International
Journal of Agriculture Innovations and Cutting-Edge Research

Exploring Genetic Variation and Quantitative Parameters in Upland Cotton (*Gossypium hirsutum* L.) by Diallel Analysis

Khatir Ali[1](Corresponding Author)**, Tehseen Ali Jilani**[2]**, Noor ul Ain**[3]**, Jalil Ahmed**[4]**, Jalal Ahmed**[5]

[1], Department of Plant Breeding and Genetics, Faculty of Agriculture, University of Agriculture Faisalabad, Pakistan, Email: *khatirali.edu@gmail.com*
[2], Department of Horticulture, Faculty of Agriculture, Gomal University, DIKhan, Pakistan, Email: *tehseenali@gu.edu.pk*
[3], Institute of Food Science and Nutrition, Faculty of Agriculture, Gomal University, DIKhan, Pakistan, Email: *noorkundi342@gmail.com*
[4], Department of Plant Breeding and Genetics, Faculty of Crop Production, Sindh Agriculture University, Tandojam, Pakistan, Email: *jaleelnawab51@gmail.com*
[5], Department of Agronomy, Sindh Agriculture University, Tandojam, Pakistan, Email: *jalalwali5@gmail.com*

Abstract

The experiment was intended to examine the cross-breeding capacity on yield and fibre characteristics in upland cotton (Gossypium hirsutum L.) using diallel analysis. A 4 × 4 diallel analysis of the four cotton varieties, viz., Lalazar, MNH-888, FH-154 and FH-175, was crossbred in the season 2023-24. In 2023-24, the hybrids (12) and their parents were planted in three replicas in an RCBD. The parents raised the crossed material, which was also raised in the experimental field of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. The data was taken using five plants of each line being selected randomly, like plant height, the number of bolls in each plant, number of monopodial branches, number of sympodial branches, seed cotton yield, boll weight, lint index and fibre characteristics, fibre length, fibre strength, and fibre fineness. The results of the data obtained were statistically processed according to the methodology of Hayman and Jinks to determine the character of the action of the genes affecting the nature of the yield and fibre traits. It was found that the fibre length, seed cotton yield and the number of monopodial branches showed partial dominance with additive gene action. Overdominance gene action was found to control plant height, number of bolls per plant, lint index, fibre strength and fibre fineness, whereas the number of sympodial branches and boll weight were found to be under total dominance. There was no epistasis whatsoever.

Keywords: Upland cotton, Diallel analysis, Combining ability, Gene action, Yield traits, Fiber quality.

DOI:	*https://zenodo.org/records/17641044*
Journal Link:	*https://jai.bwo-researches.com/index.php/jwr/index*
Paper Link:	*https://jai.bwo-researches.com/index.php/jwr/article/view/187*
Publication Process	Received: 21 Sep 2025/ Revised: 06 Nov 2025/ Accepted: 08 Nov 2025/ Published: 17 Nov 2025
ISSN:	Online [3007-0929], Print [3007-0910]

Indexing:

Publisher: BWO Research International (15162394 Canada Inc.)
https://www.bwo-researches.com

Introduction

Cotton (*Gossypium hirsutum* L.) is the greatest cash crop that is produced on a large scale in the whole world. Informative for the other parts of the world, cotton has an immense economic value in the textile industry and directly benefits rural economies in many developing countries (Abdel *et al.*, 2023). Cotton is the backbone of Pakistan's economy, and it provides raw material to the textile industry and employment opportunities for millions of people in Pakistan (Nawaz *et al.*, 2019). Increasing yield and fibre quality traits continue to be one of the main objectives with respect to cotton-based breeding programs, as those two directly impact farmers' revenue in addition to influencing textile performance (Yang *et al.*, 2020).

Yield and fibre quality are complex quantitative traits in cotton controlled by multiple genes and also greatly affected by environmental stresses (Zhang *et al.*, 2015). Genetic profiling of these traits is important for improving and selecting better cultivars in conventional and molecular breeding programs (Goren and Canavar, 2024). The combining ability analysis gives a clear depiction of additive and non-additive gene action to facilitate breeders in identifying suitable parents for hybridization (Mokadem *et al.*, 2020).

The 4 × 4 mating design, particularly the diallel cross scheme, has been utilized extensively in the partitioning of genetic variance into its components and for obtaining information on gene action for yield and fibre characters (Hayman, 1954; Jinks, 1954). These studies showed the existence of additive, dominance and overdominance gene actions, which also help to determine superior hybrid combinations for commercialization (Ujjainkar and Patil, 2021). The addition of epistatic effects leads to improving the genetic architecture, thereby leading breeders to make informed and effective selection strategies (Shar *et al.*, 2017).

Varied genetic action patterns had been reported in the literature for plant height, boll number, boll weight, lint percentage and fibre traits based on prior diallel analysis in upland cotton (Abdel *et al.*, 2023). Other research studies emphasized the additive gene action to determine the length of the fibre and yield of seed cotton, and others indicated the dominance in controlling the traits such as the boll weight and fibre strength, by dominant effects (Chakholoma *et al.*, 2022). Therefore, it is significant to conduct trait-specific studies of the action of a gene in order to develop breeding strategies for each character (Nawaz *et al.*, 2019).

There were four cotton lines that were determined as parents in the study due to the variation on the basis of their genetic variation in the yield and fibre-related traits. These lines are characterized by a broad genetic base with both the plants differing in height, boll weight, percentage of lint and fibre quality characteristics, in that they are amenable to extract genetic influence by employing a diallel examination. The study objectives were to approximate the overall and specific effects of combining ability and to determine the extent and the nature of the gene action affecting the important agronomic and fibre quality characteristics in upland cotton under various environmental situations (Rehman *et al.*, 2020). The data received from this study will help to choose better parental lines and create high-yielding cotton plants with high-quality fibres (Jarwar *et al.*, 2018).

Materials and Methods

The experiment was conducted under various conditions at the Research Field Area, Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, in 2024. Four genetically diverse genotypes (Lalazar, MNH-888, FH-154 and FH-175) were employed for the experiment. The genotypes were introduced in pots to the greenhouse in November 2023. Controlled conditions such as light, humidity and temperature were provided to the greenhouse-grown plants. Precautions against biotic and abiotic threats were taken in order to safeguard the plants. All the parents were crossed in a complete diallel mating design at the flowering stage. To avoid selfing, some flowers were bagged with craft paper bags. All precautions to prevent any foreign contamination were taken during emasculation and crossing. The parents and their direct as well as indirect crosses were as follows:

Parents: 1- Lalazar 2- MNH-888 3- FH-154 4- FH-175

Crosses:

Direct Crosses	Indirect Crosses	Self
FH-154 × FH-175	FH-175 × FH-154	FH-154 × FH-154
FH-154 × MNH-888	MNH-888 × FH-154	FH-175 × FH-175
FH-154 × Lalazar	Lalazar × FH-154	MNH-888 × MNH-888
FH-175 × MNH-888	MNH-888 × FH-175	Lalazar × Lalazar
FH-175 × Lalazar	Lalazar × FH-175	
MNH-888 × Lalazar	Lalazar × MNH-888	

Experimental layout

The self F1, direct and indirect crosses were elevated in the experimental section of the

Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. The parents and their F1 crosses were planted in the field at a complete randomized block design having three replications of F1 crosses in the 2024 normal cotton growing season. The distance between rows and between plants was 75 cm x 30cm were maintained. Three seeds were planted per hill, and the thinning was done after 2 weeks of emergence. All agronomic activities, like irrigation, fertilizer, among others, were implemented as required.

Data Collection

For each line, the following traits were taken on five plants at maturity. For the purpose of generating data for each character, the following approach was taken.

Plant height (cm)

At the end of apical growth, when plants were fully grown, plant heights in centimetres were taken with a measuring tape from the soil line to the highest point and averaged. Plant height was measured for the statistical analysis.

Number of bolls per plant

The number of bolls per plant was counted during the harvest. The numbers were counted in five plants per row, after which the average number of bolls per genotype was determined.

Monopodial branches

These are the monopodial branches with their indirect fruit on them. They are vegetative as well as referred to as shoots and are more common in the lowest part of the plant. When the plants were mature, the total number of monopodial branches was counted manually for five guarded plants, and the mean was utilized to test.

Sympodial branches

The branches with the direct fruit are called sympodial branches. The mature plant with a mean to be analyzed was counted, and the number of sympodial branches was counted when the plant was in its guarded state.

Seed cotton yield per plant

A five-plant hand-held was used to harvest cotton seed row by row. At the time, seed cotton yield per plant was measured in grammes on an electronic balance. The trait was the average value of the seed cotton yield of plants.

Boll weight (g):

The bolls were chosen at different locations and weighed separately. The average of boll weight was measured on a per-genotype and then on a per-plant basis.

Lint index (%)

Ginning of seed cotton collected in all experimental plants in a row was done using a single roller electric Ginn. The weight of lint produced on each plant obtained was weighed, and the ginning outturn calculated using the formula:

$$\text{Lint index (\%)} = \frac{\text{Weight of lint in sample}}{\text{Weight of seed cotton in sample}} \times 100$$

Fibre quality traits

A swab sample of lint was taken from the plants in an experimental setting in each row to characterize the quality of fibres. Parameters of fibre quality include fibre length, fibre strength and fibre fineness. These were fibre characteristics that were tested at the HVI (High Volume Instrument) of Cotton Research Institute AARI, Faisalabad.

Statistical analysis

ANOVA was analyzed for all the traits as per Steel *et al.* (1997). Marketable traits that exhibited signification differences among the varieties were subjected to gene action and combining ability following Hayman (1954) and Jinks (1955) (models 1 and 2). The Hayman and Jinks method is referred to as a graphical method. This is a quick approach to have knowledge of the gene action for the quantitative traits.

Diallel crossing type is highly popular, which enhances the characteristics of plants. The F_1 hybrids are produced by crossing each of the recommended parents with all the others. The goals of this work are to reach variation and to study the genetic inheritance of such a characteristic. In fact, this procedure yields accurate and unbiased estimates of the gene action for polygenic traits. The following approximations can be considered in the use of this technique:

- Parents should be homozygous
- Diploid segregation as with every other chromosome.
- No polymorphism of alleles
- No dialectal variation
- No epistasis
- Absence of linkage

In the diallel cross for exploration of information, the most reliable procedure was conceived by Hayman (1954), where the covariance of each array (Wr) was plotted against the variance (Vr). Any inclination which further checked by regression precisely indicates the presence of gene action and the degree of dominance. The triangle of dots that lie within the parabola indicates the degree of dominance and presence of the gene. Moreover, the triangle outside the dots on the right and left side of the regression line acquired a relative frequency of recessive and dominant. The means of direct and reciprocal crosses in the diallel were assumed. The variance (Vr) with a family means array and covariance (Wr) of the array with the parent's mean are calculated.

$$Vri = \sum Xi2 - \frac{\frac{(\sum Xi)2}{n}}{n-1}$$

Where,
Vri = Variance of the ith array
∑Xi2 = Sum of the squares of the ith array
∑Xi = Sum of the ith array
n = Number of observations

The data on the genetic processes were acquired by plotting the covariance (Wr) of each array versus the corresponding variance (Vr). The formula used to calculate the regression coefficient was:

$$\mathrm{Wri} = \sum \mathrm{XY} - \frac{\frac{(\sum \mathrm{X})(\sum \mathrm{Y})}{\mathrm{n}}}{\mathrm{n}-1}$$

Where,
Wri = Covariance of the ith array
∑Xi = Sum of the ith array
∑Yi = Sum of the parental means
∑XiYi = Sum of the product of the ith array and the parental mean
n = Number of observations

The data on the genetic processes were acquired by plotting the covariance (Wr) of each array versus the corresponding variance (Vr). The formula used to calculate the regression coefficient was:

$$b = cp/Vr.S.S$$

Where,

$$\text{Cp (covariance product)} = \sum \mathrm{XiYi} - \frac{\frac{(\sum \mathrm{Xi})(\sum \mathrm{Yi})}{\mathrm{n}}}{\mathrm{n}-1}$$

∑Xi ∑Yi = Product of the ith array variance and covariance
∑Xi = Sum of the ith array
∑Yi = sum of the ith array covariance with parents

$$\mathrm{Var.(Vr)} = \sum \mathrm{Xi2} - \frac{\frac{(\sum \mathrm{Xi})2}{\mathrm{n}}}{\mathrm{n}-1}$$

Var. (Vr) = variance of the ith array variances.
∑Xi2 = sum of the squares of the ith array variances.
∑Xi = sum of the ith array variances.

The significance of b from unity was checked by a t-test.

The angle of attack of the regression line fit to the array points within the parabola illustrates both dominance and gene interactions. A regression line through the covariance of each array (on the y-axis) and its respective variance (on the x-axis) was drawn, limited by the parabola. Wri was measured to construct the regression line:

$$Wrei = Wr - bvr + bvri$$

Where,
Wr = mean covariance of the ith array with the parents' means.
Vr = mean variance of the ith array
b = regression coefficient
Vri = variance of the ith array

The points of the parabola's limits were computed as:

$$Wrli = Vp \times Vri$$

Where,
Wrli = parabola limits
Vp = parental variance
Vri = variance of the ith array

The regression line touches the X-axis at the point known as the intercept, which can be estimated as:

$$a = Wr - b.Vr$$

Where,
Wr = covariance means
b = regression coefficient
Vr = variance mean
a = point of interception

The intercept corresponds to the value of the average degree of dominance. When the regression line crosses the origin (y-intercept = 0), then it is pure dominance. When the line crosses over the origin (positive intercept), this indicates dominance partially. When the trendline cuts the origin, which means the y-intercept is negative, the trend is over-prevalent. When the regression line crosses the boundaries of the parabola, it indicates insufficient dominance. With the array, the closer to the origin a point is, the more dominating genes and the further apart the point is, the higher the recessive genes are. The intermediate one suggests that there must be dominant and recessive genes.

Table 1: Analysis of variance for 4 × 4 diallel cross in Upland Cotton Mean Squares

Results and Discussion

S.O. V	**D. F**	**P. H**	**B.P. P**	**M. B**	**S. B**	**S. C. Y**	**B. W**	**L. I**	**F. L**	**F. S**	**F. F**
Replication	2	6.0 N. S	64 N. S	6*	5.17 N. S	18.45 N. S	5.75 N. S	4.73 N. S	4.11 N. S	5.16 N. S	4.23 N. S
Genotypes	15	30.38**	238.4**	6.66**	8.15*	409**	7.75*	16.5**	13.89*	33.11**	6.66*
Error	30	3.86	25.46	1.67	1.98	22.85	1.92	3.95	3.99	3.92	1.73

Results and Discussion:

As shown in Table 1 above, the ANOVA indicated the significant variation of different genotypes on the traits of interest. The results suggest that parental genotypes have significant diversity and variation in all the attributes in cotton. The diversity and variation can be used for a future crop improvement program.

Table Key: ***PH*** *= Plant Height;* ***BPP*** *= Bolls per Plant;* ***MB*** *= Monopodial Branches;* ***SB*** *= Sympodial Branches;* ***SCY*** *= Seed Cotton Yield;* ***BW*** *= Boll Weight;* ***LI*** *= Lint Index;* ***FL*** *= Fiber Length;* ***FS*** *= Fiber Strength;* ***FF*** *= Fiber Fineness;* ***N.S*** *= non-significant; * = Significant at 5%; ** = Significant at 1%.*

The data of the concerned traits in the cotton were further analyzed for gene action. The array mean of different traits has been given. The results of the traits after analyzing the given data are discussed as follows:

Plant height (cm)

Plant height plays a vital role in the overall performance and adaptability of cotton plants, as it affects canopy structure, light interception and ease of management. In this study, the selected lines FH-175, FH-154, Lalazar and MNH-888 were chosen for their contrasting plant structures and genetic backgrounds. FH-175 and FH-154 are recognized for their yield stability, Lalazar for its moderate growth and adaptability, while MNH-888 shows vigorous vegetative growth. This heterogeneity allowed them to be the best selections in comparing inheritance patterns and the ability mixture of diallel crosses.

FH-175 had the greatest general combining ability (GCA) in terms of the height of the plants, with the average being 101.11 cm, meaning it is able to pass desirable genes on to plant height. The hybrid Lalazar x FH-175 exhibited the highest SCA with an average height of 105.88 cm (Figure 1A). Lalazar is of moderate height (90 cm), which is an indication that it can be used to ensure that the plant architecture is optimum during field conditions.

The Wr-Vr graph (Figure 2A) passed the Wr-axis below the origin, which showed that the over-dominance controls the plant height of the genotypes under study. The fact that the FH-154 is closer to the source suggests that there are more dominant alleles, whereas the larger distance of FH-175 is an indication that there are more recessive genes that affect this characteristic. The resultant over-dominance can be due to complementary allele interaction between parents with opposite alleles to give taller offspring, like Lalazar × FH-175. Such results align with the findings of Shang *et al.* (2020) and Bhatti *et al.* (2020), but Goren (2024) did not report the same results, which may be caused by genetic or environmental variability. Lalazar can also be used in breeding to keep the plants at intermediate height, and FH-175 could be used as a vigorous parent line to inbreed to effect plant architectural enhancements.

Number of bolls per plant

Cotton yield is directly related to the number of bolls per plant since it is the main determinant of the lint and seed production. The parental lines to be used in the study were strategically selected due to their variability in bolls production, with FH-175 and MNH-888 being productive and considering that FH-154 and Lalazar have moderate numbers that enable a thorough study of the gene action.

Genotype FH-175 was the most GCA of the trait with an average of 40 bolls per plant, indicating that the genotype has additive genes that are favourable to form bolls. FH-154 × FH-175 had the highest SCA value, 40.91 bolls per plant. The author contends (Figure 1B) that non-additive effects, matter as dominance and gene interactions, contribute.

The Wr-Vr regression (Figure 2B) passed through the origin, which validated that over-dominance is dominant in the regulation of the trait. The closest tetramer to the origin, MNH-888, had more prominent alleles, whereas FH-154 was distant and had more recessive genes. The over-dominance is possibly due to complementary relationships between the parents in which the genes complement each other, resulting in improved setting of the boll. Lack of epistasis was also observed since the regression line had the same slope after passing through the Wr-Vr axis. These results are consistent with Bano *et al.* (2023) and Manan *et al.* (2022) and differ from Shang *et al.* (2020), maybe owing to environmental effects or genetic variations. In breeding points, FH-175 seems to be a strong general combiner to be utilized in the breeding improvement programs, but MNH-888 may be utilized in the hybrid programs aimed at the high production of bolls due to the overpowering of the inherent genes.

(Annexure A)

Number of monopodial branches

The vegetative structures within the cotton that uphold the structure of the plant and indirectly support the formation of the bolls are known as monopodial branches. Though they have bolls later than sympodial branches, they boost canopy vigour and photosynthetic potential. In the literature, genotype FH-175 had the largest general combining ability (GCA) on monopodial branches (mean = 4.43), indicating that it possesses desirable additive genes on monopodial branches. MNH-888 × FH-154 showed the highest specific combining ability (SCA) value (5.63), which represents the occurrence of non-additive gene action between the two genetically different parents (Figure 3A).

The Wr-Vr graphical representation (Figure 4A) showed that the regression point was above the origin, which implies that in the absence of full dominance, inheritance of monopodial branches is predominantly controlled by partial dominance. This is an indication that heterozygous combinations of dominant alleles of some parents are not fully expressed. This interpretation is further supported by the distribution of parental points, in which Lalazar, having a closer location to the origin, has more dominant allele frequencies, whereas FH-175, with a more distant location to the origin, has many more recessive alleles of the trait. The fact that the regression line is straight proves that there are no epistatic interactions. Manan *et al.* (2022) and Bhatti *et al.* (2020) reported similar tendencies of predominance of the monopodial branches, whereas Kumar *et al.* (2022) found the opposite pattern of predominance, as they may have used different genetic backgrounds and conditions.

Compared to the breeding perspective, MNH-888, FH-154 is a good combination of breeding that will generate high vigour genotypes with balanced monopodial growth. The addictive effects of FH-175 and dominance effects of MNH-888 might be taken advantage of through reciprocal recurrent selection or pedigree breeding, and combine structural vigour with yield efficiency.

Number of sympodial branches

Sympodial branches are the primary fruiting structures in cotton and are strongly correlated with seed cotton yield. An increased number of sympodial branches enhances boll-bearing capacity and yield potential. In this study, FH-175 again exhibited the highest GCA for sympodial branches (mean = 9.57), indicating its strong additive contribution to this yield-related trait. The cross MNH-888 × FH-154 displayed the maximum SCA (11.26), confirming the importance of non-additive effects and the potential heterotic advantage of this combination (Figure 3B).

The Wr–Vr analysis (Figure 4B) showed the regression line passing through the origin, suggesting complete dominance for this trait. This pattern implies that heterozygous combinations between certain parents fully express the dominant alleles controlling sympodial branching. The parental array positions indicate that Lalazar possesses the highest frequency of dominant alleles (being near the origin), whereas FH-175 has fewer such alleles. These findings align with Reddy et al. (2016), who also observed complete dominance for sympodial branching, though Khan et al. (2015) reported partial dominance, possibly due to genotype × environment interactions.

From a breeder's perspective, MNH-888 × FH-154 again emerged as the best performing hybrid for sympodial branches, suggesting complementary gene action between these lines. Thus, MNH-888 can be utilized as an effective parent for enhancing fibre-related and architectural traits, while Lalazar can serve as a source of dominant alleles for plant architecture improvement.

(Annexure B)

Seed Cotton Yield

Seed cotton yield is one of the most important quantitative traits determining

overall productivity and profitability in cotton. In the present study, FH-154 recorded the highest general combining ability (GCA) for seed cotton yield (mean = 95.61), suggesting its strong additive gene effects and potential as a recurrent parent for yield improvement. Among the crosses, FH-175 × FH-154 exhibited the highest specific combining ability (SCA) value (103.92), indicating the presence of favourable non-additive gene interactions between these parents (Figure 5A).

Wr-Vr graphical analysis (Figure 6A) indicated the regression line passing through the origin, which indicated that the production of seed cotton is predominantly controlled by partial dominance. The tendency is that dominant alleles are not entirely expressed in heterozygotes, resulting in intermediate performance. The interpretation is also supported by the parental array; MNH-888, which is closer to the origin, has a higher proportion of dominant alleles of yield, whereas FH-154, which is far away, has a higher proportion of recessive alleles. Hamed *et al.* (2021) and Bhatti *et al.* (2020) have also stated similar results on the partial dominance of yield traits, but Manan *et al.* (2022) have obtained the opposite findings, apparently because of environmental influences and variations in parental backgrounds.

In breeding terms, there are two alternative breeding strategies that may utilize the heterosis of early segregating generations using the cross FH-175 x FH-154 and breeding FH-154 through pedigree or selection-based mechanisms to accumulate additive genes that create better yield. The partial dominant pattern observed may indicate that retention of a certain amount of heterozygosity may increase yield stability in the changing environment.

Boll Weight

One of the vital components of yield that has a direct influence on the total production of seed cotton is Boll weight. The heavier bolls are considered to be better boll fillers and fibre maturity, which is much appreciated in commercial cotton breeding. Once more in this study, FH-154 had the highest general combining ability (GCA) on boll weight (mean = 11.68 g), which is a strong indicator of its additive genetic effect. The hybrid FH-175 x FH-154 had the highest specific combining ability (SCA) value (13.86 g), which confirmed that there are strong non-additive gene effects on this trait (Figure 5B).

Wr-Vr analysis (Figure 6B) showed that the regression line went through the origin, which means full dominance of the boll weight. This means that overpowering alleles of the parent lines will give full expression when they are combined in heterozygous conditions, and the result will be optimal heterotic performance. The pattern of the parental genotypes in a regression line indicates that Lalazar has the highest amount of frequency of dominant alleles, whereas MNH-888 has more recessive alleles. Such results are not new, as Reddy *et al.* (2016) have found total dominance in terms of boll weight, and Shahzad *et al.* (2019) have found other effects of dominance in various environmental backgrounds.

Conventionally, FH-154 stands out as a reliable donor to be used in breeding to strengthen the boll weight, whereas Lalazar can be used as a parental instance to provide dominant alleles that would improve the development of the bolls. The FH-175 x FH-154 hybrid cross seems to be especially noteworthy in breeding high-yielding superior cultivars by heterosis breeding or diallel-recurrent selection programs.

(Annexure C)

Lint Index

The economic characteristics of lint index are important since the percentage of lint outturn of the seed cotton is one economic characteristic that directly increases the yield of a fibre and increases the profitability. In the experiment, FH-175 had the most GCA effect on lint index, meaning that it has additive genes that have positive contributions when mixed in all hybrid combinations. The highest SCA value (60.53) was observed in the cross FH-154 × MNH-888, which indicates high levels of non-additive interactions between the genes and the possibility of such an interaction to develop commercial hybrids (Figure 7A).

The Wr-Vr regression line crossed the line below the origin (Figure 8A), and this is a clear indication that the lint index is controlled by over-dominance. This implies that the parental lines have dominant and complementary alleles that interact in a synergetic manner to increase lint percentage. It was also observed by Wankhade *et al.* (2020) and Liu *et al.* (2020) reported different inheritance patterns, which was probably possible because the genetic backgrounds and environmental conditions were different. The array point distribution further showed that Lalazar was the nearest to the origin, meaning that it contains the largest percentage of the dominant alleles of lint index. On the contrary, FH-154 is located at the most distant position, which indicates a higher recessive allele. These tendencies suggest that Lalazar is a genetically robust donor of lint dominance effects, and FH-154 is a donor of various recessive alleles which can establish heterotic benefits upon cross-carrying dominant affluent parents.

In breeding-wise, crosses between the FH-175 high GCA and Lalazar dominant gene source shall be given priority in improving the lint yield in terms of selection schemes that will take advantage of additive and over-dominant gene effects.

1. Fibre Length

The length of the fibre is a very important quality index that has a direct impact on the yarn strength, fineness and spinning ability. During the experiment, MNH-888 had the highest GCA value of fibre length (25.04 mm) and which confirmed that it is a strong source of desirable additive genes on fibre quality. The hybrid cross of Lalazar x MNH-888 had the largest SCA effect (29.66 mm), which means that there are strong non-additive interactions between genes that increase fibre length (Figure 7B).

The Wr-Vr graph indicated that the fibre length was controlled by partial dominance since a regression line passed above the origin (Figure 8B). This implies, there is no absolute dominance or excessive dominance, but instead there is the interaction between alleles of parents that leads to moderate expression of fibre length. These findings are reinforced by Saravanan *et al.* (2021), but Jangid (2019) found a broader spectrum of effects of dominance that is related to parental diversity, suggesting that the genetic regulation of fibre traits could be dependent on parental germplasm sources. The genotype dispersion showed that MNH-888 is the nearest one to the origin, which means that it has the greatest frequency of dominant alleles in fibre length. On the other side, FH-175 is the most distant, implying that it harbours more genes that are in recess that favour this trait. The high SCA of crosses between MNH-888 is due to the contrasting nature of these parents, which results in to increase in the fibre quality characteristics with dominance-recessive complementation.

For practical breeding, MNH-888 should be used as a core parent in programs aimed at improving fibre length, while crosses involving Lalazar × MNH-888 can be advanced for hybrid development or exploited for early-generation selection to capture dominance effects.

(Annexure D)

Fibre Strength

Fibre strength is one of the most important quality parameters of cotton, which has a direct impact on its industrial and textile use. In the study, genotype MNH-888 has the greatest general combining ability (GCA) of fibre strength, with a mean of 20.72, which means that it has strong additive gene effects of fibre strength. FH-154 × MNH-888 had the highest specific combining ability (SCA), and its value was 25.50 (Figure 9A), indicating that the hybrid was non-additive in its gene interactions.

The Wr-Vr graphical analysis (Figure 10A) indicated that the Wr-axis line was below the point of origin, which showed that over-dominance ruled the fibre strength. It is in accordance with the findings presented by Sesayro *et al.* (2023) but is in conflict with those by Zeng *et al.* (2015), who found that the effect of parental combinations and genetic backgrounds can affect the expression of fibre strength. It is important to note that the comparative position of the parental genotypes shows that Lalazar has the highest count of dominant genes, and MNH-888, which is a greater distance to the origin, has a limited count of dominant genes. That is an indication that the high level of performance observed in the hybrids with MNH-888 is due to complementary relationships between alleles of the parents.

Breeding-wise wise MNH-888 is a core parent to utilize in the enhancement of fibre strength because of the regular additive effects, and hybrid crosses like FH-154 × MNH-888 may be strategically used in order to exploit over-dominance and increase hybrid vigour. The data highlight the significance of the selection of parents not only based on the individual performance but rather based on the complementary gene action, which gives practical advice to the breeders aiming at breeding towards improving the quality of fibre.

Fibre fineness

Another trait quality to be considered is fibre fineness, because the finer fibres play a role in the excellent quality of the yarn and cloth. Genotype MNH-888 was the highest GCA in fibre fineness (mean = 4.37), and FH-175 x MNH-887 has the best SCA (5.10) in the hybrid (Figure 9B) and portrays positive non-additive interaction effects in this hybrid.

Graphical analysis (Figure 10B) of Wr-Vr also showed over-dominance to fibre fineness, which was in agreement with Shahzad et al. (2019). Nonetheless, the opposite findings presented by Nawaz et al. (2019) imply that the model of fibre fineness expression is extremely determined by the combination of alleles of parents. Genotype positions further show that Lalazar is the individual with the highest number of dominant genes with FH-175, which has gone further away from the origin, having fewer dominant genes. These positional lessons indicate why some of the crosses, especially the one between MNH-888 and FH-175, have greater fineness as a result of complementary interaction between genes.

For cotton improvement, MNH-888 should be prioritized as a donor parent for fibre fineness, while crosses such as FH-175 × MNH-888 can be utilized in hybrid programs to exploit dominance effects. The strategic selection ensures that both additive and non-additive gene actions are harnessed effectively, providing breeders with a roadmap to improve fibre fineness in new cotton cultivars.

(Annexure E)

Conclusion

To evaluate new cotton genotypes, genetic exploitation is the basic need of the time on a sustained basis. Cotton is an important cash crop of our country. Cotton yield and fibre traits are the crucial characteristics to improve for economic gains. The basic purpose of improvement is to develop such type of genotypes that are fertilizer responsive, have less input cost, are more productive, short duration and higher quality. The environment is a drastic and major obstacle in cotton production. To start any breeding program, it is necessary to know the inheritance pattern and gene action of the crop. The genetic mechanism of any trait provides more information about the inheritance and type of gene action involved. Gene action is a useful tool to know the additive, dominant and overdominant behaviour of genes. By using this type of information, we will be able to develop such type of cotton genotypes that can boost production and revolutionize cotton production. The primary aim of the experiment was to be knowledgeable of the kind of gene action that took place in different morphological and economically important yield and fibre-specific parameters such as plant height, bolls per plant, monopodial branches per plant, sympodial branches per plant, seed cotton yield, boll weight, lint index, length of fibre, strength, and fineness. The results that will be obtained through this research will come in handy when it comes to the issue of selecting the most appropriate combination of factors to increase cotton production and quality. The genotypes analysis of variance revealed that all the morphological traits regarding yield and fibre yielded significant differences across the genotypes. The Wr/Vr graphs plotting revealed that there was some sort of partial dominance in the length of the fibre, seed cotton yield and the number of monopodial branches produced by the gene. Such characters were controlled by an additive form of gene action. Such traits as the height of the plants, the number of bolls per plant, the lint index, the fibre strength and fibre fineness were controlled by over over-dominant type of gene action. The boll weight and sympodial branches were controlled by the dominant genes and had a complete form of gene action. Nonetheless, epistasis did not occur at all. Genotype Lalazar represented the dominant genes of monopodial, sympodial branches, the genes of boll weight, lint index, fibre strength and fibre fineness. Genotype MNH-888 was superior because of the dominating genes of the number of bolls, seed cotton yield and fibre length. In the case of FH-154, there were domineering genes that were observed in the case of plant height. FH-154 and FH-175 are good general combiners of the height of plants, the number of bolls, monopodial branches, and sympodial branches. MNH-888 was both a good general and a specific combiner of fibre-related characteristics. Specific combining ability had good parents in Lalazar and MNH-888.

References

Abdel, A. M. S., Sorour, F. A., Yehia, W. M. B., Kotb, H. M. K., Abdelghany, A. M., Lamlom, S. F., & Abdelsalam, N. R. (2023). Estimating the combining ability and genetic parameters for growth habit, yield, and fibre quality traits in some Egyptian cotton crosses. *BMC Plant Biology*, 23(1), 121.

Bano, M., Shakeel, A., Khalid, M. N., Ahmad, N. H., Sharif, M. S., Kanwal, S., ... & Amjad, I. (2023). Estimation of combining ability for within-boll yield components in upland cotton (*G. hirsutum* L.). *Sarhad Journal of Agriculture*, 39(1), 174-181.

Bhatti, M. H., Yousaf, M. I., Ghani, A., Arshad, M., Shehzad, A., Mumtaz, A., & Shah, S. A. S. (2020). Assessment of genetic variability and trait association in upland cotton (*G. hirsutum* L.). *International Journal of Botany Studies*, 5(2), 148-151.

Chakholoma, M., Nimbal, S., Jain, A. J., & Kumar, M. (2022). Combining ability analysis for yield and fibre quality traits in American cotton (*G. hirsutum* L.) genotypes. *Ekin Journal of Crop Breeding and Genetics*, 8(1), 61-69.

Goren, H. K. (2024). Comprehensive analysis of drought tolerance in pure lines derived from half-diallel crosses of upland cotton (*G. hirsutum* L.). *Euphytica*, 220(8), 123.

Goren, H. K., & Canavar, O. (2024). Genetic analysis of yield and fibre quality traits in cotton (*G. hirsutum* L.) under full and deficit irrigation conditions using the full diallel method. *Euphytica*, 220(7), 115.

Hamed, H. H., & Said, S. R. N. (2021). Estimation of heterosis and combining ability for yield and fibre quality traits by using line × tester analysis in cotton (*G. barbadense* L.). *Menoufia Journal of Plant Production*, 6(1), 35-51.

Hayman, B. I. (1954). The theory and analysis of diallel crosses. *Genetics*, 39(6), 789-809.

Jangid, K. (2019). Genetic parameters, correlation and path analysis of agro-morphological traits in elite genotypes of upland cotton (*G. hirsutum* L.). *International Journal of Chemical Studies*, 7(5), 1885-1889.

Jarwar, A. H., Wang, X., Wang, L., Ma, Q., & Fan, S. (2018). Genetic advancement, variability and heritability in upland cotton (*G. hirsutum* L.). *Journal of Environmental and Agricultural Sciences*, 16, 24-31.

Jinks, J. L. (1954). The analysis of continuous variation in a diallel cross of Nicotiana rustica varieties. *Genetics*, 39(6), 767-788.

Khan, S. A., Khan, N. U., Gul, R., Bibi, Z., Khan, I. U., Gul, S., & Baloch, M. (2015). Combining ability studies for yield and fibre traits in upland cotton. *Journal of Animal & Plant Sciences*, 25(3), 734-742.

Kumar, P., Nimbal, S., Budhlakoti, N., Singh, V., & Sangwan, R. S. (2022). Genetic diversity and population structure analysis for morphological traits in upland cotton (*G. hirsutum* L.). *Journal of Applied Genetics*, 63(1), 87-101.

Liu, W., Song, C., Ren, Z., Zhang, Z., Pei, X., Liu, Y., ... & Li, W. (2020). Genome-wide association study reveals the genetic basis of fibre quality traits in upland cotton (*G. hirsutum* L.). *BMC Plant Biology*, 20(1), 395.

Manan, A., Zafar, M. M., Ren, M., Khurshid, M., Sahar, A., Rehman, A., & Shakeel, A. (2022). Genetic analysis of biochemical, fibre yield and quality traits of upland cotton under high temperature. *Plant Production Science*, 25(1), 105-119.

Mokadem, S. A., Salem, M. A., Khalifa, H. S., & Salem, T. M. E. (2020). Estimation of combining ability, heterosis and heritability in some Egyptian cotton crosses. *Journal of Plant Production*, 11(2), 189-193.

Nawaz, B., Naeem, M., Malik, T. A., Muhae-Ud-Din, G., Ahmad, Q., & Sattar, S. (2019). Estimation of gene action, heritability and pattern of association among different yield-related traits in upland cotton. *International Journal of Innovative Approaches in Agricultural Research*, 3(1), 25-52.

Reddy, K. B., Reddy, V. C., Ahmed, M. L., Naidu, T. C. M., & Srinivasarao, V. (2016). Combining ability study for yield and its component traits through diallel mating design in upland cotton (*G. hirsutum* L.). *Journal of Cotton Research and Development*, 33(1), 45-53.

Rehman, A., Mustafa, N., Du, X., & Azhar, M. T. (2020). Heritability and correlation analysis of morphological and yield traits in genetically modified cotton. J*ournal of Cotton Research*, 3(1), 23.

Saravanan, K., Kumar, M., & Renganathan, V. G. (2021). Diallel analysis of yield and fibre quality traits in upland cotton (*G. hirsutum* L.). *Electronic Journal of Plant Breeding*, 12(1), 285-291.

Sesayro, M., Patel, D., & Kumar, R. (2023). Genetic analysis of yield and fibre quality traits in upland cotton (*G. hirsutum* L.) using diallel mating design. *Journal of Cotton Research*, 6(1), 22.

Shahzad, K., Li, X., Qi, T., Guo, L., Tang, H., Zhang, X., ... & Wu, J. (2019). Genetic analysis of yield and fibre quality traits in upland cotton (*G. hirsutum* L.) cultivated in different ecological regions of China. *Journal of Cotton Research*, 2(1), 14.

Shang, L., Ma, L., Wang, Y., Su, Y., Wang, X., Li, Y., & Hua, J. (2020). The main effect QTL with dominance determines heterosis for dynamic plant height in upland cotton. *G3: Genes, Genomes, Genetics*, 6(10), 3373-3379.

Shar, T., Baloch, M. J., Arain, M. A., Jatoi, W. A., & Lochi, R. (2017). Phenotypic associations, regression coefficients and heritability estimates for quantitative and fibre quality traits in upland cotton genotypes. *Advances in Agriculture and Animal Science*, 33(2), 142-152.

Steel, R. G. D., Torrie, J. H., & Dickey, D. A. (1997). Principles and procedures of statistics: A biometrical approach (3rd ed.). *McGraw-Hill*.

Ujjainkar, V. V., & Patil, V. D. (2021). Diallel analysis for seed cotton yield and fibre quality traits in upland cotton (*G. hirsutum* L.) tested over a set of environments. *International Journal of Agricultural Sciences*, 13(4), 125-132.

Wankhade, S. D., Patil, V. R., & Deosarkar, D. B. (2020). Genetic analysis of yield and fibre quality traits in upland cotton (*G.hirsutum* L.). *Journal of Pharmacognosy and Phytochemistry*, 9(5), 1659-1662.

Zeng, L., & Pettigrew, W. T. (2015). Combining ability, heritability, and genotypic correlations for lint yield and fibre quality of upland cotton in delayed planting. *Field Crops Research*, 171, 176-183.

Zhang, T., Hu, Y., Jiang, W., Fang, L., Guan, X., Chen, J., & Chen, Z. J. (2015). Sequencing of allotetraploid cotton (*G. hirsutum* L.) provides a resource for fibre improvement. *Nature Biotechnology*, 33(5), 531-537.

Yang, Z., Qanmber, G., Wang, Z., Yang, Z., & Li, F. (2020). Gossypium genomics: Trends, scope, and utilization for cotton improvement. *Trends in Plant Science*, 25(5), 488-500.

Annexure A

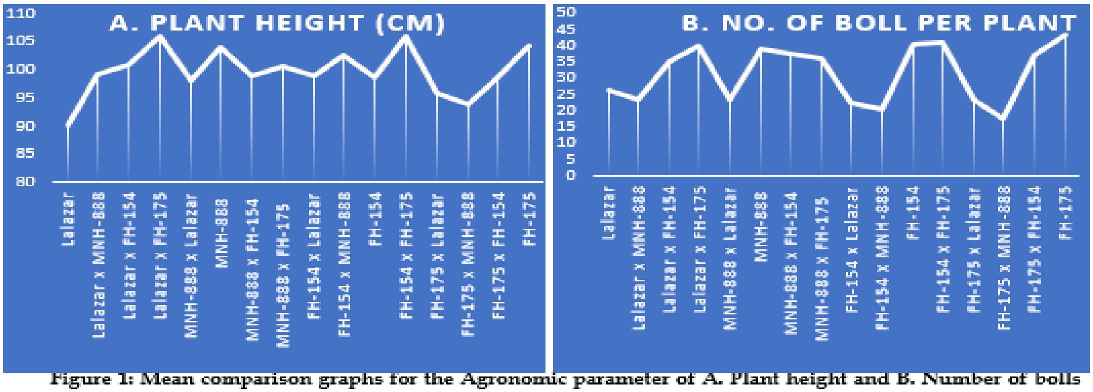

Figure 1: Mean comparison graphs for the Agronomic parameter of A. Plant height and B. Number of bolls per plant.

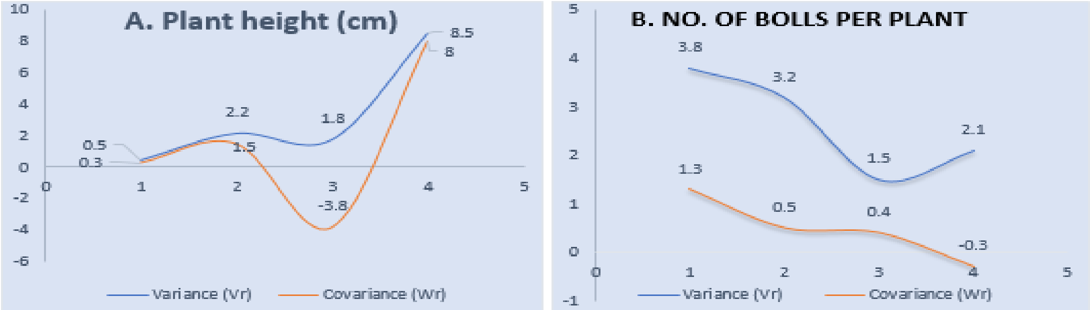

Figure 2: Variance (Vr) and Covariance (Wr) graph for the Agronomic trait of A. Plant height and B. Number of bolls per plant.

Annexure B

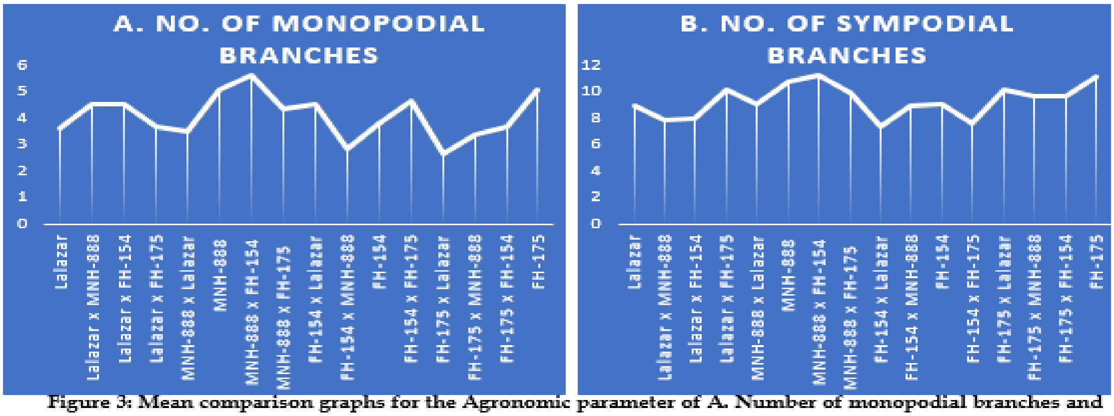

Figure 3: Mean comparison graphs for the Agronomic parameter of A. Number of monopodial branches and B. Number of sympodial branches per plant.

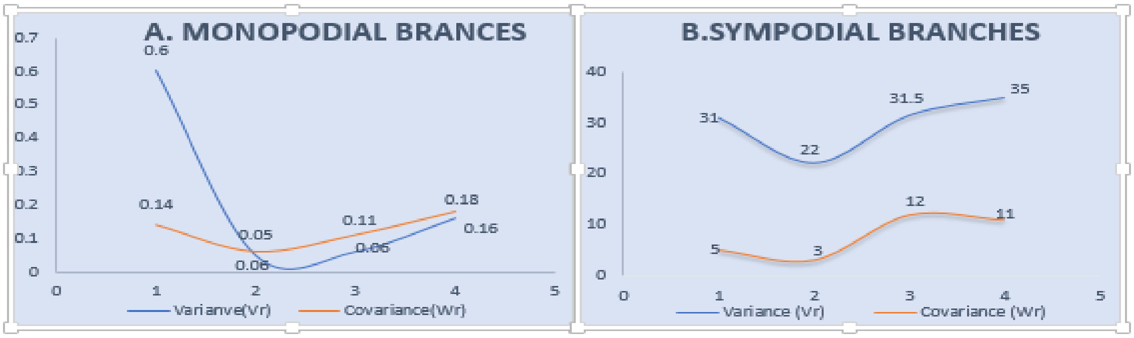

Figure 4: Variance (Vr) and Covariance (Wr) graph for the Agronomic trait of A. Number of monopodial branches and B. Number of sympodial branches per plant.

Annexure C

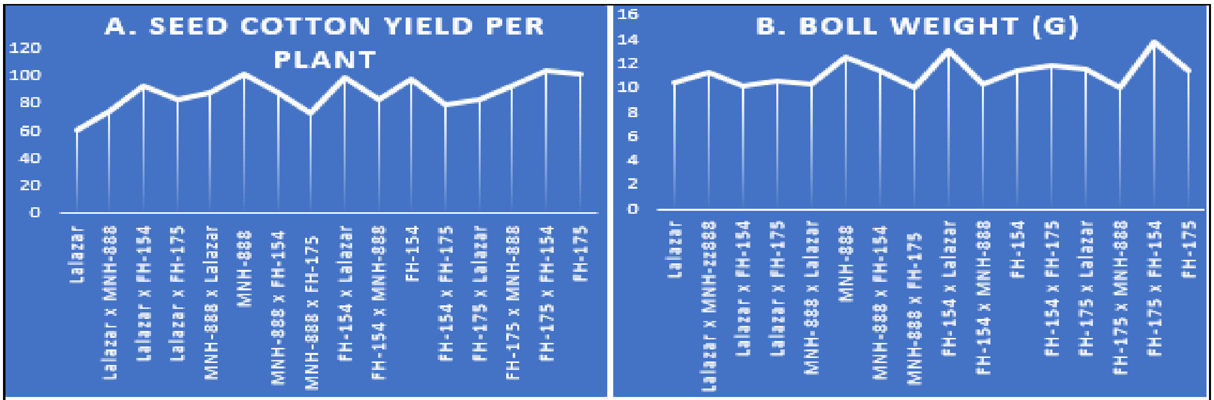

Figure 5: Mean comparison graphs for the Agronomic parameter of A. Seed cotton yield per plant and B. Boll weight.

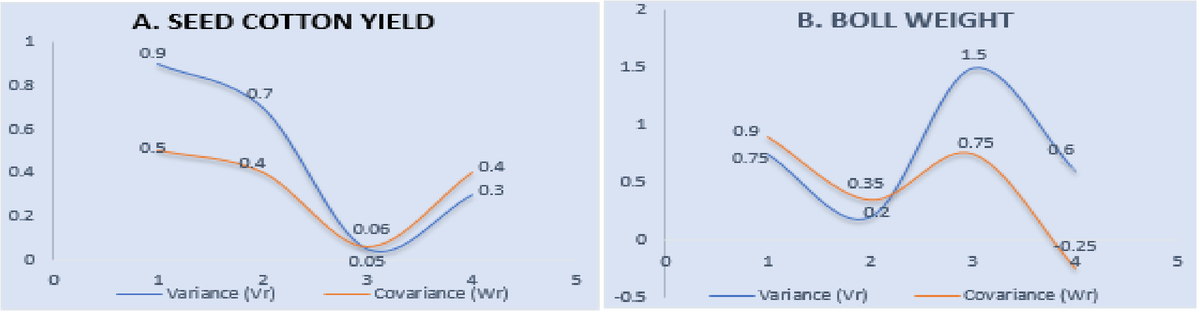

Figure 6: Variance (Vr) and Covariance (Wr) graph for the Agronomic trait of A. Seed cotton yield per plant and B. boll weight.

Annexure D

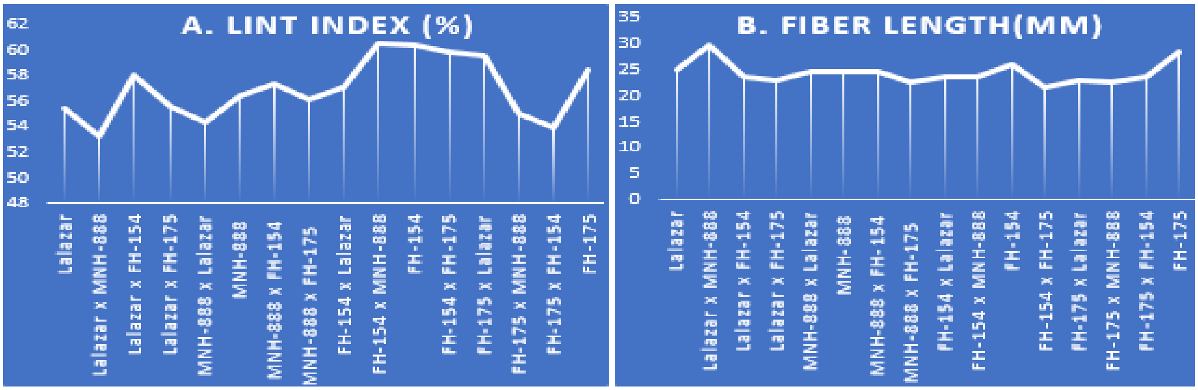

Figure 7: Mean comparison graphs for the Agronomic parameter of A. Lint index and fibre quality traits: B. Fibre length.

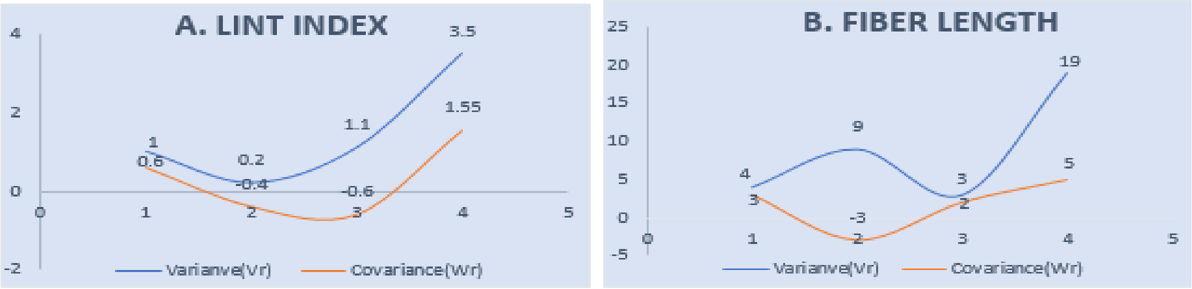

Figure 8: Variance (Vr) and Covariance (Wr) graph for the Agronomic parameter of A. Lint index and fibre quality traits: B. Fibre length.

Annexure E

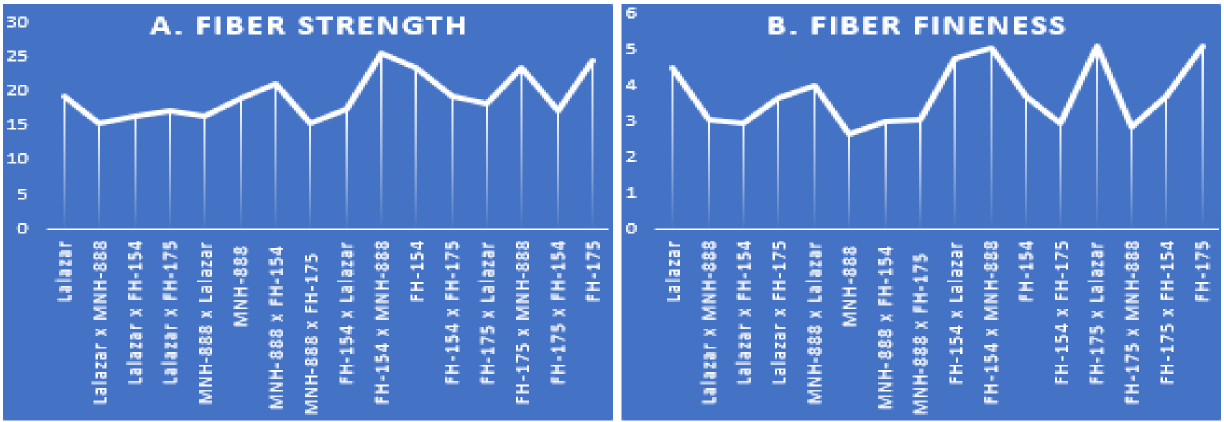

Figure 9: Mean comparison graphs for Fibre quality traits of A. Fibre strength and B. Fibre fineness.

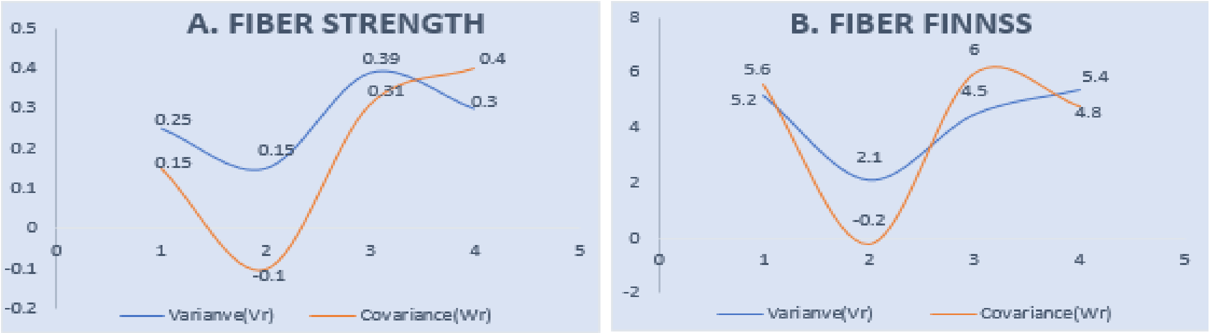

Figure 10: Variance (Vr) and Covariance (Wr) graph for Fibre quality traits of A. Fibre strength and B. Fibre fineness.