



Research Article

GENETIC VARIABILITY STUDIES IN THE F₂ POPULATIONS OF INTERSPECIFIC COTTON (*G.HIRSUTUM* L. X *G.BARBADENSE* L.) HYBRIDS

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Received: August 12, 2019; Revised: October 25, 2019; Accepted: October 26, 2019; Published: October 30, 2019

Abstract: The genetic variability present in the available germplasm may be utilized either for direct selection or for hybridization programme. The experimental material comprised of four F₂ populations along with respective parents of crops. This study was carried out in the *kharif* 2015-16 at Agricultural Research Station, Hebbali, UAS, and Dharwad. All the selected three characteristics (seed cotton yield per plant, number of bolls per plant and boll weight) of F₂ populations of four promising hybrids showed the greater phenotypic coefficient of variation (PCV) values than the genotypic coefficient of variation (GCV) values, alluding to influence of environment on the expression of these traits. Among the studied F₂ hybrid, HBS1 X Suvin (82.14% & 93.63%) showed the highest GCV and heritability value in all three characters, respectively. Simultaneously the cross FQT-37 x SB-YF-425, showed 82.14%, and 88.47% heritability in two characters *i.e.* seed cotton yield per plant and number of balls per plant respectively. High heritability was recorded for all the three traits and this high heritability was coupled with high genetic advance indicating that selection can be done based on the mean performance for the respective traits. The highest number of transgressive segregants was recorded in the F₂ generation of cross FQT-37 x SB-YF-425 (28 nos.) followed by HBS-1 x Suvin (23 nos.) and FQT-26 x Suvin (21 nos.) for the trait, seed cotton yield. These selected transgressive segregant plants can be advanced to further generations to help in isolating and stabilizing superior genotypes. All the characters *i.e.* seed cotton yield per plant, number of bolls per plant and boll weight showed high heritability with high genetic advance that revealed the substantial contribution of additive gene action in the expression of traits, which is most valuable in further selection.

Keywords: Genetic advance, GCV, Heritability, PCV, Transgressive segregants

Citation: Roy U., *et al.*, (2019) Genetic Variability Studies in the F₂ Populations of Interspecific Cotton (*G.hirsutum* L. x *G.barbadense* L.) Hybrids. International Journal of Genetics, ISSN: 0975-2862 & E-ISSN: 0975-9158, Volume 11, Issue 10, pp.- 660-663.

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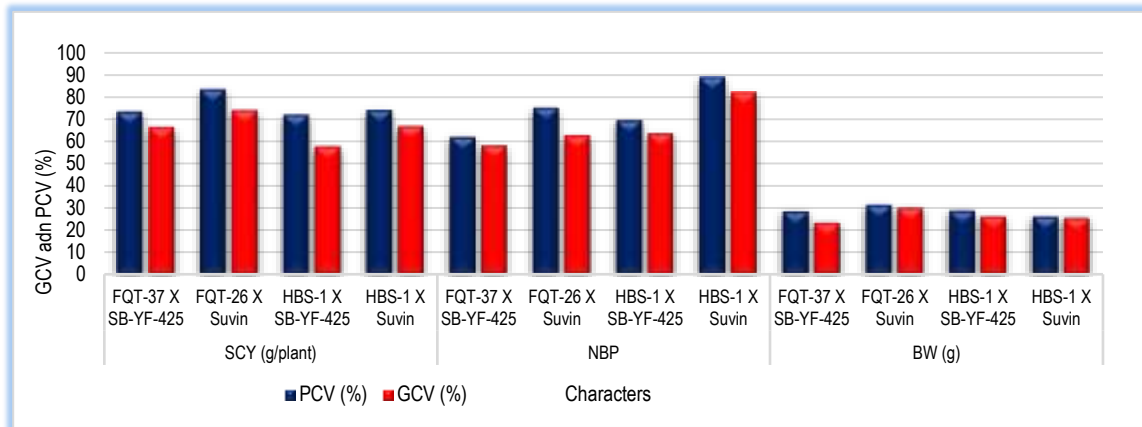
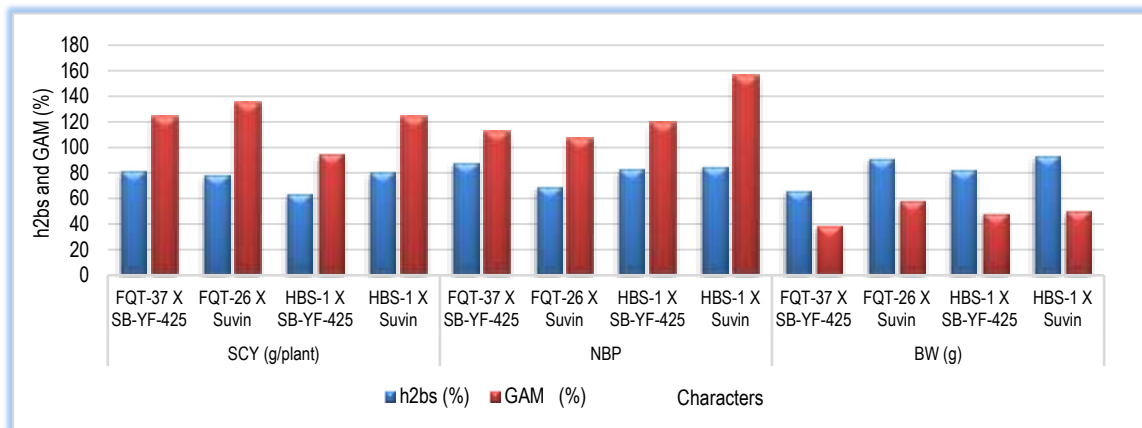
Academic Editor / Reviewer: Suleyman Cylek, Katiyar Manoj

Introduction

Cotton, a commercially important crop belongs to the family Malvaceae and genus *Gossypium*. It includes 50 species, four of which are cultivated, 44 are wild diploids and two are wild tetraploids [1]. Out of the four cultivated species, *Gossypium hirsutum* L. and *Gossypium barbadense* L. known as new world tetraploid cottons (2n = 4x = 52). India is the largest producer of cotton followed by China and USA. In India, area under cotton production is 11.8 million hectare with production of 26.8 million bales of cotton lint with an average productivity of 494 kg/ha. Gujarat stands first in production followed by Maharashtra and Telangana [2]. The genetic variability present in the available germplasm may be utilized either for direct selection or for hybridization programme which involves a choice of potential parents that can produce progeny population out yielding the parents in a set of desirable characters *i.e.*, characters related to yield. The classical experiment of Johannsen (1909) [3] demonstrated that both heritable and non-heritable agencies contributed to the somatic variations in segregating populations and that variation in pure line was entirely due to environment. Nilsson-Ehle (1909) [4] and East (1916) [5] further confirmed the work of Johannsen (1909) [3] and demonstrated how such results were obtained. Based on the study on non-segregating populations, Charles and Smith (1939), Powers (1942) and Powers *et al.* (1950) [6-8] separated genetic variance from total variance by the use of estimates of environmental variance. To start an efficient breeding program need to take the help of suitable genetic parameters such as genotypic coefficient of variation, heritability estimates, genetic advance [9]. Important function of the

heritability in the genetic study of quantitative characters is its predictive role to indicate the reliability of the phenotypic value as a guide to breeding value [10-11]. The GCV along with heritability estimates provide reliable estimates of the amount of genetic advance to be expected through phenotypic selection [12]. Therefore, assessment of available variability in a population is very important in a breeding programme. Information on the nature and magnitude of genetic variability, heritability and genetic advance is of utmost importance as it provides the basis for effective selection. Genetic variability in a population is measured by phenotypic and genotypic coefficients of variation. Selection on phenotypic basis is feasible through the improvement of genetic variability along with heritability of a character. For varietal development in cotton, selection of transgressive segregants in the early generations is desirable. The most desirable plants contain the combination of genes in the early generations would be selected and advanced.

Thus, early generation selection not only helps to reduce the burden in handling a large amount of material but also increases the possibility of picking up a desirable type in the limited screening material. An effort to identify such desirable segregants in the F₂ generation of potential crosses was done in the present study. Less knowledge of nature and magnitude of gene action controlling yield and yield attributing characters and also lack of genetic variability are implicated in the slowing of progress in developing new cotton interspecific hybrids with improved yield.

Fig-1 Estimates of PCV (%) and GCV (%) values for three characters in four F₂Fig-2 Estimates of heritability (%) and GAM (%) values for three characters in four F₂ populations, at ARS Dharwad, 2015-16

Materials and Methods

The experiment was conducted at Agricultural Research Station, Dharwad Farm in the year 2015-16; the genetic variability in F₂ generation of important interspecific productive hybrids was assessed along with the corresponding. Each F₂ population was sown in 10 rows (220 plants) and each parent was sown in 2 rows (20 plants) with 90 X 20 cm spacing. In order to assess and quantify the genetic variability among the genotypes for the characters under study, the mean and variances were analyzed based on the formula given by Singh and Chaudhary (1977) [13]. Genotypic and phenotypic components of variance were computed based on mean and variance calculated by using data of unreplicated treatments as discussed by Dabholkar (1992) [10], Sharma (1988) and Singh and Chaudhary (1977) [14]. The following parameters were estimated. Genotypic and phenotypic components of variance were computed based on mean and variance calculated by using data of unreplicated treatments by following formulae.

Phenotypic variance (σ^2_p) = Var F₂

Environmental variance (σ^2_e) = (Var P₁ + Var P₂)/2

Genotypic variance (σ^2_g) = σ^2_p - σ^2_e

The procedure adopted for calculation of different genetic parameters such as Phenotypic and genotypic coefficients of variation were worked out as suggested by Burton and Devane (1953) [12]. The broad sense heritability (h^2_{bs}) was estimated by the ratio of genotypic variance to the total phenotypic variance for all the characters as follow the method suggested by Hanson *et al.* (1956) [15]. The genetic advance and genetic advance as percent mean was categorized as given below following the method of Johnson *et al.* (1955) [3].

Results

The data recorded from individual plant observations for three characters of four F₂ populations was utilized for estimating different variability parameters, broad sense heritability and genetic advance. The results are presented in [Table-1].

Seed cotton yield per plant (g)

A wide range was observed for seed cotton yield per plant in F₂ of cross FQT-37 X

SB-YF-425 (6.00 g to 106.00 g) followed by HBS-1 X Suvin (4.00 g to 96.00 g). The mean for this trait was highest in F₂ of cross FQT-37 X SB-YF-425 (24.33 g) among the four populations. Differences between phenotypic and genotypic coefficient of variation were not significantly different from each other. The highest heritability (82.14%) was observed in F₂ of cross FQT-37 X SB-YF-425 followed by HBS-1 X Suvin (81.30%) whereas the highest GAM was recorded in F₂ of cross FQT-26 X Suvin (135.31%) and then in FQT-37 X SB-YF-425 (124.15%). Among the four F₂ populations, the F₂ of cross HBS-1 X SB-YF-425 followed by FQT-26 X Suvin, seed cotton yield per plant was largely influenced by environmental factors as indicated by large differences among the values of phenotypic and genotypic coefficients of variation, whereas F₂ of cross FQT-37 X SB-YF-425 showed less difference between PCV and GCV values indicating minimum influence of environment on this trait.

Number of bolls per plant

The range observed among FQT-37 X SB-YF-425 F₂ (3 to 28) was wider compared to the narrow range of FQT-26 X Suvin F₂ (2 to 20) population. The highest mean (8.05) and lowest mean (5.33) for this trait were recorded in F₂ of cross FQT-37 X SB-YF-425 and FQT-26 X Suvin, respectively. High heritability of 88.47 percent and 85.33 percent were observed in F₂ of crosses viz., FQT-37 X SB-YF-425 and HBS-1 X Suvin, respectively. Highest GA (9.06) and GAM (156.31) were recorded in FQT-37 X SB-YF-425 F₂ and HBS-1 X Suvin F₂ populations. Among the four populations, FQT-26 X Suvin F₂ showed more difference between phenotypic and genotypic coefficient of variation indicating high influence of environment on expression of this character whereas FQT-37 X SB-YF-425 F₂ showed less difference indicating lower influence of environment on this trait.

Boll weight (g)

The range observed for boll weight was wide in FQT-37 X SB-YF-425 F₂ (2 to 8.67) with highest mean boll weight FQT-26 X Suvin F₂ (3.99 g), among all the four populations.

Table-1 Estimates of genetic parameters for three characters in F_2 populations of four promising interspecific (HXB) crosses

Characters	Crosses	Mean	Range	V_p	V_g	PCV (%)	GCV (%)	$h^2(bs)(\%)$	GA	GAM(%)
Seed cotton yield (g/plant)	FQT-37 X SB-YF-425	24.33	6 - 106	318.69	261.79	73.37	66.4	82.14	30.2	124.15
	FQT-26 X Suvin	21.52	Apr-92	321.45	253.45	83.31	73.97	78.84	29.12	135.31
	HBS-1 X SB-YF-425	18.06	Apr-74	168.8	108.3	71.92	57.6	64.16	17.17	95.05
	HBS-1 X Suvin	20	Apr-96	315.59	256.59	74.02	66.74	81.3	29.75	123.97
Number of bolls per plant	FQT-37 X SB-YF-425	8.05	Mar-28	24.72	21.87	61.69	58.03	88.47	9.06	112.44
	FQT-26 X Suvin	5.33	Feb-20	16.04	11.14	75.07	62.56	69.45	5.73	107.41
	HBS-1 X SB-YF-425	5.35	Feb-21	13.78	11.53	69.38	63.47	83.67	6.39	119.61
	HBS-1 X Suvin	5.41	Feb-22	19.77	16.87	88.92	82.14	85.33	7.81	156.31
Boll weight (g)	FQT-37 X SB-YF-425	2.97	2 - 5.20	0.71	0.47	28.42	23.15	66.35	1.15	38.85
	FQT-26 X Suvin	3.99	2 - 8.67	1.56	1.43	31.28	29.95	91.68	2.36	59.08
	HBS-1 X SB-YF-425	3.43	2 - 6.67	0.97	0.83	28.72	26.09	82.51	1.67	48.82
	HBS-1 X Suvin	3.64	2 - 6.67	1.57	1.44	26.12	25.28	93.64	2.41	50.39

Note: V_p -Phenotypic variance, V_g -Genotypic variance, PCV-Phenotypic coefficient of variance, GCV-Genotypic coefficient of variance, GA-Genetic advance, GAM-Genetic advance on mean

Table-2 Transgressive segregants for seed cotton yield character in four F_2 populations of promising interspecific hybrids

Cross	F_2 population of cross	Mean + 2 SD (g/plant)	Total number of plants	Range of segregants (g/plant)	Plant number
I	FQT-37 X SB-YF-425	36.28	28	38-106	154, 76, 63, 120, 164, 116, 142, 57, 62, 119, 46, 136, 96, 106, 43, 86, 94, 152, 9, 74, 78, 166, 125, 17, 73, 10, 102, 153
II	FQT-26 X Suvin	45.57	21	46-92	19, 134, 38, 118, 1, 161, 140, 17, 20, 65, 159, 139, 61, 69, 94, 114, 151, 66, 131, 164, 128
III	HBS-1 X SB-YF-425	40.14	9	42-76	121, 84, 83, 58, 34, 78, 66, 61, 36
IV	HBS-1 X Suvin	40.53	23	44-96	121, 66, 95, 85, 64, 120, 132, 35, 115, 140, 44, 104, 110, 38, 46, 63, 155, 59, 114, 144, 122, 136

The heritability and GAM value observed for the trait were 93.64 percent and 59.08 percent, respectively for HBS-1 X Suvin F_2 and FQT-26 X Suvin F_2 populations and were found to be larger than in the other three populations. Phenotypic coefficients of variation were highest in FQT-26 X Suvin F_2 (31.28) followed by HBS-1 X SB-YF-425 F_2 (28.72). Whereas, coefficients of variation were highest in FQT-26 X Suvin F_2 (29.95) followed by HBS-1 X SB-YF-425 F_2 (26.09) population. In general, the differences between genotypic and phenotypic co-efficient of variation values were smaller indicating that environment has less effect on expression of this character.

Transgressive segregants

In the present study transgressive segregants were identified in segregating F_2 generations of four populations. These transgressive segregants were calculated for important character seed cotton yield per plant on the basis of mean plus two standard deviation. All these crosses with number of segregants are presented in [Table-2].

Discussions

Desirable fallout of any hybrids' study is the variability generated in the segregating generations. The F_2 generations is the first segregating generation where productive individuals can be selected and advanced to the next generations for further selection till stabilization. In the present study, the interspecific hybrids produced a range of variability across traits. An attempt to quantify the variability generated has been made here. Genotypic coefficient of variation is considered to be the most reliable than phenotypic coefficient variation for estimating genetic variability since it indicates the heritable portion of variability [Fig-1]. The F_2 progenies of the crosses FQT-26 X Suvin for seed cotton yield and F_2 progenies of cross HBS-1 X Suvin for number of bolls per plant exhibited the highest PCV and GCV values indicating that there is greater scope for selection to improve these characters in desirable direction and also among these progenies, greater diversity was found. Similarly, The GCV and PCV values for boll weight and number of bolls per plant were high in all the four populations. However, the four F_2 segregating populations F_2 progenies of cross FQT-26 X Suvin showed the highest PCV and GCV values for boll weight and seed cotton yield, respectively. Similar results were reported by Gururajan (2000), Kaushik and Kapoor (2006), Gitte et al. (2007) Magadum et al. (2012), Divya et al. (2014), Raza et al., (2016), Kumar & Katageri (2017), Kumar et al., (2017), Rajoli et al., (2017), Uma et al., (2018), Vrinda & Joshi (2018), Kalaiselvan et al., (2019), Venkatesan et al., (2019) [16-18, 20-22, 24-25, 28, 31-34]. High heritability values of more than 82 percent have been observed for seed cotton yield in the F_2 of cross FQT-37 X SB-YF-425.

High heritability was found in the four populations. Similarly, high heritability was found for number of bolls per plant. In all the four populations was found for boll weight which was governed by additive type of gene action. Same results earlier also reported by Kaushik & Kapoor (2006), Menon et al. (2008), Vineela et al. (2013), Divya et al. (2014), Venkatesha and Patil (2014), Kumar & Katageri (2017), Kumar et al., (2017), Vrinda & Joshi (2018), Muhammad et al., (2018), Kalaiselvan et al., (2019) [17, 19, 21-25, 29, 33, 34]. All the crosses contributed high heritability values for different traits like seed cotton yield, number of bolls per plant and boll weight, indicating that the traits were generally governed by additive gene action which, can be used for further selection programme. As we know genetic advance means the performance of the parental population in compared to improvement in the mean genotypic value of selected plants. Always high values of genetic gain and heritability result for effective selection. The genetic advance was high in most of the populations for the traits like seed cotton yield, number of bolls per plant and boll weight. Similarly, GAM for all the characters showed high value among the four segregating populations. Divya et al. (2014), Venkatesha & Patil (2014), Raza et al., (2016), Kumar & Katageri (2017), Vrinda & Joshi (2018) Lingaiah et al., (2018), Venkatesan et al., (2019) reported similar results [22-24, 27, 30, 32, 34]. Also, genetic advance as per mean value in all the populations exhibited higher genetic gain for all the traits under study. The high genetic advance as percent mean with high heritability will help formulate selection strategies aimed at better gains by selection. Here in all the four populations studied for three characters showed high value of genetic advance as per mean. If both heritability and GAM showed high value that indicating additive type gene action for the traits, which can be used for further selection programme [Fig-2].

Transgressive segregants

The F_2 population of the cross FQT-37 X SB-YF-425 had the highest number of transgressive segregants i.e., 28 plants for the traits seed cotton yield when mean plus two standard deviation was considered. HBS-1 X Suvin (23 nos.), FQT-26 X Suvin (21 nos.) and HBS-1 X SB-YF-425 (9 nos.) were the other populations with their transgressive segregants. The highest transgressive segregants in the F_2 of cross FQT-37 X SB-YF-425 (28 nos.) indicated high degree of dominance as gathered through line x tester analysis. So, selection for the transgressive segregants in early generations may not be beneficial. In case of the F_2 of cross FQT-37 X SB-YF-425, high x low parental combination was seen that is suitable for producing transgressive segregants. This population had the highest number of transgressive segregants for seed cotton yield which will be used in further selection procedures to generate good genetic material.

Similarly, the F₂ of cross HBS-1 X Suvin and FQT-26 X Suvin produced high number of segregants (23 nos. and 21 nos.). Both the crosses contained high x low parental combination. These can also be used in future breeding programmes [25-26].

Conclusions

As concluded that all the characters showed greater PCV values than GCV values, implying to influence of environment on the expression of these traits. High PCV and GCV values indicated the extent of variability existing for these characters. High heritability coupled with high genetic advance was observed for seed cotton yield, number of bolls per plant and boll weight indicating a good selection approach. The transgressive segregants were identified based on mean (± 2) standard deviation in four F₂ populations. The cross FQT-37 X SB-YF-425 showed highest number of transgressive segregants followed by HBS-1 X Suvin and FQT-26 X Suvin for the trait, seed cotton yield. These selected transgressive segregant plants can be used for further evaluation to identify superior genotypes.

Application of research: The findings can be put for further investigation in breeding programmes and analysed for further improvement of segregating populations in interspecific hybrids of cotton in rain-fed situation in Karnataka.

Research Category: Genetics and Plant Breeding

Abbreviations:

GCV: Genotypic co-efficient of variation,

PCV: Phenotypic co-efficient of variation

Acknowledgement / Funding: Authors are thankful to Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, 580005, India. Authors are also thankful to Hebbali Farm, UAS, Dharwad, Karnataka, 580005

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University: University of Agricultural Sciences, Dharwad, 580005, Karnataka

Research project name or number: MSc Thesis

Author Contributions: All authors equally contributed

Author statement: All authors read, reviewed, agreed and approved the final manuscript. Note-All authors agreed that- Written informed consent was obtained from all participants prior to publish / enrolment

Study area / Sample Collection: Dharwad, Karnataka

Cultivar / Variety / Breed name: *G. hirsutum* and *G. barbadense*

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.

Ethical Committee Approval Number: Nil

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