***Original Research Article***

**Evaluation of Genetic Diversity and Heterosis in Cotton (*Gossypium hirsutum* L.) genotypes: A Comprehensive Study on Yield, Fibre Quality, and Breeding Potential**

**Abstract**

The study aimed to evaluate the genetic diversity, heterosis, and variability in cotton genotypes under the climatic conditions of Guntur, Andhra Pradesh, India. A total of 11 test cross hybrids and 3 check varieties (US-7067, CRISTAL 369, and RASHI SWIFT) were evaluated for growth, yield, and fibre quality traits using Randomized Block Design (RBD). Cluster analysis grouped the genotypes into three distinct clusters, highlighting significant genetic diversity among them. Heterosis analysis revealed that H-1357 exhibited the highest positive heterosis for traits such as plant height (30.00%), number of bolls (71.77%), yield per plot (20.20%), and lint weight (25.23%), making it a superior genotype for commercial breeding. Variability analysis indicated that number of bolls (NB) and monopodial branches (MP) had high GCV (20.66% and 21.81%) and PCV (22.90% and 36.38%), suggesting a strong potential for genetic improvement. Path analysis identified yield per plant (YPL), lint weight (LW), and boll weight (BW) as the most influential traits for yield improvement, with high direct effects on yield per plot (YPO). The results suggest that H-1357 and H-1349 are the most promising hybrids for further breeding and commercial cultivation. These findings provide valuable insights for cotton improvement programs, focusing on yield enhancement, fibre quality, and genetic stability.

***Keywords:*** *Cotton genotypes, heterosis, cluster analysis, genetic variability, yield traits, path analysis*

1. **Introduction:**

Cotton (Gossypium spp.) is one of the most important fibre crops in the world, serving as a key raw material for the textile industry. Cotton, often referred to as the "King of Fibres" holds the highest economic value among all cash crops in India (**Smita, 2013**). It is the most significant cash and commercial crop, supplying nearly 75% of the raw material required by the Indian textile industry. The textile sector, which is India's leading export industry, generates revenue exceeding $10.78 billion in 2021-22, earning cotton the nickname "White Gold" (**Choudhary and Gaur, 2015**). Belonging to the genus Gossypium under the tribe Gossypieae of the Malvaceae family, cotton comprises four cultivated species: *Gossypium herbaceum* L., *G. arboreum* L., *G. hirsutum* L., and *G*. *barbadense* L. Notably, India is the only country where all four cultivated cotton species are grown. Apart from its primary use as a fibre crop, cotton is a multipurpose crop, yielding valuable by-products such as cotton seed oil, oil cake, hulls, and linters, which contribute to various industries. Globally, cotton is grown in tropical and subtropical regions, with major producers including **India, China, the United States, and Brazil.** India ranks among the top cotton-producing countries, contributing significantly to global fibre demand. As of the 2023/24 marketing year, global cotton production is projected at approximately **118.29 million 480-pound bales**. India stands as the second-largest cotton producer, contributing about **22%** of the world's total, with an estimated production of **25.4 million 480-pound bales** (**FAS-USDA(2023-24)**). In the state of Andhra Pradesh, India, cotton production for the 2023/24 season is estimated at **12 lakh bales** (1.2 million bales) (**CAI report-2024-25**). India is a world pioneer in development and commercial cultivation of cotton genotypes. In 1970, the world's first cotton genotype H4 was released, and in following years other countries obtained long-fibre quality and commercial genotype cotton varieties as well putting themselves in the genotype cotton market (**Venkateshwarlu and Da Corta., 2001**). The crop is known for its adaptability to different climatic conditions and its economic importance in both agriculture and industry. Beyond its commercial significance, cotton plays a crucial role in employment generation, supporting millions of farmers, traders, and textile workers. Continuous advancements in **breeding, biotechnology, and agronomic practices** have enhanced cotton yield, fibre quality, and resistance to pests and diseases, ensuring its continued prominence in global agriculture. There had been various advancements in the cultivation of cotton crop since the times effecting the growth and yield such as the introduction of **Bt cotton** has revolutionized cotton production by providing resistance against bollworms, reducing pesticide use, and improving yield. Countries like the **USA, India, China, and Brazil** have widely adopted Bt cotton, leading to higher productivity (**Choudhary and Gaur, 2015**). Herbicide-Tolerant (HT) cotton varieties allow farmers to use specific herbicides without damaging the crop, leading to better weed control and higher yields. Genome Editing (CRISPR-Cas9) in genetic engineering have enabled scientists to develop cotton varieties with improved fibre quality, drought tolerance, and pest resistance. The demand for **organic cotton** is rising, leading to innovations in **biopesticides, biofertilizers, and regenerative farming** practices. Global advancements in **biotechnology, precision farming, and sustainable practices** have significantly improved cotton growth, yield, and quality. As research continues, innovations in **climate resilience, pest resistance, and digital agriculture** will shape the future of cotton farming, ensuring higher productivity while minimizing environmental impact. The main objective of this study was to select the genotype with highest productivity in the central semi-arid region of Andhra Pradesh. So, in order to evaluate the genetic diversity and heterosis in Cotton (*Gossypium hirsutum* L.) genotypes the following experiment was conducted at the Field Experimental center of Research and Development of NRI Agritech Pvt Ltd & NRI Educational Institution Pvt Ltd, Nidumukkala, Tadikonda Mandal, Guntur dt, Andhra Pradesh.

1. **Material and Methods:**

The experiment was conducted at a location situated at 16.44° N latitude and 80.41° E longitude, at an altitude of 98 meters above sea level, within the UTC+5:30 (IST) time zone. The study involved eleven test cross genotypes of cotton along with three check varieties for **heterosis estimation** and comparative performance evaluation, making a total of 14 genotypes. (H-1345, H-1346, H-1347, US-7067, H-1350, H-1370, H-1348, CRISTAL 369, H-1349, H-1357, H-1368, RASHI SWIFT, H-1371, H-1378). The experimental field was structured in a Randomized Block Design (RBD) with three replications to ensure uniformity in field conditions. Each genotype was sown in four rows, with 10 plants in each row, following a spacing pattern of 90 cm between rows and 30 cm between individual plants. Each plot measured 14 × 12 feet, with a 1.5–2.0 feet buffer between adjacent plots to reduce inter-genotypic interference. All necessary agronomic and cultural practices were implemented to support healthy crop growth and development. Observations were recorded based on three randomly selected plants in each genotype in each replication for all important parameters *viz.,* plant height, monopodial branches, sympodial branches, number of bales, boll weight, lint weight, seed weight, yield per plot, yield per plant, number of 4 lobs, number of 5 lobs, number of plants per plot. These parametrics were briefly studied in the below headings giving us a better understanding on the suitable genotype for higher productivity in the Guntur region of Andhra Pradesh.

**Statistical analysis:**

The collected data were subjected to statistical analysis using RStudio software and the following analyses were performed such as Genetic Variability Analysis for Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) to assess the extent of genetic variation (**Deshmukh *et al.,* 1986**). Heritability (Broad Sense) was calculated to determine the proportion of phenotypic variance attributable to genetic factors. Genetic Advance (GA) and Genetic Advance as Percentage of Mean (GAM) were computed to evaluate the potential for selection gains (**Johnson *et al.,* 1955**).

1. **Results and discussion:**

**Growth and yield traits**:

It can be observed from the data in Table 2 that a significantly highest plant height was recorded in H-1357 genotype with 179.11cm and the statistically at par values were recorded in H-1378, H-1346, H-1349 genotypes. As per the data recorded in Table 2 the data on number of plants was non-significant and the highest number of plants were recorded in H-1357 genotype with a mean of 40 plants and the H-1349 (39.67 plants), H-1378 (39.33 plants) and check-Rashi swift (39.33 plants) were on par with H-1357 genotype. The data on monopodial branches from the Table 2 infers that significantly higher number of monopodial branches were recorded in H-1357 genotype (2.11) and the statistically on par values were recorded in Rashi swift (check), H-1349, H-1378 genotypes. The data on from Table 2 stipulates that significantly higher number of sympodial branches were recorded in H-1357 genotype with 28.22 sympodial branches and the Rashi swift (check) with 27.44, H-1349 with 27.22 and H-1347 with 26.56 were on par with H-1357 genotype. Significantly higher number of bales were recorded in H-1357 genotype with 104.33 and the Rashi swift (check) with 75.44 and H-1378 with 74.33 were on par with H-1357 genotype. As per the data recorded in Table 2 significantly highest yield per plot was recorded in H-1357 genotype with 9.82kg and the statistically at par values were recorded in H-1349 genotype with 8.85kg and H-1378 genotype with 8.84kg. It can be observed from the data in Table 2 that a significantly higher yield per plant was recorded in H-1357 genotype with 0.25gm and US-7067 (0.23gm), H-1349 (0.22gm), H-1378 (0.22gm) genotypes were statistically at par with H-1357 genotypes. Significantly higher number of 4 lobs were recorded in H-1357 genotype with 33.00. The H-1378, Rashi swift and H-1349 genotypes were statically on par with H-1357 genotype. As per the data recorded in Table 2 significantly higher number of 5 lobs were recorded in H-1357 genotype with 38.00 and H-1378 (37.67), check-Rashi swift (36.33) and H-1349 (37.00) genotypes were statistically at par with H-1357 genotype. From the data recorded in Table 2 it can be observed that a significantly highest boll weight per plant was recorded in H-1357 genotype with 6.33g and H-1349 genotype with 5.90gm was statistically on par with H-1357 genotype. As per the data recorded in Table 2 significantly highest lint weight per 10 bolls was recorded in H-1357 genotype with 20.60gm and statistically at par values were recorded in H-1349 (19.04gm), H-1378 (18.19gm). The data on seed weight per 10 bolls from Table 2 states that higher seed weight was recorded in H-1357 genotype with 38.59gm. The statistically on par values were recorded in H-1349, H-1368, H-1348, check-Rashi swift, H-1378 genotypes.

**Traits contribution to genetic divergence in genotypes:**

The pie chart in Fig.1 represents the importance of different traits in contributing to genetic divergence among the evaluated cotton genotypes. The percentage values indicate the relative contribution of each trait toward the total variation observed in the population. Boll weight (BW-21.1%), lint weight (LW-17.5%), seed weight (SW-13.2%), number of bolls (NB-10.4%) had contributed more than 50% of the total genetic deviation in 14 cotton genotypes. Other traits such as yield per plot (YPO-6.2%) and monopodia (MP-4.9%) showed moderate contributions, suggesting that yield-related traits are moderately variable but still play a role in genotype differentiation and 4lobed fruits (4LB-4%) and sympodia (SP-3.7%) contributed at similar levels, indicating their influence on structural plant development.

**Variability analysis:**

The genetic variability analysis of growth and yield traits in cotton genotypes was assessed using genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense), genetic advance (GA), and genetic advance as a percentage of the mean (GAM). Among all the traits, monopodial branches (MP) exhibited the highest GCV (21.81%) and PCV (36.38%), indicating substantial genetic and environmental influence on this trait. Similarly, number of bolls (NB) showed high GCV (20.66%) and PCV (22.90%), suggesting that selection for NB can lead to significant genetic improvements. Yield per plot (YPO) and lint weight (LW) also recorded moderate GCV values of 10.93% and 10.99%, respectively, showing that these traits have considerable genetic variability. Heritability (broad sense) was highest for plant height (PH) (0.87) and number of bolls (NB) (0.81), indicating a strong genetic influence on these traits, making them highly inheritable. Traits such as boll weight (BW) (0.72) and yield per plot (YPO) (0.72) also exhibited high heritability, suggesting that selection based on phenotypic expression can be effective for genetic improvement. Conversely, seed weight (SW) had the lowest heritability (0.17), implying a greater environmental influence on this trait. Genetic advance (GA) was highest for number of bolls per plant (NB) (24.87) and plant height (PH) (23.26), reinforcing their potential as selection criteria for breeding programs. The highest GA as a percentage of mean (GAM) was recorded for NB (38.39%) and MP (26.93%), suggesting that substantial genetic improvement can be achieved through selection for these traits. Overall, the high heritability coupled with high genetic advance for NB, PH, and YPO suggests that these traits are primarily governed by additive gene action, making them ideal for selection in cotton breeding programs. Meanwhile, traits with moderate heritability and genetic advance, such as BW and LW, indicate both additive and non-additive gene effects, requiring hybridization and selection strategies for improvement. Traits like SW, with low heritability, would require improved environmental management in addition to genetic selection for enhancement. These findings suggest that NB, PH, YPO, and MP should be prioritized in selection programs, while traits like SW and NP require additional breeding strategies to maximize genetic gains.

**Standard Heterosis in Cotton Genotypes:**

The analysis of standard heterosis in cotton genotypes, based on comparison with the check varieties (US-7067, CRISTAL 369, and RASHI SWIFT), revealed considerable variation in growth, yield, and fibre traits. The magnitude and direction of heterosis varied across different genotypes and traits, with some hybrids demonstrating positive heterosis, indicating superior performance over the check varieties, while others exhibited negative heterosis, suggesting lower trait expression. Among the studied genotypes, H-1357 exhibited the highest positive heterosis for multiple traits, including plant height (30.00%), monopodial branches (38.82%), number of bolls (71.77%), yield per plant (13.64%), boll weight (14.19%), lint weight (25.23%), and yield per plot (20.20%), indicating its superior potential as a high-yielding genotype. Similarly, H-1349 showed significant positive heterosis for monopodial branches (31.58%), number of bolls (15.98%), boll weight (6.43%), lint weight (15.74%), and yield per plot (8.32%), making it another promising genotype for yield improvement. Conversely, some hybrids exhibited negative heterosis, suggesting inferior performance compared to the check varieties. H-1371 recorded the highest negative heterosis for yield per plot (-22.64%), while H-1345 and H-1370 showed notable reductions in yield-related traits, including boll weight (-12.87% and -0.78%, respectively), lint weight (-21.34% and -2.13%), and yield per plant (-9.09% and -4.55%), indicating that these genotypes may not be ideal for commercial cultivation without further genetic improvements. In terms of fibre traits, H-1357, H-1349, and H-1378 showed positive heterosis for both 4-lobed fruit (4LB) and 5-lobed fruit (5LB), suggesting their potential for improving boll structure and fibre development. On the other hand, H-1371 and H-1370 showed negative heterosis for these traits, implying that these genotypes may require further breeding efforts to enhance fibre quality.

**Breeding implications:**

The results indicate that H-1357 and H-1349 are the most promising hybrids, showing positive heterosis across multiple growth and yield-related traits, making them ideal candidates for further evaluation and potential commercial release. Meanwhile, genotypes like H-1371 and H-1370 require additional improvement strategies to enhance their yield potential. The findings also highlight the importance of selecting hybrids with positive heterosis for yield components such as number of bolls, boll weight, and lint weight, as these traits directly influence overall productivity.

**Pearson’s correlation coefficient:**

The **Pearson’s correlation coefficients** among various growth and yield-related traits in cotton genotypes are presented in **Table 3 and Fig.1**. The correlation analysis revealed significant associations among key traits, indicating their interdependence and potential utility in selection programs. Yield per plot (YPO) exhibited a highly significant positive correlation with yield per plant (YPL) (r = 0.954\*\*\*) and lint weight (LW) (r = 0.854\*\*\*), suggesting that an increase in these traits could directly enhance overall yield. Similarly, boll weight (BW) and lint weight (LW) were strongly correlated (r = 0.963\*\*\*), indicating that heavier bolls contribute significantly to lint weight accumulation. Among the growth parameters, plant height (PH) showed a significant positive correlation with number of bolls (NB) (r = 0.786\*\*\*) and seed weight (SW) (r = 0.754\*\*), suggesting that taller plants tend to produce more bolls and heavier seeds. Likewise, number of plants (NP) displayed a strong association with monopodial branches (MP) (r = 0.956\*\*\*) and seed weight (SW) (r = 0.773\*\*), emphasizing their collective role in yield determination. Moreover, boll weight (BW) was significantly correlated with seed weight (SW) (r = 0.944\*\*\*) and lint weight (LW) (r = 0.963\*\*\*), reinforcing the importance of boll weight in improving fibre and seed yield. Traits such as 4-lobs fruit (4LB) and 5- lobs fruit (5LB) exhibited moderate correlations with other yield components, highlighting their contribution to overall fibre productivity. The findings suggest that selection for traits such as YPL, LW, and BW could significantly enhance yield performance in cotton breeding programs. The strong correlations between these traits indicate that indirect selection based on highly correlated secondary traits can be an effective breeding strategy for yield improvement.

**Path analysis:**

Path analysis provided valuable insights into the direct and indirect effects of key agronomic traits on yield per plot (YPO) in cotton genotypes. The results indicated that yield per plant (YPL), lint weight (LW), and boll weight (BW) had the strongest direct effects on YPO, making them the most critical traits for selection in breeding programs. Among these, YPL exhibited the highest direct effect (1.00001), followed by LW (0.98939) and BW (0.86892), suggesting that genotypes with higher YPL, heavier bolls, and greater lint weight are more likely to achieve increased overall yield. These findings indicate that selecting for these traits could lead to significant improvements in cotton productivity. In addition to direct effects, several traits contributed indirectly to YPO by influencing primary yield components. Plant height (PH), number of monopodia (MP), sympodia (SP), and number of bolls per plant (NB) showed moderate to strong correlations with YPO, despite their lower direct effects. PH (r = 0.701), NB (r = 0.732), and SP (r = 0.701) were particularly notable, suggesting that plants with greater height, more sympodia, and a higher number of bolls tend to yield better, primarily through their positive influence on BW, LW, and YPL. Similarly, traits like seed weight (SW) (1.00000) and number of bolls (NB) (0.78111) also played a significant role in determining final yield, reinforcing the importance of seed development and boll production in cotton genotypes. Interestingly, while 4-lobed fruit (4LB) and 5-lobed fruit (5LB) had relatively lower direct effects, they contributed to YPO through their influence on boll and fibre traits. The positive association between BW and LW (0.963) and SW (0.944) further suggests that genotypes with larger, heavier bolls tend to produce greater lint and seed yield, making boll characteristics a vital consideration in selection. The strong correlation of LW with YPO (0.854) emphasizes the importance of fibre -related traits in determining overall yield potential. These findings indicate that a multi-trait selection approach is necessary for effective cotton breeding. While YPL, LW, and BW should be the primary selection criteria due to their strong direct effects, other traits such as PH, SP, NB, and SW should not be overlooked, as they contribute indirectly to yield through their influence on key fibre and boll characteristics.

**Cluster Analysis of Cotton Genotypes:**

The cluster analysis was performed to classify cotton genotypes based on their genetic similarity and variability. The hierarchical clustering dendrogram and the elbow method graph were used to determine the optimal number of clusters. Based on the within-cluster sum of squares (WCSS) values, the genotypes were grouped into three distinct clusters, highlighting the genetic diversity among them. Cluster 1 contained 7 genotypes with a WCSS of 249.745, indicating a relatively moderate level of genetic variation within this group. Cluster 2 was the smallest, with only 1 genotype, showing no intra-cluster variability (WCSS = 0). Cluster 3 comprised 6 genotypes and exhibited the highest WCSS value (511.245), suggesting a greater level of genetic divergence among the genotypes within this cluster.

* The dendrogram in Fig.4 revealed clear genetic relationships among the genotypes, with closer branches representing genotypes with high genetic similarity. The elbow method suggested that three clusters were optimal, as the WCSS values showed a sharp decline up to three clusters and then plateaued, indicating that additional clusters would not significantly improve the grouping structure.

**Selection and Improvement Prospects:**

The presence of genotypic diversity across the clusters suggests that genotypes from different clusters can be used as potential parents for hybridization programs to maximize heterosis. The genotypes in Cluster 3, which exhibited the highest intra-cluster variability, could serve as valuable sources of novel genetic variations for improving yield and fibre quality traits. Conversely, the genotypes in Cluster 2, which showed no intra-cluster variability, may be genetically uniform and could be used for stabilizing specific traits in breeding programs.

* The cluster means provide insights into how different groups of cotton genotypes vary in their growth, yield, and fibre-related traits. Based on the data, the three clusters showed distinct trait variations, which help identify potential breeding strategies.
1. **Cluster 1 (7 genotypes):**
* Lowest plant height (PH) (136.37 cm) and lowest number of bolls (NB) (55.76) suggest that these genotypes may have shorter growth periods and lower boll production.
* Moderate lint weight (LW) (15.41 g) and seed weight (SW) (34.06 g) indicate that these genotypes have a balanced fibre and seed yield, though not the highest.
* Lowest yield per plot (YPO) (7.39 kg) suggests that these genotypes may be less productive compared to the others.
1. **Cluster 2 (1 genotype** **– homogeneous cluster):**
* Tallest plants (PH = 179.11 cm), highest NB (104.33), and highest lint weight (LW = 20.6 g) suggest that this genotype is a high-yielding, late-maturing variety.
* Highest seed weight (SW = 38.59 g) and highest yield per plot (YPO = 9.82 kg) indicate that this genotype produces the best fibre and seed output, making it an elite selection candidate.
1. **Cluster 3 (6 genotypes)**:
* Intermediate values for PH (147.13 cm), NB (68.70), and YPO (8.13 kg) suggest these genotypes have moderate growth duration and yield potential.
* Boll weight (BW = 5.62 g) is higher than Cluster 1 but lower than Cluster 2, indicating that these genotypes could benefit from targeted selection for boll weight improvement.

**Future Breeding Directions:**

Cluster 2 represents the best-performing genotype with the highest yield, fibre weight, and boll production. It could be used as a parent in breeding programs to transfer high-yield traits. Cluster 1 genotypes may be suitable for early-maturing varieties but require improvement in yield-related traits. Cluster 3 consists of genotypes with moderate performance, making them ideal for hybridization with high-yielding genotypes from Cluster 2 to enhance productivity.

**Table 1:** **Mean sum of squares of 14 cotton genotypes**

|  |
| --- |
| **Mean Sum of Squares** |
| **Characters** | **Genotypes (df=13)** | **Replication (df=2)** | **Error (df=26)** |
| **Plant height** | 464.17 | 31.24 | 22.75 |
| **No.of plants** | 7.80 | 0.74 | 2.66 |
| **Monopodial branches** | 0.53 | 0.15 | 0.20 |
| **Sympodial branches** | 5.70 | 1.96 | 1.62 |
| **No.of boles** | 578.12 | 8.39 | 40.96 |
| **Yield per plant** | 0.00 | 0.00 | 0.00 |
| **4 Lobs** | 16.69 | 1.52 | 4.68 |
| **5 Lobs** | 11.72 | 0.88 | 4.80 |
| **Boll weight** | 0.35 | 0.25 | 0.04 |
| **Lint weight** | 12.31 | 3.11 | 2.61 |
| **Seed weight** | 7.94 | 16.24 | 4.90 |
| **Yield per plot** | 2.50 | 0.76 | 0.28 |

**Table 2:** **Means of growth and yield parameters of 14 cotton genotypes**

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Genotypes** | **Ph** | **Np** | **Mp** | **Sp** | **Nb** | **Ypo** | **Ypl** | **4 lb** | **5lb** | **Bw** | **Lw** | **Sw** |
| **H-1345** | 135.56 | 37.33 | 1.00 | 24.11 | 57.56 | 6.96 | 0.19 | 28.67 | 35.67 | 4.83 | 12.94 | 31.09 |
| **H-1346** | 147.11 | 36.67 | 1.00 | 25.33 | 69.33 | 7.23 | 0.20 | 29.33 | 34.00 | 5.33 | 14.17 | 34.69 |
| **H-1347** | 137.11 | 37.33 | 1.67 | 26.56 | 58.56 | 6.85 | 0.18 | 31.00 | 35.67 | 5.30 | 13.88 | 34.91 |
| **US-7067** | 139.89 | 36.67 | 1.00 | 26.11 | 50.33 | 8.29 | 0.23 | 29.00 | 33.00 | 5.50 | 16.04 | 34.02 |
| **H-1350** | 141.78 | 38.67 | 1.67 | 23.56 | 65.56 | 7.71 | 0.20 | 30.67 | 36.33 | 5.37 | 15.58 | 33.73 |
| **H-1370** | 133.89 | 37.00 | 1.00 | 24.28 | 58.67 | 7.66 | 0.21 | 25.00 | 32.00 | 5.50 | 16.10 | 34.60 |
| **H-1348** | 143.78 | 39.00 | 1.67 | 26.22 | 55.11 | 7.81 | 0.20 | 31.00 | 32.67 | 5.67 | 16.83 | 35.35 |
| **CRISTAL 369** | 132.33 | 37.33 | 1.56 | 26.28 | 56.44 | 7.86 | 0.21 | 28.67 | 35.00 | 5.40 | 15.97 | 33.76 |
| **H-1349** | 146.22 | 39.67 | 2.00 | 27.22 | 70.44 | 8.85 | 0.22 | 32.33 | 37.00 | 5.90 | 19.04 | 36.23 |
| **H-1357** | 179.11 | 40.00 | 2.11 | 28.22 | 104.33 | 9.82 | 0.25 | 33.00 | 38.00 | 6.33 | 20.60 | 38.59 |
| **H-1368** | 158.78 | 38.67 | 1.67 | 26.33 | 57.11 | 7.78 | 0.20 | 27.00 | 33.00 | 5.60 | 16.19 | 35.54 |
| **RASHI SWIFT** | 141.11 | 39.33 | 2.00 | 27.44 | 75.44 | 8.36 | 0.21 | 32.33 | 36.33 | 5.73 | 17.34 | 35.32 |
| **H-1371** | 132.00 | 37.33 | 1.11 | 24.33 | 53.67 | 6.32 | 0.17 | 28.00 | 33.33 | 5.53 | 16.14 | 34.71 |
| **H-1378** | 147.78 | 39.33 | 1.89 | 26.33 | 74.33 | 8.84 | 0.22 | 32.67 | 37.67 | 5.77 | 18.19 | 35.25 |
| **Maximum** | 180.67 | 40 | 2.67 | 28.67 | 104.67 | 0.27 | 35.00 | 40.00 | 6.50 | 21.34 | 40.04 | 10.79 |
| **Minimum** | 124 | 34 | 0.33 | 22.67 | 47.00 | 0.14 | 24.00 | 30.00 | 4.50 | 11.20 | 29.51 | 5.41 |
| **Grand mean** | 144.03 | 37.40 | 1.52 | 25.88 | 64.78 | 0.21 | 29.90 | 34.98 | 5.55 | 16.36 | 34.84 | 7.88 |
| **SEm** | 2.75 | 0.94 | 0.26 | 0.73 | 3.70 | 0.01 | 1.25 | 1.27 | 0.12 | 0.93 | 1.28 | 0.31 |
| **CD (5%)** | 8.01 | 2.74 | 0.75 | 2.13 | 10.74 | 0.03 | 3.63 | 3.68 | 0.34 | 2.71 | 3.72 | 0.89 |
| **CD (1%)** | 10.82 | 3.70 | 1.01 | 2.88 | 14.52 | 0.04 | 4.91 | 4.97 | 0.46 | 3.67 | 5.02 | 1.21 |

Ph-Plant height, Np-Number of plants per plot, Mp-Monopodial branches, Sm-Sympodial branches, Nb-Number of bales, Ypo-Yield per plot, Ypl-yield per plant, 4 lb-Number of 4 lobed fruits, 5 lb-number of 5 lobed fruits, Bw-Boll weight, Lw-Lint weight per 10 bolls, Sw-Seed weight per 10 bolls.



**Fig.1: Contribution of different traits on the road to variations in 14 cotton genotypes**

**Note: For abbreviations of different traits see Table 2**

 **Table 3: Variability analysis of growth and yield traits in cotton genotypes**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Characters** | **GCV** | **PCV** | **H2 (Broad sense)** | **GA** | **GA % of mean** |
| **Plant height** | 8.42 | 9.05 | 0.87 | 23.26 | 16.15 |
| **Number of plants** | 3.50 | 5.59 | 0.39 | 1.69 | 4.51 |
| **Monopodial branches** | 21.81 | 36.38 | 0.36 | 0.41 | 26.93 |
| **Sympodial branches** | 4.51 | 6.67 | 0.46 | 1.63 | 6.29 |
| **Number of Bolls** | 20.66 | 22.90 | 0.81 | 24.87 | 38.39 |
| **Yield per plant** | 8.36 | 11.83 | 0.50 | 0.03 | 12.17 |
| **4 lobs** | 6.69 | 9.85 | 0.46 | 2.80 | 9.36 |
| **5 lobs** | 4.34 | 7.62 | 0.32 | 1.78 | 5.09 |
| **Boll weight** | 5.78 | 6.83 | 0.72 | 0.56 | 10.08 |
| **Lint weight** | 10.99 | 14.78 | 0.55 | 2.76 | 16.85 |
| **Seed weight** | 2.89 | 6.98 | 0.17 | 0.86 | 2.46 |
| **Yield per plot** | 10.93 | 12.85 | 0.72 | 1.51 | 19.16 |

**GCV-** Genotypic coefficient of variation, **PCV-** Phenotypic coefficient of variation, **H2(Broad sense)-** Heritability (broad sense), **GA-**Genetic Advance, **GA % of mean**- Genetic advance as a percentage of the mean.

**Table 4: Standard heterosis against check varieties in cotton genotypes**

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **GENOTYPES** | **Ph** | **Np** | **Mp** | **Sp** | **Nb** | **Ypl** | **4lb** | **5lb** | **Bw** | **Lw** | **Sw** | **Ypo** |
| **H-1345** | -1.61 | -6.30 | -34.21 | -9.39 | -5.23 | -9.09 | -4.43 | **2.57** | -12.87 | -21.34 | -9.53 | -14.81 |
| **H-1346** | **6.77** | -4.51 | -34.21 | -4.81 | **14.15** | -9.09 | -2.23 | -2.23 | -3.85 | -13.86 | **0.94** | -11.51 |
| **H-1347** | -0.48 | **1.81** | **9.87** | -0.19 | -3.58 | -18.18 | **3.33** | **2.57** | -4.39 | -15.62 | **1.58** | -16.16 |
| **H-1350** | **2.91** | **1.81** | **9.87** | -11.46 | **7.94** | -9.09 | **2.23** | **4.47** | -3.13 | -5.29 | -1.85 | -5.63 |
| **H-1370** | -2.82 | -2.70 | -34.21 | -8.76 | -3.40 | -4.55 | -16.67 | -7.98 | -0.78 | -2.13 | **0.68** | -6.24 |
| **H-1348** | **4.36** | **4.51** | **9.87** | -1.47 | -9.26 | -9.09 | **3.33** | -6.06 | **2.29** | **2.31** | **2.86** | -4.41 |
| **H-1349** | **6.13** | **6.30** | **31.58** | **2.29** | **15.98** | **4.55** | **7.77** | **6.39** | **6.43** | **15.74** | **5.42** | **8.32** |
| **H-1357** | **30.00** | **7.22** | **38.82** | **6.05** | **71.77** | **13.64** | **10.00** | **9.27** | **14.19** | **25.23** | **12.29** | **20.20** |
| **H-1368** | **15.24** | **2.70** | **9.87** | -1.05 | -5.97 | -9.09 | -10.00 | -5.11 | **1.02** | -1.58 | **3.41** | -4.77 |
| **H-1371** | -4.19 | -0.89 | -26.97 | -8.57 | -11.63 | -22.73 | -6.67 | -4.16 | -0.24 | -1.88 | **1.00** | -22.64 |
| **H-1378** | **7.26** | **5.41** | **24.34** | -1.05 | **22.38** | **4.55** | **8.90** | **8.32** | **4.09** | **10.58** | **2.57** | **8.20** |

**Note: For abbreviations of different traits see Table 2**

**Table 5:** **Pearson’s correlation coefficients in 14 cotton genotypes**

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Ph** | **Np** | **Mp** | **Sp** | **Nb** | **Ypl** | **4lb** | **5lb** | **Bw** | **Lw** | **Sw** | **Ypo** |
| **Ph** | **1.000** | 0.556\* | 0.549\* | 0.591\* | 0.786\*\*\* | 0.590\* | 0.431 NS | 0.404 NS | 0.713\*\* | 0.636\* | 0.754\*\* | 0.701\*\* |
| **Np** |  | **1.000** | 0.956\*\*\* | 0.677\*\* | 0.589\* | 0.404 NS | 0.698\*\* | 0.55\* | 0.804\*\*\* | 0.795\*\*\* | 0.773\*\* | 0.647\* |
| **Mp** |  |  | **1.000** | 0.716\*\* | 0.629\* | 0.455 NS | 0.768\*\* | 0.693\*\* | 0.698\*\* | 0.705\*\* | 0.663\*\* | 0.671\*\* |
| **Sp** |  |  |  | **1.000** | 0.559\* | 0.602\* | 0.619\* | 0.422 NS | 0.722\*\* | 0.658\* | 0.734\*\* | 0.701\*\* |
| **Nb** |  |  |  |  | **1.000** | 0.658\* | 0.645\* | 0.731\*\* | 0.704\*\* | 0.681\*\* | 0.694\*\* | 0.732\*\* |
| **Ypl** |  |  |  |  |  | **1.000** | 0.468 NS | 0.487 NS | 0.648\* | 0.726\*\* | 0.479 NS | 0.954\*\*\* |
| **4lb** |  |  |  |  |  |  | **1.000** | 0.812 \*\*\* | 0.517 NS | 0.527 NS | 0.466 NS | 0.583\* |
| **5lb** |  |  |  |  |  |  |  | **1.000** | 0.353 NS | 0.432 NS | 0.286 NS | 0.548\* |
| **Bw** |  |  |  |  |  |  |  |  | **1.000** | 0.963\*\*\* | 0.944\*\*\* | 0.801\*\*\* |
| **Lw** |  |  |  |  |  |  |  |  |  | **1.000** | 0.831\*\*\* | 0.854\*\*\* |
| **Sw** |  |  |  |  |  |  |  |  |  |  | **1.000** | 0.659\* |
| **Ypo** |  |  |  |  |  |  |  |  |  |  |  | **1.000** |



**Fig.2: Heat map on Pearson’s correlation coefficient in 14 cotton genotypes**

**Note: For abbreviations of different traits see Table 2**

**Table 6:** **Path analysis on direct and indirect effects of traits on yield in 14 cotton genotypes**

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Ph** | **Np** | **Mp** | **Sp** | **Nb** | **Ypl** | **4lb** | **5lb** | **Bw** | **Lw** | **Sw** | **Ypo** |
| **Ph** | **0.61479** | 0.26656 | 0.08647 | -0.48638 | -0.58857 | 0.7797 | 0.00822 | 0.16805 | 0.83381 | -0.23003 | -0.69528 | 0.75734\*\* |
| **Np** | 0.4245 | **0.38604** | 0.18169 | -0.58531 | -0.52514 | 0.67956 | 0.01653 | 0.28579 | 1.05405 | -0.36004 | -0.69881 | 0.85886\*\* |
| **Mp** | 0.45292 | 0.59763 | **0.11737** | -0.77678 | -0.6277 | 0.79075 | 0.01913 | 0.41344 | 0.97107 | -0.31257 | -0.70661 | 0.93865\*\* |
| **Sp** | 0.43913 | 0.33183 | 0.13389 | **-0.68094** | -0.4806 | 0.96976 | 0.01356 | 0.23279 | 0.93725 | -0.28493 | -0.68859 | 0.92315\*\* |
| **Nb** | 0.51908 | 0.29082 | 0.10568 | -0.46947 | **-0.69709** | 0.75768 | 0.01204 | 0.32096 | 0.83383 | -0.25474 | -0.63768 | 0.78111\*\* |
| **Ypl** | 0.46652 | 0.25532 | 0.09032 | -0.64268 | -0.51404 | **1.0275** | 0.00899 | 0.25064 | 0.86584 | -0.33141 | -0.47699 | 1.00001\*\* |
| **4lb** | 0.32952 | 0.41589 | 0.14632 | -0.6021 | -0.5469 | 0.60179 | **0.01534** | 0.4176 | 0.73162 | -0.22296 | -0.55223 | 0.73389\*\* |
| **5lb** | 0.32165 | 0.34349 | 0.15107 | -0.49351 | -0.69655 | 0.80179 | 0.01995 | **0.3212** | 0.55201 | -0.23234 | -0.29136 | 0.7974\*\* |
| **Bw** | 0.47458 | 0.37672 | 0.10551 | -0.59086 | -0.53813 | 0.85674 | 0.01039 | 0.16415 | **1.08004** | -0.35617 | -0.71405 | 0.86892\*\* |
| **Lw** | 0.43888 | 0.43134 | 0.11385 | -0.60211 | -0.55108 | 1.05676 | 0.01062 | 0.23159 | 1.19392 | **-0.32223** | -1.01214 | 0.98939\*\* |
| **Sw** | 0.77436 | 0.48871 | 0.15024 | -0.84943 | -0.80529 | 0.80211 | 0.01535 | 0.16954 | 1.39725 | -0.59084 | **-0.552** | 1.00000\*\* |
| **Ypo** | 0.61479 | 0.26656 | 0.08647 | -0.48638 | -0.58857 | 0.7797 | 0.00822 | 0.16805 | 0.83381 | -0.23003 | -0.69528 | **0.75734\*\*** |

**Note: For abbreviations of different traits see Table 2**



**Fig.3: Line graph representing optimal number of clusters through elbow method**

**Table 7: Tabular representation of number of members in the clusters and their within-cluster sum of squares (WCSS) values**

|  |
| --- |
| **Within Cluster Sum of Squares** |
| **Cluster No** | **No. of Members** | **Within SS** |
| **1** | 7 (1, 3, 4, 6, 7, 8, 13) | 249.745 |
| **2** | 1 (10) | 0 |
| **3** | 6 (2, 5, 9, 11, 12, 14) | 511.245 |
| **Total** | 14 | 760.99 |

**Table 8: Inter and Intra cluster distances in between the genotypes**

|  |  |  |  |
| --- | --- | --- | --- |
| **Inter Cluster Distances** |  |  |  |
| **Cluster No** | **1** | **2** | **3** |  | **Cluster** | **Intra-cluster Distance** |
| **1** | 7.55 |  |  |  | **1** | 7.55 |
| **2** | 65.52 | 0.00 |  |  | **2** | 0.00 (Only one sample) |
| **3** | 17.22 | 48.38 | 10.7 |  | **3** | 10.7 |



**Fig.4: Dendrogram based on the cluster analysis of 12 different traits showing relationship among 14 cotton genotypes**

**Table 9: Representation of traits in different clusters on the basis of mean value. Grand mean displayed the mean value of a trait from all three clusters**

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Cluster No** | **PH** | **NP** | **MP** | **SP** | **NB** | **YPL** | **4LB** | **5LB** | **BW** | **LW** | **SW** | **YPO** |
| **1** | 136.37 | 36.57 | 1.29 | 25.41 | 55.76 | 0.20 | 28.76 | 33.91 | 5.39 | 15.41 | 34.06 | 7.39 |
| **2** | 179.11 | 39.67 | 2.11 | 28.22 | 104.33 | 0.25 | 33.00 | 38.00 | 6.33 | 20.60 | 38.59 | 9.82 |
| **3** | 147.13 | 38.00 | 1.71 | 26.04 | 68.70 | 0.21 | 30.72 | 35.72 | 5.62 | 16.75 | 35.13 | 8.13 |
| **G. mean** | 154.20 | 38.08 | 1.70 | 26.56 | 76.27 | 0.22 | 30.83 | 35.88 | 5.78 | 17.59 | 35.93 | 8.45 |

**Note: For abbreviations of different traits see Table 2**

**Discussions:**

The present study provides comprehensive insights into the genetic diversity, heterosis, and variability of cotton genotypes, aiming to identify promising hybrids for yield and fibre improvement. The findings highlight the significance of heterotic effects, genetic variability, and trait associations in determining superior cotton genotypes for commercial cultivation and breeding programs.

**Genetic Variability and Trait selection:**

The high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for monopodial branches (MP) (21.81% and 36.38%) and number of bolls (NB) (20.66% and 22.90%) indicate the presence of substantial genetic variation, allowing for efficient selection in breeding programs. The high heritability (broad sense) observed in PH (0.87), NB (0.81), and YPO (0.72) suggests that these traits are highly inheritable, indicating the predominance of additive gene action, which facilitates effective selection. These findings are consistent with reports from previous studies that observed high heritability and genetic advance for yield-related traits in cotton genotypes (**Monisha, K. 2018 and Irum *et al.,* 2013**).

**Heterosis and performance of genotypes:**

The analysis of standard heterosis revealed that certain hybrids significantly outperformed the check varieties for growth, yield, and fibre traits. H-1357 exhibited the highest positive heterosis for plant height (30.00%), number of bolls per plant (71.77%), yield per plot (20.20%), and lint weight (25.23%), making it a superior hybrid for breeding programs. These results align with previous studies indicating that heterosis breeding plays a crucial role in improving yield potential and fibre quality in cotton (**Srinivas *et al.,* (2015)**). The presence of both positive and negative heterosis suggests that non-additive gene action influences the inheritance of these traits, making hybridization an effective approach for yield enhancement (**Karthickeyan *et al.,* 2025**).

**Path Analysis and Trait Relationships:**

The path coefficient analysis identified yield per plant (YPL), lint weight (LW), and boll weight (BW) as the most influential traits, exhibiting strong direct effects on yield per plot (YPO). The positive correlation between boll weight and lint weight (r = 0.963) and seed weight (r = 0.944) further suggests that larger bolls contribute to higher fibre and seed production, emphasizing the importance of these traits in selection programs. These results are in agreement with previous research that reported boll weight and lint weight as major determinants of cotton yield performance (**Srinivas *et al.,* (2015)**). The presence of strong indirect effects from plant height (PH), number of monopodial branches (MP), and number of sympodial branches (SP) suggests that these growth traits influence yield through their impact on reproductive structures.

**Cluster Analysis and Genetic Diversity:**

The hierarchical cluster analysis grouped the genotypes into three distinct clusters, demonstrating considerable genetic diversity among the evaluated hybrids. The presence of high-yielding genotypes in Cluster 2 suggests that these hybrids possess elite genetic potential for commercial cultivation. Meanwhile, Cluster 3 genotypes displayed moderate performance, indicating their suitability for hybridization with high-yielding genotypes to exploit genetic variability. The high within-cluster sum of squares (WCSS) in Cluster 3 further suggests that these genotypes exhibit greater genetic divergence, making them ideal candidates for selection in breeding programs aimed at enhancing adaptability and stress tolerance (**Jarwar *et al.,* 2019**).

**Significance:**

The following study “Evaluation of Genetic Diversity and Heterosis in Cotton (*Gossypium hirsutum* L.) genotypes: A Comprehensive Study on Yield, Fibre Quality, and Breeding Potential” offers important information for programs aimed at improving cotton. According to the study, H-1357 and H-1349 are two promising cotton hybrids that show superior traits for commercial breeding, with an emphasis on genetic stability, fibre quality, and yield enhancement. The results guarantee higher productivity, fibre quality, and economic viability for cotton farmers, which advances cotton breeding. Because these characteristics have a direct impact on overall productivity, it also emphasises how crucial it is to choose hybrids with positive heterosis for yield components like the number of bolls, boll weight, and lint weight.

**Conclusion:**

This study provided a comprehensive evaluation of growth, yield, and fibre-related traits in cotton genotypes, identifying key genotypes for future breeding programs. Cluster analysis classified the genotypes into three distinct clusters, demonstrating significant genetic variability. The heterosis analysis highlighted that H-1357 exhibited the highest positive heterosis for most traits, including plant height, number of bolls, yield per plot, and lint weight, making it an ideal candidate for hybridization and commercial cultivation. Path analysis confirmed that YPL, BW, and LW had the strongest direct effects on yield per plot, suggesting that these traits should be prioritized in selection programs. Variability analysis showed high heritability and genetic advance for key traits like NB, PH, and YPO, indicating their potential for significant genetic improvement. The findings of this study emphasize the need for a multi-trait selection approach, integrating high-yielding hybrids, genetically diverse parental lines, and superior fibre quality traits. The genotypes identified in Cluster 3 with high variability and those in Cluster 2 with elite yield potential can serve as valuable breeding materials. Future research should focus on stabilizing high-yielding hybrids and exploring genetic mechanisms governing fibre quality and yield stability. The results contribute to cotton breeding advancements, ensuring increased productivity, fibre quality, and economic viability for cotton farmers.

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