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# Selection Response, Heritability and Genetic Variability Studies in Upland Cotton

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## ABSTRACT

The present study was undertaken for the estimation of heritability, genetic variability and genetic advance of yield contributing traits in $F_3$ generation of upland cotton (Gossypiumhirsutum L.). The $F_3$ generations of ten crosses along with their parents were sown in non-replicated field trail. The data was recorded on maturity for node of first fruiting branch, total number of nodes/plant, plant height (cm), monopodial branches per plant, sympodial branches per plant, total number of fruiting points, number of bolls/plant, boll retention percentage, average boll weight, yield per plant (kg), lint percentage and fiber length (mm). The heritability in broad-sense, genetic advance and genetic variability estimates presented in table-3, table-4 and table-5 suggested that the highest heritability in broad–sense coupled with good genetic advance and genetic variability was present for plant height (83.78%, 10.51 and 39.75), boll retention percentage (81.78%, 4.54 and 8.18), fiber length (96.06%, 1.82 and 1.125), nodes per plant (84.15%, 4.48 and 7.97) and average boll weight (88.39, %, 0.61 and 0.137) respectively. From these results it is evident that improvement in these traits could be achieved through selection in segregating generations.

**KEY WORDS:** Heritability, genetic variability, genetic advance, selection response, Gossypiumhirsutum,

## 1. INTRODUCTION

Cotton is an important cash crop in the world (Chary and Leffler, 1984), the major cotton producing countries of the world are USA, China, India, Pakistan, Uzbekistan, Egypt, Argentina, Australia, Greece, Brazil and Turkey. These countries contribute about 80% to the cotton production. Being an agrarian country, economy of Pakistan almost entirely depends on agriculture. Cotton, main source of foreign exchange is exclusively known as silver fiber as it is major cash crop of Pakistan, its share in GDP is 1.6% and value added in agriculture owing to this single crop is about 7.8%. In Pakistan, 2835 thousand hectare area was under cotton cultivation during 2011-12 (Anonymous 2011-12). Cotton is not only export earning crop but also provides raw material to domestic textile industry which comprises of 1139 ginning factories, 503 textile mills and about 5000 oil expelling units (Mahmood 1999). Apart from a fiber crop its share in domestic edible oil industry is 60-70% (Khan *et al.* 2009). Domestic industry demands cotton with improved traits that motivates the breeder to improve the quality and yield of cotton crop.

In order to develop high yielding varieties of cotton, the genetic information on different quantitative and qualitative traits may be helpful for cotton breeders to improve genetic architecture of the plant in particular direction for improving and maintaining the proper crop production level (Nadeem &Azhar 2004, Ali & Khan 2007, and Abbas *et al.* 2008). The use of existing genetic variability in the breeding material and the creation of new variability along with its genetic understanding is of crucial importance for this purpose in a breeding program (Basal &Turgut, 2005; Abbas *et al.* 2008; Ali *et al.* 2008; and Ali and Awan 2009).

The degree to which the given trait is transmitted to next generation can be best visualized by the estimates of heritability, thus heritability coupled with genetic advance and genetic variability could be the suitable tool for plant breeder to select the suitable breeding method in order to improve the genetic makeup of cotton plant. The breeding program of any crop mainly depends on the presence of genetic variability present in the breeding materials.

Many investigators (Khan and Azhar 2000; Chandio *et al.* 2003; and Bloach 2004) reported that high heritability for different agronomic traits of upland cotton helped cotton breeders to exploit different breeding procedures for enhancement of yield and quality related traits of upland cotton. Basal and Tuegut, 2005; Joshi et al.

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2006; Rauf et al. 2006; estimated the high heritability and genetic advance for number of traits i.e. lint percentage, fiber length, seed cotton yield and number of bolls per plant. Similarly Elsiddig*et al.* 2007; Ali *et al.* 2010; reported moderate to high heritability for seed cotton yield, seed index, boll weight, lint yield, bolls per plant, average boll weight and fiber fineness. Basbag and Gencer (2004) found that among yield related traits bolls per plant had low heritability, whereas other characters had moderate heritability. Nistor and Nistor (1999) determined high broad-sense heritability (89%) for staple length. Ahmad *et al.* (2006) determined moderate to high heritability estimates and genetic advance for plant height and seed cotton yield per plant. Ulloa (2006) revealed that the GOT showed highest heritability (95%) followed by staple length (80%). Heritability is an important statistical tool used by the breeders for effective selection of the genetic variation from the total phenotypic variation. Heritability is considered as a good index of transmission of characters from parents to their offspring. The effectiveness of selection is dependent on the magnitude of heritability. The heritability estimates express the reliability of phenotypic value, as a guide to the breeding value and its determination is obviously of fundamental importance in any breeding program.

The present study was undertaken by non replicated yield trail to determine heritability, genetic advance and genetic variability of different yield and quality traits in upland cotton. This information would be helpful to cotton breeders in future breeding program.

## 2. MATERIAL AND METHODS

**Plant material:** The $F_3$ generation of upland cotton (*Gossypium. hirsutum* L.) obtained from ten crosses (S 09 × CIM 534, CRSM 2007 × MNH 6070, CIM 534 × IUB 1524, MNH 786 × IUB 09, MNH 6070 × CIM 473, IUB 09 × N 111, IUB 09 × MNH 6070, CRS 2007 × IUB 1524, CIM 534 × IUB 09 and CIM 707 × IUB 1524) along with their parental material were provided by the department of Plant Breeding and Genetics, University College of Agriculture and Environmental Sciences, The Islamia University of Bahawalpur.

**Field Experiment:** The $F_3$ families along with their parents were sown in non-replicated yield trail in the field research area of Department of Plant Breeding and Genetics, University college of Agriculture and Environmental sciences, the Islamia University of Bahawalpur. Two rows (10m long) of parents and eight rows of their cross were sown by dibbling method. Plant to plant and row to row and distance was maintained as 30 cm and 75 cm respectively. The agronomic and plant protection measures were adopted in standard fashion.

**Collection of data:** On maturity the data was recorded for 150 consecutive plants of each cross while the data of 20 plants was recorded for each of the parent. The data was maintained for plant height (cm), node of first fruiting branch, total number of nodes per plant, monopodial branches per plant, sympodial branches per plant, total fruiting points per plant, number of bolls per plant, boll retention percentage, average boll weight per plant (gm), Seed cotton yield per plant (gm), lint percentage and fiber length (mm).

- **Plant Height:** Plant height was recorded in cm at maturity. The measurement was taken from the ground level to the tip of the main shoot.
- **Node of first fruiting branch:** First fruiting node from the base of each plant of each cross was recorded.
- **Total number of nodes per plant:** Total number of nodes above zero node on each plant of every cross were counted.
- **Monopodial Branches per plant:** Vegetative branches/ indirect fruiting branches that arise from the main stem are called monopodial branches per plant these were counted and recorded for each plant.
- **Sympodial branches per plant:** Fruiting branches that bears direct fruiting are called sympodial branches that were counted in each plant.
- **Total number of fruiting points:** All the open and shaded bolls were counted and added in order to calculate the total number of fruiting points per plant.
- **Number of bolls per plant:** The numbers of matured bolls were counted and record was maintained for each plant.
- **Boll Retention percentage:** The boll retention percentage was calculated by dividing the total number of bolls from each plant of every cross on the fruiting points per plant and multiplied by hundred.

$$\text{Boll retention percentage} = \frac{\text{Total number of bolls per plant}}{\text{Fruiting points per plant}} \times 100$$

- **Average boll weight (gm):** Average boll weight was recorded by dividing total seed cotton weight from each plant of every cross on total number mature/opened bolls that were picked.

$$\text{Average boll weight per plant} = \frac{\text{Total seed cotton yield per plant}}{\text{Number of bolls per plant}}$$

- **Seed Cotton yield per plant (gm):** Seed cotton yield per plant was recorded by weighing total seed cotton of each plant recorded in grams.
- **Lint Percentage (G.O.T):**From each plant 50gm dry seed cotton was weighed and was ginned on roller ginning machine. Lint percentage from each plant was recorded by following formula.
$$\text{Lint percentage} = \frac{\text{Weight of lint sample}}{\text{Weight of seed cotton sample}} \times 100$$
- **Staple length (mm):**Staple length was measured in millimeters by the tuft method.

**Statistical procedure:** The recorded data were subjected for statistical analysis by way of calculating mean, standard deviation, variance for parents and $F_3$ generation. Genetic advance study was undertaken and Heritability estimates for the traits were calculated by using the formula given by Cahaner and Hillil (1980).

Variance was calculated by the following formula

$$\mathrm{Vr} = \frac{\sum x^2 - (\sum x)^2/n}{n-1}$$

Where

Vr = Variance

n = Number of genotypes

x = Mean value of genotypes

The genetic variability ($\mathrm{Var_gF_3}$) and heritability were calculated by the formulas given by Cahaner and Hillel (1980).

$$\mathrm{Var_gF_3} = \mathrm{VF_3} - \sqrt{\mathrm{VrP_1} \times \mathrm{VrP_2}}$$

$$h^2_{(b.s)} = \frac{\mathrm{VrF_3} - \mathrm{VrP}}{\mathrm{VrF_3}}$$

Whereas

$h^2_{(b.s)}$ = The estimates of broad-sense heritability from $F_3$ generation.

$\mathrm{VrF_3}$ = Phenotypic variance of a trait in $F_3$ generation

VrP = Average variance of a trait within pure-bred parental line.

Genetic advance was calculated by the formula:

$$\mathrm{GA} = \mathrm{SDF_3} \times h^2_{(b.s)} \times \mathrm{I}$$

Whereas

GA = genetic advance

$\mathrm{SDF_3}$ = standard deviation of $F_3$

$h^2_{(b.s)}$ = heritability in broad-sense

I = constant value that reflects selection intensity.

## 3. RESULTS AND DISCUSSION

**Means and variance of parents and $F_3$ generation:** The means of parents and their $F_3$ generations are presented in table-1 which suggested that among the parental population the highest mean value for node of first fruiting branch (6.67) was recorded for the parent CRS-2007, the parent MNH-6070 showed highest mean value for the plant height (178.2 cm). CIM-707 showed highest mean value for the fiber length (30.4 mm), nodes/plant (47.06) and number of sympodial branches per plant (40.22). The parent MNH-6070 showed highest mean value for the traits number of bolls per plant (131.4), seed cotton yield per plant (175.36gm) and ginning out turn percentage (39.76%). The parent IUB-1709 showed highest mean value for the traits boll retention percentage (53.67%) and average boll weight (3.27gm). The parent N-111 showed high mean value for monopodial branches per plant (4.78), while IUB-1524 showed highest mean value for fruiting point per plant (230.4). The $F_3$ generation of cross CIM-534 × IUB-1524 showed highest mean values for node of first fruiting branch (6.76), nodes per plant (46.71), monopodial branches per plant (7.61) and number of bolls per plant (84.38). The mean values for sympodial branches per plant (39.17) and ginning out turn percentage (41.27 %) were highest in the parental combination of CIM-707 × IUB-1524. The cross IUB-1709 × N-111 showed highest means for fruiting points per plant (167.64) and seed cotton yield per plant (110.94 gm). The parental combinations CIM-534 × IUB-1709, IUB-1709 × MNH-6070, CRS-2007 × IUB-1524 and MNH-6070 × CIM-473 showed highest mean values for boll retention percentage (57.39%) plant height (169.02cm), average boll weight (3.19gm) and fiber length (26.24 mm) respectively.

The estimate of variances among parental population presented in Table-2 suggested that for plant height (9.64 cm), boll retention percentage (4.12%) and seed cotton yield per plant (65.95gm) estimates were high in the genotype CRS-2007. The estimates of variance for the genotype CIM-534 was found best for monopodial branches per plant (0.92), number of bolls per plant (4.64) and lint percentage (0.79%). The genotype IUB-09 showed highest variance for the traits fruiting point per plant (4.92) and average boll weight (0.046gm) while the genotype N-111 showed highest variance estimates for node of first fruiting branch (1.83) and nodes per plant (3.81). The genotype MNH-786 showed highest variance for sympodial branches per plant (4.41), while CIM-707 showed highest variance estimates for staple length (0.341mm). The estimates of variance for $F_3$ generation presented in Table-2 suggested highest variance for plant height (56.04cm), nodes per plant (12.41) and ginning out turn percentage (4.36%) in the parental combination of CRS-2007 × IUB-1524. The estimates of variance for $F_3$ generation of the cross S-09 × CIM-534 was found best for node of first fruiting branches (3.61) and monopodial branches per plant (2.29) whereas fruiting points per plant (14.68) and number of bolls per plant (13.06) the estimates of variance were highest in the cross CIM-707 × IUB-1524. The parental combination IUB-09 × N-111 was found best for boll retention percentage and fiber length as the estimates of variance for these traits were 11.42% and 2.1mm respectively. Within the parental combinations of MNH-786 × IUB-09, CRS-2007 × MNH-6070 and CIM-534 × IUB-1524 the estimates of variance were found highest for sympodial branches per plant (17.74), average boll weight (0.155gm) and seed cotton yield per plant (131.25g) respectively. As the estimated variance of $F_3$population for all the traits were high as compared to their parents which suggests the presence of homozygosity among the parental population and variation due to environment is also very low whereas high variance of $F_3$ population for all traits is indication for the presence of high genetic variability within the population. Similar observations in cotton was reported by Dheva and Potdukhe (2002) and Preetha and Raveendran (2007). Kowsalya and Raveendran (1996), Do Thi Ha An et al. (2006) reported low genotypic and phenotypic variance for staple length in segregating generation and concluded that selection could be practiced in early segregating population of greater genetic variability for improvement in this trait.

**Genetic variability, Heritability and Genetic advance of $F_3$ generation:** The heritability in broad-sense is an important tool to ease the selection procedure, the degree to which a given trait would be transmitted to the next generation is best visualized by the estimates of heritability. According to Johnson et al. (1955) highly heritable traits if observe high genetic advance could be useful in order to predict the behavior of segregating generation. It can be inferred that those traits can be selected in early generations and selection will prove true in the fixation of the said traits. The estimates of genetic variability, Heritability and genetic advance are represented in table-3, table-4 and table-5 respectively.

1. **Node of First Fruiting branch:** Breeding for earliness in cotton is prime objective for cultivation in wheat-cotton-wheat crop rotation. There are different morphological traits that can be used to determine the earliness in cotton, node of first fruiting branch (NFB) is a good indication for estimating the earliness of genotype. The lower value indicates the onset of reproductive phase. This trait is least affected by the environment. So the selection of early maturing genotype from segregating generation by node of first fruiting branch is helpful for breeder. Estimates of heritability in broad-sense, genetic advance and genetic variability are presented in figure-3, figure-4 and figure-5 revealed that highest heritability in broad-sense coupled with good genetic advance and genetic variability were found in parental combination of S-09 × CIM-534 (65%, 2.17 and 2.34 ) followed by the cross CIM-534 × IUB-1524 (64%, 2.05 and 2.13), CIM-707 × IUB-1524 (53.75%), CIM-534 × IUB-09 (50.85%, 1.44, 1.33) as has been reported by Ray and Richmond (1996). Apart from this lowest heritability in broad-sense coupled with genetic advance and genetic variability was found in the cross combination of IUB-09 × N-111 (27.51%, 0.73 and 0.63) as reported by Jain (1980). The results of present study suggested that the lower node of first fruiting branch among the population of above mentioned crosses could be achieved through selection.
2. **Plant Height:** The estimates of Heritability in Broad-sense, genetic variability and genetic advance presented in tables suggested that for the trait plant height the highest heritability in broad-sense was found in the parental combination of IUB-09 × MNH-6070 (83.78%) followed by the cross CRS-2007 × IUB-1524 (83.66%), CIM-707 × IUB-1524 (79.95%), CRS-2007 × MNH-6070 (78.04%) as reported by Qayyum *et al.* (1998), Akbar *et al.* (1994) and Batool *et al.* (2010) . Apart from this lowest heritability for plant height was found in the cross combination of IUB-09 × N-111 (56.1%) whereas for plant height genetic advance and genetic variability estimates for these crosses were IUB-09 × MNH-6070 (10.51, 39.75), CRS-2007 × IUB-1524 (11.02, 46.89), CIM-707 × IUB-1524 (8.3, 28.07), CRS-2007 × MNH-6070 (8.81, 32.19) and IUB-09 × N-111 (3.39, 8.91) as reported by Soomro *et al.* (2010) . these results suggested that the selection of desired character plant height can efficiently be performed in the populations of these crosses. The genetic variance was found highly heritable and was also larger than

environmental variances. Therefore, for morpho-yield traits the said breeding material can safely be used in future breeding programs and has the room for further improvement.

3. **Nodes per plant:** The number of nodes is influenced by genetics and environmental factors. Final plant height is also a function of the extension of main stem nodes. The highest heritability in broad-sense coupled with high genetic advance and genetic variability presented in figure-3. Figure-4 and figure-5 showed highest heritability in broad-sense for nodes per plant was 84.15% for the cross CRS-2007 × MNH-6070 followed by 83.64%, 83.19%, 78.28% for the cross combinations of MNH-6070 × CIM-473, IUB-09 × MNH-6070, CRS-2007 × IUB-1524 as reported by Dhamayanathi *et al.* (2010).Apart from this lowest heritability in broad-sense was 69.19% for the parental combination of IUB-09 × N-111. The genetic advance and genetic variability studies revealed that for the cross CRS-2007 × MNH-6070 the genetic advance and genetic variability were 4.48 and 7.97 whereas good genetic advance and genetic variability was found for the combinations MNH-6070 × CIM-473(4.47, 7.99), IUB-09 × MNH-6070 (4.62, 8.65), CRS-2007 × IUB-1524 (4.85, 9.74) and low genetic advance and genetic variability was found for cross IUB-09 × N-111(3.95, 7.34). These suggested that the selection of desired character nodes per plant can efficiently be performed in the populations of these crosses. This recommends that in improving the seed cotton yield of genotypes, this character could be considered as selection criteria.
4. **Monopodial Branches per plant:** Monopodial branches are also called vegetative branches which develop from auxiliary buds. These branches give appearance like the main stem and bears indirect fruiting bearing branches. Monopodial branches per plant have key role in determining the earliness of cotton genotype. With increase in number of monopodial branches vegetative growth phase of the cotton plant also increases which causes delay in the reproductive phase thus it results late maturity. As breeders aim is to develop early maturing genotypes thus selection in early segregating generations can be practiced to develop genotypes with fewer numbers of monopodial branches which would favor earliness in cotton. Highest heritability in broad-sense combined with greater genetic advance and good genetic variability was fond in the parental combination of IUB-09 × N-111 (78.19%, 1.99, and 1.65) followed by parental combinations of MNH-6070 × CIM-473 (75.74%, 1.54, and 1.01), CRS-2007 × MNH-6070 (73.02%, 1.58 and 1.13), S-09 × CIM-534 (70.96%, 1.88 and 1.67) respectively as reported by Sing and Singh (1981) and Seth and Singh (1984). Apart from this lowest values of heritability in broad-sense coupled with genetic advance and genetic variability was found in the cross combination of CIM-534 × IUB-09 (55.81%, 1.288 and 0.97). High values of heritability in broad sense with appreciable genetic advance and Genetic variability for these parental combinations suggests that selection could be useful practiced for this trait to develop new strains with decreased in number of monopodial branches.
5. **Sympodial Branches per plant:** Sympodial branches are direct fruit bearing branches thus also called fruiting branches of the cotton. Trait sympodial branches per plant is of great agronomic importance because these branches bear direct bolls, so higher the number of fruiting branches greater will be number of bolls per plant and as a result yield per plant would also be improved. As breeder emphasis is to develop high yielding cultivars thus selection for the increase in sympodial branches per plant could be helpful in segregating generations. Highest heritability in broad-sense combined with higher genetic advance and good genetic variability was fond in parental combination of CIM-534×IUB-09 (79.91%, 5.5 and 12.33) followed by the parental combinations of CRS-2007×IUB-1524 (79.15%, 5.04 and 10.46), CRS-2007×MNH-6070 (78%, 4.69 and 9.2), MNH-786×IUB-09(77%, 5.71 and 13.62) respectively as reported by Khan and Tariq (1984),Khorgade and Ekbote (1981) and Ikram*et al.* (1993). Apart from this lowest values of heritability in broad-sense coupled with genetic advance and genetic variability was found in the cross combination of CIM-707 × IUB-1524 (37.69%, 2.42 and 6.69). these results suggested that higher yield can be obtained by greater number of nodes on main stem which bears sympodial branches per plant.
6. **Number of fruiting point per plant:** Highest heritability in broad-sense together with greater genetic advance and good genetic variability was fond in parental combination of CIM-707×IUB-1524 (78.54%, 5.29 and 11.54) followed by the parental combinations of CIM-534×IUB-1524 (75.05%, 4.03 and 7.05), S-09×CIM-534 (69.64%, 4.22 and 8.53 ), CRS-2007×MNH-6070 (69.55%, 4.26 and 8.43) respectively as reported by Dhamayanathi *et al.* (2010) whereas lowest values of heritability in broad-sense coupled with genetic advance and genetic variability was found in the cross combination of MNH-786 × IUB-09 (51.81%, 2.75 and 4.75). These results recommended that the selection for desirable character number of fruiting point per plant can efficiently be performed in the populations of these crosses.
7. **Number of bolls per plant:** Breeding high yielding cultivars is the main objective of plant breeders. In cotton there are different morphological traits that determine high seed cotton yield. The trait, number of

bolls per plant is directly associated with seed cotton yield, higher the number of bolls per plant greater will be the seed cotton yield. Selection of genotypes in segregating generations with higher number of bolls per plant could be the fruitful tool for plant breeder. Highest heritability in broad-sense joined with greater genetic advance and good genetic variability was fond in parental combination of CIM-707×IUB-1524 (77.18%, 4.908 and 10.2) followed by the parental combinations of CIM-534×IUB-1524 (71.8%, 4.38 and 8.85), IUB-09×N-111 (70.63%, 4.4 and 8.98 ), MNH-6070×CIM-473 (69.9%, 4.28 and 8.48) respectively as reported by Soomro *et al.* (2010), Desalegn *et al.* (2009), Ahmad *et al.* (2006), Kumaresan *et al.* (2000) and Esmail *et al.* 1999. Apart from this lowest values of heritability in broad-sense coupled with genetic advance and genetic variability was found in the cross combination of S-09 × CIM-534 (46.6%, 2.32 and 3.75). Therefore for the successful breeding program in improvement of this trait it is preferred to access the heritability and genetic advance in each cross of $F_3$ generation which would be helpful in order to know the extent of genetic variation and potential for improvement in segregating generations.

8. **Boll retention percentage:** The seed cotton yield directly depends on the number of bolls per plant, which is the function of flower production and boll retention. Thus for improvement of seed cotton yield per plant breeder can utilize different selection procedures to develop varieties with high flower production and boll retention percentage. Highest heritability in broad-sense attached with maximum genetic advance and good genetic variability was fond in parental combination of IUB-09×MNH-6070 (81.78%, 4.54 and 8.18) followed by the parental combinations of CIM-534×IUB-09 (81.69%, 4.58 and 8.32), S-09×CIM-534 (80.98%, 4.45 and 7.94 ), IUB-09×N-111 (80.69%, 4.79 and 9.3) respectively as reported by(Ray and Richmond 1966). Whereas lowest values of heritability in broad-sense coupled with genetic advance and genetic variability was found in the cross combination of CRS-2007 × MNH-6070 (69.74%, 3.92 and 7.31). The results suggested that selection will be useful for improvement of this trait.
9. **Average boll weight per plant:** Boll weight is an important agronomic trait as this trait is directly associated with seed cotton yield. Increased boll weight in new cotton genotypes is one of the prime objective of plant breeder. Highest heritability in broad-sense combined with high genetic advance and good genetic variability was fond in parental combination of CRS-2007×MNH-6070 (88.39%, 0.61 and 0.137) followed by the parental combinations of MNH-6070×CIM-473 (85%, 0.52 and 0.102), CRS-2007×IUB-1524 (77.73%, 0.453 and 0.086 ), CIM-707×IUB-1524 (73.75%, 0.36 and 0.062) respectively as reported by Ahmad *et al.* (2006), Elsiddig *et al.* (2007), Esmail (1999), Shanti *et al.* (1999). Apart from this lowest values of heritability in broad-sense coupled with genetic advance and genetic variability was found in the cross combination of IUB-09 × MNH-6070 (50%, 0.224 and 0.035).
10. **Seed cotton yield per plant:** Seed cotton yield per plant is an important agronomic trait in upland cotton so improvement in this trait is the primary objective of plant breeder. Highest heritability in broad-sense combined with high genetic advance and good genetic variability was fond in parental combination of MNH-786×IUB-09 (74.6%, 14.14 and 86.87) followed by the parental combinations of CIM-534×IUB-1524 (74.5%, 15.01 and 100.76), IUB-09×N-111 (69.76%, 12.5 and 72.44), MNH-6070×CIM-473 (68.5%, 13.26 and 85.35) respectively as reported by Ahmad *et al.* (2006), Elsiddig *et al.* (2007) and Esmail *et al.* (1999) whereas lowest values of heritability in broad-sense coupled with genetic advance and genetic variability was found in the cross combination of CRS-2007 × MNH-6070 (42.78%, 7.6 and 44.155).
11. **Lint percentage (G.O.T):** Lint percentage is the percentage of ginned lint obtained from a mass of seed cotton. Economically, high ginning out-turn is desirable trait and it is useful indicator to evaluate the performance of genotype. The trait lint percentage is associated with the lint yield of the genotype. As the plant breeder emphasized for the development of high yielding cultivar thus different breeding approaches could be practiced to know the extent of heritable variation for improvement in this trait. Highest heritability in broad-sense along with high genetic advance and good genetic variability was fond in parental combination of IUB-09×N-111 (93.07%, 2.64 and 2.42) followed by the parental combinations of CRS-2007×IUB-1524 (91.86%, 3.37 and 4.02), C1M-707×IUB-1524 (91.35%, 2.73 and 2.64), MNH-786×IUB-09 (89%, 2.73 and 2.67) respectively as described by Khan *et al.* (2010), Desalegn et al. (2009), Basal *et al.* (2005), Jagtap and Mehtari (1998) and Yankun *et al.* (1988) whereas lowest values of heritability in broad-sense coupled with genetic advance and genetic variability was found in the cross combination of CRS-2007 × MNH-6070 (81%, 2.36 and 2.21).
12. **Staple Length:** In cotton among the fiber quality traits the staple length is of great importance in textile industry. With the advancement of spinning technology improved staple length is needed for good spinning. This trait is greatly influenced by the environmental conditions. For the improvement in this trait breeders need to identify the degree of variation within the population thus selection in segregating

generation could be practiced. Highest heritability in broad-sense along with high genetic advance and good genetic variability was fond in parental combination of IUB-09×MNH-6070 (96.06%, 1.82 and 1.125) followed by the parental combinations of CIM-534×IUB-1524 (95.96%, 2.11 and 1.51), C1M-534×IUB-09 (95.8%, 1.87 and 1.1), MNH-6070×CIM-473 (95.43%, 1.82 and 1.11) respectively as reported by Azhar *et al.* (2010), Kumari and Subbaramamma (2006), Joshi *et al.* (2006), Killi*et al.* (2005) and Baloch (2004) whereas lowest values of heritability in broad-sense coupled with genetic advance and genetic variability was found in the cross combination of S-09 × CIM-534 (86.64%, 1.66 and 1.07).

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## Table-1. Means of parents and $F_3$

| Cross | NFB | Plant height (cm) | Nodes/ plant | MB/ plant | SB/ plant | Fruiting points/ plant | Bolls/ plant | Bolls retention % | Av boll wt/ plant (gm) | SCY/ plant (gm) | GOT % | FL/ plant (mm) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **P1** | 6.27 | 149.27 | 43.21 | 3.13 | 31.06 | 138.27 | 55.06 | 42.15 | 3.24 | 126.84 | 35.89 | 27.71 |
| **P2** | 6.07 | 151.00 | 39.66 | 3.06 | 30.20 | 142.33 | 89.93 | 40.09 | 2.82 | 138.44 | 39.06 | 27.1 |
| **S-09×CIM-534** | **6.69** | 141.47 | 45.17 | 7.39 | 33.96 | 157.26 | 63.23 | 52.33 | 2.76 | 88.18 | 40.10 | 26.85 |
| **P1** | 6.67 | 150.06 | 39.86 | 2.87 | 39.67 | 201.13 | 82.06 | 50.07 | 2.87 | 151.53 | 38.18 | 26.81 |
| **P2** | 5.87 | 178.2 | 39.73 | 2.53 | 40.13 | 213.4 | 131.4 | 40.74 | 2.97 | 175.36 | 39.76 | 28.98 |
| **CRS-2007× MNH-6070** | **6.75** | 155.55 | 40.82 | 7.32 | 38.5 | 161.23 | 67.99 | 41.38 | 3.03 | 74.42 | 40.57 | 27.06 |
| **P1** | 6.07 | 151.00 | 39.66 | 3.06 | 30.20 | 142.33 | 89.93 | 40.09 | 2.82 | 138.44 | 39.06 | 27.1 |
| **P2** | 6.13 | 158.66 | 42.13 | 2.53 | 37.12 | 230.4 | 100.53 | 50.36 | 2.08 | 156.01 | 37.87 | 29.79 |
| **CIM-534 ×IUB-1524** | **6.76** | 143.23 | 46.71 | 7.61 | 37.95 | 145.51 | 84.38 | 43.12 | 3.08 | 70.94 | 40.44 | 27.55 |
| **$P_2$** | 6.40 | 141.41 | 43.44 | 2.93 | 37.11 | 151.12 | 108.93 | 51.27 | 3.09 | 166.02 | 38.41 | 27.83 |
| **P2** | 6.27 | 153.06 | 47 | 2.8 | 39.53 | 153.73 | 89.2 | 53.67 | 3.27 | 127.40 | 38.99 | 29.51 |
| **MNH-786 × IUB-09** | **6.07** | 142.14 | 39.33 | 7.23 | 35.43 | 142.12 | 64.6 | 51.52 | 3.12 | 69.37 | 40.78 | 27.96 |
| **P1** | 5.87 | 178.2 | 39.73 | 2.53 | 40.13 | 213.4 | 131.4 | 40.74 | 2.97 | 175.36 | 39.76 | 28.98 |
| **P2** | 6.06 | 138.27 | 39.21 | 2.66 | 31.06 | 142.22 | 101.00 | 41.11 | 2.34 | 135.62 | 39.74 | 28.51 |
| **MNH6070 × CIM473** | **6.14** | 150.02 | 42.12 | 6.39 | 38.13 | 138.03 | 64.11 | 50.07 | 3.12 | 85.54 | 41.29 | 26.32 |
| **$P_1$** | 6.27 | 153.06 | 47 | 3.12 | 32.87 | 157.73 | 89.2 | 53.67 | 3.27 | 127.46 | 38.99 | 29.51 |
| **$P_2$** | 6.53 | 151.80 | 39.33 | 4.78 | 34.12 | 138.06 | 100.46 | 50.06 | 2.79 | 152.31 | 38.15 | 28.23 |
| **IUB-1709 × N-111** | 6.60 | 144.99 | 44.11 | 2.23 | 31.11 | 167.64 | 68.92 | 45.24 | 2.85 | 110.94 | 40.16 | 28.27 |
| **P1** | 6.27 | 153.06 | 47 | 2.8 | 39.53 | 153.73 | 89.2 | 53.67 | 3.27 | 127.46 | 38.99 | 29.51 |

Continued

## Table 1. Mean of Parents and $F_3$

| Cross | NFB | plant height | Nodes/ plant | MB/plant | SB/plant | Fruiting points/ plant | Bolls/ plant | Bolls retention % | Av boll wt/ plant | SCY/ Plant | GOT% | FL/plant (mm) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **P2** | 5.87 | 178.2 | 39.73 | 2.53 | 40.13 | 213.4 | 131.4 | 40.74 | 2.97 | 175.36 | 39.74 | 28.98 |
| **IUB-1709 × MNH-6070** | 6.75 | 169.02 | 44.91 | 5.23 | 36.19 | 155.16 | 66.14 | 48.95 | 3.18 | 72.41 | 40.23 | 26.83 |
| **P1** | 6.67 | 150.06 | 39.86 | 2.87 | 39.67 | 201.13 | 82.06 | 50.07 | 2.87 | 151.53 | 38.18 | 26.81 |
| **P2** | 6.13 | 158.66 | 42.13 | 2.53 | 37.12 | 230.4 | 100.53 | 50.36 | 2.08 | 156.01 | 37.87 | 29.79 |
| **CRS-2007 × IUB-1524** | 6.23 | 144.64 | 41.90 | 3.38 | 37.00 | 166.84 | 64.03 | 52.58 | 3.19 | 75.33 | 39.11 | 27.12 |
| **P1** | 6.07 | 151.00 | 39.66 | 3.06 | 30.20 | 142.33 | 89.93 | 40.09 | 2.82 | 138.44 | 39.06 | 27.1 |
| **P2** | 6.27 | 153.06 | 47 | 2.8 | 39.53 | 153.73 | 89.2 | 53.67 | 3.27 | 127.46 | 38.99 | 29.51 |
| **CIM-534 × IUB-1709** | 6.2 | 134.33 | 41.06 | 3.92 | 33.19 | 165.38 | 68.21 | 57.39 | 2.09 | 85.22 | 40.2 | 26.27 |
| **P1** | 6.65 | 140.2 | 47.06 | 4.11 | 40.22 | 162.8 | 95.53 | 45.61 | 2.69 | 104.274 | 39.14 | 30.4 |
| **P2** | 6.13 | 156.4 | 42.13 | 4.12 | 37.38 | 230.4 | 100.53 | 50.36 | 2.08 | 156.01 | 37.87 | 29.79 |
| **CIM-707 × IUB-1524** | 6.45 | 143.86 | 40.78 | 3.21 | 39.17 | 164.52 | 64.3 | 56.89 | 2.87 | 75.33 | 41.27 | 26.24 |

## Table-2. Variance of Parents and $F_3$

| Cross | NFB | plant height (cm) | Nodes/ plant | MB/ plant | SB/ plant | Fruiting points/ plant | Bolls/ plant | Bolls retention % | Av boll wt/ plant (gm) | SCY/ plant (gm) | GOT % | FL/plant (mm) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **P1** | 1.49 | 6.92 | 2.71 | 0.41 | 2.92 | 4.92 | 3.92 | 1.57 | 0.039 | 42.37 | 0.33 | 0.27 |
| **P2** | 1.066 | 9.14 | 2.38 | 0.92 | 2.31 | 2.31 | 4.64 | 2.15 | 0.028 | 47.19 | 0.79 | 0.048 |
| **S-09×CIM-534** | 3.61 | 30.12 | 10.12 | 2.29 | 10.63 | 11.91 | 8.02 | 9.78 | 0.073 | 122.52 | 3.33 | 1.19 |
| **P1** | 1.52 | 9.64 | 2.27 | 0.55 | 2.09 | 3.84 | 4.35 | 4.12 | 0.017 | 65.95 | 0.47 | 0.039 |
| **P2** | 1.409 | 8.46 | 0.64 | 0.27 | 2.98 | 3.54 | 3.83 | 2.07 | 0.019 | 50.84 | 0.58 | 0.036 |
| **CRS-2007× MNH-6070** | 2.63 | 41.23 | 9.18 | 1.52 | 11.7 | 12.12 | 12.87 | 10.23 | 0.155 | 102.06 | 2.73 | 0.82 |
| **P1** | 1.066 | 9.14 | 2.38 | 0.92 | 2.31 | 1.81 | 4.64 | 2.15 | 0.028 | 47.19 | 0.79 | 0.048 |
| **P2** | 1.27 | 8.67 | 3.12 | 0.27 | 3.38 | 2.84 | 2.12 | 2.49 | 0.032 | 19.69 | 0.24 | 0.079 |
| **CIM-534 ×IUB-** | 3.3 | 38.12 | 11.11 | 1.31 | 11.53 | 9.32 | 11.99 | 9.92 | 0.078 | 131.25 | 3.11 | 1.57 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **1524** | | | | | | | | | | | | |
| **P1** | 1.4 | 6.79 | 2.11 | 0.35 | 4.41 | 3.87 | 4.49 | 3.91 | 0.021 | 26.21 | 0.47 | 0.051 |
| **P2** | 1.49 | 6.92 | 2.71 | 0.6 | 3.84 | 4.92 | 4.31 | 1.57 | 0.046 | 32.79 | 0.16 | 0.056 |
| **MNH-786 × IUB-09** | 2.5 | 21.17 | 10.62 | 1.26 | 17.74 | 9.12 | 9.34 | 10.51 | 0.089 | 116.19 | 3.04 | 1.04 |
| **P1** | 1.409 | 8.46 | 0.64 | 0.27 | 2.98 | 3.54 | 3.83 | 2.07 | 0.019 | 50.84 | 0.58 | 0.036 |
| **P2** | 0.8 | 6.92 | 2.38 | 0.38 | 3.21 | 4.12 | 3.46 | 2.55 | 0.017 | 25.68 | 0.23 | 0.071 |
| **MNH6070 × CIM473** | 2.23 | 24.12 | 9.23 | 1.34 | 9.98 | 10.27 | 12.13 | 10.55 | 0.12 | 121.49 | 2.83 | 1.17 |
| **P1** | 1.49 | 6.92 | 2.71 | 0.41 | 2.92 | 4.92 | 4.31 | 1.57 | 0.046 | 32.79 | 0.16 | 0.056 |
| **P2** | 1.83 | 7.03 | 3.81 | 0.51 | 3.11 | 4.78 | 3.12 | 2.84 | 0.01 | 29.97 | 0.2 | 0.35 |
| **IUB-1709 × N-111** | 2.29 | 15.89 | 10.56 | 2.11 | 11.52 | 12.44 | 12.65 | 11.42 | 0.063 | 103.79 | 2.6 | 2.1 |
| **P1** | 1.49 | 6.92 | 2.71 | 0.6 | 3.84 | 4.92 | 4.31 | 1.57 | 0.046 | 32.79 | 0.16 | 0.056 |
| **P2** | 1.409 | 8.46 | 0.64 | 0.27 | 2.98 | 3.54 | 3.83 | 2.07 | 0.019 | 50.84 | 0.58 | 0.036 |
| **IUB-1709 × MNH-6070** | 2.63 | 47.41 | 9.97 | 1.51 | 12.34 | 13.64 | 11.25 | 9.99 | 0.065 | 100.15 | 2.65 | 1.17 |

### Table -2. Variance of Parents and $F_3$

| Cross | NFB | Plant height (cm) | Nodes/ plant | MB/ plant | SB/ plant | Fruiting points per plant | Bolls/ plant | Bolls retention % | Av boll wt/ plant | SCY/ plant | GOT % | FL/ plant (mm) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **P1** | 1.52 | 9.64 | 2.27 | 0.55 | 2.09 | 3.84 | 4.35 | 4.12 | 0.017 | 65.95 | 0.47 | 0.039 |
| **P2** | 1.27 | 8.67 | 3.12 | 0.27 | 3.38 | 2.84 | 2.12 | 2.49 | 0.032 | 19.69 | 0.24 | 0.079 |
| **CRS-2007× MNH-6070** | 2.54 | 56.04 | 12.41 | 2.12 | 13.12 | 9.35 | 9.66 | 10.24 | 0.11 | 122.42 | 4.36 | 0.92 |
| **P1** | 1.066 | 9.14 | 2.38 | 0.92 | 2.31 | 1.81 | 4.64 | 2.15 | 0.028 | 47.19 | 0.79 | 0.048 |
| **P2** | 1.49 | 6.92 | 2.71 | 0.6 | 3.84 | 4.92 | 4.06 | 1.57 | 0.027 | 32.79 | 0.16 | 0.056 |
| **CIM-534 × IUB-09** | 2.6 | 21.24 | 10.9 | 1.72 | 15.31 | 9.78 | 12.93 | 10.16 | 0.067 | 121.69 | 3.96 | 1.24 |
| **P1** | 0.95 | 5.31 | 2.14 | 1.78 | 13.33 | 3.46 | 3.84 | 2.84 | 0.01 | 49.48 | 0.26 | 0.341 |
| **P2** | 1.27 | 8.67 | 3.12 | 0.27 | 3.38 | 2.84 | 2.12 | 2.49 | 0.032 | 19.69 | 0.24 | 0.079 |
| **CIM-707 × IUB-1524** | 2.4 | 34.86 | 11.23 | 2.45 | 13.41 | 14.68 | 13.06 | 11.2 | 0.08 | 101.7 | 2.89 | 1.69 |

### Table-3. Genetic variability of various traits of upland cotton:

| Cross | NFB | plant height (cm) | Nodes/ plant | MB/ plant | SB/plant | Fruiting points/ plant | Bolls/ plant | Bolls retention % | Av boll wt/ plant (gm) | SCY/ plant (gm) | GOT% | FL/ plant (mm) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **S-09 × CIM-534** | 2.34 | 26.11 | 7.58 | 1.67 | 8.03 | 8.53 | 3.75 | 7.94 | 0.039 | 77.8 | 2.81 | 1.07 |
| **CRS-2007 ×MNH-6070** | 1.16 | 32.19 | 7.97 | 1.13 | 9.2 | 8.43 | 8.78 | 7.31 | 0.137 | 44.155 | 2.21 | 0.78 |
| **CIM-534 ×IUB-1524** | 2.13 | 33.89 | 8.38 | 0.811 | 8.73 | 7.05 | 8.85 | 7.60 | 0.048 | 100.76 | 2.67 | 1.51 |
| **MNH-786 × IUB-09** | 1.05 | 17.46 | 8.22 | 0.801 | 13.62 | 4.75 | 4.94 | 8.30 | 0.06 | 86.87 | 2.76 | 0.98 |
| **MNH-6070 × CIM-473** | 1.16 | 16.46 | 7.99 | 1.01 | 6.88 | 6.45 | 8.48 | 8.25 | 0.102 | 85.35 | 2.46 | 1.11 |
| **IUB-09 × N-111** | 0.63 | 8.91 | 7.34 | 1.65 | 8.50 | 7.59 | 8.98 | 9.3 | 0.041 | 72.44 | 2.42 | 1.96 |
| **IUB-09 × MNH-6070** | 1.18 | 39.75 | 8.65 | 1.11 | 8.95 | 9.46 | 7.18 | 8.18 | 0.035 | 59.32 | 2.34 | 1.125 |
| **CRS-2007 × IUB-1524** | 1.15 | 46.89 | 9.74 | 1.73 | 10.46 | 6.04 | 6.62 | 7.03 | 0.086 | 86.38 | 4.02 | 0.86 |
| **CIM-534 × IUB-09** | 1.33 | 13.28 | 8.36 | 0.97 | 12.33 | 6.79 | 8.45 | 8.32 | 0.04 | 82.35 | 3.61 | 1.1 |
| **CIM-707 × IUB-1524** | 1.30 | 28.07 | 8.64 | 1.75 | 6.69 | 11.54 | 10.2 | 8.54 | 0.062 | 70.48 | 2.64 | 1.52 |

### Table-4. Heritability of F$_3$ Generation of various traits of upland cotton:

| Cross | NFB | plant height (cm) | Nodes/ plant | MB/ plant | SB/plant | Fruiting points per plant | Bolls/ plant | Bolls retention % | Av boll wt/ plant (gm) | SCY/ Plant (gm) | GOT% | FL/ plant (mm) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **S-09×CIM-534** | 65 | 73.33 | 74.85 | 70.96 | 75 | 69.64 | 46.6 | 80.98 | 54 | 63.5 | 83 | 86.64 |
| **CRS-2007× MNH-6070** | 44 | 78.04 | 84.15 | 73.02 | 78 | 69.55 | 68 | 69.74 | 88.39 | 42.78 | 81 | 95.42 |
| **CIM-534 ×IUB-1524** | 64 | 76.63 | 75.24 | 54.58 | 75 | 75.05 | 71.8 | 76.61 | 62 | 74.5 | 83 | 95.96 |
| **MNH-786 × IUB-09** | 42.2 | 67.61 | 77.3 | 62.3 | 77 | 51.81 | 52.89 | 73.92 | 62.35 | 74.6 | 89 | 94.86 |
| **MNH6070 × CIM473** | 50.4 | 68.11 | 83.64 | 75.74 | 68.9 | 62.7 | 69.9 | 78.1 | 85 | 68.5 | 86 | 95.43 |
| **IUB-09 × N-111** | 27.51 | 56.1 | 69.13 | 78.19 | 73.82 | 61.01 | 70.63 | 80.69 | 55.56 | 69.76 | 93.07 | 90.33 |
| **IUB-09 × MNH-6070** | 44.89 | 83.78 | 83.19 | 71.19 | 72.36 | 68.98 | 63.82 | 81.78 | 50 | 58.22 | 86.03 | 96.06 |
| **CRS-2007 × IUB-1524** | 45.1 | 83.66 | 78.28 | 61.32 | 79.15 | 64.27 | 66.51 | 67.72 | 77.73 | 65.02 | 91.86 | 93.6 |
| **CIM-534 × IUB-09** | 50.85 | 62.19 | 76.65 | 55.81 | 79.91 | 65.59 | 66.35 | 81.69 | 58.91 | 67.13 | 88.01 | 95.8 |
| **CIM-707 × IUB-1524** | 53.75 | 79.95 | 76.58 | 58.16 | 37.69 | 78.54 | 77.18 | 76.21 | 73.75 | 65.9 | 91.35 | 87.6 |

**Table-5. Genetic advance of $F_3$ Generation of various traits of upland cotton:**

| Cross | NFB | plant height (cm) | Nodes/ plant | MB/ plant | SB/ Plant | Fruiting points/ plant | Bolls/ Plant | Bolls retention % | Av boll wt/ plant (gm) | SCY/ Plant (gm) | GOT % | FL/ plant (mm) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **S-09×CIM-534** | 2.17 | 7.08 | 4.19 | 1.88 | 4.3 | 4.22 | 2.32 | 4.45 | 0.26 | 12.37 | 2.67 | 1.66 |
| **CRS-2007× MNH-6070** | 1.25 | 8.81 | 4.48 | 1.58 | 4.69 | 4.26 | 4.29 | 3.92 | 0.61 | 7.6 | 2.36 | 1.52 |
| **CIM-534 ×IUB-1524** | 2.05 | 8.32 | 4.41 | 1.09 | 4.48 | 4.03 | 4.38 | 4.24 | 0.3 | 15.01 | 2.58 | 2.11 |
| **MNH-786 × IUB-09** | 1.17 | 5.47 | 4.43 | 1.23 | 5.71 | 2.75 | 2.84 | 4.21 | 0.32 | 14.14 | 2.73 | 1.702 |
| **MNH6070 × CIM473** | 1.32 | 5.88 | 4.47 | 1.54 | 3.83 | 3.58 | 4.28 | 4.46 | 0.52 | 13.26 | 2.55 | 1.82 |
| **IUB-09 × N-111** | 0.73 | 3.93 | 3.95 | 1.99 | 4.41 | 3.78 | 4.4 | 4.79 | 0.245 | 12.5 | 2.64 | 2.3 |
| **IUB-09 × MNH-6070** | 1.27 | 10.51 | 4.62 | 1.53 | 4.47 | 4.48 | 3.76 | 4.54 | 0.224 | 10.25 | 2.46 | 1.82 |
| **CRS-2007 × IUB-1524** | 1.26 | 11.02 | 4.85 | 1.57 | 5.04 | 3.45 | 3.63 | 3.81 | 0.453 | 12.66 | 3.37 | 1.58 |
| **CIM-534 × IUB-09** | 1.44 | 5.04 | 4.45 | 1.288 | 5.50 | 3.61 | 4.19 | 4.58 | 0.265 | 13.03 | 3.08 | 1.87 |
| **CIM-707 × IUB-1524** | 1.46 | 8.3 | 4.51 | 1.602 | 2.42 | 5.29 | 4.908 | 4.48 | 0.36 | 11.69 | 2.73 | 2.01 |