Original Article

J Genet Appl Biotechnol, 2026: *e2026020*
DOI: https://doi.org/10.66432/kdf4sr93
Received: 23 Oct 2025; Revised: 10 Jan 2026; Accepted: 18 Jan 2026; Published online: 28 Feb 2026

Correlation analysis of several economic traits of upland cotton (*Gossypium hirsutum* L.)

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Abstract

Cotton is a leading natural source of textile fiber. It is highly susceptible to biotic & abiotic stresses, which decreases cotton production every year. The purpose of this research is to assess the correlation among yield related characters and fibre traits, that help in preliminary selection of desirable characters and genetically diverse parental line for future breeding of cotton. Eighteen varieties of upland cotton were cultivated in RCBD in three repetitions in fields of Plant Breeding and Genetics, University of Agriculture Faisalabad. Data was recorded for several agronomic traits of upland cotton. i.e. Bolls per plant, height of the plant, sympodial branches, seeds per boll, monopodial branches, 100 seed weight, boll weight, strength of fiber (g/tex), lint index, GOT (%), Seed cotton yield (g) and fiber fineness (µg /inch), fiber length (mm) Agglomerative hierarchical clustering was performed to group diverse genotypes into distinct clusters by using ward's minimum variance method. Significant variation was observed among all genotypes through analysis of variance. Bolls/plant, weight of boll, sympodial branches and 100 seed weight revealed significantly positive relationship with seed cotton yield. It also revealed positive relationship with fibre fineness, However bolls per plant displayed strong negative correlation with fiber length. Traits exhibiting positive association to yield of seed cotton can be selected to be utilized in breeding programs for producing high yield cultivars. Eighteen varieties were classified into four groups. Cluster III is the biggest cluster, which is sub divided into two sub-clusters i.e. Cluster IIIa & Cluster IIIb, which comprises of eight and two genotypes respectively followed by Cluster I and Cluster IV comprised of 3 genotypes in each. However, Cluster II is the smallest cluster consisting of only two genotypes.

Keywords: Seed cotton yield, correlation analysis, hierarchical clustering
How to cite this article: Perveen S, Fatima A, Zia A, Rehman AU. Correlation analysis of several economic traits of upland cotton (*Gossypium hirsutum* L.). *J. Genet. Appl. Biotechnol.* 2026: e2026020. https://doi.org/10.66432/kdf4sr93

Introduction

Cotton is the major cash crop, which has significant contribution in economic growth of Pakistan. It is the primary source for fiber, fuel and seed cake. It is crucial for Pakistan's economy being a primary source of foreign exchange earnings. It provides employment to large population, that are engaged in agriculture, textile mills and ginning factories. Cotton products have remarkable share of ~ 60% in total exports and 50% of labor in textile industry (1). Cotton fiber provides foundation to the largest textile business across the world by generating annual revenue of 599 billion dollars worldwide (2). Nearly 1.5 million people of Pakistan obtained their livelihoods from cotton cultivation (3). Cotton was cultivated on an area of 2.4 million hectare (ha) as compared to 2.1 million hectares (ha) last year, which causes significant increase of production by 108.2% to 10.2 million bales as compared to last year i.e. 4.9 million bales. It contributes about 0.7% to GDP and 2.9% value addition in agriculture (4, 5). Although, cotton production has increased noticeably but its maximum potential has not been achieved so far due to various factors including reduced genetic diversity, climate change, cotton leaf curl disease (CLCuD), instability in input and output cost and weed crop competition. Hence, Researchers need to develop highly productive cotton genotypes to meet the future demands of the textile industry by estimating the extent of correlation among the traits and their association with fiber quality and yield parameters (6).

Yield is a complicated character that is highly affected by biotic & abiotic stresses. Stresses have negative effect on overall crop yield, due to which demand of good quality fiber and genotypes higher yield by textile industry is increasing day by day. Traits of cotton are linked with each other, so breeders need to know the interaction among several quantitative characters of upland cotton to identify desirable traits (7). Correlation helps in the determination of positive or negative inter-relationship among various characters (8). This study is mainly focused to assess phenotypic association among several yield contributing characters along with fiber quality parameters. It provides preliminary guidelines for the identification of desirable characters. Hierarchical clustering was performed to identify genetically diverse upland cotton genotypes that may serve as potential parental lines for future breeding programs under local environmental conditions.

Materials and Methods

This study was performed during kharif season in 2024-2025 in fields of Plant Breeding and Genetics, University of Agriculture, Faisalabad; located at 31º 25N' latitude and 184.4m altitude above sea level. Eighteen varieties of upland cotton namely; NIAB-820, VH-148, FH-177, CRS-456, FH-118, NS-121, FH-114, CIM-602, FH-4243, VH-283, S-3, CIM-598, FH-175, VH-295, FH-187, VH-329, CIM-599 and As-01 were cultivated in the Randomized Complete Block Design each with 3 repetitions. The plant-plant and row- row distance was maintained at 30cm and 75cm respectively. All suggested agricultural practices i.e. thinning, application of fertilizers, weedicides, pesticides and timely irrigation were performed for the management of weeds and pests according to the requirements to achieve healthy plants. Five guarded plants were chosen randomly from each genotype. Data was recorded for several traits namely, boll weight (g), monopodial branches, bolls/plant, number of seeds/boll, plant height (cm), sympodial branches, lint index (g), 100 seed weight (g), strength of fiber (g/tex), GOT (%), fiber fineness (µg/inch), fiber length (mm) and yield of seed cotton (g). Spin lab High Volume Instrument (HVI-900) was used for fiber analysis.

Statistical analysis

Analysis of variance was performed for each character to estimate significant variation among all observed genotypes as suggested by (9). Significant data was subjected to correlation to estimate degree of phenotypic association among various economic characters following Pearson correlation method (10). Statistix 8.1 was used to perform ANOVA and correlation analysis (11). Furthermore, hierarchical clustering was performed to reduce disparities within the clusters by using Ward's minimal variance approach (12). Minitab 17 was used to perform cluster analysis.

Results

Result of Analysis of variance, correlation and cluster analysis of all observed genotypes for various characters namely, sympodial branches, lint index, bolls/plant, monopodial branches, fiber fineness, 100 seed weight, GOT, fiber strength, boll weight, and staple length are mentioned below.

Monopodial branches

ANOVA for monopodial branches showed non-significant differences at 5% level of significance among observed varieties. Mean values for monopodial branches varied from 1 to 2.67 as displayed in graph (Figure 1). The genotypes including VH-295 (2.2) and S-3 (2.17) exhibited maximum monopodial branches, while minimum branches were exhibited by CIM-599 (1.07) and NIAB-820 (1.00).

Table 1. Mean squares of ANOVA for several yield contributing traits and fiber parameters

S.O.V	Replication	Genotypes	Error
DF	2	17	34
MB	0.56	0.40^{NS}	0.28
SB	1.02	24.9**	7.44
PH	320.9	608.4**	167.7
BW	0.45	0.66**	0.24
SI	0.08	0.76**	0.15
LI	107.8	266.6**	88.48
GOT%	27.18	31.46**	13.42
NOB	7.07	153.5**	54.68
SPB	51.34	52.03*	18.08
SCY	107.8	266.5**	88.48
FL	2.06	5.54*	1.84
FS	0.52	88.5**	1.39
FF	0.03	2.02**	0.1

*P <0.05= Significant; **P <0.01= Highly significant; ^{NS} P >0.05= Non-Significant; MB (Monopodial branches); BW (Boll weight); SB (Sympodial branches); GOT (Ginning out turn); PH (Plant height); NOB (Number of bolls); SI (Seed index); LI (Lint index); FS (Fiber strength); FF (Fiber fineness); SPB (Seeds per boll); FL (Fiber length); SCY (Seed cotton yield).

Sympodial branches

ANOVA for sympodial branches showed significant variation at 5% significance level among all observed varieties. Mean values for fruiting branches ranged from 26.2 to 30.23 as depicted in Figure 1. Genotypes namely, VH-148 exhibited highest number of sympodial branches i.e. 33 followed by S-3 (33), VH-148 and CIM-598 (31.2). However, genotypes including FH-114 (28.4) and CRS-456 (28.3) revealed lowest sympodial branches.

Plant height (mm)

ANOVA for plant height exhibited considerable differences at 5% significance level among all observed varieties. Mean values of plant height varied from 96cm to144.3cm. Maximum plant height was displayed by VH-148 (144.3cm) followed by VH-295 (140.1cm) and S-3 (130.1cm), while the genotypes including FH-4243 minimum plant height i.e. 104.1cm followed by FH-114 and FH-175.

Bolls per plant

ANOVA for bolls plant-1 showed significant variation at 5% significance level among all observed genotypes. Mean values for bolls/ plant ranged from 18.8 to 46.05. The highest bolls were demonstrated by NIAB-820 (46.05) VH-329 (42.27), while the genotypes including CRS-456 (19.23) and FH-114 (18.8) had minimum bolls (Figure 1).

Boll weight

ANOVA for boll weight exhibited significant variation at 5% level of significance among all the genotypes. Mean values of boll weight varied from 1.23g to 3.19g. Highest boll weight was depicted by VH-148 (3.19g) followed by CRS-456 (2.1g) and minimum boll weight was observed in FH-175 i.e. 1.23.

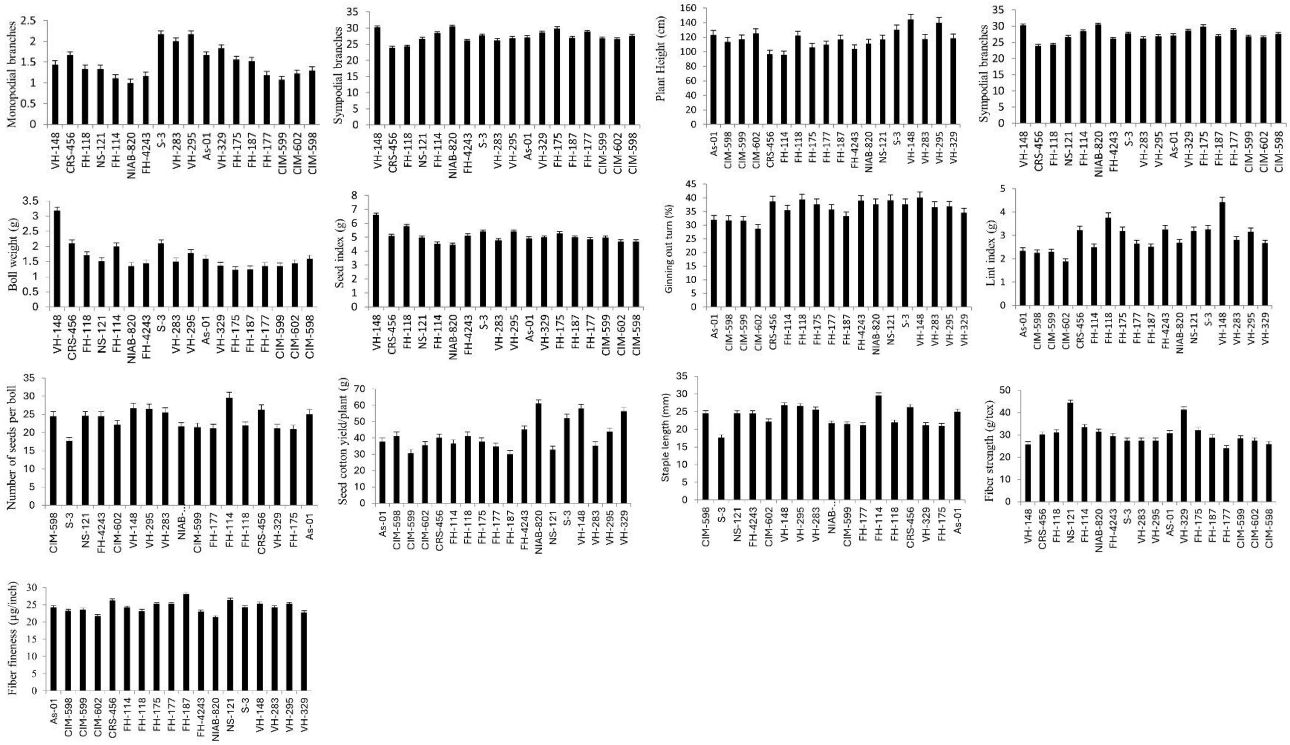

Figure 1: Mean Performances of economic characters and fiber related parameters among varieties of cotton. Error bars indicate standard error.

Seed index

ANOVA for 100 seed weight showed significant differences at 5% significance level among all observed varieties. Mean values of seed index varied from 4.45g to 6.6g are displayed in Figure 1. Genotypes namely, NIAB-820 (4.45g) exhibited lowest seed index followed by FH-114 (4.46g) and CIM-608 (4.68g), while the highest seed index were depicted by VH-148 (6.6g) followed by FH-118 (5.78g) and FH-175.

Ginning out turn (GOT)

ANOVA for GOT% revealed significant variation at 5% significance level among all observed varieties. Average values for GOT ranged from 28.79% to 40.12%. The lowest GOT was revealed by genotypes CIM-599 and CIM-602 i.e. 31.62% and 28.79% respectively, while the genotypes including VH-148 (40.12%) and FH-118 (39.44%) revealed highest GOT.

Lint index (g)

ANOVA for lint index showed significant variation at 5% significance level among all observed varieties. Average values for lint index varied from 1.89g to 4.21g (Figure 1). The lowest lint index was demonstrated by genotypes CIM-602 and CIM-598 i.e. 1.89g and 2.25g respectively, while genotypes including VH-148 (4.21g) depicted highest lint index followed by FH-118 (3.77g).

Seeds per boll

ANOVA for seeds/boll exhibited considerable differences at 5% significance level among all observed varieties. Mean values for number of seeds boll-1 ranges from 13.15 to 29.609 are shown in Figure 1. The lowest seed per boll was recorded in genotypes FH-187 and FH-175 i.e. 13.15 and 13.542 respectively, while the genotypes namely FH-114 (29.609) and CRS-456 (23.306) revealed highest seeds per boll.

Seed cotton yield (g)

ANOVA for seed cotton yield exhibited significant variation at 5% significance level among all varieties. Average values for yield varied from 30.1 to 61.04g. The genotypes namely, CIM-599 (30.71) and FH-187 (30.1) had lowest yield. While highest crop yield was exhibited by NIAB-820 (61.04) and VH-148 (58.2) among all observed genotypes (Figure 1).

Fiber length (mm)

ANOVA for staple length exhibited significant variation at 5% significance level among all the varieties. Mean values for staple length varied from 21.4mm to 28.133mm are shown in Figure 1. The lowest staple length was demonstrated by varieties NIAB-820 and CIM-602 i.e. 21.4 and 21.767 respectively, however, the genotypes including FH-187 (28.133) and NS-121 (26.467) exhibited highest maximum fiber length.

Fiber strength (g/tex)

ANOVA for staple length exhibited significant variation at 5% significance level among all the varieties. Mean values for fiber strength ranged 24.2g/tex to 44.267g/tex are depicted in Figure 1. The minimum strength of fiber was recorded in genotypes FH-177 and CIM-598 i.e. 24.2g/tex and 25g/tex respectively, while NS-121 (44.267) revealed highest fiber strength followed by VH-329 (41.3).

Fiber fineness (µg/inch)

ANOVA for staple length exhibited significant variation at 5% significance level among all the genotypes. Average values of genotypes for staple fineness ranged from 3µg/inch to 6.7µg/inch. The minimum staple fineness was recorded in genotypes FH-187 and S-3 i.e. 3µg/inch and 4.2µg/inch respectively, while the genotypes including FH-177 (6.76) and FH-4243 (5.1667) revealed highest maximum fineness.

Correlation analysis

The results of correlation for several characters are displayed in Figure 2. Correlation exhibited that crop yield displayed considerably linear relationship to boll weight (0.503), sympodial branches (0.542), bolls/plant (0.674), plant height (0.53) and lint index (0.570). However, it exhibited inverse relationship with fibre length (-0.42) and non fruiting branches (-0.007). Fruiting branches revealed considerably linear correlation by bolls/plant (0.821). Seed index showed considerably direct relationship with weight of boll (0.703), seed cotton yield (0.546) and negatively correlated with seeds/boll (-0.29) and fiber strength (-0.19). Plant height displayed considerable positive relation with 100 seed weight (0.507), lint index (0.4712) and crop yield (0.53). It also revealed weakest positive relationship with several other traits including fruiting branches (0.035) and boll weight (0.33), but this relationship is not significant due to which these traits do not have any significant impact on yield. Bolls produced by each plant demonstrated significant linear association with sympodial branches (0.821) and yield (0.674), however non-significant negative linkage was observed between bolls/plant with seeds per boll (-0.386), seed index (-0.232) and weight of boll (-0.232). Boll weight revealed considerable positive relation with seeds per boll (0.822), 100 seed weight (0.703) and non-significant weak negative correlation to sympodial branches (-0.176), bolls/plant (-0.232), strength of fiber (-0.237), monopodial branches (-0.383) staple fineness (-0.051) and GOT (-0.025). 100 seed weight exhibited moderately significant linear relationship with lint index (0.491), seeds/ boll (0.364) and yield (0.546). GOT had negative association to yield (-0.227) and seeds boll-1 (-0.130). Plant height and lint index revealed positive relationship with each other i.e. (0.471). Fiber length exhibited strong positive correlation with boll mass (0.429) and 100 seed weight (0.506) and inversely associated with bolls (-0.479) and fibre fineness (-0.536). Fiber fineness exhibited strong direct correlation by lint index (0.52) and inversely correlated to plant height (-0.285) and GOT (-0.239). Strength of fiber revealed non-significant positive relation by fruiting branches (0.056), bolls/plant (0.13), staple length (0.013) and staple fineness (0.001) and negatively correlated with non fruiting branches per plant (-0.013), plant height (-0.276), weight of boll (-0.237) and seed index (-0.19).

Cluster analysis

Cluster analysis is a multivariate analysis that is utilized to classify genotypes in distinct groups on the basis of similarity in most of the characters. In this study, eighteen varieties were classified into 4 groups (Figure 3; Table 2). Cluster III is the largest cluster comprised of two sub clusters i.e. cluster III(a) and Cluster III(b). Cluster III(a) comprised of 8 varieties namely 3, 9, 18, 4, 14, 16, 13 & 15 out of which 14 and 16 revealed least genetic diversity with higher similarity level. Genotypes with higher similarity index are genetically less diverse. However, Cluster IIIb is comprised of 2 genotypes 11 & 17. Cluster I comprised of three genotypes (1, 8 & 10) followed by 2 genotypes in cluster II (2 & 5) and 3 genotypes in Custer-IV (6, 7 & 12) as displayed in table 2. Genotypes showing greater distance from the horizontal axis revealed higher genetic diversity such as the genotype 6 exhibited maximum genetic diversity with minimum similarity followed by genotypes 7 & 12. Genotypes grouped in Cluster 3 have less genetic diversity, while the maximum genetic variation was exhibited by the genotypes grouped in Cluster-IV.

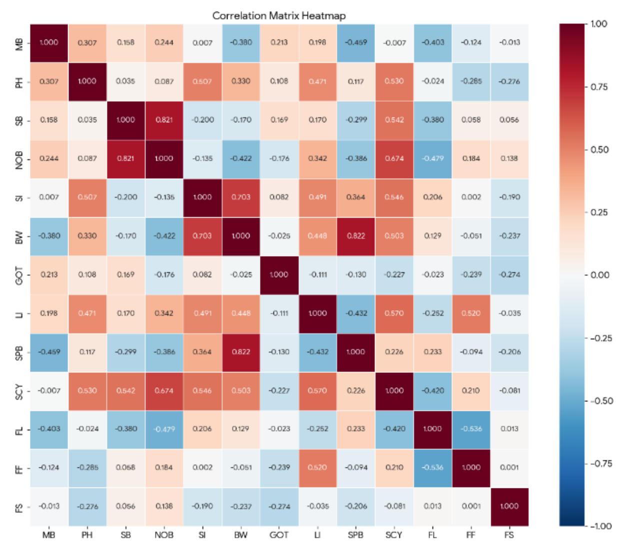

Figure 2: Correlation analysis for several yield contributing traits and fiber related parameters of Gossypium hirsutum L. MB (Monopodial branches); BW (Boll weight); SB (Sympodial branches); GOT (Ginning out turn); PH (Plant height); NOB (Number of bolls); SI (Seed index); LI (Lint index); FS (Fiber strength); FF (Fiber fineness); SPB (Seeds per boll); FL (Fiber length); SCY (Seed cotton yield).

Discussion

Results of correlation exhibited that plant with maximum bolls/plant, fruiting branches, boll weight, lint index and plant height showed higher yield of cotton. Which suggests that these traits have linear association with seed cotton yield. Similar findings were also reported by various scientists (13-15). They found positive relationship of yield with fruiting branches, seed index, bolls/plant, plant height and boll weight. However, plant with higher bolls per plant and fruiting branches also demonstrated positive correlation with each other. A positive association was also discovered among bolls per plant and sympodial branches, which suggested that plant with maximum fruiting branches had higher bolls/plant, that ultimately enhance crop yield (16, 17). Linear relationship of yield with boll weight, lint index and sympodial branches was also observed (18). These results indicated that traits including boll weigh, fruiting branches, bolls per plant and 100 seed weight are highly reliable parameters that can be selected to utilize in future breeding programs to enhance the overall crop yield. Number of bolls had linear association with seed cotton yield and inversely related to GOT, boll weight and seeds per boll. Increases in bolls/plant lead to significant drop in boll weight, which is in accordance with results reported earlier (17, 19). However, plant with maximum bolls/plant had higher yield but a smaller number of seeds, boll weight and GOT. Negative relationship between bolls per plant and seeds/boll were observed by (20). 100 seed weight revealed positive relationship to number of bolls, plant height and lint index, which suggested that plant with highest 100 seed weight exhibited higher plant height and lint index due to their linear association with each other. Similar findings were also observed earlier (20, 21). For fiber related parameters fibre length exhibited negative correlation with bolls/plant. Hence, it was suggested that plant with maximum bolls exhibited minimum fiber length due to the presence of inverse correlation between these traits. An increase in number of bolls enhances utilization of nutrients essential for boll development, which limits availability of nutrients for fiber elongation. Similar results were also found by other scientists (22, 23). Staple fineness and lint index exhibited considerably positive correlation with each other, while it shows negative relationship with staple length. It suggested that plant with maximum fiber fineness exhibited higher lint index and minimum staple length. A linear association of lint index with staple fineness was also reported earlier (24). The varying performance of distinct varieties emphasizes the ability to utilize these complementary parameters through hybridization results in producing breeding lines that result in maximum crop yield with best fiber quality traits. Eighteen genotypes were classified into 4 distinct groups through cluster analysis on the basis of similarity in most of the observed economic characters. Multivariate analysis has proved an effective approach to group genotypes in distinct groups on basis of similarity in most of parameters to assess genetic variation among observed genotypes (11, 25, 26). Esmail et al. also reported 2 distinct clusters with two sub-clusters in each (13). Similarly, 4 distinct groups were exhibited by Amna et al. and 7 clusters were observed by Asha et al. (27, 28).

Conclusion

The experiment was conducted to identify association among several yield related characters and fiber quality traits. Genetic diversity among all observed cotton cultivars was determined through cluster analysis. It was concluded from results that fiber index, bolls, fruiting branches plant height and boll weight revealed significantly positive correlation with yield. However, seed cotton yield exhibited indirect correlation with staple length and strength of fiber. Height of the plant had considerably positive correlation with seed index and lint index, sympodial branches. Bolls showed considerably positive interrelationship with each other. The boll weight displayed significantly linear correlation with lint index and seeds/ boll. Fibe length and staple fineness had strong negative correlation to each other. VH-148 and NIAB-820 were best performing varieties in terms of seed cotton yield. VH-329 were best for fiber related parameters namely fiber fineness and strength of fiber.

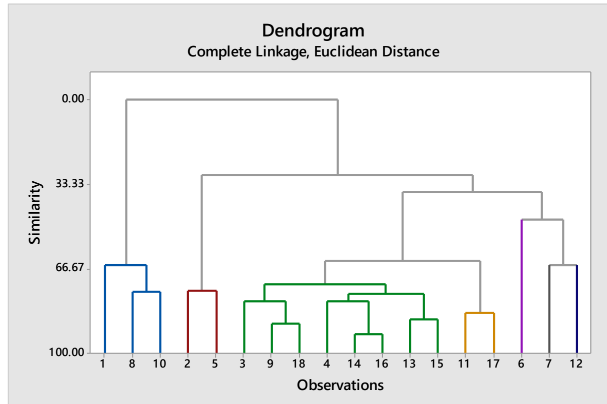

Figure 3: Dendrogram representing clustering of eighteen genotypes of upland cotton

Table 2. Classification of eighteen genotypes into seven distinct clusters

Cluster	Genotypes
Cluster I	VH-148, S-3, VH-295
Cluster II	CRS-456, FH-114
Cluster III a	FH-118, VH-283, CIM-598, NS-121, FH-187, CIM-599, FH-175, FH-177
Cluster III b	AS-01, CIM-602
Cluster IV	NIAB-820, FH-4243, VH-329

Disclaimer: None.
Conflicts of Interest: The authors declare no conflict of interest.
Source of Funding: None
Ethics approval statement: Not Applicable
Authors' Contribution Statements: SP: Execution of experiment, Statistical analysis, data collection: AF, AZ: Execution of experiment, data collection, AUR: Proofread the manuscript

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