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ESTIMATION OF YIELD STABILITY AND VARIETAL SCREENING IN COTTON-SOYBEAN INTERCROPPING SYSTEM

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ABSTRACT

Compared to growing them separately as sole crops, intercropping cotton and soybeans can increase yield stability, profitability, and productivity. On the stability of yields in cotton-soybean intercropping systems, however, there is less data. The intention behind this The goal of the study is to assess crop output and identify the best genotype pairings for intercropping between soybeans and cotton. Two distinct genotypes of cotton and two genotypes of soybeans were used in field experiments utilizing a split-plot design under RCBD with three replications, in both solo and intercropping patterns. Plant height (cm), the number of nodes per plant, the number of monopodial branches, the hundred seed weight (g), the seed weight (g) per plant, the g of seed cotton yield (per plant), and the number of cotton sympodial branches were recorded. Plant height (cm), number of pods per plant, fresh and dry plant weight (g), leaf area (cm2), number of seeds per pod, and hundred seed weight (g) are the characteristics that were determined for soybeans. Treatment changes were quantified using ANOVA, and associations between disparate features were found using correlation analysis. The study found significant differences in key traits between soybean and cotton genotypes and treatments at D.G. Khan. SCYPP positively correlated with BoPP, NON, PH, and SWP in cotton, while YPP significantly correlated with HSW, PH, DPW, and NPP in soybean. MNH-1020 and NARC-21 were recommended for maximum yield under intercropping. The results will be useful in formulating suggestions for the ideal crop spacing and variety matching when intercropping soybeans and cotton.

INTRODUCTION

Intercropping is considered as traditional agriculture technique in which two or more crops are cultivated in parallel, so they coexist and interact with the agro-ecosystem for eloquent portion of life cycle. These promising strategies used to increase agriculture productivity and yield (Maitra and Gitari, 2020). Various positive results of intercropping have been reported. The following are the main advantages of the intercropping: The main reason of using intercropping all over world, that it produced yield more than pure cropping on the same land. It is reported that wheat and beans intercrops had been more than pure cropping (Ghanbari-Bonjar and Lee, 2002). In intercropping system, production increases due to increase in growth rate while decrease in weeds, pests, diseases as well as more efficiently use of resources (Eskandari, 2012a). The main advantages of intercropping in comparison to pure cropping are because of its interaction between components and environmental resources. When the components of an intercrop consume disparate natural resources from one another in a complementary way, compared to a pure cropping, the efficiency of resource usage increases, leading to an enhanced yield (Mahapatra, 2010). As farmers have limited resources so it is very important to stable income and yield of agriculture systems. If multiple crops are cultivated together and fail to yield a product, then other crop may be able to produce it which lowers the risk of loss. Therefore, in case of multiple cropping, risk of agronomy failure is less than pure cropping (Eskandari *et al.*, 2009). Given the rising input costs associated with cotton cultivation, which reduce profits, it is one of the promising ways to increase crop yield and profitability per unit of cultivated area. Therefore, research into combining cotton cultivation with other crops that yield higher returns is necessary. According to Nyawade et al. (2020), intercropping improves soil quality by reducing crop failure risk and climate variability, enhancing biodiversity, and guaranteeing more efficient use of resources. The intercropping system's viability or failure is dependent on some companion crop considerations, making their choice crucial. These include factors about each companion crop's plant tent's geometry and planting timing, the maturity of the Intercropping crops and the yield from the intercropping system (Maitra *et al.*, 2020). Gossypium hirsutum L., commonly known as cotton, is a vital industrial crop that is a member of the Malvasia family. This crop serves two purposes: it is cultivated for oil and fiber, which are obtained from rose cotton, the primary raw material used to manufacture cotton textiles to meet industry demands. Millions of families are employed in both the cultivation and manufacturing stages of this industry (Iftikhar H. Bhatti et al., 2013). Because its seeds have a high percentage of oil, the soybean, Glycine max L., a member of the legume family Fabaceae, is one of the major leguminous crops grown worldwide and has eloquent economic value, where the seeds' protein content ranges from 30 to 50% and their percentage is between 14 and 24 percent. By fixing atmospheric nitrogen through the soil's root nodes and giving the plant food and other requirements for growth, its cultivation enhances the soil's qualities and increases its fertility. Additionally, the crop's competition with easily decomposable biomass added to the soil (Dwivedi *et al.,* 2015) demonstrated how intercropping helps to maintain the soil, fight the jungle, and boost yield.

Materials and Methods

The Following research was conducted at three disparate locations across South Punjab at research sites of MNS University of Agriculture, Multan, National Research Center for Intercropping (NRCI) Islamia University Bahawalpur and Ghazi University, Dera Ghazi Khan. Genotypes were collected from NRCI, IUB and Cotton Research Institute, Multan. These genotypes were grown using split plot design with three treatments and 3 replications for each of cotton and soybean which included Sole Cotton/Sole Soybean Cropping, one row of soybean and one row of cotton on each bed and one cotton plant after one soybean plant in every row. Soil was prepared by 2 ploughings followed by planking and bed formation. DAP and Urea were applied at the rate of 1 bag per acre Both of these crops were sown by dibbling on edges of beds with plant to plant distance kept at 10 cm for soybean and 15 cm for cotton. Pendimethaline was sprayed as pre-emergence weedicide. Irrigation was applied at standard rate. Bayer Oberon and Buprofezon were applied for white fly and bollworms control as per recommended dosages.

List of Genotypes

Sr.No.	**Cotton Genotypes**	**Sr.No.**	**Soybean Genotypes**
1	MNH-1020	1	NARC-21
2	MNH-886	2	NARC-22

Data Collection

Data Collection of Cotton Crop

Data were collected from 5 plants per genotype in each replication and average was calculated for further analysis.

Plant Height (cm)

Plant height was measured in centimeters at maturity using measuring scale from base to the tip of each plant.

Number of Nodes Per Plant

Numbers of nodes per plant were counted at maturity from base to the tip of stem.

Number of Monopodial Branches

Number of Monopodial Branches were counted manually at the maturity of crop.

Number of Bolls Per Plant

Number of bolls per plant were counted at maturity from each and every branches and stem of the plant.

Number of Sympodial Branches

Number of Sympodial branches per plant were counted at the maturity of crop.

Seed Cotton Yield Per Plant (g)

Seed cotton yield per plant was measured using portable electric weight balance (G&G® Electrical Scale JJ224BC) and observation was recorded in grams.

100-Seed Weight (g)

Hundred seed weight was calculated using electric weight balance (G&G® Electrical Scale JJ224BC) and observation was recorded in grams.

Seed Weight Per Plant (g)

Seed weight per plant was calculated by weighing all the seeds obtained from single plant at maturity using an electric weight balance (G&G® Electrical Scale JJ224BC) and observation was recorded in grams.

Data Collection of Soybean Crop

Data were collected from 5 plants per genotype in each replication and average was calculated for further analysis. Plant Height (cm)

Plant height

The plant height at maturity was measured in centimeters from the base to the tip of the stem using a measuring scale.

Fresh Weight of Plant (g)

Fresh weight of plant was calculated by weighing the whole plant using electric weight balance (G&G® Electrical Scale JJ224BC) and observation was recorded in grams.

Dry Weight of Plant (g)

Dry weight of plant was calculated by keeping the plant in dry oven for 24 hours and weighing the whole plant using electric weight balance (G&G® Electrical Scale JJ224BC) and observation was recorded in grams.

Leaf Area (cm^2)

Leaf area was estimated by multiplying the length and width of each leaf.

Number of Pods Per Plant

All pods picked from a plant were tallied independently for each entry in a repetition, and the average of three plants was calculated.

Number of Seeds Per Pod

Three pods from each selected plant were manually threshed and total seeds were counted from each entry in a repeat and average was taken.

100-Seed Weight (g)

Each genotype had 100 seeds counted, and the weight in grams was recorded using a weighing balance (G&G® Electrical Scale JJ224BC).

Yield Per Plant (g)

All seeds from a single plant were weighed in grams as plant yield using a weighing balance (G&G® Electrical Scale JJ224BC), and the average of three plants was calculated.

Statistical Analysis

Data were subjected to ANOVA and Least Eloquent Difference was calculated using Rstudio Software. Principal Component Analysis was computed to evaluate the performance of genotypes at disparate locations using Rstudio Software. Genotypic and Phenotypic Correlation Coefficients were also calculated using Rstudio Software.

Result and Discussion

The results showed significant differences among genotypes for studied traits of both soybean and cotton The study also found significant relationships among BoPP, NON, PH and SWP with SCYPP for cotton. Sahar et al., 2021 also reported significant relationships among NON and PH with SCYPP. While HSW, PH and NPP with

YPP for soybean. Akram et al., 2016 found significant relationships among PH and NPP with YPP. These traits maybe improved for improvement in yield under intercropping. For intercropping at Multan, Soybean will give more productivity while sown in 1RCS pattern while cotton will excel while sown in 1PCS system. MNH-1020 performed better for key yield traits than MNH-886. NARC-21 performed better for key yield traits than NARC-22. So MNH-1020 for cotton and NARC-21 for soybean are recommended to grow at Multan for max. yield under intercropping. At 2nd location (NRCI Bahawalpur), ANOVA revealed significant differences among key traits for genotypes and treatment for both soybean and cotton while the interaction was also significant for cotton. Correlations revealed that SCYPP had eloquent and positive association with BoPP, NON, PH and SWP in cotton. For soybean, YPP had Eloquent and significant relation with HSW, PH and NPP. These traits maybe improved for improvement in yield under intercropping. For intercropping at Bahawalpur, Soybean will give more productivity while sown in 1RCS pattern while cotton will excel while sown in 1PCS system. MNH-1020 performed better for key yield traits than MNH-886. NARC-21 performed better for key yield traits than NARC-22. So MNH-1020 for cotton and NARC-21 for soybean are recommended to grow at Bahawalpur for max. yield under intercropping. ANOVA showed significant differences among key traits for genotypes for soybean and genotypes and treatments for cotton while the interaction was also significant for cotton and soybean at D.G. Khan. Correlations revealed that SCYPP had eloquent and positive association with BoPP, NON, PH and SWP in cotton. For soybean, YPP had Eloquent and significant relation with HSW, PH, DPW and NPP. These traits maybe improved for improvement in yield under intercropping. For intercropping at Bahawalpur, Soybean will give more productivity while sown in 1RCS pattern while cotton will excel while sown in 1PCS system. MNH-1020 performed better for key yield traits than MNH-886. NARC-21 performed better for key yield traits than NARC-22. So MNH-1020 for cotton and NARC-21 for soybean are recommended to grow at D.G. Khan for max. yield under intercropping. Principal Component Analysis (PCA) provides valuable insights into the correlations between several samples (MNH-886, MNH-1020, and MNH-102) from three regions: Bahawalpur, DG Khan, and Multan. The first two principal components (PC1 and PC2) account for 75% of total variation in the data, thereby reducing the multidimensional dataset to two dimensions. The samples from DG Khan (green) are distributed along the negative side of PC1 and PC2, indicating that this group is impacted by distinct variables than the other groups. DG Khan's samples, in particular, are strongly related with variables such as HS and SB, implying that these characteristics play an important role in characterizing this population. In contrast, samples from Bahawalpur (red) are positioned more favorably along PC1 and PC2, showing that factors such as BoPP, PH, and NON have a greater impact on these samples. Based on these data, it seems that the Bahawalpur group differs from the DG Khan group. Multan's samples (blue) are closer to the center of the biplot, indicating a more equal contribution from the factors; yet, they are strongly related with SCYPP and SWP. This central placement suggests that, while Multan's samples have some similarities with Bahawalpur and DG Khan, they also have distinct features influenced by these specific factors. Overall, the PCA biplot demonstrates that, while there is some overlap across the groups, there are significant differences, notably in the variables linked with PC1 and PC2. This difference demonstrates how particular factors are more significant in certain locations, resulting in clustering of samples from the same region and an obvious separation between them. This Principal Component Analysis (PCA) for Soybean depicts the associations between variables and groups using the first two principal components (PC1 and PC2), which together account for 82.8% of the total variance (56.7% for PC1 and 26.1% for PC2). The graphic shows ellipses representing distinct groups—Bahawalpur (red), DG Khan (green), and Multan (blue), demonstrating how samples cluster depending on these components. The arrows (vectors) labeled PH, FBW, HSW, SPP, PPP, and LA represent each variable's contribution to the components, with SPP and LA substantially correlated with PC1 and FBW with PC2. In contrast, PH and HSW have a negative connection with PC2. Variables with same direction and closeness are positively correlated, and samples near vectors are more connected with those variables. For example, Bahawalpur is more related with FBW and SPP, but Multan is more connected with LA. The groups' distinct locations indicate distinctions recorded by the main components, emphasizing the variety in samples from Bahawalpur, DG Khan, and Multan.

Correlation coefficients for various traits among cotton genotypes at Multan

Results for correlation coefficients are presented in table 7. These results show that PH had positive and eloquent association with BoPP, number of nodes, SCYPP and SWP. PH had positive and non-eloquent association with MB and negative and non-eloquent association with SB and HSW. NON exhibited positive and eloquent association with BoPP, PH, SCYPP and SWP. Similar findings were also reported by Joshi et al. (2006) and Gnanasekaran et al., 2020. It had positive and non-eloquent association with MB and negative and non-eloquent association with SB and HSW. MB had positive and eloquent association with HSW and positive and non-eloquent association with number of nodes, plant height, SB and SWP. It had negative and non-eloquent association with BoPP and seed cotton YPP. BoPP had positive and eloquent association with number of nodes, PH, SCYPP and SWP. It had negative and non-eloquent association with MB, HSW and SB. SB exhibited positive and non-eloquent association with HSW, MB and SWP while negative and non-eloquent association with BoPP, number of nodes, PH and seed cotton YPP. SCYPP had positive and eloquent association with BoPP, number of nodes, PH and SWP. It has negative and non-eloquent association with SB, MB and HSW. HSW exhibited positive and eloquent association with MB while positive and non-eloquent association with SB and SWP however negative and non-eloquent association was observed with BoPP, number of nodes, PH and seed cotton YPP. SWP had positive and eloquent association with BoPP, number of nodes, PH and seed cotton YPP. It had positive and non-eloquent association with HSW, MB and SB. Similar results were reported by Sakthi et al. (2007) and Rao and Gopinath (2013). The positive and eloquent correlation of BoPP, number of nodes, PH and SCYPP indicates that the yield in intercropping of cotton with soybean can be enhanced by improving these traits in upcoming new cultivars.

Correlation coefficients for various traits among soybean genotypes at Multan

Table 8 expresses the correlation coefficients for soybean. Results show that PH posed positive and eloquent relationship with NPP, FPW, HSW and YPP. It posed positive and non-eloquent relationship with DPW and SPP. FPW had positive and eloquent relationship with DPW and PH while positive and non-eloquent with rest ones except SPP with negative and non-eloquent relation. DPW posed positive and eloquent relationship with FPW. It posed positive and non-eloquent relationship with left ones except SPP that had negative and non-eloquent association. LA posed positive and non-eloquent relationship with PH, FPW and DPW. It had negative and eloquent relationship with HSW and NPP while non-eloquent with SPP and YPP. NPP posed positive and eloquent relationship with PH, HSW and YPP and positive and non-eloquent with FPW, DPW. It had negative and eloquent relationship with LA while non-eloquent with SPP. SPP posed positive and non-eloquent relationship with PH and HSW while negative and non-eloquent with all others. HSW posed positive and eloquent relationship with PH, NPP and YPP and negative and eloquent with LA. It had positive and non-eloquent relationship with FPW and SPP. YPP posed positive and eloquent relation with PH, HSW and NPP. It had positive and non-eloquent relationship with DPW and FPW and negative and non-eloquent with LA and SPP. Positive and eloquent correlation of these traits indicates that the yield in intercropping of cotton with soybean can be enhanced by improving these traits in upcoming new cultivars

Correlation coefficients for various traits among cotton genotypes at NRCI Bahawalpur

Results for correlation coefficients are presented in table 9. PH exhibited positive and eloquent interrelationship with BoPP, NON, SCYPP and SWP while positive and non-eloquent association was observed with MB. It had negative and non-eloquent association with SB and HSW. NON had positive and eloquent association with BoPP, PH, SCYPP and SWP and positive and non-eloquent association was observed with MB. Similar results were reported by Rao and Gopinath (2013). It showed negative and non-eloquent association with SB and HSW. MB had positive and eloquent association with HSW while positive and non-eloquent association was observed for number of nodes, PH, SB and SWP. It also showed negative and non-eloquent association with BoPP and seed cotton YPP. BoPP expressed positive and eloquent association with PH, number of nodes, SCYPP and SWP. It posed negative and non-eloquent association with SB, MB and HSW. SB posed positive and eloquent association with SCYPP and SWP. It had positive and non-eloquent association with MB and HSW while negative and non-eloquent with PH, number of nodes and BoPP. SCYPP posed positive and eloquent association with PH, number of nodes, BoPP and SWP. It posed negative and non-eloquent association with MB, SB and HSW. HSW posed positive and eloquent relationship with MB and SB and SWP were positively but non-eloquently related. It also posed negative relationship with seed cotton YPP, PH, number of nodes and BoPP. SWP posed positive and eloquent association with PH, number of nodes, BoPP and seed cotton YPP. It had positive but non-eloquent relationship with SB, MB and HSW. Similar findings were also reported by Joshi et al. (2006) and Sakthi et al. (2007). Positive and eloquent correlation of these traits indicates that the yield in intercropping of cotton with soybean can be enhanced by improving these traits in upcoming new cultivars.

Correlation coefficients for various traits among soybean genotypes at NRCI Bahawalpur

Table 10 expresses the correlation coefficients for soybean. Results show that PH posed positive and eloquent relationship with NPP, HSW and YPP. It posed positive and non-eloquent relationship with FPW, DPW, and LA however negative and non-eloquent with SPP. FPW had positive and eloquent relationship with DPW and positive and non-eloquent with rest ones. DPW posed positive and eloquent relationship with FPW and YPP. It posed positive and non-eloquent relationship with left ones except SPP that had negative and non-eloquent association. LA posed positive and non-eloquent relationship with PH, FPW and DPW. It had negative and eloquent relationship with HSW and non-eloquent with NPP, SPP and YPP. NPP posed positive and eloquent relationship with PH, HSW and YPP and positive and non-eloquent with FPW, DPW and SPP. It had negative and non-eloquent relationship with LA. SPP posed positive and non-eloquent relationship with FPW, NPP and HSW while negative and non-eloquent with PH, DPW, LA and YPP. HSW posed positive and eloquent relationship with PH, NPP and YPP and negative and eloquent with LA. It had positive and non-eloquent relationship with FPW and DPW but negative and non-eloquent with SPP. YPP posed positive and eloquent relation with PH, HSW and NPP. It had positive and non-eloquent relationship with DPW and FPW and negative and non-eloquent with LA and SPP. Positive and eloquent correlation of these traits indicates that the yield in intercropping of cotton with soybean can be enhanced by improving these traits in upcoming new cultivars.

Correlation coefficients for various traits among cotton genotypes at Dera Ghazi Khan

Results for correlation coefficients are shown in table 11. PH posed positive and eloquent relationship with number of nodes, BoPP, SCYPP and SWP while positive and eloquent with MB. It also posed negative and non-eloquent relationship with SB and HSW. Number of nodes posed positive and eloquent relationship with PH, BoPP, SCYPP and SWP. Similar results were reported by Sakthi et al. (2007).It had positive and non-eloquent relationship with MB while SB and HSW posed negative and non-eloquent relationship. MB posed positive and eloquent association with HSW and positive and non-eloquent relationship with PH, number of nodes, SB and SWP. It also posed negative and non-eloquent relationship with

SCYPP and BoPP. BoPP posed positive and eloquent relationship with number of nodes, PH, seed cotton YPP and SWP. Negative and non-eloquent relationship was found in SB, MB and HSW. SB posed positive and non-eloquent relationship with HSW, MB and SWP while it had negative and non-eloquent relationship with PH, number of nodes, SCYPP and BoPP. SCYPP expressed positive and eloquent relationship with PH, number of nodes, BoPP and SWP. It posed negative and non-eloquent association with SB, MB and HSW. HSW posed positive and eloquent relationship with MB and positive and non-eloquent relationship with SB and SWP. PH, NON, BoPP and SCYPP had negative and non-eloquent relationship with HSW. SWP posed positive and eloquent relationship with PH, number of nodes, BoPP and SCYPP and positive and non-eloquent relation with SB and MB and HSW. Positive and eloquent correlation of these traits indicates that the yield in intercropping of cotton with soybean can be enhanced by improving these traits in upcoming new cultivars.

Correlation coefficients for various traits among soybean genotypes at Dera Ghazi Khan

Table 12 expresses the correlation coefficients for soybean. Results show that PH posed positive and eloquent relationship with NPP, HSW and YPP. It posed positive and non-eloquent relationship with FPW, DPW, and LA however negative and non-eloquent with SPP. FPW had positive and eloquent relationship with DPW and positive and non-eloquent with rest ones. DPW posed positive and eloquent relationship with FPW and YPP. It posed positive and non-eloquent relationship with left ones. LA posed positive and non-eloquent relationship with PH, FPW, DPW and SPP. It had negative and eloquent relationship with HSW and non-eloquent with NPP and YPP. NPP posed positive and eloquent relationship with PH, HSW and YPP and positive and non-eloquent with FPW and DPW. It had negative and non-eloquent relationship with LA and SPP. SPP posed positive and non-eloquent relationship with FPW, DPW, LA and YPP while negative and non-eloquent with PH, NPP and HSW. HSW posed positive and eloquent relationship with PH, NPP and YPP and negative and eloquent with LA. It had positive and non-eloquent relationship with FPW and DPW but negative and non-eloquent with SPP. YPP posed positive and eloquent relation with PH, DPW, HSW and NPP. It had positive and non-eloquent relationship with SPP and FPW and negative and non-eloquent with LA. Positive and eloquent correlation of these traits indicates that the yield in intercropping of cotton with soybean can be enhanced by improving these traits in breeding programs to elevate those new and upcoming cultivars. These findings suggest that selecting for higher seed weight, taller plants, and more pods per plant could be beneficial strategies for improving soybean while BoPP, NON, SWP and PH maybe improved for improving cotton yield.

SOV	DF	Mean Squares							
		PH	NON	MB	BoPP	SB	SCYPP	HSW	SWP
Block	2	20.6	4.667	0.01427	25.53	22.320	15.185	4.5833	30.76
Genotype	2	374.4*	90.167*	0.46220	316.93	35.600*	15.006	12.1277	407.16**
Error Block*Genotype	4	32.9	10.833	0.13388	116.68	4.372	43.487	3.3857	13.29
Treatment	1	45.4	2.722	0.39161	170.16*	190.971*	255.96**	28.0051**	4.54
Genotype*Treatment	2	3508.3*	132.389*	0.11689	709.93**	4.147	78.67**	23.0419**	133.80
Error	6	552.5	23.667	0.07279	23.36	22.771	3.797	0.3687	35.28

SOV	DF	Mean Squares							
		PH	NON	MB	BoPP	SB	SCYPP	HSW	SWP
Block	2	17.06	4.667	0.01762	17.73	18.447	18.746	3.1828	48.07

Table 1. ANOVA for traits in Cotton genotypes at Multan

Table 2. ANOVA for traits in Soybean genotypes at Multan

SOV	DF	Mean Squares							
		PH	FPW	DPW	LA	NPP	SPP	HSW	YPP
Block	2	2.056	216.1	123.50	5.167	186.17	0.100	3.72	4.66
Genotype	2	196.722	4364.1*	841.17**	108.667**	892.67**	0.010	32.88*	216.16
Error Block*Genotype	4	30.556	533.4	36.17	4.083	35.08	0.165	1.97	1.33
Treatment	1	76.056*	14.2	12.50	56.889**	0.22	0.008	1.38	0.50
Genotype*Treatment	2	6.056	1259.4**	120.50	14.889	20.22	0.003	0.22	23.16
Error	6	9.056	97.8	118.17	3.889	60.22	0.023	3.11	4.44

Table 3. ANOVA for traits in Cotton genotypes at Bahawalpur

Genotype	2	309.39*	90.167	0.57062	220.09	29.422	18.526	8.4220	636.19
Error Block*Genotype	4	27.22	10.833	0.16528	81.03	3.613	53.688	2.3512	20.77
Treatment	1	37.56*	2.722	0.48347	118.17	157.827	316.010	19.4480	7.09
Genotype*Treatment	2	2899.39*	132.389	0.14431	493.01	3.427	97.126	16.0013	209.06
Error	6	456.61	23.667	0.08986	16.22	18.819	4.688	0.2561	55.12

Table 4. ANOVA for traits in Soybean genotypes at Bahawalpur

SOV	**DF**	Mean Squares							
		PH	**FPW**	**DPW**	**LA**	**NPP**	**SPP**	**HSW**	**YPP**
Block	2	2.667	72.2	134.72	7.389	222.72	0.039	4.667	8.667
Genotype	2	181.167*	4405.6*	1176.39**	115.38**	1114.39**	0.006	35.167*	258.66**
Error Block*Genotype	4	24.583	447.2	34.72	3.556	27.31	0.070	2.083	3.083
Treatment	1	88.889*	22.2	5.56	80.22**	3.56	0.224	0.889	2.000
Genotype*Treatment	2	7.389	1705.6**	234.72	19.056	41.06	0.015	0.389	28.667*
Error	6	11.722	144.4	137.50	4.944	41.89	0.067	3.389	2.944

Table 5. ANOVA for traits in Cotton genotypes at DG Khan

SOV	**DF**	**Mean Squares**							
		PH	**NON**	**MB**	**BoPP**	**SB**	**SCYPP**	**HSW**	**SWP**
Block	2	24.6	4.667	0.011	29.96	26.563	11.998	5.379	23.553
Genotype	2	445.5*	90.167*	0.365	371.95	42.367*	11.857	14.233	311.73**
Error Block*Genotype	4	39.2	10.833	0.105	136.94	5.203	34.360	3.973	10.176
Treatment	1	54.1	2.722	0.309	199.71*	227.271*	202.24**	32.86**	3.476
Genotype*Treatment	2	4175.1*	132.389*	0.092	833.19**	4.935	62.16**	27.04**	102.440
Error	6	657.5	23.667	0.057	27.42	27.099	3.000	0.433	27.011

Table 6. ANOVA for traits in Soybean genotypes at DG Khan

SOV	**DF**	**Mean Squares**							
		PH	**FPW**	**DPW**	**LA**	**NPP**	**SPP**	**HSW**	**YPP**
Block	2	2.056	87.5	134.72	7.389	230.22	0.240	4.667	7.722
Genotype	2	207.389*	4116.7*	1068.06**	115.38**	1109.39**	0.015	35.167*	236.05**
Error Block*Genotype	4	25.889	429.2	43.06	3.556	40.22	0.025	2.083	1.056

Treatment	1	98.000*	5.6	5.56	80.22**	0.50	0.001	0.889	0.889
Genotype*Treatment	2	5.167	1605.6**	184.72	19.056	32.17	0.168	0.389	14.38*
Error	6	13.278	143.1	112.50	4.944	39.11	0.159	3.389	1.722

Table 7. Correlation Coefficients for various traits among Cotton genotypes at Multan

	BoPP	HSW	MB	NON	PH	SB	SCYPP
HSW	-0.2944						
MB	-0.2244	0.7493**					
NON	0.8372**	-0.0966	0.0999				
PH	0.7524**	-0.0926	0.1111	0.9055**			
SB	-0.0716	0.3262	0.1895	-0.0476	-0.1450		
SCYPP	0.7912**	-0.3966	-0.3073	0.5870*	0.5096*	-0.4491	
SWP	0.7275**	0.1942	0.2188	0.7903**	0.6261**	0.0785	0.4621*

* *= Eloquent at 0.01 probability level *= Eloquent at 0.05 probability level

PH= Plant height, SB= Sympodial Branches, NON= Number of Nodes, MB= Monopodial Branches, HSW= Hundred Seed Weight, SCYPP= Seed Cotton Yield Per Plant, SWP= Seed Weight per Plant

Table 8. Correlation Coefficients for various traits among Soybean genotypes at Multan

	HSW	PH	DPW	FPW	LA	NPP	SPP
PH	0.5360*						
DPW	0.1917	0.3917					
FPW	0.2872	0.4644*	0.8773**				
LA	-0.5484*	0.0392	0.3144	0.2864			
NPP	0.6587**	0.5885*	0.1428	0.2457	-0.514*		
SPP	0.0173	0.0528	-0.1243	-0.3212	-0.0468	-0.0452	
YPP	0.6863**	0.6850**	0.3027	0.3526	-0.3914	0.7592**	-0.1487

* *= Eloquent at 0.01 probability level *= Eloquent at 0.05 probability level

PH= Plant height, DPW= Dry Plant Weight, FPW= Fresh Plant Weight, LA= Leaf Area, NPP= Number of Pods Per Plant, SPP= Seeds Per Pod, YPP= Yield Per Plant

Table 9. Correlation Coefficients for various traits among Cotton genotypes at NRCI BahawalPur

	BoPP	HSW	MB	NON	PH	SB	SCYPP
HSW	-0.2944						
MB	-0.2244	0.7493**					
NON	0.8372**	-0.0966	0.0999				
PH	0.7524**	-0.0926	0.1111	0.9055**			
SB	-0.0716	0.3262	0.1895	-0.0476	-0.1450		
SCYPP	0.7912**	-0.3966	-0.3073	0.5870*	0.5096*	-0.4491	
SWP	0.7275**	0.1942	0.2188	0.7903**	0.6261**	0.0785	0.4621*

* *= Eloquent at 0.01 probability level *= Eloquent at 0.05 probability level

PH= Plant height, SB= Sympodial Branches, NON= Number of Nodes, MB= Monopodial Branches, HSW= Hundred Seed Weight, SCYPP= Seed Cotton Yield Per Plant, SWP= Seed Weight per Plant

Table 10. Correlation Coefficients for various traits among Soybean genotypes at NRCI BahawalPur

	HSW	PH	DPW	FPW	LA	NPP	SPP
PH	0.5578*						
DPW	0.1770	0.3246					
FPW	0.2358	0.3105	0.8927**				
LA	-0.4706*	0.0672	0.3454	0.3921			
NPP	0.7618**	0.6711**	0.2311	0.2269	-0.4405		
SPP	0.0938	-0.3395	-0.0353	0.0061	-0.2447	0.1208	
YPP	0.7214**	0.7121**	0.3109	0.2807	-0.2696	0.7854**	-0.1572

* *= Eloquent at 0.01 probability level *= Eloquent at 0.05 probability level

PH= Plant height, DPW= Dry Plant Weight, FPW= Fresh Plant Weight, LA= Leaf Area, NPP= Number of Pods Per Plant, SPP= Seeds Per Pod, YPP= Yield Per Plant

Table 11. Correlation Coefficients for various traits among Cotton genotypes at Dera Ghazi Khan

	BoPP	HSW	MB	NON	PH	SB	SCYPP
HSW	-0.2944						
MB	-0.2244	0.7493**					
NON	0.8372**	-0.0966	0.0999				
PH	0.7524**	-0.0926	0.1111	0.9055**			
SB	-0.0716	0.3262	0.1895	-0.0476	-0.1450		
SCYPP	0.7912**	-0.3966	-0.3073	0.5870*	0.5096*	-0.4491	
SWP	0.7275**	0.1942	0.2188	0.7903**	0.6261**	0.0785	0.4621*

* *= Eloquent at 0.01 probability level *= Eloquent at 0.05 probability level

PH= Plant height, SB= Sympodial Branches, NON= Number of Nodes, MB= Monopodial Branches, HSW= Hundred Seed Weight, SCYPP= Seed Cotton Yield Per Plant, SWP= Seed Weight per Plant

Table 12. Correlation Coefficients for various traits among Soybean genotypes at Dera Ghazi Khan

	HSW	PH	DPW	FPW	LA	NPP	SPP
PH	0.5640**						
DPW	0.2902	0.3980					
FPW	0.2400	0.3353	0.8952**				
LA	-0.4706*	0.0760	0.2654	0.3865			
NPP	0.7567**	0.6708**	0.3276	0.2059	-0.4485		
SPP	-0.2806	-0.2266	0.0794	0.2520	0.2943	-0.2135	
YPP	0.7415**	0.7254**	0.4556*	0.3603	-0.2496	0.7805**	0.0035

* *= Eloquent at 0.01 probability level *= Eloquent at 0.05 probability level

PH= Plant height, DPW= Dry Plant Weight, FPW= Fresh Plant Weight, LA= Leaf Area, NPP= Number of Pods Per Plant, SPP= Seeds Per Pod, YPP= Yield Per Plant

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