Variability Studies for Physio Morphological and Yield Components Traits in American Cotton (Gossypium Hirsutum.L)

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Abstract: The present investigation was conducted to elicit information on extent of genetic variability, heritability and genetic advance for twenty-one characters in 84 intrahirsutum cotton hybrids (Gossypium hirsutum.L) plus two checks which were derived by involving twelve lines and seven testers in line X tester fashion. These lines were developed from new heterotic genepools. These 84 intrahirsutum cotton hybrids along with two checks were evaluated during kharif 2010-11. Wide variability was observed incase of number of sympodia, specific leaf weight, crop growth rate at peak flowering stage, crop growth rate at boll formation stage, crop growth rate at maturity stage. High heritability accompanied by high genetic advance was observed in case of plant height, number of monopodia, number of sympodia, relative water content, specific leaf weight, crop growth rate at boll formation stage, crop growth rate at maturity stage, crop growth rate at maturity stage, boll weight, seed index and lint index indicating the role of additive gene action in the inheritance of these traits and directional selection could be profitably applied on these traits in the genetically diverse material.

Keywords: Variability, heritability, genetic advance, American cotton

I.

Introduction

The success of any breeding programme depends upon the quantum of genetic variability present in the population. Wider range of variability helps in selecting a desired genotype. Therefore for successful improvement of any crop, it is necessary to have knowledge of variability present in the available genetic material.

Cotton is an important fibre crop of global importance which is grown in tropical and subtropical regions of more than 60 countries of the world. Despite threat from synthetic fibre or man made fibre, cotton retains its reputation as "queen of the fibre plants". For multiple uses of lint and by-products, cotton is also referred to as "white gold". In any crop improvement programme, knowledge on nature of gene action and inheritance of traits is essential so as to choose a suitable breeding methodology in crop improvement. Presence of wider spectrum of variability will enhance the chances of selection as ideal genotype. Besides genetic variability, information on heritability and genetic advance measure the relative degree to which a trait is transmitted to its off spring thereby aids the breeder to employ a suitable breeding technique to achieve the objectives. Keeping the above points in view the present investigation was undertaken with an objective to find out the extent of genetic variability, heritability and genetic advance.

II. Material and Methods

The experimental material used in the present study consisted of 84 intra-hirsutum derived from 12 lines i.e RAH 100-32, SC 7, RAH 370, GCOT 16, RAH 178-4, RACH 99-152, SM 1, RAH 97- 612, RAH 111, NAWAB, RAH 178, RAC 99152 and 7 testers SC 68, SC7-IPS, SC 40, SC 79, C11, NAWAB 8, SC 31 which were isolated from new heterotic gene pools through line x tester fashion (Kempthorne 1957) along with two checks i.e., Mallika Bt and RAHH 95. The experiment was laid in randomized block design in 2 replications at Agriculture college students' farm during *kharif* 2010-11. Each entry was sown in one row of 7.2m length spaced at 90cm apart between the rows and 60cm within the row.

The crop was maintained as per the standard agronomic practices recommended for the region. Need based plant protection measures were taken up against pests and diseases. Data was collected on 5 randomly selected competitive plants per replication per genotype for plant height (cm), number of monopodia per plant, number of sympodia per plant, relative water content (%), specific leaf weight (mg/cm²), crop growth rate at peak flowering stage (g/m²/day), crop growth rate at boll formation stage (g/m²/day), crop growth rate at maturity stage (g/m²/day), number of bolls per plant, boll weight (g), seed index (g), lint index (g), lint yield per plant (g) and seed cotton yield per plant (g).

However, data on days to 50% flowering, 2.5%span length(mm), micronaire(10-6g/inch),bundle strength (g/tex) uniformity ratio(%) and fibre elongation were recorded on plot basis. Phenotypic and genotypic coefficient of variations (pcv and gcv) were computed according to Burton (1952). As suggested by

Siva Subramanian and Madhav Menon (1973), GCV and PCV were categorized. Heritability in broad sense was estimated as per Allard (1960) and classified as per Johnson *et al.*, (1955). Genetic advance as percent of mean was computed and classified as per Johnson *et al.*,(1955).

III. Results and Discussion

The analysis of variance revealed significant differences among 86 intra - hirsutum hybrids of cotton (*Gossypium hirsutum*. L) evaluated for 21 characters indicated existence of genetic variability in the material studied. Thus the data collected from diverse material will yield reliable information. The details are presented in table1 and 2.

 Table 1. Analysis of variance for yield and yield component traits in cotton (Gossypium hirsutum L.)

Source	d. f.	Plant height (cm)	Days to 50% flower ing	No. of monopo dia plant ⁻¹	No. of sympod ia plant ⁻¹	Relativ e water conten t (%)	Specifi c leaf weight (mg/c m ²)	C.G.R at peak flowerin g (g/m²/da y)	C.G.R at boll formati on (g/m ² /da y)	C.G.R at maturit y (g/m ² /da y)	No. of bolls plant ⁻¹
			Me	ean sum of so	quares						
Replicatio ns	1	10.207	0.703	0.002	0.123	1.492	0.001	0.081	0.096**	0.019	19.156
Treatmen ts	85	666.312 **	8.160**	0.092**	17.925 [*]	133.61 9**	5.789**	0.839**	2.068**	0.370**	39.280 [*]
Error	85	12.897	0.915	0.025	1.057	2.349	0.008	0.036	0.042	0.013	10.785

* ** Significant at 5% and 1% level, respectively.

Sourc e	d. f.	Boll weight (g)	Ginnin g out- turn (%)	Seed index (g)	Lint index (g)	2.5% span length (mm)	Micro naire (10 ⁻⁶ g/in)	Bundl e streng th (g/tex)	Unifor mity ratio	Fibre elonga tion (%)	Lint yield plant ⁻¹ (g)	Seed cotton yield plant ⁻¹ (g)
				Mean su	im of squares							
Repli catio ns	1	0.004	0.123	0.029	0.004	0.377	0.034	0.170	0.103	0.023	3.730	17.396
Treat ments	8 5	0.469**	10.410 [*]	2.477**	1.273**	4.354**	0.372**	2.652**	6.160**	0.094**	76.607* *	428.191**
Error	8 5	0.006	0.205	0.023	0.005	0.567	0.024	0.823	1.295	0.018	19.488	140.893

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

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					variation		(broad sense)	as per cent of	
			Minimum	Maximum	PCV (%)	GCV (%)	(70)	mean	
1	Plant height (cm)	122.37	87.70	161.80	15.06	14.77	96.20	29.84	
2	Days to 50% flowering	55.17	53.00	62.00	3.86	3.45	79.83	6.35	
3	Number of monopodia plant ⁻¹	1.00	0.60	1.50	24.13	18.20	56.89	28.27	
4	Number of <u>sympodia</u> plant ⁻¹	14.48	9.40	20.80	21.28	20.06	88.87	38.96	
5	Relative water content (%)	81.34	58.11	95.22	10.14	9.96	96.54	20.16	
6	Specific leaf weight (mg/cm ²)	5.78	2.68	9.75	29.47	29.43	99.72	60.54	
7	CGR at peak flowering (g/m ² /day)	2.92	2.12	7.34	22.66	21.71	91.83	42.86	
8	CGR at boll formation (g/m ² /day)	3.59	2.36	9.17	28.62	28.05	96.03	56.61	
9	CGR at maturity (g/m ² /day)	1.81	1.15	3.44	24.17	23.35	93.38	46.49	
10	Number of bolls plant ⁻¹	35.65	26.75	46.40	14.04	10.59	56.92	16.46	
11	Boll weight (g)	4.10	3.15	5.47	11.89	11.73	97.33	23.84	

PCV = Phenotypic coefficient of variation GCV = Genotypic coefficient of variation

Thus the magnitude of difference between PCV and GCV was relatively low for all the traits except number of monopodia, number of bolls, lint yield per plant and seed cotton yield per plant, which revealed the least influence of environment on these traits. The magnitude of PCV was higher than GCV in case of number of monopodia, number of bolls, lint yield per plant and seed cotton yield per plant which revealed the influence of environment on these traits. Wider variability was observed in case of number of sympodia per plant (Neelima et al., 2008), specific leaf weight (Narsireddy and Ratnakumri, 2004) and C.G.R at peak flowering stage, C.G.R at boll formation stage, C.G.R at maturity stage (Saidu Bazi,2011) which indicated their amenability towards directional selection. The traits, plant height, number of bolls per plant, boll weight, seed index, lint index and lint yield per plant recorded moderate variability. Contrary to this wider genetic variability was reported by Sivaprasad et al., (2004b), Neelima et al., (2005), Tuteja et al., (2006a), Do Thi Ha An et al., (2008) and Saidu Bazi (2011). This might be due to differences in breeding material tested under different environments. While the other traits exhibited low variability.

Moderate to high heritability coupled with high genetic advance as percent of mean was observed in case of plant height, number of sympodia, boll weight, seed index and lint index (Ravikesavan et al., 2008; Do Thi Ha An et al, 2008 and Saidu Bazi 2011) number of monopodia (vijaya Lakshmi 2007) relative water content (Kumari and Chamundeswari 2005), specific leaf weight (Narsireddy and Ratnakumari 2004), crop growth rate at peak flowering stage, crop growth rate at boll formation stage, crop growth rate at maturity stage (Girijarani 2000 and saidu Bazi 2011), revealing the role of additive gene action in the inheritance of these traits and the scope for improvement of these traits through simple selection procedures aiming to exploit the additive gene effects.

If the heritability in broad sense was mainly due to non-additive affects (dominance and / or epistasis), the genetic gain will be low as seen in the case of days to 50% flowering and 2.5% span length (Ravi Kesavan et al., 2008; Do Thi Ha An et al., 2008), uniformity ratio (Saidu Bazi 2011) and fibre elongation (Kulkarni et al.,2010) which need to be improved by cyclic hybridization, heterosis breeding, diallel selective mating system and biparental mating system duly adopting standard selection procedures.

Moderate to high heritability along with moderate genetic advance was observed in case of number of bolls per plant, lint yield per plant and seed cotton yield per plant (Do Thi Ha An et al., 2008 and Saidu Bazi 2011) ginning out-turn, and micronaire (Ravikesavan et al., 2008, revealed the involvement of both additive and non-additive gene action in the inheritance of these traits and offers the best possibility of improvement of these traits through progeny selection or any modified selection procedures aiming to exploit the additive gene effects.

IV. Conclusion

The genetic variability studies revealed that the material used in present investigation possessed variability which provides scope for selection by breeder. Wider genetic variability was observed for number of sympodia per plant, specific leaf weight, crop growth rate at peak flowering stage, crop growth rate at boll formation stage and crop growth rate at maturity stage, whereas, it was moderate for plant height, number of bolls per plant, boll weight, seed index, lint index and lint yield per plant. This indicated ample scope for genetic improvement of these traits through hybridization and subsequent directional selection. High PCV and moderate GCV was observed for number of monopodia while moderate PCV and low GCV was observed in case of relative water content, micronaire and seed cotton yield per plant revealing the influence of environment, while remaining traits have recorded low values.

Acknowledgement

I am thankful to ANGRAU for providing financial assistance in the form of fellowship during my course of study.

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