00**	2273929.00**	67.78**
Treatments	50	165.37**	783.98**	12.27**	57.33**	76.89**	0.24**	204.44**	1724.94**	5.17**	14537579.94**	12575137.16**	205994.92**
Error	50	4.17	115.01	3.26	4.56	25.85	0.08	2.17	17.85	0.02	723386.70	615218.15	8428.07

**= Significant at 5%

Where,

d.f.	= Degrees of freedom	PB	= Primary branches	SW	= 100 seed weight
DFP	= Days to 50% flowering	SB	= Secondary branches	FP	= Total flowers produced
DM	= Days to maturity	PBL	= Pod bearing length	FD	= Total buds, flowers and pods dropped
PH	= Plant height	SPP	= Seeds per plant	PPP	= Pods per plant

Table 2: Genetic variability parameters in 51 genotypes of pigeonpea for floral abscission studies

Sl. No.	Variability parameters	Range		Mean \pm S.Em	Variance		Co-efficient of variation (%)		h ² bs (%)	GA (%)	GAM (%)
		Min.	Max.		Gen.	Phen.	Gen.	Phen.			
1	Days to 50% flowering	78.00	122.50	103.53 \pm 1.43	80.60	84.77	8.67	8.89	95.08	18.03	17.42
2	Days to maturity	126.00	176.00	154.48 \pm 1.03	101.14	103.30	6.51	6.58	97.90	20.50	13.27
3	Plant height (cm)	84.84	172.60	121.95 \pm 7.51	334.49	449.50	15.00	17.39	74.41	32.50	26.65
4	Primary branches	3.67	15.67	10.01 \pm 1.26	4.51	7.76	21.21	27.84	58.06	3.33	33.30
5	Secondary branches	2.42	26.84	11.94 \pm 1.49	26.39	30.94	43.01	46.58	85.27	9.77	81.82
6	Pod bearing length (cm)	15.00	37.50	27.01 \pm 3.56	25.52	51.37	18.70	26.54	49.68	7.33	27.16
7	No. of seeds per pod	3.00	4.67	3.37 \pm 0.20	0.08	0.16	8.27	11.88	48.43	0.40	11.85
8	Seed yield per plant (g)	19.84	167.99	65.81 \pm 2.96	853.54	871.39	44.40	44.86	97.95	59.56	90.51
9	100 seed wt (g)	8.00	16.50	10.42 \pm 0.11	2.57	2.60	15.39	15.46	99.06	3.29	31.55
10	Total flowers produced	621.75	13104.00	4958.71 \pm 595.48	6907096.62	7630483.32	53.00	55.71	90.52	5150.94	103.88
11	No. of buds, flowers and pods dropped	308.25	12195.00	4121.82 \pm 549.16	5979959.51	6595177.65	59.33	62.30	90.67	4796.81	116.38
12	No. of mature pods per plant	264.00	1569.00	836.89 \pm 64.28	98783.43	107211.50	37.56	39.12	92.14	621.48	74.26

Where, h²bs = Heritability in broad sense S.Em = Standard error of mean

GA = Genetic advance

Gen. = Genotypic

Phen. = Phenotypic

GAM = Genetic advance as per cent mean

Table 3: Genotypic variation for flower production and abscission in pigeonpea

Sl. no.	Genotype	Total flowers produced	Total buds, flowers and pods dropped	Total pods produced	% flower drop	% pod set	Flowers produced to pod set Ratio
Advanced genotypes							
1	AKT-9913	1210.00	946.00	264.00	78.18	21.82	4.6:1
2	GRG-140	1125.75	792.25	333.50	70.37	29.63	3.4:1
3	GRG-2013	802.50	382.00	420.50	47.60	52.40	1.9:1
4	ICP-8793	2399.25	1825.25	574.00	76.08	23.92	4.2:1
5	ICP-11320	1499.25	795.00	704.25	53.03	46.97	2.1:1
6	IC-407476	2228.00	1662.00	566.00	74.60	25.40	3.9:1
7	JKM-197	9833.75	8798.50	1035.25	89.47	10.53	9.5:1
8	RAJA	1137.00	308.25	828.75	27.11	72.89	1.4:1
9	BAHAR	621.75	328.50	293.25	52.84	47.16	2.1:1
10	ICP-8793-1	5199.00	4313.63	885.38	82.97	17.03	5.9:1
11	ICP-7035	5760.00	5202.00	558.00	90.31	9.69	10.3:1
12	GPHR-8-11	3103.00	2211.00	892.00	71.25	28.75	3.5:1
13	ICP-13101	2870.85	2170.50	700.35	75.60	24.40	4.1:1
14	BDN-2008-1	7897.00	6928.25	968.75	87.73	12.27	8.2:1
15	ICP-86053	6778.50	5622.75	1155.75	82.95	17.05	5.9:1
16	GRG-177	13104.00	12195.00	909.00	93.06	6.94	14.4:1
17	GRG-152	4832.00	3775.50	1056.50	78.13	21.87	4.6:1
18	GRG-222	5200.50	4327.50	873.00	83.21	16.79	6.0:1
19	GRG-111	6070.50	5402.75	667.75	89.00	11.00	9.1:1
20	GRG-617	4664.88	3919.38	745.50	84.02	15.98	6.3:1
21	ICPL-15015	5159.33	3956.25	1203.08	76.68	23.32	4.3:1
22	ICP-2376	3110.00	2634.00	476.00	84.69	15.31	6.5:1
23	ICPL-14001	5863.50	4956.75	906.75	84.54	15.46	6.5:1
24	PRG-176	3136.50	2382.00	754.50	75.94	24.06	4.2:1
25	ICPL-332	4621.80	4006.80	615.00	86.69	13.31	7.5:1
26	ICPL-161	2816.00	2347.50	468.50	83.36	16.64	6.0:1
27	TS-3R	8730.38	7878.00	852.38	90.24	9.76	10.2:1
28	GRG-811	3302.50	2571.00	731.50	77.85	22.15	4.5:1
29	BSMR-736	6721.50	5355.00	1366.50	79.67	20.33	4.9:1
30	ASHA	5590.50	4300.00	1290.50	76.92	23.08	4.3:1
31	MARUTI	11935.50	10366.50	1569.00	86.85	13.15	7.6:1
32	BDN-711	3592.50	2986.50	606.00	83.13	16.87	5.9:1
33	LRG-41	5351.25	3787.50	1563.75	70.78	29.22	3.4:1
34	GC-11-39	2324.00	1982.00	342.00	85.28	14.72	6.8:1
35	ICPL 87	2892.50	2536.50	356.00	87.69	12.31	8.1:1
36	TS-3	4277.10	3378.00	899.10	78.98	21.02	4.8:1
37	WRP-R-29-4	6252.50	5281.00	971.50	84.46	15.54	6.4:1
Hybrids							
38	ICPH-3477	9518.50	8625.00	893.50	90.61	9.39	10.7:1
39	MPH-10-5	6251.00	5296.50	954.50	84.73	15.27	6.5:1
40	NTH-77	5811.50	5172.00	639.50	89.00	11.00	9.1:1
41	ICPH-2751	5048.50	3931.50	1117.00	77.88	22.12	4.5:1
42	ICPH-3762	6240.38	5100.00	1140.38	81.73	18.27	5.5:1
43	ICPH-2433	3782.25	3367.50	414.75	89.03	10.97	9.1:1
Land races							
44	KARI TOGARI	6197.50	5341.00	856.50	86.18	13.82	7.2:1
45	BENNUR LOCAL	7625.25	6300.00	1325.25	82.62	17.38	5.8:1
46	GULYAL WHITE	4153.75	3337.25	816.50	80.34	19.66	5.1:1
47	GULYAL RED	8124.00	7136.00	988.00	87.84	12.16	8.2:1
48	RAICHUR PINK	5587.25	4230.00	1357.25	75.71	24.29	4.1:1
49	CHAPLE	3773.50	3013.00	760.50	79.85	20.15	4.9:1
50	JAMADAR LOCAL	3591.38	2660.25	931.13	74.07	25.93	3.9:1
51	KATTI BEEJA	5174.75	4091.75	1083.00	79.07	20.93	4.8:1
Overall mean		4958.71	4121.82	836.89	79.21	20.79	
SD		2901.96	2707.71	325.19			

Where, SD = Standard Deviation

Total number of flowers produced

Total number of flowers produced for the entries investigated showed wide differences ranging from 621.75 (BAHAR) to 13104.0 (GRG-177) with mean of 4958.71. High genotypic and phenotypic coefficients of variability (53.0 and 55.71 per cent respectively) with high heritability of 90.52%, high GA of 5150.94 and high GAM of 103.88% were observed. High genotypic and phenotypic coefficients of variability with a low difference between the genotypic and

phenotypic variation suggest presence of low influence of environment on the trait. High heritability coupled with high GAM is suggestive of high response to appropriate selection procedures and thus selection for this trait will result in high genetic gain (Table 3).

Total number of buds, flowers and pods dropped

The total number of buds, flowers and pods dropped in the entries investigated ranged from 308.25 (RAJA) to 12195.0 (GRG-177) with mean value of 4121.82. The genotypic

and phenotypic coefficients of variability were as high as 59.32 and 62.30 per cent respectively with high heritability of 90.67%, higher GA of 4796.81% and high GAM of 116.38%. The high genotypic and phenotypic coefficients of variability with low difference between genotypic and phenotypic variation indicate less influence of non-genetic factors. High heritability coupled with high GAM is suggestive of high response to appropriate selection procedures and selection for this trait will result in high genetic gain only when selection is carried towards lesser GAM and heritability of the trait.

Per cent flower drop represents the amount of total loss of flowers from the total flowers produced. Genotype GRG-177 showed the highest flower drop (93.06%) and genotype RAJA showed the lowest flower drop (27.11%) with a mean of 4039.91 ± 2702.71 . Large variations were found with respect to flower drop. This is due to genotypic variability and could be resulted from internal hormonal changes like ABA (Abscisic acid), Ethylene, Proline *etc.* and external factors like moisture content, availability of nutrients at flowering and pod filling stage, effect of pest and diseases, source to sink relationship, photosynthetic rate *etc.* Selection against this trait should be done to achieve improvement in yield. Genotypes RAJA, GRG-2013, ICP-11320 and BAHAR showed lesser flower produced to pod set ratio indicating more number of pods set for total flowers produced and effective utilization of photosynthates. These genotypes can be utilized in further breeding programmes to improve yield.

Total number of mature pods per plant

Total number of mature pods per plant of the entries investigated for floral abscission ranged from 264 (AKT-9913) to 1569 (MARUTI) with mean of 836.89. The genotypic and phenotypic coefficients of variability were recorded to be high *i.e.*, 37.56 and 39.12 per cent respectively with high heritability of 92.14%, high GA and GAM of 621.48 and 74.26% respectively. High GCV, PCV and low difference between genotypic

and phenotypic variances indicate that the trait is less influenced by environmental factors. High heritability coupled with high genetic advance as per cent mean was suggestive of influence of additive gene action. The research results are in agreement with previous studies conducted by Sarsamkar *et al.*, Vange and Egbe¹⁴, Bhadru, Sharma *et al.*¹⁰ and Rao *et al.*⁸ whereas, Vanisree *et al.*¹⁵ and Yogendra *et al.*¹⁶ obtained low heritability for the trait (Table 3).

Per cent pod set represents the total pods set from the total flowers produced. Total number of mature pods per plant forms an important basis for selection. Genotype RAJA showed the highest pod set (72.89%) and genotype GRG-177 showed the lowest pod set (9.94%) with a mean of 805.07 ± 325.19 . The trait showed high heritability indicating genetic governance of the trait which will help in selection in further breeding programmes. Large variations were found with respect to pod set. This variation can be utilized to study the genes involved in trait expression and in developing mapping populations. The genotypes expressing higher number of pod set per cent are considered to have high reproductive efficiency. This higher efficiency can be utilized to improve the yield of pigeonpea. The lower pod set per cent indicates reproductive inefficiency of the genotypes. Per cent flowers produced to per cent pods set in Advanced genotypes, hybrids and landraces are presented in Figure 1, and 3 respectively.

The genotypes JKM-197, ICP-86053, GRG-152, ICPL-15015, BSMR-736, ASHA, MARUTI, LRG-41 and the hybrids ICPH-3762, ICPH-2751 showed higher number of mature pods per plant. Land races like Bennur local, Raichur Pink and Katti Beeja also showed higher number of pods per plant indicating their high reproductive efficiency.

Flowers produced to pods set ratio

The ratio of number of flowers produced to number of pods set indicates the total number of flowers produced to set one pod. This forms important criteria to analyse the amount of flower drop in a genotype and understand the

variations for flower drop between different genotypes. Ratio of total number of flowers produced to total number of pods set ranged from 1.4:1 (RAJA) to 14.4:1 (GRG-177). Results pertaining to this are represented in Table 3.

A total of 37 advanced genotypes were studied for their flower abscission pattern. The genotype GRG-177 showed the highest ratio (14.4:1) which indicated that out of 14.4 flowers produced one pod is set or it requires production of 14.4 flowers to set one pod. Whereas, genotype RAJA showed the lowest ratio (1.4:1) which indicated it requires production of 1.4 flowers to set one pod. Ten genotypes were in the range of 4.1:1 to 4.9:1 and seven genotypes were in the range of 6:1 to 6.8:1.

A total of six hybrids were evaluated for flower abscission. The lowest ratio was 4.5:1 showed by the genotype ICPH-2751 followed by genotype ICPH-3762 (5.5:1) and the highest ratio was 10.7:1 showed by genotype ICPH-3477.

A total of eight landraces were evaluated for flower abscission. The landrace Jamadar local showed the lowest ratio of 3.9:1 and genotype Gulyal red showed the highest ratio of 8.2:1. Five genotypes were in range of 3.9:1 to 5.1:1.

This genetic variation is due to differential response of genotypes to source-sink relationship. The character flower production and abscission showed high heritability indicating genetic governance of the trait. The genotypes which are contrasting for this trait can be further used to study the number of genes governing the floral abscission. The genotypes with more floral abscission and fewer pod set shows their reproductive inefficiency in terms of improper use of photosynthates. In contrast, the genotypes with less floral abscission and more pod set are preferred as they exhibit high reproductive efficiency without wasting photosynthates of plant. The genotypes GRG-152, ICPH-2751, ICPH-3762 and ICPL-15015 were found to be good in terms of their reproductive efficiency.

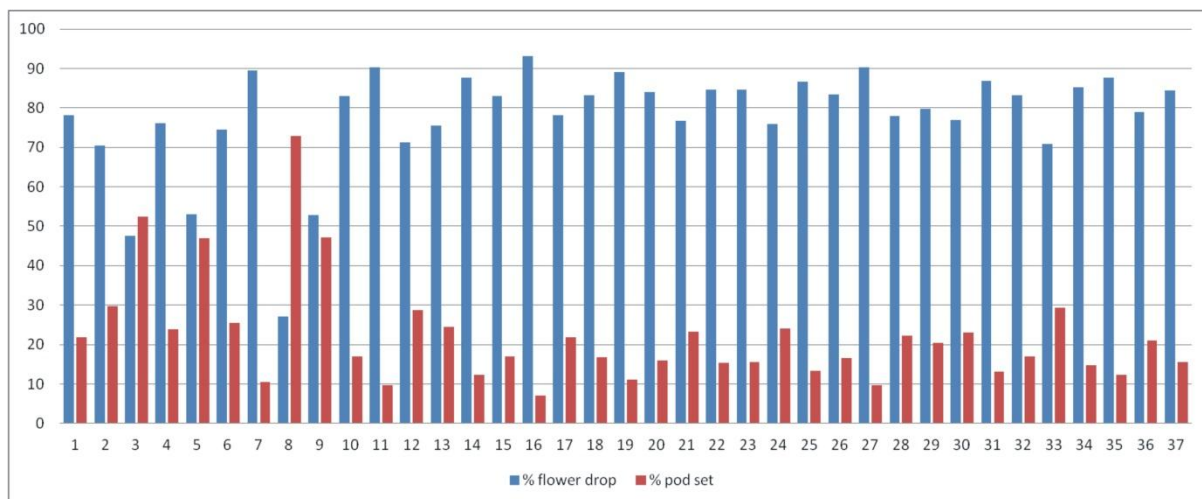


Fig. 1: Per cent flower drop and per cent pod set in Advanced genotypes

LEGEND:

37.WRP-29-4

Sl.	Genotype
1	AKT-9913
2	GRG-140
3	GRG-2013
4	ICP-8793
5	ICP-11320
6	IC-407476
7	JKM-197
8	RAJA
9	BAHAR
10	ICP-8793-1
11	ICP-7035
12	GPBR-8-11
13	ICP-13101
14	BDN-2008-1
15	ICP-86053
16	GRG-177
17	GRG-152
18	GRG-222
19	GRG-111
20	GRG-617
21	ICPL-15015
22	ICP-2376
23	ICPL-14001
24	PRG-176
25	ICPL-332
26	ICPL-161
27	TS-3R
28	GRG-811
29	BSMR-736
30	ASHA
31	MARUTI
32	BDN-711
33	LRG-41
34	GC-11-39
35	ICPL 87
36	TS-3

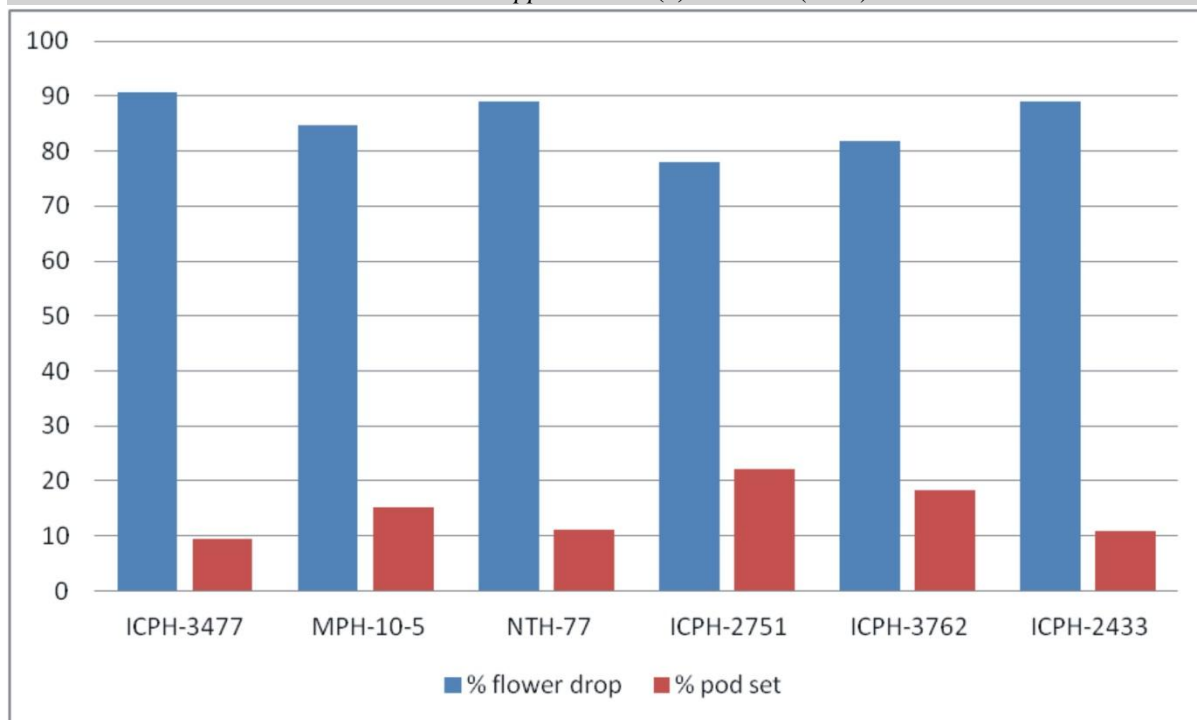


Fig. 2: Per cent flower drop and per cent pod set in Hybrids

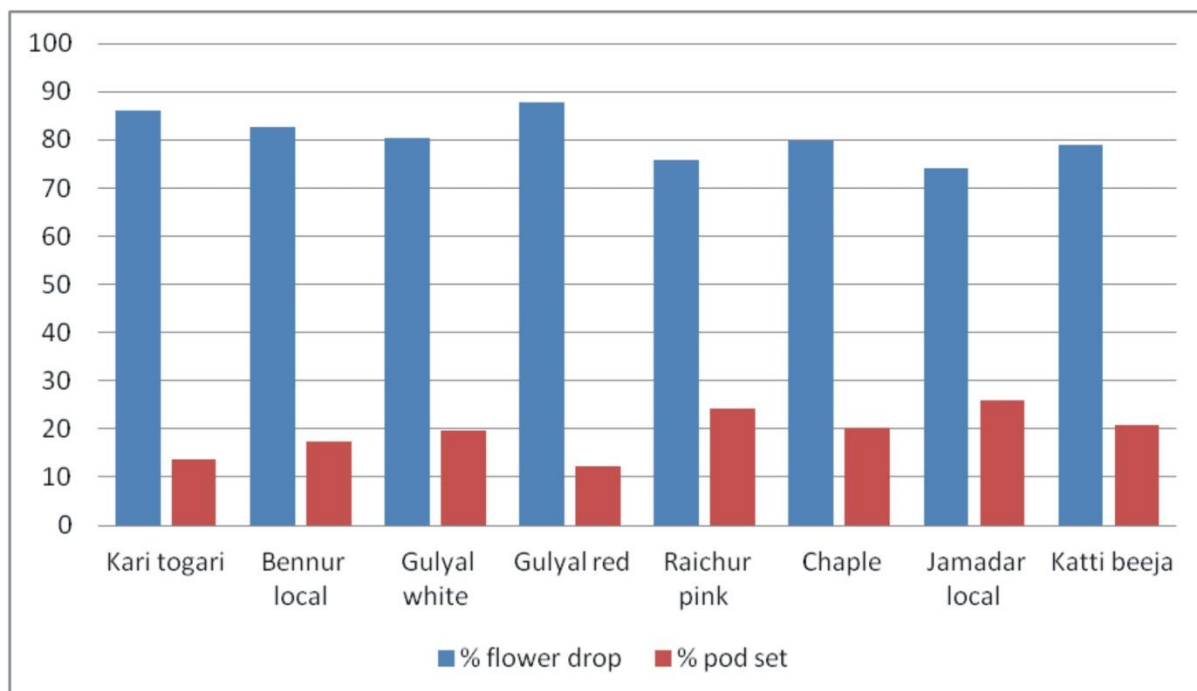


Fig. 3: Per cent flower drop and per cent pod set in Landraces

CONCLUSIONS

Wide variation for per cent flower drop and per cent pod set were obtained for the genotypes studied and this was clearly reflected in the ratio of flowers produced to pods set. The genotypes contrasting to the trait flower abscission like RAJA and GRG-177 can be used in crossing to identify number of

genes governing the trait and developing mapping population. Advanced genotypes Raja, GRG-2013, Bahar, ICP-11320, ICP-13101, ICP-8793, PRG-176, ICPL-15015, Asha and GRG-811; Hybrid ICPH-2751 and landrace Jamadar local and Raichur pink were found potential as they showed less per cent flower drop compared to other genotypes.

Hence, these genotypes can be further used in breeding programmes.

Advanced genotypes Maruti, LRG-41, BSMR-736, Asha, ICPL-15015, ICP-86053, GRG-152 and JKM-197 showed good number of pods set per plant. Similarly hybrids ICPH-2751 and ICPH-3762 and landraces Raichur pink, Bennur local and Katti beeja showed good number of pods set per plant. Hence, these genotypes can be further used as parents in breeding programmes or in crop improvement programmes.

Genotype GRG-152 was not only showed a significantly higher number of pods per plant, but also was found resistant to *Fusarium* wilt and moderately resistant to SMD (test results of separate trial). Similarly genotypes ICPH-2751, ICPH-3762 and ICPL-15015 showed similar properties as like GRG-152. Hence, these genotypes were found to have high potentiality in improving yields of pigeonpea with good quality and they can be utilized in further breeding programmes and release.

The genotype in the solitary cluster VI was Maruthi showing the highest number of flowers produced, flowers dropped and pod set making it the most unique genotype among the 51 genotypes studied. It can be further utilized in breeding programmes.

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