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Genetic variability studies for fibre yield and its attributes in roselle (*Hibiscus sabdariffa* L.)

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Abstract
Genetic variability analysis was studied in a set of 52 diverse genotypes of roselle (*Hibiscus sabdariffa* L.) during *kharif*, 2018 at Agricultural Research Station, Amadalavalasa, Srikakulam District, Andhra Pradesh for 11 quantitative traits. Analysis of variance indicated significant differences among 52 genotypes for all the characters under study. High PCV and GCV was recorded for green fresh weight per plant and dry fibre yield per plant. Moderate PCV and GCV was recorded for plant height and fibre wood ratio. Low PCV and GCV was recorded for days to 50% flowering. High Heritability coupled with high genetic advance as percent of mean was recorded for green fresh weight per plant, dry stick weight per plant and dry fibre yield per plant.

Keywords: Genetic variability, heritability, genetic advance as percent of mean, roselle

Introduction
Roselle (*Hibiscus sabdariffa* L.) is an annual erect, bushy, herbaceous shrub grown as annual or biennial plant belonging to family Malvaceae. It is a self pollinated crop with chromosome number, 2n=4x=72 mostly cultivated in tropical and sub-tropical regions for bast fibre, paper pulp or edible calyces, leaves and seeds (Sabiel *et al*., 2014; Osman *et al*., 2011) [13, 12]. It is commonly known by different names in different countries namely Roselle, Karkade, Razelle, Sorrel, Red Sorrel, Jamaica Sorrel, Indian Sorrel, Guinea, Sorrel, Sour -Sour, and Queens land jelly plant (Naim and Ahmed, 2010; Mahadevan *et al.*, 2009) [11, 10]. Roselle is one of the important and popular medicinal plant having several properties. The fresh calyces are filled with greater amount of ascorbic acid and also rich in riboflavin, niacin, carotene, calcium and iron while dry calyces contains antimicrobial as well as antioxidant activities due to its phenolic compounds: flavonoids, gossypetine, hibiciscetine and saddaretine. Seeds of roselle have been found to be a good source of protein (Anokwuru *et al.*, 2011) [2].
The acquisition of germplasm and valuation of genetic variability is a fundamental step in any crop improvement programme. Yield being a complex character governed by many genes and being influenced by the environment, so the variability acquired for these characters is the sum of heredity effects by the genes and also by the environment. Hence, it becomes paramount important to partition the variability into heritable and non heritable components measured as PCV and GCV, heritability and genetic advance as percent of mean. In this context, the present investigation was undertaken to study the genetic variability for fibre yield and its attributing characters in roselle.

Material and methods
52 diversified genotypes (geographically and genetically) of roselle were evaluated at Agriculture Research Station, Amadalavalasa. The experiment was laid out in Randomized Block Design with three replications during *kharif* 2018-19. Each genotype was sown in single row of 4.5m length with a spacing of 40 X 10 cm. The data was collected from randomly selected 5 plants in a row of each replication. All the fibre yield parameters were recorded at the time of harvesting. Fibre was extracted by standard method of retting.
Data was recorded for 11 quantitative characters *viz*., days to 50% flowering, plant height, base diameter, mid diameter, petiole length, number of nodes per plant, internode length, green fresh weight per plant, dry stick weight per plant, fibre wood ratio and dry fibre yield per plant. GCV and PCV were calculated by using the formulae suggested by Burton and Devane (1953) [4]. Heritability and genetic advance were calculated by using the formulae given by Allard (1960) [1].

Table 1: Analysis of variance for 11 characters for 52 genotypes in roselle (*Hibiscus sabdariffa* L.)

Mean sum of squares								
S. No	**Sources**	**Df**	**DF**	**PH**	**BD**	**MD**	**PL**	**NODES**
1	Replications	2	39.87	322.23	0.12	0.13	0.37	7.96
2	Treatments	51	3.58	3013.01 *	6.39**	3.78**	1.28*	50.25*
3	Error	102	2.24	659.87	0.99	0.65	0.34	14.76

Table 1: Cont ...

Mean sum of squares							
S. No	**Sources**	**df**	**IL**	**GFW**	**DSW**	**FWR**	**DFY**
1	Replications	2	0.55	897.33	19.94	0.0061	1.00
2	Treatments	51	0.75*	11193.17**	172.39**	0.0102**	27.29**
3	Error	102	0.22	1243.69	20.55	0.0019	2.31

* Significant at 5% level
** Significant at 1% level

Table 2: Estimates of genetic variability parameters of yield component attributes in roselle (*Hibiscus sabdariffa* L.)

S. No	Characters	Mean	Range	GCV	PCV	Heritability ($h^{2)}$	GAM
1	DF	130.92	128.66 – 133.33	0.50	1.25	16.5	1.76
2	PH	257.35	171.66 – 309.66	10.88	14.76	54.3	16.52
3	BD	15.50	10.45 – 18.35	8.64	10.76	64.5	14.29
4	MD	11.10	7.73 – 13.86	9.19	11.71	61.6	14.87
5	PL	9.82	8.42 – 11.06	2.25	10.27	4.80	1.01
6	NODES	49.16	36.40 – 57.93	6.99	10.48	44.5	9.61
7	IL	5.64	4.76 – 7.30	7.41	11.16	44.1	10.13
8	GFW	264.62	92.00- 401.33	21.76	25.51	72.7	38.23
9	DSW	36.41	20.66 – 58.26	19.53	23.16	71.1	33.94
10	FWR	0.39	0.26 – 0.56	13.35	17.62	57.5	20.85
11	DFY	13.95	9.66 – 23.53	20.68	23.38	78.3	37.71

DF-Days to 50% flowering; PH-Plant height; BD-Base diameter; MD-Mid diameter; PL- Petiole length; IL-Internode length; GFW-Green fresh weight per plant; DSW- Dry stick weight per plant; FWR- Fibre wood ratio; DFYP-Dry fibre yield per plant.

Results and discussion

The analysis of variance for 11 quantitative characters of selected genotypes of roselle was furnished in Table 1. significant difference was observed for all the characters indicating the presence of substantial variability for the characters under study. Wider genetic variability with moderate PCV and GCV was observed for plant height and fibre wood ratio, whereas high PCV and high GCV was observed for green fresh weight per plant and dry fibre yield per plant. The results were similar with the earlier reports of Krishnaveni and Murthy (2000) [8], Kameswararao (2002) [7], Kumar and Appalaswamy (2014) [9] and Satyanarayana *et al*. (2017) [14]. Narrow genetic variability with low PCV and low GCV was observed for all the remaining characters. Similar results were observed by the earlier reports of Guptaji and Subramanyam (1997) [6], Elasdig *et al*. (2013) [5] and Sabiel *et al*. (2014) [13].

High heritability coupled with high genetic advance as percent of mean is high for green fresh weight per plant, dry stick weight per plant and dry fibre yield per plant. Similar results were found by Satyanarayana *et al*. (2015) [15] and Satyanarayana *et al*. (2017) [14] indicating preponderance of additive gene action in controlling the character and improvement can be anticipated by simple direct selection. High heritability coupled with moderate genetic advance as percent of mean is high for base diameter and mid diameter indicating operation of additive and non additive gene actions. This implies that the further improvement for these characters can be made through mass selection, progeny selection or any modified selection procedure aiming to exploit the additive gene effect. Moderate heritability coupled with moderate genetic advance as percent of mean is observed for plant height, internode length and fibre wood ratio indicating additive gene action. Low heritability coupled with low genetic advance as percent of mean was observed for days to 50% flowering, number of nodes per plant and petiole length indicating the preponderance of non additive gene action and influence of environment and direct selection for these characters may not be effective. Similar results were reported by Anuradha and Venkateswararao (1993) [3], Satyanarayana *et al.* 2015 [15].

Conclusion

From my present study high variability with high heritability coupled with high genetic advance as percent of mean were recorded for green fresh weight per plant and dry fibre yield per plant indicated preponderance of additive gene action and hence selection for these traits would be rewarding.

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