ESTIMATION OF GENETIC VARIABILITY PARAMETERS IN SEGREGATING F$_2$ GENERATION OF COTTON

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خلاصہ

جینیاتی تغیرات اور ورثہ پن کا مطالعہ F2 میں روئی کی الگ الگ نسل میں دو کراس USD16-3058 x CRIS-671 اور USD16-3058 x MNH-1026 میں حاصل کی گئی پیداوار، جیننگ اور فائبر کی خصوصیات کے لئے سنٹرل کاٹن ریسرچ انسٹی ٹیوٹ سکرند میں کی گئی۔ مطالعے کے تحت موجود تمام خصلتوں کے لئے کافی حد تک تغیر پایا گیا، جس نے مطلوبہ سمت میں خصلتوں میں بہتری لانے کی کافی گنجائش کا اشارہ کیا۔ دونوں کراس کے امتزاج میں، بولس فی پلانٹ، بول وزن اور کپاس کی پیداوار فی پلانٹ کے لئے اعلی سے اعتدال پسند فینوٹائپک اور جینوٹائپک کا جغرافیہ حاصل کیا گیا۔ جبکہ، درمیانے درجے کے فینوٹائپک گتانک میں تغیر اور کم جینوٹوپک گتانک میں تغیرات مائکرونیر ویلیو کے لئے ریکارڈ کیا گیا تھا اور کم شرح جننگ، بنیادی لمبائی اور فائبر کی طاقت کے لئے نوٹ کیا گیا تھا۔ لہذا انتخاب فینوٹائپک بنیادوں پر قابل قدر ہوگا۔ اعلی جینیاتی پیش قدمی کے ساتھ اعلی اعزازی بولس پلانٹ، بال وزن اور بیج کپاس کی پیداوار کے لئے دونوں تجاوزات میں ریکارڈ کی گئیں۔ تجویز کیا گیا ہے کہ اس طرح کے خدوخال کو عمومی طور پر اضافی جینوں کے ساتھ کنٹرول کیا جاتا ہے، جس نے تجویز پیش کی ہے کہ ان خصوصیات میں بہتری بڑے پیمانے پر اور ممکن ہے نسبتا انتخاب کراس- 1 میں جی او ٹی اور بنیادی لمبائی کے لئے اعتدال پسند جینیاتی پیش قدمی کے ساتھ اعلی وراثت جو خوبیوں کی وکالت کرتی ہے وہ دونوں اضافی اور غیر اضافی جینوں کے ساتھ وراثت میں ملتی ہیں۔ جبکہ، کراس 2 میں کم جینیاتی پیشگی کے ساتھ اعلی وراثیت جی او ٹی اور فائبر کرداروں کے لئے غیر اضافی جین عمل کی وجہ سے نوٹ کی گئی تھی۔

Abstract

The study of genetic variability and heritability was carried out in segregating F$_2$ generation of cotton in two crosses USD16-3058 x CRIS-671 and USD16-3058 x MNH-1026 at Central Cotton Research Institute Sakrand for yield, ginning outturn and fiber traits. The substantial range of variation was noted for all the traits under study, which indicated sufficient scope for taking improvement of traits in desirable direction. In both the cross combinations, high to moderate phenotypic and genotypic coefficient was obtained for bolls plant^{-1}, boll weight and seed cotton yield plant^{-1}. Whereas, medium phenotypic coefficient of variation and low genotypic coefficient of variation was recorded for micronaire value and low value was noted for ginning outturn, staple length and fiber strength. Therefore selection would be worthwhile on phenotypic basis. High heritability coupled with higher genetic advance was recorded for bolls plant^{-1}, boll weight and seed cotton yield plant^{-1} in both crosses suggested that such traits are generally controlled with additive genes, which proposed the improvement in these traits is likely through mass and progeny selection. High heritability with moderate genetic advance for GOT and staple length in cross-1 which advocated the traits are inherited with both additive and non-additive genes. Whereas, higher heritability with low genetic advance in cross-2 was noted for GOT and fiber characters due to non-additive gene action.

Keywords: Genetic Variability, Heritability, Genetic Advance, Genotypic and Phenotypic Coefficient of Variation

Introduction

Cotton is known as white gold as well as silver fiber of Pakistan. It is grown in Major areas of Sindh and Punjab and brings cash profit for the farmers. Cotton provides raw material to the textile industries and create employments to both rural and urban areas. In Pakistan during last year cotton crop were sown under area of 2.985 million hectares with the production of 12.72 million bales (Cotton Review, 2020).Yearly economic impact of cotton crops is more than 600 billion dollars globally Ashraf *et al.,* (2018). Through conventional breeding approach, hybridization is main source to create artificial genetic variability of cotton breeder to workout selection procedures, because of continuous variation due to heredity.For any breeding program diverse germplasm is essential, it is a precious material which provides the source of genetic variability. The knowledge about genetic parameters i.e. phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV), genetic advance and heritability is important to assess the characters for genetic improvement. These genetic parameters are practical tools which help the breeder to plan appropriate breeding strategy to achieve the objectives. Burton (1952), Swarup and Chaugle (1962) designated that heredity coupled with genetic variability would provide an amount of genetic advance which probably help in selection. Sivasu bramanian and Menon

(1973) quantified that <%10 phenotypic and genotypic coefficient of variations are low, 10-20% considered as moderate and >20% high. Robinson *et al.,* (1949) classified that from 0-30% heritability measured as low, while 30-60% as moderate and >60% is high. However, Johanson *et al.* (1955) quantified genetic advance over mean with <10% as low, 10-20% as moderate and more than 20% revealed as high.

Material and Method

The experiment was conducted at the field of Central Cotton Research Institute Sakrand. Breeding material comprised on three diverse parents USD16-3058 female parent, CRIS-671 and MNH-1026 male parent. Created two hybrids USD16-3058 x CRIS-671 and USD16-3058 x MNH-1026 during cotton season 2018 and F_1 generation were selfed in glass house. However, non-replicated F_2 generation was sown in the field conditions during 2019, the row to row and plant to plant spacing was maintained at 75cm and 30cm respectively. The recommended, cultural, agronomical and plant protection measures were followed as per need. The 15 plants were tagged from parents and 10% plants were tagged from F_2 population for data recording. The traits were studied for bolls plant^{-1}, boll weight (g), seed cotton yield plant^{-1}, ginning outturn%, staple length, fiber strength and micronaire value. The mean and variance were statistically analyzed according to method given by Singh and Choudhry (1977). The phenotypic and genotypic coefficient of variation was calculated according to method outlined by Burton and Devane (1953). Heritability broad sense was calculated by following the formula suggested by Hanson *et al.,* (1956). However, genetic advance was estimated suggested by Johanson *et al.,* (1955).

Result and Discussion

The estimated mean, range, phenotypic variance, genotypic variance, phenotypic coefficient of variance (PCV), genotypic coefficient of variation (GCV), heritability (h^2), genetic advance and genetic advance over mean percent of cross USD16-3058 x CRIS-671 and USD16-3058 x MNH-1026 are presented in table 1, Fig.1 and Fig.2. Substantial range of variation was noted for all the traits under study, which indicated sufficient scope for taking improvement of traits in desirable direction. In F_2 segregating generation, selection of best genotypes is principle objective that considered in breeding program. As selection should perform in F_2 generation on the basis desirable crosses and best progenies within the population. This approach will efficiently exploit the transgressive variability existing within a cross Larner (1958). For any breeding strategy, the cross with higher mean value was comparatively effective in recognizing superior segregants Finkner *et al.,* (1973). As it is helpful to remove undesirable crosses Natarajan (1992). Allard (1960) emphasized that genetic potential of progeny is not only rely on mean, but also degree of genetic variability should be considered.

The genetic variability parameters (Table 1 and Fig.1) indicated that for bolls plant^{-1} cross C_2 (USD16-3058 x MNH-1026) had average mean value but higher phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was noted (32.2 and 26.5) and C_1 (USD16-3058 x CRIS-671) produced high mean with high phenotypic and genotypic coefficient of variation (23.8 and 20.7). For the character boll weight, C_2 attained high mean value (3.5) with high PCV (22.1) and moderate GCV (18.4) and C_1 also attained high mean performance (3.3) but moderate PCV and GCV (19.7 and 16.8 respectively). For the trait seed cotton yield plant^{-1} both cross obtained high mean value, while results of genetic variability parameters, C_2 had high PCV (21.8) with moderate GCV value (17.5). C_1 showed high mean value (134) with moderate PCV and GCV values (16.9 and 14.1) for seed cotton yield. The distance between phenotypic and genotypic coefficient of variation did not differ significantly from each other which indicated that traits were very less affected by environment. Therefore selection would be worthwhile on phenotypic basis. The range and mean performance can propose an idea regarding variability but coefficient of variation is more reliable as it is dependent on unit of measurement. The selection would also be fruitful, if high mean with high variability and high mean with moderate variability characters are chosen, as such group have the potential to produce more suitable transgressive segregants as compared with low mean with low variability. Similar findings of high to moderate Phenotypic and genotypic coefficient of variation (PCV & GCV) in F_2 generation of cotton were reported by Alkudsi *et al.,* (2013), Jawahar and Patil (2017), Lokesh kumar and Patil (2018), Ahsan and Mahmood (2019) and Roy *et al.,* (2019). The least significant difference among the PCV and GVA was obtained by Erande *et al.,* (2014). The mean performance, phenotypic and genotypic coefficient of variation for ginning outturn and fiber quality characters are depicted in Table 1 and Fig.1 which exhibited that traits ginning outturn, staple length, fiber strength and micronaire value produced moderate mean values, whereas, variability parameters (PCV and GCV) were low for all these traits except micronaire value which suggested less variability in the traits. Joshi and Patil (2018) and Lokesh kumar and Patil (2018) found similar results with low PCV and GCV for GOT and fiber traits in F_2 generation.

Heritability (h^2) and genetic advance over mean percent of cross-1 and cross-2 for all the characters are presented in Fig. 2. High broad sense heritability was found in C_1 (USD16-3058 x CRIS-671) for all the

characters except fiber strength and micronaire value. Although, C_2 (USD16-3058 x MNH-1026) also produced high heritability for all the characters studied excluding micronaire value. The assessment of heritability (h^2) is not alone useful on prediction subsequent effect for selection of appropriate individuals, because it contain the effect of both additive as well as non-additive genes. Therefore, heritability coupled with genetic advance would be more helpful than alone heritability. Genetic advance over mean per cent for all the characters are presented in Fig.2 which specified that cross-1 (USD16-3058 x CRIS-671) showed higher genetic advance over mean percent for bolls plant^{-1}, boll weight and seed cotton yield plant^{-1}. Although, moderate genetic advance was noted for ginning outturn, staple length and micronaire value in cross-1, while, low genetic advance was observed for fiber strength. The cross-2 (USD16-3058 x MNH-1026) also attained high genetic advance over mean percent for bolls plant^{-1}, boll weight and seed cotton yield plant^{-1} and low genetic advance for ginning outturn, staple length, fiber strength and micronaire value. High heritability along with higher genetic advance was found for bolls plant^{-1}, boll weight and seed cotton yield plant^{-1}in both the crosses (C_1 and C_2) suggested that these traits are generally controlled with additive genes, which proposed the improvement in these traits is likely through mass and progeny selection. Result of high heritability coupled with moderate genetic advance was noted for the trait ginning outturn and staple length in cross-1 which advocated the traits are inherited with both additive and non-additive genes. Whereas, high heritability with low genetic advance and moderate heritability with low genetic advance are due to non-additive gene action. Earlier workers, Alkudsi *et al.,* (2013), Ahsan *et al.,* (2015), Muhammad *et al.,* (2015), Jawahar and Patil (2017), Kumar and Katageri (2017), Joshi and Patil (2018) and Lokesh kumar and Patil (2018), Ahsan and Mahmood (2019) also found similar results with high heritability and high genetic advance, higher heritability with moderate genetic advance, high heritability with low genetic advance and moderate heritability with low genetic advance for yield, ginning outturn and fiber characters of cotton.

Table 1. Genetic variability parameters in F_2 crosses. C_1 (USD16-3058 x CRIS-671) and C_2 (USD16-3058 x MNH-1026).

Traits	Crosses	Range		Mean	$\sigma^2 P$	$\sigma^2 G$	GA
		Min.	Max.				
Bolls Plant^{-1}	C_1	18	54	39	86.2	65.2	12.3
	C_2	17	47	30.5	96.7	65.1	11.2
Boll Weight (g)	C_1	2.1	4.2	3.3	0.42	0.31	0.83
	C_2	2.1	4.6	3.5	0.59	0.41	0.94
Seed Cotton Yield Plant^{-1}	C_1	93	183	134	510.3	356.8	27.72
	C_2	83	180	123	720.5	460.8	30.1
Ginning outturn%	C_1	34.2	43.5	39.6	6.5	6.1	4.14
	C_2	35.1	42.5	38	4.8	4.4	3.5
Staple length(mm)	C_1	23.4	31.5	28.2	4.6	4.3	3.5
	C_2	24.3	30.4	27.7	3.1	2.7	2.7
Fiber Strength(g tex^{-1})	C_1	26.4	33.5	30	2.7	1.6	1.32
	C_2	26.4	31.5	28.8	2.6	1.6	1.7
Micronaire Value(µg inch^{-1})	C_1	3.4	4.9	4.1	0.2	0.12	0.48
	C_2	3.6	5.1	4.2	0.29	0.12	0.39
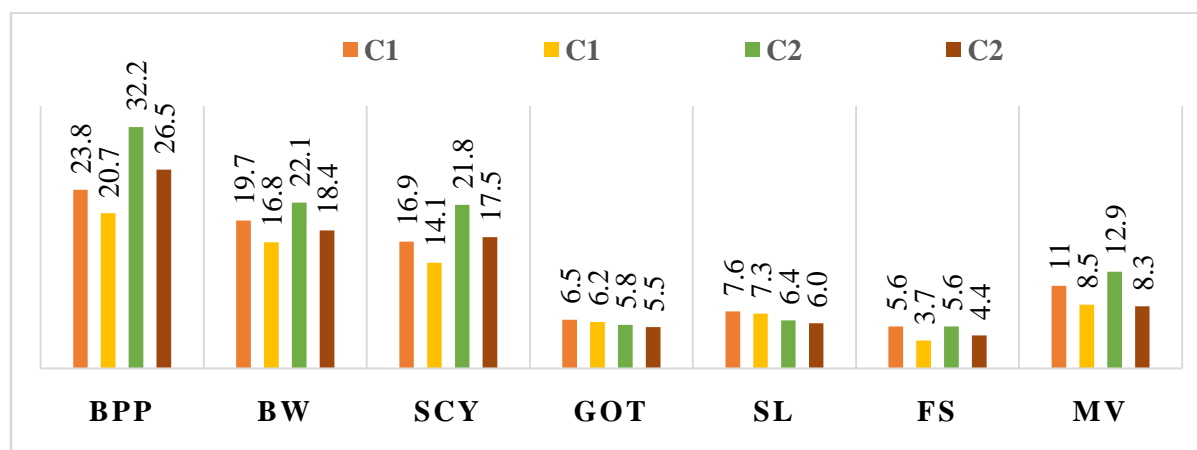
Fig. 1. Phenotypic and Genotypic Coefficient of Variation of C_1 (USD16-3058 x CRIS-671) and C_2 (USD16-3058 x MNH-126).
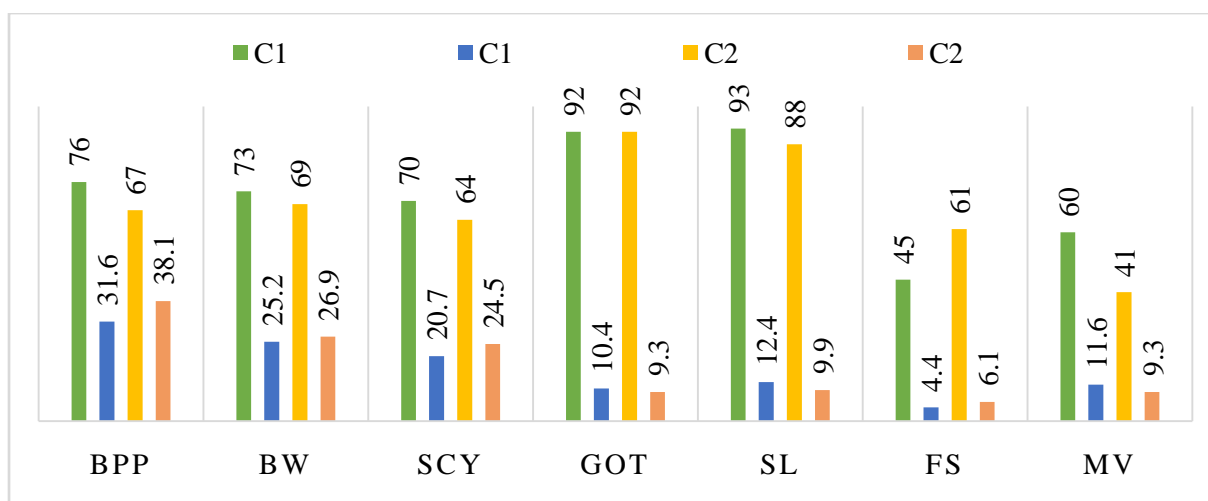
Fig. 2. Heritability (h^2) and Genetic Advance over mean % of C_1 (USD16-3058 x CRIS-671) and C_2 (USD16-3058 x MNH-126).

Conclusion

The study was conducted to evaluate the genetic variability and heritability in F_2 segregating generation of cotton for yield, ginning outturn and fiber traits. It was concluded that in both cross combinations, high to moderate, medium to low and low to low phenotypic and genotypic coefficient of variation was observed for various traits. Therefore selection would be effective on phenotypic basis. However, high heritability coupled with higher genetic advance for yield and its contributing traits indicated that traits are generally inherited due to additive genes, which proposed the improvement through mass and progeny selection. High heritability with moderate genetic advance for GOT and staple length in cross-1 which advocated the traits are inherited with both additive and non-additive genes. Whereas, higher heritability with low genetic advance in cross-2 was noted for GOT and fiber characters due to non-additive gene action.

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