Genetic variability and heritability estimates in F2 populations of intra hirsutum for various traits

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Abstract

Background: Plant breeders are more interested in genetic variance rather than phenotypic variance because that is more amenable to selection and brings further improvement in the desirable characters. Therefore the current investigation was laid out to estimate heritability and genetic advance among F2 progenies of cotton based on these parameters of cotton, *i.e.* days to 1st boll formation, days to 1st boll opening, boll formed at 90 days after sowing, plant height, sympodial branches plant^{-1}, bolls plant^{-1}, boll weight (g), seed cotton yield plant^{-1} (g), GOT (%) and staple length.

Result: The mean square of genotypes demonstrated substantial difference for most of the characters except plant height, sympodial branches plant^{-1} and staple length. Based on average performance variety Mehran recorded better performance for most of the components while in F$_2$ progenies Mehran x Koonj and CRIS-508 x CRIS-510 were noted with superior result for various traits. In case of heritability estimation Bakhtawar x CRIS-508 showed maximum heritability (77.80%) for days to 1st boll opening, (82.03%) heritability bolls formed at 90 days after sowing (84.89%) for staple length. Mehran x Koonj expressed maximum (88.78%) heritability for sympodial branches plant^{-1} and (90.52%) for GOT (%). Koonj x CRIS-510 contributed high (82.83%) heritability for plant height, and Bakhtawar x CRIS-510 showed high heritability for seed cotton yield . considering genetic gain Mehran x CRIS-508 was noted with maximum genetic progression for plenty of the parameters.

Conclusions: Mehran variety performed better for boll formation at 90 days after sowing, boll weight (g), seed cotton yield and staple length. Among the F$_2$ progenies Mehran x Koonj, Mehran x CRIS-508 and Bakhtawar x CRIS-508 recorded better mean performance for most of the traits. Regarding heritability estimation F$_2$ progenies Mehran x CRIS-508, Mehran x Koonj, Koonj x CRIS-510 and Bakhtawar x CRIS-510 showed high heritability and genetic gain for various traits that could be useful for further improvement.

Introduction

Cotton is essential fiber crop among the world which is mostly cultivated for fiber and oil purpose and play a chief role for the advancement of the country's economy with concern to textile development it is also known as white gold (Komala et al. 2018). Cotton crop is globally most important crop which is grown in both tropical and sub-tropical areas of the world it is also categorized necessary for Pakistan. Pakistan is ranked 4th position for productivity. Furthermore seed of the cotton is utilized for edible oil and feeding for animals in the form of seed cake (Shakeel et al. 2015). Cotton shares 0.8% in the GDP and 4.5% in agriculture sector while the production of the cotton is low in Pakistan due to various biotic and abiotic factors. The yield of cotton has been decreased to 9.86 million bales and the cultivated region is 2.373 thousand hectares. Declined up in cotton yield 17.5% which results to reduce cotton ginning by 12.74% (Anonymous 2019−20). The world population is increasing every day. Therefore, in order to meet the needs of the textile industry, crop yields must be increased. Using different breeding tools is one way to meet the needs of the textile industry (Farooq et al. 2018).

The states of Pakistan heavily depends on textile industries and sectors. Cotton crop is leading crop among fiber producing crops in Pakistan its usage for millions peoples clothing and considered in broad range in various sectors for by products (Khan et al. 2015). The value of this crop is reflected higher in textile sectors which is globally considered white gold (Hampannavar et al. 2020). The American cotton also known as tetraploid cotton that is significantly contributes in the economy of the country because it provides raw material to different textile industries for exporting. This crop has greater value for sufficient clothing material, edible oil and the proteins amount various chemical industries relies on its raw materials (Sahito et al. 2015).

Plant breeders are more interested to contain available genotypes for continuing various efforts to develop new cultivars that is highly essential to maintain cotton production. In breeding approaches the existence of sufficient extent of genetic variation is more efficient criteria for selection, thus it is essential to recognize the existence variation in a population to adopt suitable breeding technologies. Different types of the gene actions which controls the characters improvement (Tiwari et al. 2019). The quantitative traits controlled by many genes which depends upon the characters association and heritability thus it is essential to understand these parameters before starting any breeding program (Tabasum et al. 2012). Genetic progression is directly associated heritability to response to selection (Sootaher et al. 2020).

Genetic variation is necessary for breeders to conduct the various types' of the selection based on genotypic and phenotypic variation. The coefficient of variance contributes only the magnitude of available variation but does not provide any evidence about heritable portion. Thus heritability along with genetic progression assisted to find out fixed selection pressure quantity of advance changes with extent of heritability. Moreover selection criteria depends upon the study of characters linkage. Phenotypic association designated the magnitude of relation between two variables whereas the genotypic linkage gives information about inherent correlation between the genes governing them. (Rao et al. 2021).

Genetic variation is mainly described as total examined variability that occurs due to phenotypes in plant populations which leads to genetic changes among them. The ratio of genetic variance over phenotypic variation that is called heritability in broad sense on the other hand it regulates the extent of transmission in parameters from parental lines to their progenies (Baloch et al., 2018). Characters controlled by additive genes which are significant parameters of heritability. It is prominent technique to measure between the components of parents and their offspring. (Baloch et al. 2018) stated the genotypic variation along with maximum heritability estimation for the trait of seed cotton yield and its attributes concluded that these parameters can be developed through hybridization through transgressive selection.

Materials And Methods

Experimental trial was conducted at the Cotton Research Institute, Tandojam in randomized complete block design (RCBD) with three replications during 2020. The breeding material for the present study comprised five parents/varieties Bakhtawar, Mehran, Koonj, CRIS-508 and CRIS-510 and their ten F_2 progenies of cotton (*Gossypium hirsutum* L. which are namely as Bakhtawar ×Mehran , Bakhtawar ×Koonj , Bakhtawar ×CRIS-508, Bakhtawar ×CRIS-510, Mehran ×Koonj, Mehran ×CRIS-508, Mehran ×CRIS-510,

Koonj ×CRIS-508, Koonj ×CRIS-510 and CRIS-508 ×CRIS-510. The seed of ten intra-hirsutum ten F_2 population and their ten parents was sown in the field by diblling method .Three seeds per hill were dibbled, however after 15 days, seedling were thinned to one per hill to ensure uniform and reduced plant competition for optimum plant growth and development. The distance between plant to plant was kept at 30cm whereas row to row at 75cm. All the agronomic practices were done at proper time. The inputs like fertilizer, irrigation and insecticides were applied as and when required.

Collection of data

Days to 1st boll formation

Number of days were counted from planting to the appearance of first boll formation. Average of the days were calculated from five plants of each replication.

Days to 1st boll opening

The number of days was recorded from sowing date to 1st boll opening.

Bolls formation after 90 days of sowing

Earliness percentage of boll formation was recorded after 90 days of sowing from the total bolls formed at 90 days.

Plant height (cm)

The final plant height was measured from index plant in centimeters the height of the plant was measured with the help of measuring rod and their average was calculated from five plants of each replications.

Sympodial branches plant[-1]:

In cotton, buds generally emerge from axils of leaf. The upper ones are called axillary buds and lower ones as extra axillary bud. The extra axillary bud gives rise to sympodial branches which bears fruits. Number of sympodial branches per plant was counted per plant from tagged plants at the time of maturity.

Boll plant[-1]:

The total number of bolls were counted from tagged plants and recorded as number of productive bolls.

Bolls weight (g):

Boll size per plant was calculated by dividing the seed cotton yield per plant with the number of productive bolls per plant. The average boll weight was calculated by the formula given below

$$\text{Boll weight (g)} = \frac{\text{weight of seed cotton yield per plant (g)}}{\text{Number of bolls per plant}}$$

Seed cotton yield plant^{-1} (g):

At maturity time, mature bolls were picked in paper bags and seed cotton was kept separately from each plant. Picking was done after 10: A.M. when the due was over. Weight of seed cotton yield per plant was taken in grams with the help of electronic balance in the laboratory.

Ginning outturn (%):

Ginning outturn percentage is the ratio of lint to seed cotton sample after ginning. The samples were first dried under the sun then ginned with electric saw gin machine. The ginning outturn percentage (G.O.T.) was calculated by using the following formula

$$\text{G.O.T \%} = \frac{\text{Weight of lint (g)}}{\text{Weight of seed cotton (g)}} \times 100$$

Staple length (mm):

Staple length or fiber length is the most important quality parameter in cotton. Four samples of lint from each plant were run in the digital fibro graph and the automated measurements from the screen were recorded in millimeters.

Statistical Analysis:

The present research was carried out to determine genetic parameters of some quantitative traits in intra-hirsutum crosses of upland cotton (*Gossypium hirsutum* L.) through genetic analysis developed by Falconer (1889). ANOVA was done according to statistical procedures developed by Gomez and Gomez (1984).

The genetic parameters studied were:
1. Genetic variance ($\delta^2 g$)
2. Heritability percentage in broad sense (h^2)
3. Genetic Advance (GA)

The genetic parameters for all the characters were determined as under:
1. $\text{Mean} = \dfrac{X}{n}$

2. Variance $(S^2) = \dfrac{\Sigma(x^2)-(\Sigma x)^2/n}{n-1}$

3. Standard deviation $= \delta^2 F_2 - \delta^2 e$

5. Genetic variance $(\delta^2 g) = \delta^2 F_2 - \delta^2 e$

6. Environmental variance $(\delta^2 e) = \dfrac{\delta^2 P_1 + \delta^2 P_2}{2}$

7. Heritability percentage $(h^2) = \dfrac{\delta^2 g}{\delta^2 F_2} \times 100$

8. Genetic gain or Genetic advance $(GA) = K \times H \times \sqrt{\delta^2 p}$

Where:
SD= Phenotype standard deviation
K = Constant for selection difference at 10% selection intensity
$\delta^2 e$ = Environmental variance
$\delta^2 g$ = Genetic variance
$\delta^2 P_1$ = Variance of parent one
$\delta^2 P_2$ = Variance of parent two
H = Heritability coefficient
$h^2\%$ = heritability percentage in broad sense
GA = Genetic advance
S^2 = Variance
Σ = Sigma (latin alphabetical word) means summation.
X = mean
X = variable.

Results

Analysis of variance

The result regarding analysis of variance for various traits of cotton is presented in (Table 1). The mean square of genotypes differed significantly for the characters number of days to 1st boll formation, days to 1st boll opening, boll formed at 90 days after sowing, bolls plant[-1], boll weight (g), seed cotton yield plant[-1] (g) and GOT (%).while plant height, sympodial branches plant[-1] and staple length were non-significant.

Mean performance of cotton genotypes for different traits.

Mean performance of ten F_2 progenies along with parental lines is summarized in (Table 2). The results revealed that most of the F_2 progenies reflected higher mean values than their parents for all the studied

traits. Considering days to 1st boll formation among the F$_2$ progenies CRIS-508 ×CRIS-510 recorded maximum mean value (55.80) while in parental population CRIS-508 resulted maximum days (57.00). In case of days to 1st boll opening F$_2$ crosses CRIS-508 ×CRIS-510 demonstrated maximum value (85.93) while CRIS-508 was on the top (86.93) among the parental lines. Regarding boll formation to 90 days the maximum value was noted in Mehran × Koonj (32.73) among the F$_2$ progenies while the variety Bakhtawar exposed high value (19.80) among the parental population. In case of plant height with concern to F$_2$ progenies cross CRIS-508 ×CRIS-510 produced maximum plant height (137.93). While in parents' genotype CRIS-508 demonstrated maximum plant height (153.87). The number of sympodial branches per plant result indicate that among the progenies Bakhtawar ×Koonj produced higher number of sympodial branches (33.00), while in parental lines CRIS-510 recorded maximum numbers (29.60). With regards to Bolls plant^{-1} F$_2$ progenies Mehran ×Koonj consisted maximum number of Bolls plant^{-1} (53.13), however the variety Bakhtawar demonstrated maximum number of bolls (50.13) in parental accessions. For the parameter of boll weight maximum boll weight was reported in Bakhtawar ×Mehran (3.28) among the F$_2$ progenies, whereas variety CRIS-510 showed maximum weight (3.08) in parental population. Seed cotton yield per plant among the crosses Mehran ×CRIS-510 recorded maximum seed cotton yield plant^{-1} (g) (132.43), however genotype Mehran produced maximum yield (144.07) among the parental lines. Ginning outturn percentage the maximum value for this parameter was observed in Koonj ×CRIS-510 (38.84) among the combinations, while CRIS-508 recorded higher value (38.96) in the parental lines. In case of staple length Among the F$_2$ combinations Bakhtawar × Koonj demonstrated maximum staple length (32.17), however the variety Mehran recorded maximum value (28.90) among the parental lines. The F$_2$ progenies CRIS-508 ×CRIS-510, Mehran ×CRIS-508 and Mehran x Koonj the parental lines CRIS-508 and Mehran possessed better performance for most of the traits theses crosses along with genotypes may considered in different breeding programs for further development of the parameters.

Estimation of Heritability and Genetic advance

The breeding objectives in any economically valuable crop are to evolve new varieties possessing most of the desirable traits. For the improvement in any plant character, plant breeders heavily rely on the availability of genetic variability in a segregating population. It is the additive portion of genetic variability which is heritable from one generation to the next. Quantitative traits which are controlled by polygenes are largely influenced by environmental factors. The environmental variation is non-heritable hence it is neglected. Present research was aimed to estimate genetic variability, heritability percentage in broad sense and genetic advance at 10% selection pressure in intra-hirsutum F$_2$ populations for ten quantitative traits. Estimates of heritability and genetic advance for various traits of cotton are given in (Tables 3). The results for days to 1st boll formation for all the ten F$_2$ progenies revealed that most of the progenies displayed moderate to high genetic variance varied from 45.02-102.32. Though heritability percentage in majority of the progenies was high to medium, yet six progenies, Mehran ×Koonj, Bakhtawar ×CRIS-510, Bakhtawar ×CRIS-508, Mehran ×CRIS-508, Koonj ×CRIS-510 and CRIS-508 ×CRIS-510 estimated high heritability 84.56, 76.91, 73.50, 43.00 and 61.63% respectively. With regards to days to 1st boll opening exposed that most of the progenies exhibited moderate to high genetic variance varied from 66.17-217.46.

Though heritability percentage in majority of the progenies recorded moderate to high heritability which is ranged from 43.05-77.80% respectively. However, maximum genetic advance of 17.64 was exhibited by the progeny Bakhtawar ×CRIS-510. The results for Boll formation at 90 days after sowing demonstrated that most of the progenies a fair amount of genetic variance (GV) varied from 64.06-221.73. Regarding heritability percentage in broad sense, except few progenies, majority have expressed low to high heritability percentages ranging from 9.53 to 82.03. Among the progenies Bakhtawar ×CRIS-508 and Koonj ×CRIS-510 displayed maximum heritability and genetic advance respectively (82.03 and 13.63). Considering plant height which represented the range for genetic variance varied from 134.3-265.28. Whereas heritability percentage in broad sense, except few progenies, majority have stated moderate to high heritability percentages ranging from 42.67 to 82.83%. However the Koonj ×CRIS-510 showed maximum heritability (82.83%) and Bakhtawar ×CRIS-508 indicated greater value for genetic gain (23.15). For parameter of sympodial branches per plant which comprised the range for genotypic variance f 79.52-207.46 and contributed low to high heritability (27.61-88.78%). Among the progenies, Mehran x Koonj exposed maximum (88.78%) heritability while Bakhtawar x CRIS-510 displayed highest genetic potential (23.34). In case of bolls plant^{-1} generally, all the progenies exhibited fairly high genetic variances (32.26 to 711.42) while the heritability percentage in broad sense, majority of combinations expressed low to moderate heritability percentages ranging from 10.34 to 55.67. The Koonj x CRIS-510, Bakhtawar x Mehran, Koonj ×CRIS-508 ranked top scorer for heritability (55.67, 49.85 and 47.47%) and Mehran ×Koonj consisted higher value for genetic progression (10.19). The results regarding Boll weight of ten F_2 progenies exhibited fairly high genetic variances (09.23 to 21.01). However the heritability percentage in broad sense, expressed low to high heritability percentages ranging from 24.53 to 88.55 for all the combinations. Seed cotton yield demonstrated range for genetic variances (118.21 to 275.14) whereas heritability percentages was ranged from 43.31 to 80.06%. Among the F2 progenies, Bakhtawar ×CRIS-510 recorded high heritability (80.06%) while high genetic potential (25.38) was reported in Mehran ×Koonj. In case of ginning turnout displayed genetic variances varied from (25.08 to 113.69). Regarding heritability percentage in broad sense, progenies showed low to high heritability percentages varied from 1.74 to 90.52. The Mehran ×Koonj recorded maximum heritability and genetic advance respectively (90.52 and 23.07). The result for staple length designated genetic variance range 38.70 to 81.77. Heritability percentage in broad sense in most of the progenies varied from low to high 14.26 to 84.89% which was associated with reasonable genetic advance ranging from 2.14 to 24.94.

Discussion

The analysis of variance showed significant difference among the genotypes (consisted of ten F_2 progenies and their five parental lines) for all the traits. This suggested that significant mean differences existed in the breeding material studied. Sahar et al, (2021) noted considerable difference for most of the yield and fiber traits in upland cotton whereas Ishaq et al, (2021) also recorded sufficient variation in F2 progenies of American cotton.

Mean comparison for quantitative characters

Phenotypic yield and fiber quality parameters are important which makes sustainable resources for enhancing yield and assisted to improve marketing quality regarding lint and oil (Anjani et al. 2020). Based on average performance fifteen genotypes including (five parental lines and ten F2 progenies) recorded remarkable performance for many of the attributes. Considering days to first boll formation which is more significant with concern to the period for the development of reproductive stage among the F2 progenies CRIS-508 x CRIS-510 recorded maximum value and variety CRIS-508 was on the top among parents. Days to first boll opening has greater contribution for estimating shortest period CRIS-508 x CRIS-510 combination was reported with greater value while the CRIS-508 displayed higher value among the parental lines. Boll formation after 90 days is highly significant for estimating boll formation in particular time period among the F2 progenies Mehran x Koonj exhibited higher value whereas genotypes Mehran and Bakhtawar were reported with greater value among the parental lines. Batool et al, (2010) reported similar findings for days to first flowering. Plant height is important symbol which permits the yield plant to resist clearly with weeds and other purposes such as proper distribution of photosynthesis CRIS-508 x CRIS-510 was reported with taller plants, while variety CRIS-508 reported taller Plant among the parental lines Abro et al (2021) reported almost similar findings for plant height in F4 combinations and their parents. Sympodial branches were noted in maximum number in F2 hybrid Bakhtawar x Koonj whereas genotype CRIS-510 was remained on the top among the parents. Bolls per plant the greater numbers of boll were observed in Mehran x Koonj however the parent Bakhtawar was noticed in maximum numbers. Khokhar et al (2017) stated almost similar results for number of bolls and sympodial branches in various genotypes of cotton. Boll weight is also highly economic parameter of cotton that effects different sizes i.e. larger, smaller, medium which directly impacts on seed cotton yield. Bakhtawar x Mehran was noticed with maximum boll weight among the F2 progenies however the CRIS-510 was on the top among parental lines.   Seed cotton yield is a complicated parameter controlled by many genes. Thus it depends upon other associative parameters which is used to increase the yield potential and selection approaches for further cotton breeding. Mehran x Koonj recorded maximum seed cotton yield among the F2 hybrids while the variety Mehran was reported with maximum value in parents. Considering ginning turnout highest ginning turnout was exposed by Mehran x CRIS-508 among F2 progenies while the genotype CRIS-508 recorded higher value in parental lines. In case of staple length which is valuable for textile sectors longest staple length was reserved Bakhtawar x Koonj among F2 hybrids while the Mehran consisted longest fiber length among the parental lines. Nazir et al (2020) reported similar results for the trait of fiber length in various genotypes of upland cotton. Our findings are agreed with the research of Khokhar et al (2017) where they observed almost similar results for bolls per plant and boll weight.

Estimation of Heritability and Genetic advance

The research of inheritance of any genotypes in plant breeding that assisted to breeder to accomplish better yield and development of novel genotypes. Sootaher et al (2020). Regarding heritability and genetic gain estimation for the character of days to first boll formation it was ranged from low to high heritability for all the combinations with low genetic advance. Batool et al (2010) observed low to high heritability for this parameter. In case of days to first boll opening all the crosses possessed range from low to high heritability with low to moderate genetic progression. Considering boll formation after 90 days which was

noted with range from low to high heritability and low to moderate genetic advance. Regarding plant height all the combinatios exposed range from low to high heritability with low to high genetic progression. Abro et al (2020) observed highest heritability with highest genetic gain for plant height high heritability for this trait indicated that it could be effective for further improvement. Considering sympodial branches that was noted from low to high heritability with low to high genetic gain. Sehar et al (2021) noticed high heritability with maximum genetic advance by observing different genotypes in upland cotton Kumar et al. (2017) and Kumbhar et al. (2020). Recorded superior performance regarding heritability and genetic gain appropriate result was founded by Anjani et al. (2020) result indicated that sympodial branches can be appropriate parameter for future breeding. For the character of bolls per plant that was reported with low to moderate heritability with low genetic gain. Rao et al (2021) reported moderate heritability with low genetic gain for this parameter these values indicated this parameter more needs regarding further improvement. Considering boll weight that was exhibited range from low to high heritability with low genetic progression. Farooq et al. (2018) and Saleem et al. (2020) carried out research in various cotton genotypes for estimating genetic and inheritance of quantitative characters utilizing numerous segregating progenies in which they indicated that the segregating progenies provided more genetic perception into polygenic parameters such as bolls per plant, boll size and boll weight. Abro et al (2021) reported moderate to high heritability with low genetic gain for boll weight in F4 populations of upland cotton. In case of seed cotton yield moderate to high heritability observed with low to high genetic progression. High heritability denoted that seed cotton yield is less influenced by environmental factors for most of the F2 progenies. Kaleri et al. (2016) exposed that the variations were noted for seed cotton yield was governed by inheritance and less effected by environments. Hampannavar et al. (2020) stated high heritability and maximum genetic progression for this parameter. Considering ginning turnout most of the F2 progenies were reported low heritability with low to high genetic gain except Mehran x Koonj that comprised highest heritability indicating that this F2 hybrid has greater value regarding ginning turnout Komala et al. (2018) demonstrated that selection on wide based for the improvement of segregating progenies it is necessary to notice moderate and high heritability to make better variations in hybridization program. Lingling et al. (2020) noted the good results for this parameter in upland cotton. Regarding staple length that was noticed range from low to high heritability with low to high genetic advance Nazir et al. (2020) stated that quality of fiber is improved by many countries as compare to Pakistan, thus the betterment for fiber quality is the main aim of breeder. Pandiyan et al. (2019) reported high heritability with moderate genetic gain by estimating 53 genotypes of American cotton.

Conclusion

Genetic variability and heritability estimates are very important parameters from plant breeding perspective for the improvement of any quantitative traits. Thus, heritability estimate is an indication of the degree of transmission of characters from one generation to the next. Among the F_2 progeny Mehran x CRIS-508, Mehran x Koonj, Koonj x CRIS-510 and Bakhtawar x CRIS-510 showed high heritability for various traits could serve potential segregating populations in further selfing generations.

Declarations

Authors'contributions

Farman Ali kaleri and Wajid Ali Jatoi conducted the experiments and data analysis. Saleem Raza drafted the manuscript. Shah Nawaz Mari, Shahnaz Memon, Majid Hussain Kaleri in data collection and analysed the data.Lubna Rajput and Muhammad Kashif Sarwar revise the manuscript.

Availability of data and materials

The datasets used and analyzed during the current study are available from the corresponding author on reasonable request.

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no conflict of interest.

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Tables

Table-1. Mean squares from ANOVA for quantitative traits of cotton genotype

Traits	Mean squares					
	Replications	Genotypes	Parents (P)	Crosses (C)	P vs V	Error
Degrees of freedom	02	14	05	09	36.36**	28
Days to 1st boll formation	0.86	24.85**	38.87**	16.92**	2.24*	0.73
Days to 1st 1st boll opening	0.77	19.79**	51.96**	7.447**	27.78**	0.84
Bolls formation at 90 days	20.67	59.848**	5.357**	87.63**	523.16**	3.93
Plant height	329.96	560.80	1015.90	362.71**	0.72	436.09
Sympodial branches plant^{-1}	101.55	98.76	37.73**	136.78	4.11	74.92
Boll plant^{-1}	36.36	138.509**	64.28**	186.43**	0.01	33.02
Boll weight	0.047	0.296**	0.321**	0.317**	0.11	0.035
Seed cotton yield plant^{-1}	14.61	1022.60**	886.87**	1196.53**	6.48	59.15
GOT %	0.228	5.847**	1.758**	7.59**	3.358**	0.24
Staple length	9.228	7.90	1.498	11.25	36.36**	5.06

**,* = significant at 0.01 and 0.05 probability levels respectively

Table 2.   Mean performance of cotton genotypes for yield and its related traits.

Genotypes	FBF	BO	BF	PH	SB	BP	BW	SCY	GOT	SL
Parents										
Bakhtawar	56.43	85.13	19.80	106.47	27.97	50.13	2.73	136.67	37.45	27.84
Mehran	52.13	81.47	16.67	132.33	22.33	42.00	3.43	144.07	37.81	28.90
Koonj	48.23	76.13	19.80	119.60	21.40	38.13	2.59	99.59	37.00	26.97
CRIS-508	57.00	86.93	18.07	153.87	26.27	41.73	2.86	119.30	38.96	27.82
CRIS-510	54.77	83.60	19.13	140.93	29.60	39.73	3.08	122.43	38.35	28.27
Bakhtawar	56.43	85.13	19.80	106.47	27.97	50.13	2.73	136.67	37.45	27.84
F_2 Crosses										
Bakhtawar x Mehran	49.67	82.87	20.00	119.53	20.87	37.80	3.28	123.53	37.96	27.57
Bakhtawar x Koonj	49.87	83.13	15.60	119.40	33.00	40.13	3.03	126.31	35.16	32.17
Bakhtawar x CRIS-508	51.07	82.87	13.73	134.00	23.67	39.13	3.26	122.57	35.84	28.77
Bakhtawar x CRIS-510	51.40	82.80	20.53	110.93	20.67	49.07	2.63	128.56	35.54	31.83
Mehran x Koonj	49.07	82.33	32.73	106.07	21.00	53.13	3.16	167.83	37.94	28.53
Mehran x CRIS-508	54.07	84.40	24.53	128.40	28.80	26.98	3.30	128.93	39.65	27.90
Mehran x CRIS-510	54.87	84.53	20.40	131.73	23.80	47.07	2.83	132.43	37.66	27.43
Koonj x CRIS-508	49.93	80.07	19.93	113.47	21.00	32.93	2.67	87.49	37.33	27.30
Koonj x CRIS-510	52.33	82.33	20.80	132.60	25.67	44.93	2.51	112.62	38.84	26.47
CRIS-508 x CRIS-510	55.80	85.93	15.33	137.93	24.00	45.87	2.51	114.81	35.18	27.40
LSD at 5%	1.42	1.53	3.31	34.92	14.47	9.61	0.31	12.86	0.82	3.76

Whereas BF: first boll formation, BO: boll opening first, BF: boll formation after 90 days, PH: plant height, BP: the boll number per plant, SB: sympodial branches per plant, BW: boll weight, SCY: seed cotton yield, GOT: ginning outturn and SL: staple length

Table 3. The values of genetic variance (d^2g), heritability percentage (h^2) in broad sense and genetic advance (GA) of upland cotton F_2 progenies

Traits	F$_2$ progenies	Genotypic variance (GV)	Heritability (h2b.s.)	Genetic advance (GA)
Days to first flower	Bakhtawar ×Mehran	49.71	17.99	5.83
	Bakhtawar ×Koonj	87.82	21.58	8.06
	Bakhtawar ×CRIS-508	58.54	73.99	4.43
	Bakhtawar ×CRIS-510	46.60	76.91	5.29
	Mehran × Koonj	79.78	84.56	3.94
	Mehran × CRIS-508	102.32	73.50	3.33
	Mehran × CRIS-510	53.55	55.10	4.93
	Koonj × CRIS-508	45.02	61.86	9.21
	Koonj ×CRIS-510	82.27	43.00	2.77
	CRIS-508 ×CRIS-510	50.89	61.63	6.61
Days to first boll opening	Bakhtawar ×Mehran	175.33	71.10	11.60
	Bakhtawar ×Koonj	189.42	75.63	8.24
	Bakhtawar ×CRIS-508	135.57	77.80	11.38
	Bakhtawar ×CRIS-510	170.76	25.83	17.64
	Mehran × Koonj	140.90	52.22	13.11
	Mehran × CRIS-508	217.46	43.05	14.53
	Mehran × CRIS-510	189.72	71.26	11.87
	Koonj × CRIS-508	66.17	64.15	5.85
	Koonj ×CRIS-510	82.08	77.06	14.58
	CRIS-508 ×CRIS-510	111.30	51.51	12.28
Boll formation at 90	Bakhtawar	64.06	16.06	5.65

days	×Mehran			
	Bakhtawar ×Koonj	148.96	61.32	6.82
	Bakhtawar ×CRIS-508	130.19	82.03	8.06
	Bakhtawar ×CRIS-510	141.39	9.85	3.55
	Mehran × Koonj	221.73	68.31	9.08
	Mehran × CRIS-508	199.26	49.77	10.48
	Mehran × CRIS-510	120.18	27.19	10.06
	Koonj × CRIS-508	117.80	9.53	3.34
	Koonj ×CRIS-510	115.36	79.26	13.63
	CRIS-508 ×CRIS-510	111.21	70.43	12.81
Plant height	Bakhtawar ×Mehran	195.30	42.67	9.76
	Bakhtawar ×Koonj	226.26	71.77	6.74
	Bakhtawar ×CRIS-508	265.82	61.03	23.15
	Bakhtawar ×CRIS-510	197.12	46.04	17.89
	Mehran × Koonj	159.42	74.42	7.32
	Mehran × CRIS-508	134.30	59.58	22.03
	Mehran × CRIS-510	136.84	77.71	17.86
	Koonj × CRIS-508	117.80	9.53	3.34
	Koonj ×CRIS-510	115.36	79.26	13.63
	CRIS-508 ×CRIS-510	111.21	70.43	12.81
Sympodial branches	Bakhtawar ×Mehran	201.13	86.26	16.96
	Bakhtawar ×Koonj	79.52	74.72	6.02
	Bakhtawar ×CRIS-508	173.99	31.12	12.95

	Bakhtawar ×CRIS-510	393.88	69.11	23.34
	Mehran × Koonj	238.70	88.78	23.24
	Mehran × CRIS-508	139.25	77.09	22.94
	Mehran × CRIS-510	191.59	38.77	15.17
	Koonj × CRIS-508	136.27	30.94	11.43
	Koonj ×CRIS-510	144.90	27.61	11.13
	CRIS-508 ×CRIS-510	207.46	66.05	15.22

Contd……….
(Table 3)

Traits	F$_2$ progenies	Genotypic variance (GV)	Heritability (h2 b.s.)	Genetic advance (GA)
Bolls per plant	Bakhtawar ×Mehran	711.42	49.85	3.15
	Bakhtawar ×Koonj	557.53	39.10	5.98
	Bakhtawar ×CRIS-508	552.26	33.81	4.05
	Bakhtawar ×CRIS-510	32.26	10.34	1.16
	Mehran × Koonj	121.92	42.98	10.19
	Mehran × CRIS-508	222.07	14.51	9.99
	Mehran × CRIS-510	542.24	24.50	3.29
	Koonj × CRIS-508	514.29	47.47	2.50
	Koonj ×CRIS-510	114.35	55.67	4.48
	CRIS-508 ×CRIS-510	441.02	20.99	1.93
Boll weight	Bakhtawar ×Mehran	21.01	49.40	0.54
	Bakhtawar ×Koonj	14.22	37.24	2.21
	Bakhtawar ×CRIS-508	12.06	20.82	1.15
	Bakhtawar ×CRIS-510	11.58	22.80	1.06
	Mehran × Koonj	10.79	77.91	0.44
	Mehran × CRIS-508	10.93	88.55	0.50
	Mehran × CRIS-510	12.63	32.77	1.63
	Koonj × CRIS-508	09.32	24.53	0.21
	Koonj ×CRIS-510	11.80	28.42	1.26
	CRIS-508 ×CRIS-510	12.54	40.23	1.78

Seed cotton yield	Bakhtawar ×Mehran	248.08	43.61	4.76
	Bakhtawar ×Koonj	215.00	72.32	10.04
	Bakhtawar ×CRIS-508	236.01	79.56	20.62
	Bakhtawar ×CRIS-510	210.21	80.06	21.14
	Mehran × Koonj	118.21	43.31	25.38
	Mehran × CRIS-508	275.41	55.27	11.95
	Mehran × CRIS-510	142.54	61.95	14.55
	Koonj × CRIS-508	233.37	57.97	9.22
	Koonj ×CRIS-510	228.47	61.80	3.57
	CRIS-508 ×CRIS-510	160.85	44.10	2.42
Ginning turnout	Bakhtawar ×Mehran	25.08	1.74	1.16
	Bakhtawar ×Koonj	68.78	10.27	6.48
	Bakhtawar ×CRIS-508	78.76	13.65	8.61
	Bakhtawar ×CRIS-510	102.40	7.67	14.93
	Mehran × Koonj	78.67	90.52	23.07
	Mehran × CRIS-508	77.68	39.34	27.45
	Mehran × CRIS-510	78.89	52.16	24.65
	Koonj × CRIS-508	113.69	22.51	14.79
	Koonj ×CRIS-510	52.43	29.99	20.50
	CRIS-508 ×CRIS-510	57.13	20.78	12.86
Staple length	Bakhtawar ×Mehran	45.21	55.95	12.89
	Bakhtawar ×Koonj	81.77	19.84	14.99
	Bakhtawar ×CRIS-508	45.48	84.89	12.48

Bakhtawar ×CRIS-510	54.59	14.26	2.14
Mehran × Koonj	54.48	54.24	22.13
Mehran × CRIS-508	38.70	34.97	12.44
Mehran × CRIS-510	55.15	77.33	23.54
Koonj × CRIS-508	46.28	52.18	11.05
Koonj ×CRIS-510	51.72	17.38	13.44
CRIS-508 ×CRIS-510	74.98	50.49	24.94