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Research Note

Evaluation of genetic parameters of agro-morpho-quality traits in American cotton (*Gossypium hirsutum* L.)

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Abstract

In the present study, forty American cotton (*Gossypium hirsutum* L.) genotypes of diverse origin were evaluated to observe the genetic variability, heritability and genetic advance for yield and fibre quality traits. The analysis of variance study indicated the presence of significant difference among all the traits. The highest PCV and GCV were observed for the number of monopodia per plant, followed by seed cotton yield per plant. Genotypic coefficients of variation had a similar trend as the phenotypic coefficient of variation indicating a less environmental effect on the expression of the traits. High heritability along with high genetic advance was observed in seed cotton yield per plant. The high heritability was recorded for the traits *viz*., days to 50% flowering, the number of monopodia per plant, the number of sympodia per plant, boll weight, seed index, ginning outturn, 2.5% span length, bundle strength and seed cotton yield per plant. The high genetic advance was also observed for seed cotton yield per plant indicating the use of simple selection for the improvement of this character in the future breeding programmes.

Keywords

genetic variability, cotton, heritability, genetic advance

Cotton is the king of fibre crops and assumes a place of pride in the Indian economy which continues to be the predominant fibre in the Indian textile scene, despite stiff competition from the man-made synthetic fibres. In India, cotton is cultivated in an area of 122.00 lakh ha with production and productivity of 377.0 lakh bales (1 bale = 170 kg) and 524 kg/ha, respectively. In Andhra Pradesh cotton occupies an area of about 5.44 lakh ha with a production of 22.0 lakh bales and average productivity of 688.0 kg/ha (AICCIP Annual Report, 2017-18). The genus *Gossypium* is having 50 species among which 4 are cultivable with spinnable lint, while 44 are wild diploids and two are wild tetraploids. Out of the four cultivated species, *G. hirsutum* L. and *G. barbadense* L. are called as new world cotton which are tetraploid ($2n = 4x = 52$), whereas, *G. herbaceum* L. and *G. arboreum* L. are diploid ($2n = 2x = 26$) and are known as old-world cotton. Among the two cultivated tetraploid species, upland cotton (*G. hirsutum*) is considered the most important one for its wide adaptability, high yielding and better spinning ability as demarcated by the release of the number of stable varieties/hybrids. Yield and fibre quality are the two important criteria which decide the sustainability of the variety or hybrid for commercial cultivation. The precious evaluation of the genetic diversity of the excellent germplasm will provide a guide for choosing parents and predicting the degree of inheritance, variation and level of heterosis, which are essential for reaching the breeding goal. Genetic variability is pre-requisite for plant breeders to exercise selection. Heritability itself provides no indication about the genetic progress that would result from the selection. However, at a fixed selection pressure, the amount of advance varies with the magnitude of heritability. Hence, the present study was planned to assess the variability, heritability and genetic advance for various yield, yield components and fibre quality characters in a set of 40 genotypes. Such information may be fruitful in formulating efficient selection programme for synthesis and development of new cotton genotypes with improved yield and its contributing traits.

The experiment was conducted at the Regional Agricultural Research Station, Lam, Guntur, during *Kharif* 2017-18. Forty *G. hirsutum* cotton genotypes were planted in Randomized Block Design with three replications. Uniform spacing of 105 cm x 60 cm and all the recommended field operations were carried out for raising a good crop. In each replication, five competitive plants were randomly selected and observations were recorded for 14 characters *viz*., plant height (cm), days to 50% flowering, the number of monopodia per plant, the number of sympodia per plant, the number of bolls per plant, boll weight (g), seed index (g), lint index (g), ginning outturn (%), 2.5% span length (mm), uniformity ratio, micronaire value (10^{-6} g/inch), bundle strength (g/tex) and seed cotton yield per plant (g). The mean data was used for statistical analysis. Genotypic and phenotypic coefficient of variation was calculated using the method suggested by Burton (1952). Heritability in a broad sense was calculated by the method of Hanson *et al*. (1956) and the genetic advance was categorized based on reports of Johnson *et al*. (1955).

The analysis of variance showed highly significant differences among the genotypes for all the characters studied and infers the existence of considerable genetic diversity among genotypes (**Table 1**). The mean performances and phenotypic coefficients of variation, genotypic coefficients of variation, heritability in the broad sense and genetic advance as a percentage of mean were estimated for fourteen characters and are furnished in **Table 2.** The improvement of crop mainly depends upon the nature and magnitude of genetic variability present in the base population (Kusugal *et al*., 2014).The genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) showed wide variation for the characters studied (Table 2). Similar results were also reported by Sakthi *et al*. (2007), Khan *et al*. (2010) and Soomro *et al*. (2010) for seed cotton yield per plant.

Table 1. Analysis of variance for yield and yield components in cotton (*Gossypium hirsutum* L.) mean sum of squares

Source	d.f.	Plant Height (cm)	Days to 50% Flowering	Monopodia Per Plant	Sympodia Per Plant	Bolls/ Plant	Boll Weight (g)	Seed Index (g)
Replications	2	102.1648	2.5083	0.0413	0.1166	1.7028	0.0585	0.5728
Varieties	39	504.6003**	33.6306**	2.1872**	12.3834**	52.4236**	0.3904**	1.9567**
Error	98	99.8318	1.2434	0.0924	1.7686	26.0024	0.0467	0.2684

Source	d.f.	Lint Index (g)	Ginning Outturn (%)	2.5% Span Length (mm)	Uniformity Ratio (%)	Micronaire (10^{-6} g/inch)	Bundle Strength (g/Tex)	Seed Cotton Yield/Plant (g)
Replications	2	0.3535	0.2521	0.0003	0.0333	0.0092	0.0251	3.0850
Varieties	39	1.7266**	10.6704**	5.7172**	4.4596**	0.3300**	4.1021**	1040.8245**
Error	98	0.3290	1.5887	0.4911	2.7000	0.0889	0.6502	122.1462

High PCV and GCV values were recorded for the number of monopodia per plant (38.01 and 35.72). High to moderate PCV and GCV were recorded for seed cotton yield (22.06 and 18.65). Asha *et al*. (2013) reported high PCV and GCV for the number of monopodia per plant followed by the number of bolls per plant and seed cotton yield per plant. PCV and GCV values were moderate for the number of sympodia (14.28 and 11.66) and lint index (14.33 and 10.97). Moderate to low PCV and GCV were recorded for plant height (10.52 and 7.97), the number of bolls per plant (14.96 and 7.52), boll weight (11.00 to 9.27) and seed index (10.45 and 8.60). Similar results were reported by Altaher and Singh (2003), Vijaya Lakshmi *et al*. (2008) and Asha *et al*. (2013). Low PCV and GCV were recorded for days to 50% flowering (5.72 and 5.41), ginning outturn (6.62 and 5.36), 2.5% span length (5.44 and 4.80%), uniformity ratio (3.73 and 1.57%), micronaire value (9.77 and 6.73%) and bundle strength (5.89 and 4.71%) which indicated that the presence of low variability for these traits in the studied material. Kavithamani and Amalabalu (2017) also reported low PCV and GCV for days to 50% flowering, 2.5% span length and micronaire value. Dahiphale and Deshmukh (2018) recorded low PCV and GCV for 2.5% span length. Similar suggestions were also given by Sajid and Tanwar (2008) and Refazy and Razak (2013).

In a population, the observed variability is a combined measure of genetic and environmental causes, whereas the genetic heritability is the only estimate heritable from generation to generation. However, themeasure of heritability alone does not give an idea about the expected gain in the next generation but, it has to be considered in conjunction with genetic advance. The traits which expressed high heritability and high genetic advance as a percentage of mean could be used as a powerful tool in the selection process.High to moderate heritability coupled with high to moderate genetic advance as per cent of

Table 2 Mean, genetic variability, heritability (broad sense) and genetic advance as per cent of mean for seed cotton yield and yield components in cotton (*Gossypium hirsutum* L.)

S.No.	Character	Mean	Range		Coefficient of variation		Heritability (%) (broad sense)	Genetic Advance as per cent of mean
			Minimum	Maximun	PCV	GCV		
1	**Plant Height (cm)**	145.60	112.83	174.70	10.52	7.97	57.5	18.14
2	**Days to 50% Flowering**	60.64	54.67	73.00	5.72	5.41	89.7	6.40
3	**Monopodia Per Plant**	2.34	0.87	4.63	38.01	35.72	88.3	1.61
4	**Sympodia Per Plant**	16.13	11.00	20.00	14.28	11.66	66.7	3.16
5	**Bolls/ Plant**	39.42	27.67	49.33	14.96	7.52	25.3	3.07
6	**Boll Weight (g)**	3.65	3.07	4.81	11.00	9.27	71.0	0.58
7	**Seed Index (g)**	8.72	7.14	10.23	10.45	8.60	67.7	1.27
8	**Lint Index (g)**	6.22	4.43	7.91	14.33	10.97	58.6	1.07
9	**Ginning outturn (%)**	32.44	27.43	35.58	6.62	5.36	65.6	2.90
10	**2.5% Span Length (mm)**	27.47	24.13	30.07	5.44	4.80	78.0	2.40
11	**Uniformity Ratio (%)**	48.61	45.33	50.67	3.73	1.57	17.8	0.66
12	**Micronaire (10^{-6} g/inch)**	4.21	3.43	4.87	9.77	6.73	47.5	0.40
13	**Bundle Strength (g/tex)**	22.77	20.30	25.83	5.89	4.71	63.9	1.76
14	**Seed Cotton Yield per Plant (g)**	93.78	51.27	139.32	22.06	18.65	71.5	30.47

mean was observed for seed cotton yield per plant (71.5 and 30.47), plant height (57.5 and 18.14) which indicates the preponderance of additive gene action and hence direct phenotypic selection may be useful. These results were similar to the results reported by Srinivas and Bhadru (2015) and Patel *et al*. (2014). Moderate to low heritability was recorded for lint index (58.6 and 1.07) and micronaire value (47.5 and 0.40) revealing the role of additive and non-additive gene actions. High heritability coupled with low genetic advance was recorded for the traits, days to 50% flowering (89.70 and 6.40), the number of monopodia per plant (88.3 and 1.61), the number of sympodia (66.70 and 3.16), boll weight (71.00 and 58.80), ginning outturn (65.60 and 2.90), 2.5% span length (78.00 and 2.40) and bundle strength (63.90 and 1.76) indicating the role of non-additive gene actions in the inheritance of these traits and the non-additive component may be exploited through heterosis breeding. The traits, the number of bolls per plant and uniformity ratio showed low heritability with low genetic advance. These results are in accordance with results reported by Sunayana *et al*. (2017), Kavithamani and Amalabalu (2017) and Kulkarni *et al*. (2010).

The accessions with high mean performance are generally preferred for all the traits except for days to 50% flowering since earliness is the preferred attribute and early flowering was taken into consideration. From the results of the present study, it can be concluded that direct selection can be done for most of the yield attributing traits since it exhibited high genetic variability and a high range of variation. A high PCV over GCV for the characters studied indicated that environment influence on the expression of the characters under study. The high heritability was observed for traits *viz*., days to 50% flowering, the number of monopodia per plant, the number of sympodia per plant, boll weight, seed index, ginning outturn, 2.5% span length, bundle strength and seed cotton yield per plant. High genetic advance with high heritability was observed for seed cotton yield per plant indicated that simple selection can resort for the improvement of this character in the future cotton improvement programmes.

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