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Genetic Variability for Earliness Traits in Upland Cotton

Muhammad Abubakar[*1], Muhammad Zahid[1], Fajar Raheem[1], Noor Ul Ain[1], Asma Rafi[1] Zahid Akram[1] and Ume Ruqia Zainab[2]

[1]Department of Plant Breeding and Genetics, University of Agriculture Faisalabad

[2]Department of Botany, University of Agriculture Faisalabad

*Correspondence
abubakaruca879@gmail.com

Abstract

Cotton is a warm-season, perennial shrub and commonly referred to as "white gold." It is a member of the *Gossypium* genus, which is classified into the Malvaceae family. Genetic variability in the germplasm is a prerequisite before starting any breeding programs. Genetics variabilities studies of available cotton genotypes will facilitate for the selection of potential parent for the improvement of cotton. A group of 14 cotton genotypes (PB-94, PB-96, PB-97, PB-101, PB-113, PB-126, PB-128, PB-130, PB-132, PB-133, PB-136, PB-137, FH-490 and LALAZAR) were analyzed to evaluate the genetic variability of cotton. This experiment was carried out at the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. A randomized complete block design with two replications was used for the experiment. Data was recorded for plant height, internodal distance, number of bolls per plant, boll weight, earliness index, the node number of the first sympodial branch having effective boll, number of monopodial branches per plant, number of sympodial branches per plant, the node of the first sympodial branch, seed index, seed cotton yield, number of seeds per boll, ginning out turn, fiber length, fiber strength, and fiber uniformity. Significant results were observed among genotypes for all attributes. The genotype PB-136 showed the highest potential for seed index while PB-130 expressed the best performance for fiber length and fiber uniformity. PB-132 and PB-113 showed highest potential for internodal distance and seed cotton yield respectively. These results showed the potential of studied genotypes for using in future breeding program for the development if high yielding cotton varieties.

K E Y W O R D S
Breeding program, Fiber quality, Earliness index, Seed cotton yield

1 | INTRODUCTION

Cotton is a warm-season, perennial shrub that is grown annually and commonly referred to as "white gold." Cotton is known as the king of natural fibers due to its renewable fiber properties (Zafar et al., 2024). In Pakistan, 1.5 million people cultivate cotton. Out of total cultivated area 60% in Punjab region and 35% in Sindh region. The textile industry employs 40% of the labor force with ten million employees working in various areas including 1,050 ginneries, 430 mills and 350 cottonseed oil refineries (Rehman and Anderson, 2021).

China takes the lead as the top global producer of cotton, with an impressive production of 6,423 metric tons. India is second with 6,162 metric tons, while the United States ranks third with a production of 3,181 metric tons. Brazil comes in fourth place with a production of 2,341 metric tons and Pakistan is fifth globally with a production of 980 metric tons (US Department of Agriculture, 2021-2022).

Pakistan is among the top five cotton producing countries globally and the export of cotton and textile products accounts for approximately 60% of the country's total exports (Zafar et al., 2023). The cotton sector contributes about 0.6% to Pakistan's GDP and 2.4% to the value added in agriculture. However, in recent years, cotton cultivation has decreased and other crops like sugarcane, maize, potato, and rice have taken its place. During the 2021-22 season, the area under cotton cultivation shrank by 6.8% to 1,937 thousand hectares from 2,079 thousand hectares in the previous year. Nevertheless, cotton production increased by 17.9% to 8.329 million bales compared to the previous year's 7.064 million bales due to favorable weather conditions, efficient input supplies, improved crop

management practices and high cotton prices in both domestic and international markets (GOP, 2021-22).

As the world population is growing, there is an increasing need to increase crop production in order to fulfil the requirements of the textile industry. To achieve this, a variety of breeding techniques should be employed (Farooq et al. 2015). To increase cotton production, it is essential to address the limitations that hinder its growth such as the use of low-quality cultivars, improper sowing times, low plant population and various biotic and abiotic stressors, along with poor-quality seeds. Maintaining high quality and yield is a vital factor for all crops, including cotton (Fang et al. 2017; Zafar et al. 2023; Chattha et al. 2021).

Breeding cotton for success involves identifying and utilizing promising genotypes through hybridization and selecting desirable genes and gene complexes. To achieve this accurate understanding of genetic variability, heritability of traits and correlations among desirable traits is necessary. This information forms a reliable foundation for improving crops (Khan et al. 2009; Chattha et al. 2017).

The development of new cotton varieties is highly dependent on the presence of genetic variability, which can be achieved through the crossing of genetically diverse plants. It is important to consider that traits that contribute to yield are interconnected with each other (Haq et al. 2017; Bilal et al. 2022). This genetic variation is capable of being passed down from parents to their offspring, thereby affecting the expression of the trait in future generations.

Due to the continuous growth of the global population, the demand for textiles has risen which has resulted in the need to enhance crop productivity. Therefore, the primary objective of this study is to assess the genetic variability among diverse upland cotton genotypes to produce superior quality fibers that can meet the specific requirements of the textile industry.

2   METERIAL AND METHOD

The study was conducted at the Department of Plant Breeding and Genetics research field at the University of Agriculture Faisalabad, utilizing 14 upland cotton genotypes. The experiment was carried out during the cotton sowing season in 2022, using randomized complete block design (RCBD) with two replications for each variety and maintaining the recommended plant-to-plant distance of 30cm and row-to-row distance of 75cm. Data was collected from randomly selected five plants from each replication of each genotype. Throughout the growth cycle the appropriate agronomic practices were followed including weeding, thinning, hoeing, proper irrigation and plant protection using recommended chemicals until harvesting.

Data were Recorded for the following Traits
Plant Height (cm)

At the time of maturity, the height of the plants was measured using a measuring tape, from zero node to the point at which the apical growth of the main stem had ceased. The measurement was taken in centimeters and the average height per plant was calculated for use in statistical analysis.

Internodal Distance (cm)

The portion of stem between two nodes is called the internode. The internodal distance was determined between the two nodes of a plant. The internodal distance was determined in centimeters with the help of measuring tape. The average internodal distance per plants was estimated for the statistical analysis.

Number of Bolls per Plant

During each picking, the number of picked bolls was recorded. Upon completion of the final picking, the total numbers of bolls were calculated, and the average number was calculated for use in statistical analysis.

Boll Weight (g)

The weights of five bolls were measured from each of the selected plants chosen randomly and subsequently, the average weight of these bolls was calculated.

Earliness Index

The calculation of the earliness index for the genotype was done using the formula provided below;

Earliness index = (Yield of first picking) / (Total Yield) x 100
For statistical purposes, the mean values of the earliness index were calculated for all five plants.

Node Number of First Sympodial Branch having Effective Boll

To determine the node number of the first effective boll, a branch that bears the first effective boll was identified and its node number was counted. The mean value of the node number of the first effective boll was recorded for statistical analysis based on the five selected plants.

Number of Monopodial Branches per Plant

Monopodial branches, also known as vegetative branches, are those that do not bear fruit directly and are formed at the base of the cotton plant, typically in the first few nodes. Numbers of monopodial branches on each selected plant were counted.

Number of Sympodial Branches per Plant

Fruiting branches are known as sympodial branches as they directly bear fruit. Sympodial branches also develop on the secondary branches of monopodial branches and produce fruit directly. Once a plant has a sympodial branch growing from a main stem node, it cannot produce any more monopodial branches above that node. Sympodial branches on each selected plant were counted.

Node of First Sympodial Branch

The node number of the first fruit-bearing sympodial branch was determined for five plants that were randomly selected. The mean value of these node numbers was recorded for statistical analysis.

Seed Index (g)

To determine the seed index, a sample of gin-dried seeds that were both lint-free and disease-free was taken. One hundred seeds were then randomly selected from this sample and weighed on an electronic balance. This weight measurement of the hundred seeds was referred to as the seed index.

Seed Cotton Yield (g)

To measure the yield of seed cotton, the crop in the field was allowed to fully mature. The first picking of seed cotton was done after 90 days of sowing, when there was no moisture in the crop. The second picking was carried out three weeks after the first picking. The combined weight of the seed cotton obtained from both pickings of five randomly selected plants was measured in grams using an electronic weighing balance. The mean values of these measurements for each genotype were calculated for statistical analysis.

Statistical Analysis

Analysis of variance was done by following Fischer's technique Steel et al. (1997). The mean performance of genotypes was drawn through Microsoft excel.

3   RESULTS AND DISCUSSION

Analysis of variance reveals whether genetic differences are significant, non-significant or highly significant. There is no reason to continue analyzing the data if results are non-significant because the genotypes do not differ significantly.

Plant Height

The results revealed that genotypes showed significant difference for plant height as shown in the Table 1. Maximum height was observed in PB-128 (146 cm) and the minimum value of height was observed in PB-132 (123 cm) genotypes according to mean performances (Fig. 1). The range of plant height varied from 146 cm to 123 cm. Mawblei et al. (2022) and Bano et al. (2023) evaluated the genetic variability and reported results those were similar for plant height.

Table 1: MS values for various traits in cotton genotypes

Sources of variation	Replication	Genotype	Error
DF	1	13	13
Plant height	96.57	85.43*	17.91
Internodal distance	0.1	0.31*	0.02
Bolls per plant	11.06	127.7*	13.52
Boll weight	0.0005	0.11*	0.01
Earliness index	49.63	146.93**	9.84
Sympodial branch having effective boll	0.2	5.48*	0.53
Node of first sympodial branch	0.96	1.41*	0.24
Seed index	0.20571	0.433*	0.07341
Seed cotton yield	758.58	1524.4*	188.59
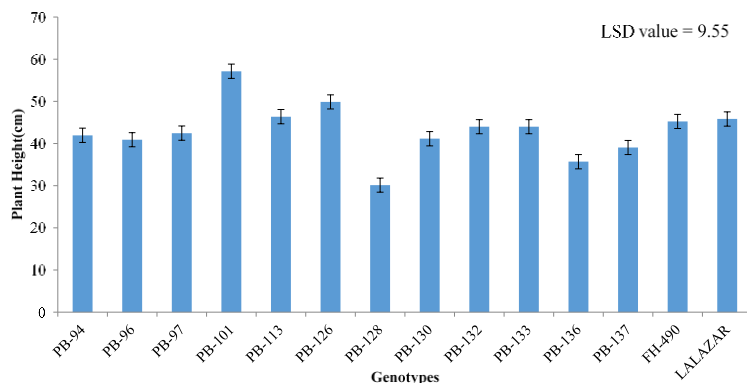
Fig. 1: Mean performances of 14 genotypes of cotton for plant height.

Internodal Distance

Analysis of variance demonstrated the significant difference among the genotypes for Inter nodal distance (Table 1). Largest inter nodal distance was observed in PB-130 (4.89 cm). The minimum distance was seen in PB-137 (3.45 cm) according to mean performance (Fig. 2). The range of Inter nodal distance varies from 4.89 cm to 3.45 cm. The findings are consistent with studies of Monisha (2018) and Mawblei et al. (2022)
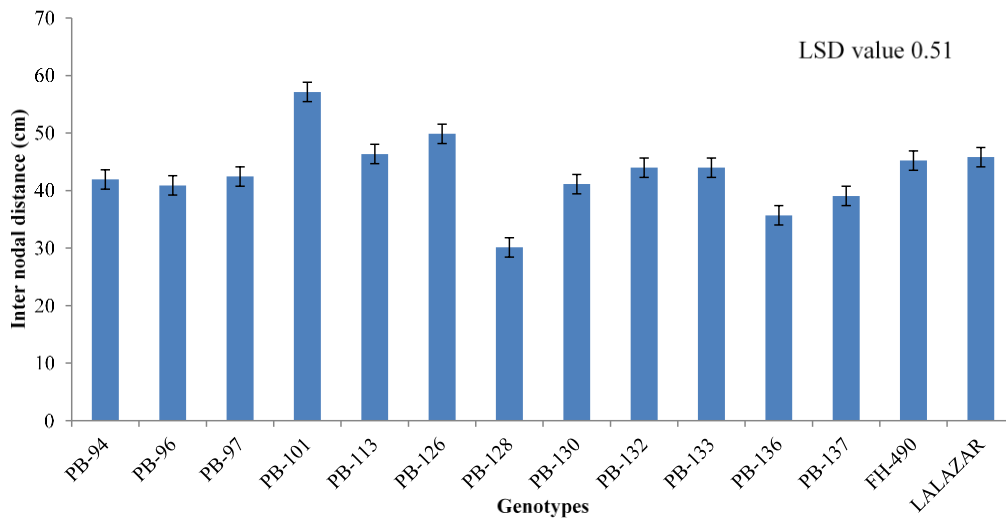
Number of Bolls per Plant

Results revealed that among fourteen cotton genotypes, the trait number of bolls per plant showed a significant difference as shown in Table 1. The maximum number of bolls per plant was observed in FH-490 (83.6) and the minimum value of the number of bolls per plant was observed in PB-132 (56.6) according to mean performances (Fig. 3). The range of the number of bolls

per plant is varied from 83.6 to 56.6. The calculated value of genetic advance mean was 29.35. Pujer et al. (2014) and Venkatesha and Patil (2014) researched cotton genetic diversity and found significant results for the number of bolls per plant.
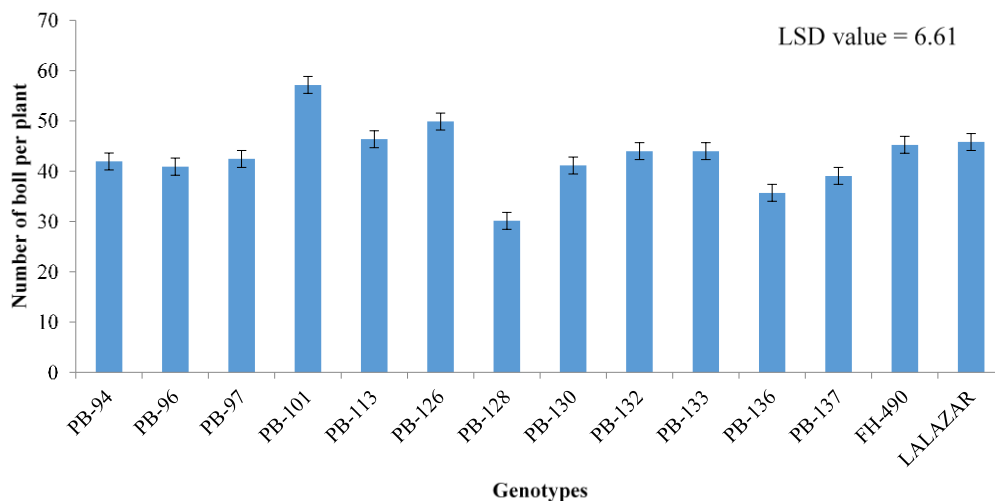
Boll Weight

Mean square results from investigation of variance depicted highly significant variation among genotypes for boll weight per plant (Table 1). Mean values of boll weight per plant were ranged from 4.01 to 3.08. The highest mean values were depicted by genotype PB-113 (4.01 g) and the lowest by PB-130 (3.08 g) as shown in the Fig. 4.4. Genetic advance mean (23.56) values were also observed. Higher phenotypic and genotypic variance was calculated for boll weight.
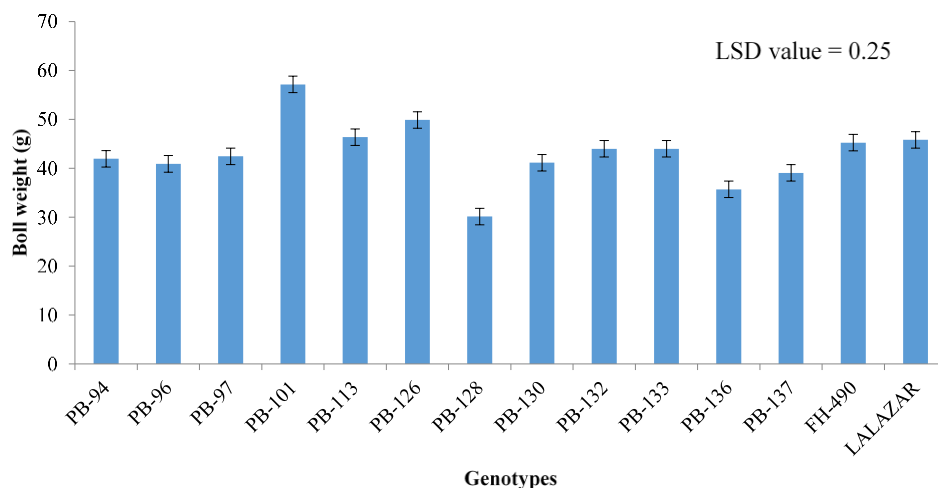
Similar results were showed by Ranganatha et al. (2013), Baloch et al. (2017) and Gnanasekaran et al. (2018) for boll weight for cotton genotypes.
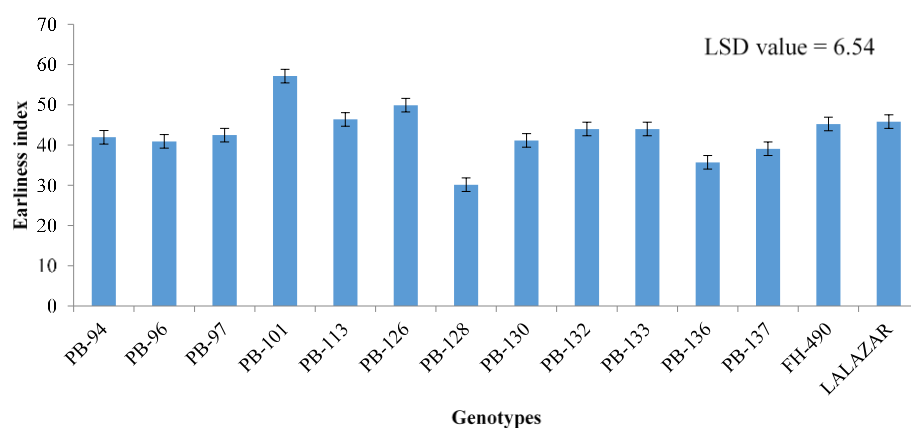

Fig. 2: Mean performances of 14 genotypes of cotton for internodal distance.

Fig. 3: Mean performances of 14 genotypes of cotton for number of boll per plant.

Fig. 4: Mean performances of 14 genotypes of cotton for boll weight.

Fig. 5: Mean performances of 14 genotypes of cotton for earliness index.

Earliness Index

There are significant differences among the genotypes in terms of the earliness index (Table 1). The greater earliness index was recorded in PB-130 (67.06) and the lowest earliness index was recorded in PB-94 (42.73) as given in Fig. 4.5. The phenotypic variance is slightly higher than the genotypic variance. The same outcomes were assessed by Farooq et al. (2018).

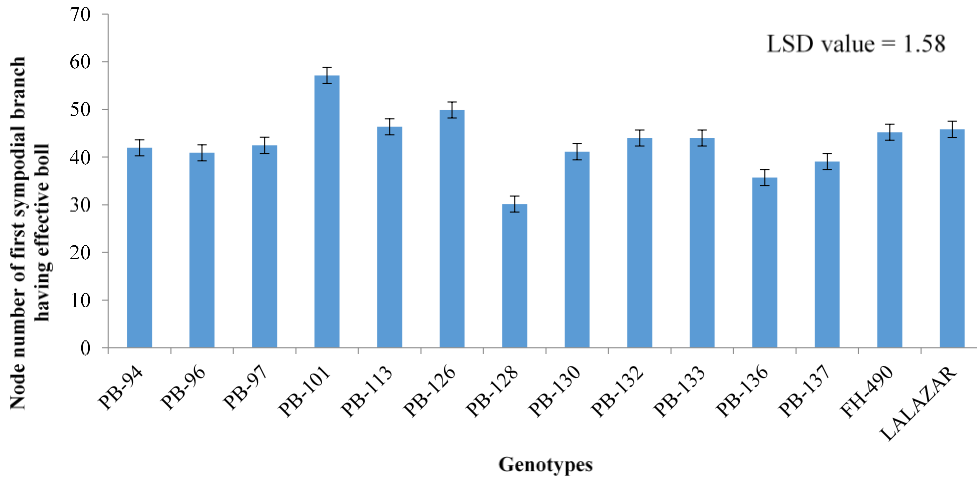## Node Number of First Sympodial Branch having Effective Boll

According to the analysis of variance, the results indicated that there were significant differences observed among the 14 genotypes of upland cotton in the case of node number of the first sympodial branch having an effective boll (Table 1.). The greater value of the node number of the first sympodial branch having effective boll was observed in PB-130 (12.1) and the lower value of the node number of the first sympodial branch having effective boll was observed in PB-133 (5.7) according to the mean performance of genotypes as given in Fig. 6. Highly significant results were shown by Bano et al. (2023) for node number of the first sympodial branch having effective boll.
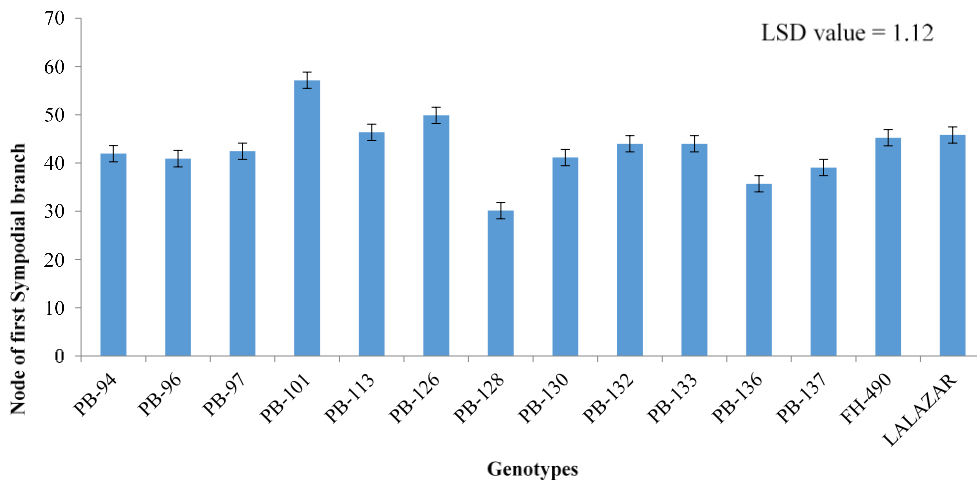
Node of First Sympodial Branch

Mean square results from the investigation of variance depicted highly significant variation among genotypes for the node of first sympodial branch (Table 1). Mean square values for the node of first sympodial branch ranged from 4.8 to 7.9. The highest mean values were depicted by genotypes LALAZAR (7.9) and the lowest by PB-94 (4.8) as shown in Fig. 7. The similar results were revealed by Bednarz et al. (2000).
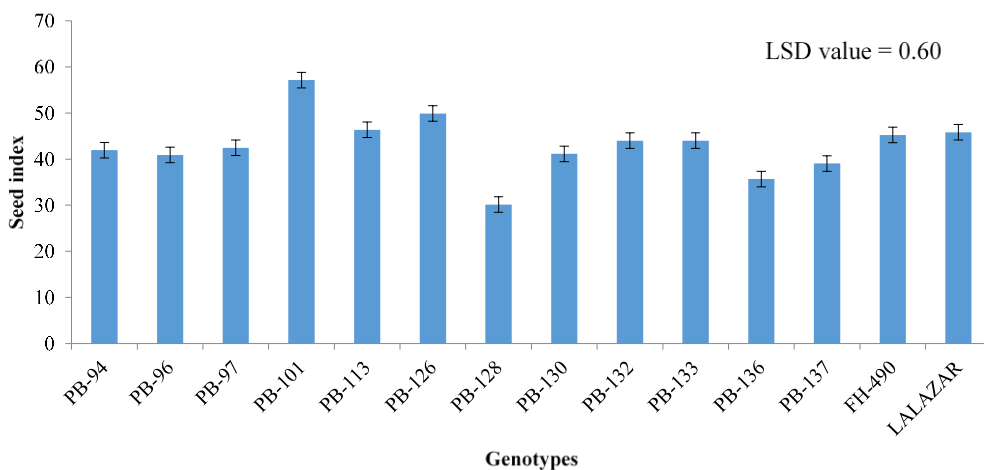
Seed Index

Mean square results from the investigation of variance depicted highly significant variation among genotypes for seed index (Table 1). Mean square values for the seed index ranged from 8.1 to 9.7. The highest mean values were depicted by genotypes PB-136 (9.7) and the lowest mean values were depicted by genotypes PB-128 (8.1) as shown in Fig. 4.10. Genotypes demonstrated variable results for the seed index and may be used in the future for cultivars development (Kumar and Katageri 2017). Manan et al. (2022) observed strong heritability assessment and high genetic progress for the seed index.

Fig. 6: Mean performances of 14 genotypes of cotton for node number of first sympodial branch having effective boll.

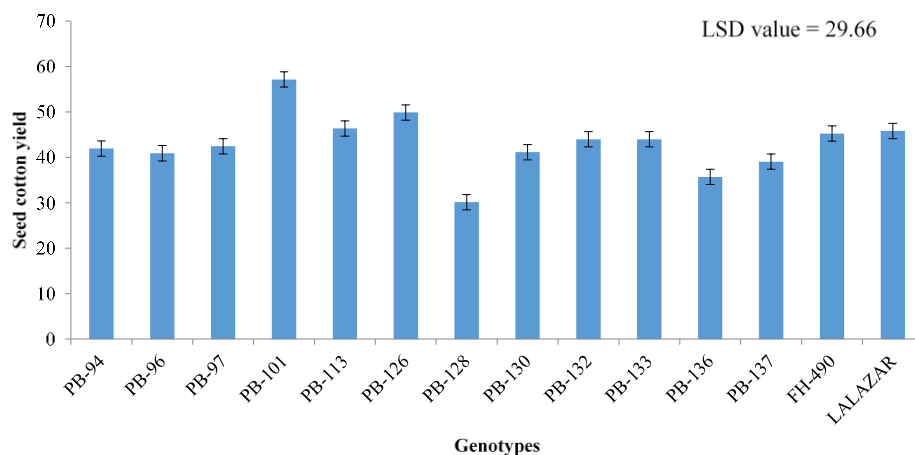**Fig. 7:** Mean performances of 14 genotypes of cotton for node of first sympodial branch

Fig. 8: Mean performances of 14 genotypes of cotton for seed index

Seed Cotton Yield

Mean square results from the investigation of variance depicted highly significant variation among genotypes for seed cotton yield (Table 1). Mean square values for seed cotton yield ranged from 118.69 to 199.08. The highest mean values were depicted by genotype PB-94 (199.08) and the lowest by PB-137 (118.69) as shown in Fig. 9. Genotypes showed a diverse significant result which predicts the importance of traits for further experiments with respect to yield components. Abro et al. (2021), Mawblei et al. (2022) and Meena et al. (2022) observed similar results.

Conclusion

Although, all of the lines performed well across a variety of parameters, with bulk PB-113 standing out in key areas like as internodal distance and seed cotton production. Notably, compared to other lines, PB-113 produced more seed cotton. Finally, PB-113 produced good results and may be valuable in future breeding efforts.

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