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Estimation of mean performance of parents and their hybrids for yield related traits in *Gossypium hirsutum* L.

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Cotton (*Gossypium hirsutum* L.) is an important fiber crop and plays an important role in Pakistan's economy as a cash crop. Cotton crop is cultivated primarily for fiber. The main objective of all cotton breeders is the production of a new variety with high yield and fiber quality. The current experiment was be conducted in the research area of Department of Plant Breeding and Genetics, University of Agriculture Faisalabad. Crosses were made of four varieties AGC-999, IR-3701, VH-37 and AS-01 by full Diallel mating design in the greenhouse during winter season. Evaluation of 12 crosses and 4 parental varieties were proceeded in the field during Kharif season of 2019 under RCBD (Randomized completely blocked Design) design with three replications. The data for agronomic characters and yield related traits as plant height, number of branches, number of bolls, number of nodes, seed cotton yield, ginning out turn, seed index and lint index was recorded. Mean data of seed cotton yield for all the genotypes indicated that the parent AS-01 provided the maximum yield (93.73 grams) among the parents while AGC-999 × IR-3701 had the maximum yield (82 grams) among the crosses. While VH-37, VH-37 × AS-01 and AS—01 × AGC-999 had the minimum value among parents and crosses respectively. These genotypes

Keywords: Cotton, mean performance, seed cotton yield, hybrid.

INTRODUCTION

Cotton (*G. hirsutum* L.) is a worldwide pre-eminent fiber and natural crop that stretches to one of the largest textile industries in the world with an annual economic effect of at least $600 billion worldwide. Pakistan's cotton and cotton products account for nearly 60% of its overseas earnings (Chaudhry *et al*., 2022). *Gossypium hirsutum*, or "upland" cotton, accounts for more than 90% of the world's cotton production and its cultivars are widely distributed worldwide, ranging from tropical to temperate latitudes in around 40 countries, with China, the United States, Brazil and Pakistan being the main producers (Hassan *et al*., 2021).

The genus of cotton has 50 species in which only four are cultivated, Gossypium hirsutum covers 90%, *G. barbadense* 9%, *G. herbacium* and *G. arboreum* are sown only 1% of the world cotton growing areas. These 50 species belong to eight diploid genera A, B, C, D, E, F, G, K and one tetraploid AD genome (Mudasir *et al*., 2021). American Diploid Species have two sections and six subsections of Subgenus *Houzingenia*, whose species collectively comprise the New World D-genome diploids. These species belong to the American taxonomy and have been thoroughly collected and studied that's why their taxonomy is well known than other diploid species. Western Mexico is the center of diversity for the 13 species of D-genome (Shuli *et al*., 2018).

Gossypium hirsutum is considered as the allotetraploid (2n = 4x=52) among species of the cotton because it was developed by the crossing of two diploid species *Gossypium Raimondi* and *Gossypium americana* and it is at top in the area wise cultivation lagging the *Gossypium barbadense*. It is cultivated on 5 % area of the world cotton cultivation, remaining 5% of the world cotton is fulfilled by *Gossypium arboreum* and *Gossypium herbaceum* (Bakhsh *et al*., 2005).

Fiber of cotton is a single cell that is very helpful in the study of fiber such as biosynthesis and expansion of cellulose. Fiber

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of cotton is very famous in the world due to its quality and soft fiber for the textile industries. *Gossypium arboreum* has a main role, that is also known as the "Nirma" famous for the long and soft fiber, is cultivated in the Sanghar district, Sindh Province of the Pakistan (Mansoor *et al*., 2003).

MATERIALS AND METHODS

The material for this research comprised of the four varieties as parent AGC-999, IR-3701, VH-37, AS-01 and their twelve crosses were made by crossing in all possible combination as full diallel mating design that is AGC-999 × IR-3701, AGC-999 × VH-37, AGC-999 × AS-01, IR-3701 × VH-37, IR-3701 × AS-01, IR-3701 × AGC-999, VH-37 × AS-01, VH-37 × AGC-999, VH-37 × IR-3701, AS—01 × AGC-999, AS-01 × IR-3701, AS-01 × VH-37. The research was conducted in the research area of Department of Plant Breeding and Genetics, University of Agriculture Faisalabad

At the time of maturity data of the following characters was noted:

1. Plant height (cm)
2. Monopodial branches
3. Sympodial branches
4. Number of nodes
5. Node of first fruiting branch
6. Number of bolls per plant
7. Seed cotton yield (g)
8. Boll weight (g)
9. G.O.T (%)
10. Seed index (g)
11. Lint index (g)

***Statistical Analysis*:** The collected data from the field was subjected to statistical analysis of variance technique by using Minitab software.

RESULTS AND DISCUSSION

***Plant height*:** Plant height has an important role in the cotton crop. Mostly medium height plants are preferred over the tall plants due to many factors of negativity. Analysis of the variances showed highly significant differences among the genotypes for the observed trait (Table 1).

In the parents, genotype AS-01 has the maximum mean value for the plant height (102.83 cm) whereas AGC-999 showed the minimum mean value for the plant height that was 101 cm. Among F_1 population maximum mean value was for the AGC-999 × IR-3701 (105.93 cm) and minimum mean value was of VH-37 × AS-01 (87 cm) (Fig. 1). Similar results were found by (Abbas, 2020 (Ashokkumar *et al*., 2010; Geng *et al*., 2021).

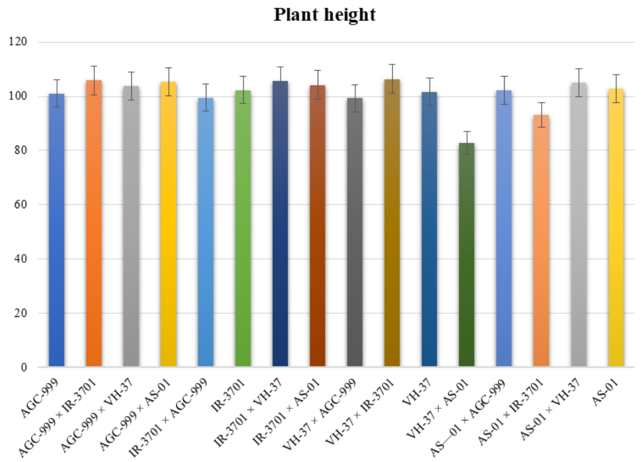

Figure 1. Mean values for plant height.

***Monopodial Branches*:** Monopodial branches are known as the vegetative branches of the cotton crop. Usually the less numbers of monopodial branches are required in the cotton due to many yield and growth impact factors. In this research genotypes were significant that said there were differences among the genotypes that were also useful to control the variation (Table 1). The maximum mean value for the monopodial branches among parents was for AGC-999 (3.9 branches) but minimum value had the parent VH-37 (1.87 branches) and in the crosses, the cross AGC-999 × IR-3701 had the higher mean value (3.5), the cross AS-01 × VH-37 had the lower mean value (2.0) for the monopodial branches (Figure 2). Similar results were found by (Ali *et al*., 2019; Baloch *et al*., 2015; EL-SEOUDY *et al*., 2014).

***Sympodial Branches*:** Sympodial branches are the direct fruiting branches and more these branches more will be the yield of plants. The maximum mean value for the sympodial branches among parents was for AGC-999 (16.1 branches) but minimum value had the parent IR-3701 (12.34 branches) and in the crosses, the cross AGC-999 × IR-3701 had the higher mean value (15.19), the cross IR-3701 × AS-01 had the lower mean value (5.04) for the sympodial branches (Figure 3). Similar results were found by (Razzaq *et al*., 2021; Islam *et al*., 2021; Sawarkar *et al*., 2015).

Table 1. Analysis of variance for all attributes.

SOV	DF	PH	MB	SB	NN	FFB	BPP	SCY	BW	GOT	SI	LI
Replication	2	34.16	0.29	11.68	11.70	14.87	110.2	10.24	0.80	10.41	0.0	7.68
Genotypes	15	106.37**	1.28*	34.86**	67.11*	36.43**	25.62*	1815.59**	0.69**	52.38*	0.01**	10.18**
Error	30	11.17	0.08	4.71	16.09	5.43	4.10	14.52	0.06	11.73	0.0	1.35
Total	47											

Plant height (PH), Monopodial branches (MB), Sympodial branches (SB), Number of nodes (NN), Node of first fruiting branch (FFB), Number of bolls per plant (BPP), Seed cotton yield (SCY), Boll weight (BW), Ginning out turn (GOT), Seed index (SI), Lint index (g)

Data was analyzed and the analysis showed that genotypes were highly significant in terms of sympodial branches. So, the genotypes were widely different from each other's (Table 1).

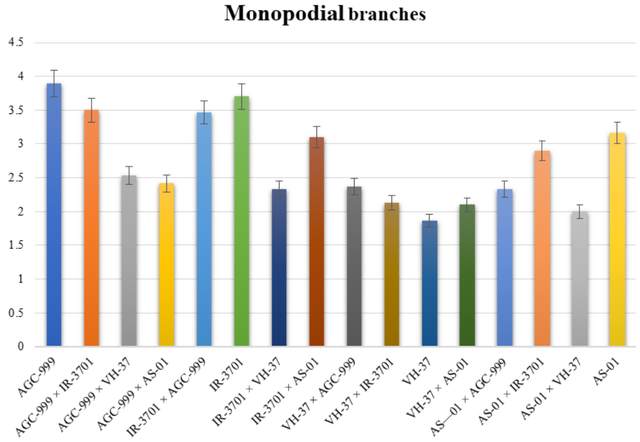

Figure 2. Mean values for monopodial branches

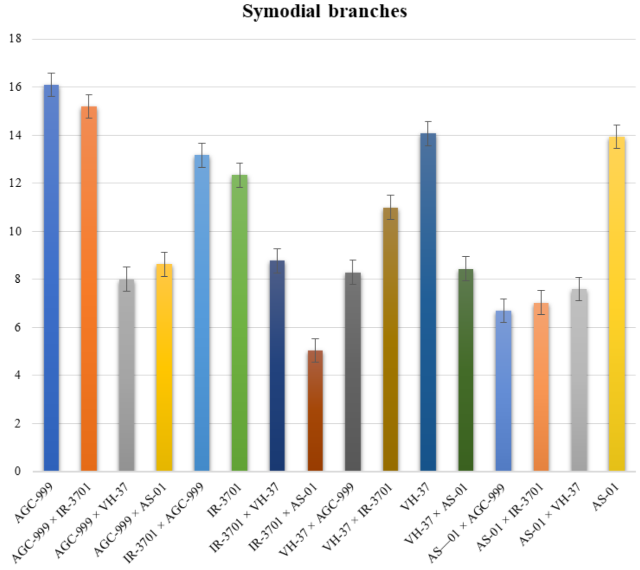

Figure 3. Mean values for sympodial branches

***Total number of nodes*:** Node is a point from which leaves or branches are produced on the plants. Nodes are present on the main stem as well as on the monopodial and sympodial branches. Average of the nodes was calculated and putted in the graph. Graphical data showed that the maximum nodes among parents were on the AS-01 with total nodes 34.33 and minimum nodes were on the VH-37 with total nodes of 32.23. Among crosses, the cross AGC-999 × IR-3701had the more nodes 39.33 and the cross AS-01 × IR-3701 had the minimum nodes 19 among all the genotypes (Figure 4). Similar results were found by (Raania & Zafar, 2009; Baloch *et al*., 2010; Monicashree *et al*., 2017). Analysis of variance showed that genotypes were significant, in this trait (Table 1).

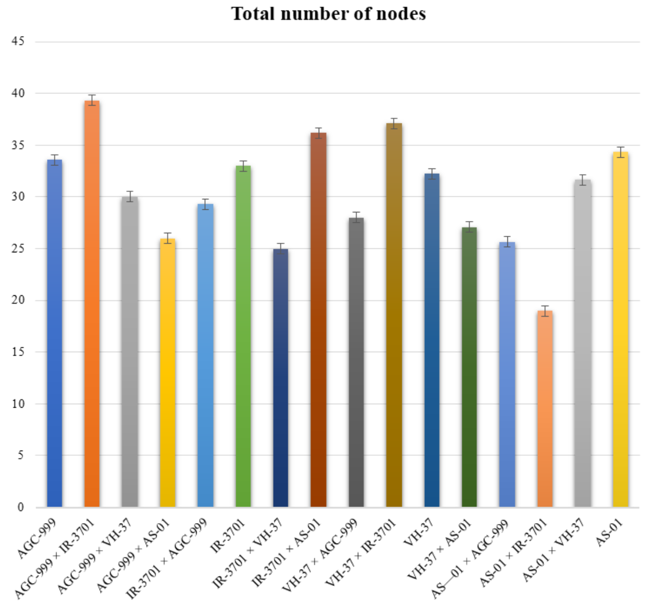

Figure 4. Mean values for the total number of nodes

***Node of first fruiting branch*:**Node of first fruiting branch mean the node from zero node on which the first true fruiting branch exist of a plant or genotype. The mean values were arranged in graph form that showed that among parents' maximum nodes of first fruiting branch was at the genotype VH-37 (16.13) and minimum value represented by IR-37 (12.43). While in the crosses the top position was obtained by the IR-3701 × AS-01 (16.33) and at lower position was IR-3701 × AGC-999 (5) (Figure 5). Similar results were found by (Kouser *et al*., 2019; Makhdoom *et al*., 2019).

Data of this trait was subjected to the analysis and analysis of variance showed that replications were significant, but genotypes were highly significant. Significant replications said that blocking is necessary to control the soil fertility level and genotypes had wide differences among them (Table 1).

***Number of bolls per plant*:**Opened bolls were calculated and subjected to the analysis. Analysis of variance revealed that genotypes were significant. Genotypes had different means in this research for the number of bolls per plant (Table 1).

The mean data of the parents and crosses is presented in the graph 4.6.1. This indicated that the maximum number of bolls among the parents was for the AS-01, 19.33 bolls per plant and minimum value was for the VH-37 keeping the 14.73 bolls of each plant. In the crosses, cross IR-3701 × AS-01 had the more bolls (14) as compared to other crosses and the cross AGC-999 × VH-37 had the lowest bolls among crosses (Figure 6). Similar results were found by (Razzaq *et al*., 2020; Rani *et al*., 2020; Rauf *et al*., 2006).

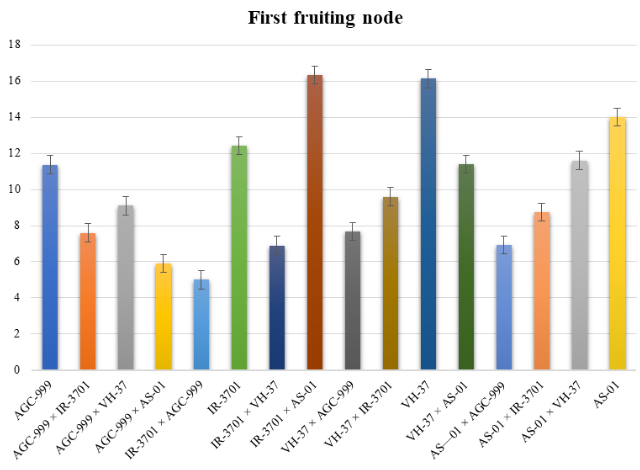

Figure 5. Mean values for the first fruiting node.

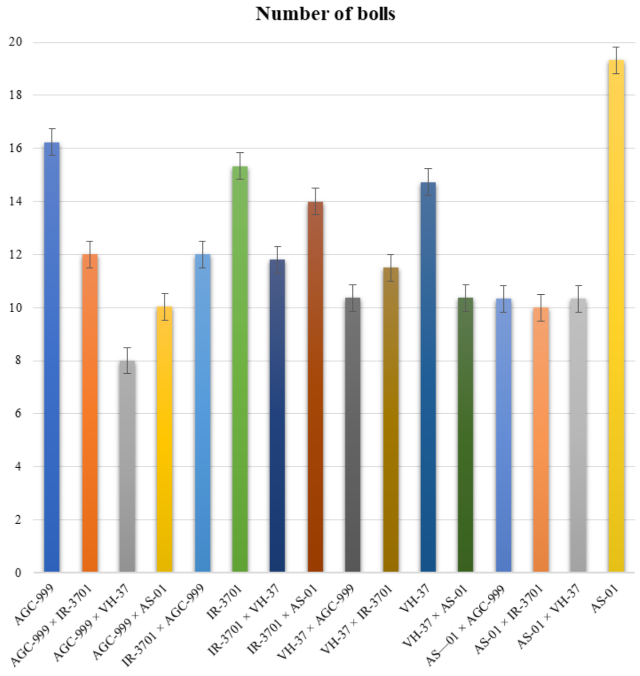

Figure 6. Mean values for number of bolls

Seed cotton yield: Total yield is the main and important factor for any crop but in cotton seed cotton yield is desired by the cotton industries or all other linked departments. So, it the main focused trait by breeder that how to improve the yield that's why data was analyzed. Analysis of variance showed that genotypes were highly significant for seed cotton yield. Its mean that great genetic variability was present in the genotypes that is utmost required to run any breeding scheme (Table 1).

Mean data of all the genotypes is compared in the graph that indicated that the parent AS-01 provided the maximum yield (93.73 grams) among the parents while AGC-999 × IR-3701 had the maximum yield (82 grams) among the crosses. While VH-37, VH-37 × AS-01 and AS—01 × AGC-999 had the minimum value among parents and crosses respectively (Figure 7). Similar results were found by (Said *et al*., 2019; Majeedano *et al*., 2014; Mudhalvan *et al*., 2021).

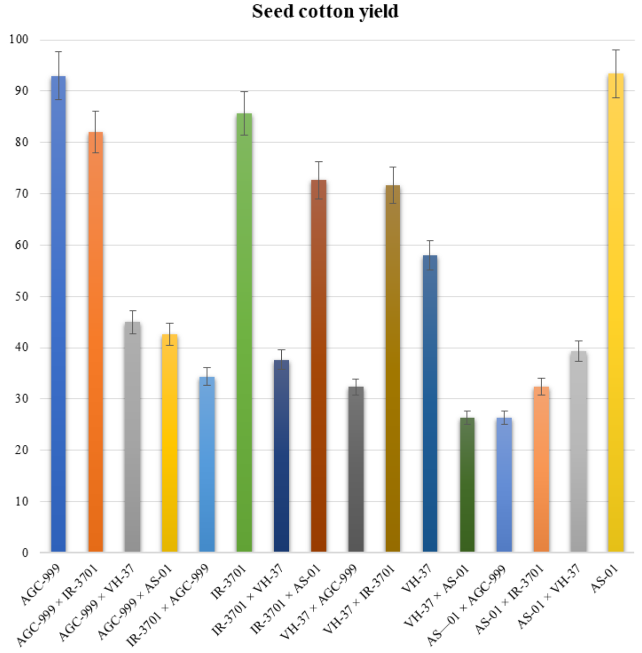

Figure 7. Mean values for the seed cotton yield

Boll weight: Seed cotton yield is directly related to boll weight. More boll weight more will be yield. The maximum boll weight was obtained by the AS-01 (4.1 gm) and lower value parent was VH-37 (3.1 gm). In the crosses IR-3701 × AS-01 had the maximum boll weight (4.22 gm) and AGC-999 × VH-37 had lower value boll weight (2.8) among crosses as well as in the total genotypes (Figure 8). Similar results were found by (Muhammad Mubashar Zafar, *et al*., 2022; Majeedano *et al*., 2014). Analysis of variance showed that genotypes were highly significant (Table 1).

G.O.T. (Ginning out turn): Percentage of lint is known as the ginning out turn that's mean when a sample of seed cotton is ginned then weight of the lint is calculated in percentage. In this research the maximum G.O.T. was obtained by the AS-01 (39.66 %) and minimum G.O.T. was gained by the IR-3701 (37%). In the crosses the maximum lint percentage was gained by the AGC-999 × AS-01 (38.15 %) and minimum value was for the VH-37 × AGC-999 (27.67 %) (Figure 9). Similar results were found by (Muhammad Mubashar Zafar *et al*., 2022; Khokhar *et al*., 2017).

Analysis of variance showed that genotypes were significant, having the differences in their mean values but replications were nonsignificant. In this regard replications had no effect in the variability of genotypes all of the variation was due to genetics and environment had negligible share (Table 1).

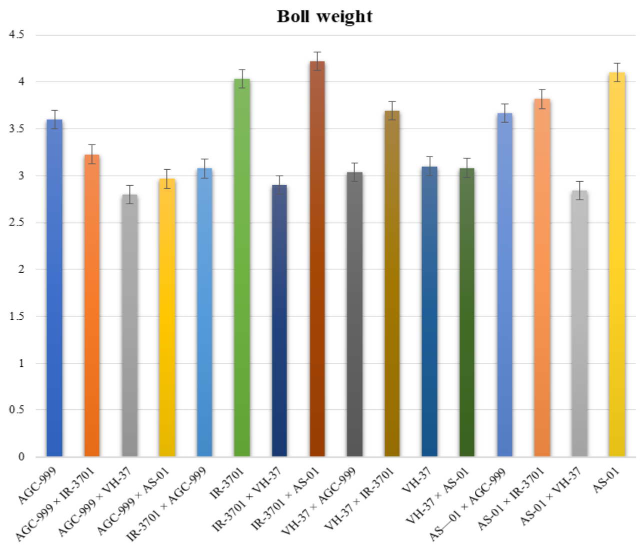

Figure 8. Mean values for boll weight

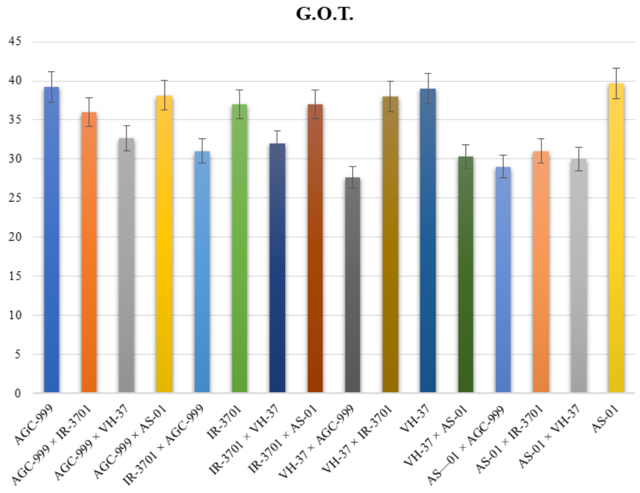

Figure 9. Mean values for the G. O. T.

Seed index**:** It is the 100 seed wight of a sample. 100 seeds were randomly selected, weighted and average of them was represented in the graphical form. The highest weight in the parents was obtained by the AGC-999 (4.99 gm) and lower value was obtained by the IR-3701 (4.87 gm). Similarly in the crosses the highest value for seed index got two crosses AGC-999 × VH-37 and IR-3701 × AS-01 the same value (5.09 gm) (Fig. 10). Similar results were found by (Muhammad Mohsin Zafar *et al*., 2022; Khan *et al*., 2009; Khokhar *et al*., 2017). Analysis of variance showed that genotypes were highly significant, having the differences in their mean values but replications were non-significant. Replications had no effect in the variability of genotypes all of the variation was due to genetics and environment had negligible effect (Table 1).

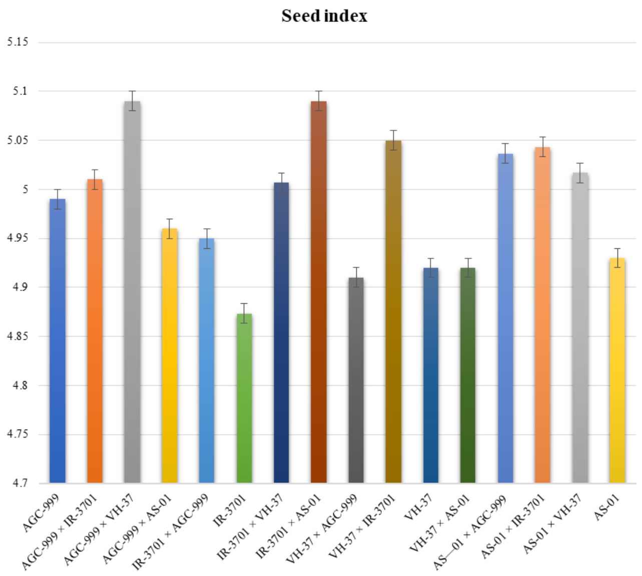

Figure 10. Mean values for the seed index

Lint index**:** Lint index plays a vital role in the selection of good varieties for the textile mills. More of the greater value for lint index then more will be the fine variety to be used in the fabrics of high quality. In this research the highest value was obtained by the parent AGC-999 (9 gm) and lower value in parent was gone to VH-37 (6.4 gm) but in crosses maximum value was gained by the IR-3701 × AGC-999 (5.37 gm) and minimum value was obtained by the AS-01 × IR-3701 (2.06 gm), performed very poor in regards of lint index (Figure 11). Similar results were found by (Manan *et al*., 2022; Hosseini, 2014; Kumar *et al*., 2014).

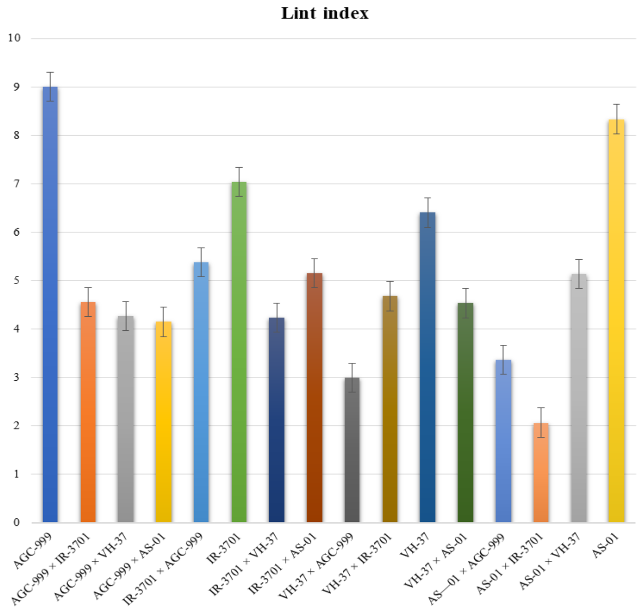

Figure 11. Mean values for the lint index

Data of the lint index was subjected to the analysis and analysis of variance showed that genotypes were highly significant. This means that variation in the genotypes were also due to environment although genotypes had their own genetic variability (Table 1).

***Conclusion*:** The results of this study showed that AS-01 had the maximum yield among the parents while AGC-999 × IR-3701 had the maximum yield among the crosses. AS-01 Parent and the cross combination AGC-999 × IR-3701 can be used for further breeding programs to boost up the yield potential of future genotypes.

***Authors' contributions*:** Muhammad Naveed performed this research. Tariq Manzoor Khan supervised this research. Remaining authors equally contribute in formatting, editing, revision and proof reading of this article

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