

INHERITANCE OF QUANTITATIVE TRAITS AND EVALUATION OF SELECTION EFFICIENCY FOR THE DEVELOPMENT OF PROMISING COTTON (*GOSSYPIMUM HIRSUTUM* L.) GENOTYPES

Namozov Zuxriddin Abdikarimovich

Mustaqil-tadqiqotchi

<https://orcid.org/0009-0009-4328-3286>

Abstract

The improvement of cotton productivity depends largely on the effective utilization of genetic variability and the identification of quantitative traits that can respond efficiently to selection. The present study focuses on the inheritance of economically important quantitative traits and the evaluation of their significance for selection in *Gossypium hirsutum* L. breeding material. Major morphological, yield-related, and fiber traits, including plant height, number of fruiting branches, number of bolls per plant, boll weight, seed cotton yield, fiber percentage, and fiber length, were considered. Genetic and phenotypic variability, heritability, genetic advance, and relationships among quantitative traits were used as major criteria for determining their breeding value. The integrated evaluation showed that the efficiency of selection depends not only on the magnitude of phenotypic variability but also on the genetic contribution to trait expression and relationships among yield components. Traits characterized by substantial genetic variability, relatively high heritability, and favorable associations with productivity can be considered valuable selection criteria. The combined assessment of quantitative traits provides a reliable basis for identifying promising breeding material and developing cotton genotypes combining productivity with desirable fiber characteristics. The results emphasize the importance of integrating genetic parameters and phenotypic evaluation in cotton breeding programs aimed at developing improved varieties.

Keywords: *Gossypium hirsutum* L., cotton, quantitative traits, inheritance, genetic variability, heritability, genetic advance, selection efficiency, breeding.

Introduction

Cotton (*Gossypium hirsutum* L.) is one of the world's most important industrial crops and represents the major natural source of textile fiber. Upland cotton accounts for the predominant proportion of global cotton production because of its high adaptability, productivity, and acceptable fiber quality. Increasing demand for high-quality raw materials and the influence of changing environmental conditions require the development of cotton varieties combining high yield potential, fiber quality, adaptability, and stability.

The development of improved varieties depends on the availability and efficient utilization of genetic variation. In breeding populations, economically

important characteristics such as plant height, fruiting branch number, boll number, boll weight, seed cotton yield, fiber percentage, and fiber length are generally quantitative in nature. Their expression is controlled by multiple genes and is influenced to different degrees by environmental conditions. Therefore, direct phenotypic evaluation alone may not provide sufficient information about the genetic value of breeding material.

Genetic variability is a prerequisite for successful selection. The magnitude of genotypic variation determines the potential for genetic improvement, whereas phenotypic variation represents the combined effects of genotype and environment. Comparison of genotypic and phenotypic variation makes it possible to estimate the relative influence of environmental factors on trait expression.

Heritability is another important genetic parameter used to predict the reliability of phenotypic selection. High heritability indicates that a considerable proportion of observed variation is associated with genetic differences among genotypes. Nevertheless, heritability should not be interpreted independently. Its combination with genetic advance provides more useful information about the expected response to selection and the potential contribution of transmissible genetic effects.

Yield is one of the most complex quantitative characteristics in cotton. It results from interactions among several morphological and reproductive components. Therefore, selection for yield should consider not only final seed cotton productivity but also traits contributing to yield formation. Relationships among boll number, boll weight, fruiting branch number, plant architecture, and fiber characteristics can provide additional criteria for indirect selection.

The efficiency of cotton breeding can consequently be improved by integrating information on phenotypic performance, genetic variability, heritability, genetic advance, and relationships among economically important traits. Such an approach facilitates the identification of genotypes with favorable combinations of characteristics and increases the probability of selecting valuable parental material and advanced breeding lines.

The objective of the present study was to assess the inheritance and genetic variability of major quantitative traits in *Gossypium hirsutum* L., evaluate their potential response to selection, and determine their importance for identifying promising genotypes suitable for the development of improved cotton varieties.

Materials and Methods

Plant material and experimental evaluation

The study was conducted using *Gossypium hirsutum* L. genotypes representing breeding material with variation in morphological, productivity, and fiber characteristics. The genotypes were evaluated under field conditions during the growing season.

Phenological and morphological observations were performed at appropriate stages of plant development. Representative plants were selected for biometric measurements to characterize within- and between-genotype variation.

The principal quantitative characteristics evaluated included plant height, number of fruiting branches per plant, number of bolls per plant, average boll weight, seed cotton yield, fiber percentage, and fiber length. These traits were selected because of their direct or indirect importance for productivity, plant architecture, and technological fiber quality.

Evaluation of genetic variability

Phenotypic variation was considered to consist of genetic and environmental components. Genotypic and phenotypic coefficients of variation were used to compare the relative magnitude of variation among quantitative characteristics.

A small difference between GCV and PCV was interpreted as an indication of comparatively limited environmental influence, whereas a greater difference indicated stronger environmental modification of phenotypic expression.

Heritability and genetic advance

Broad-sense heritability was estimated as the proportion of phenotypic variance attributable to genetic variance:

$$H^2 = \sigma^2g / \sigma^2p \times 100$$

The expected genetic advance was considered together with heritability to evaluate the potential effectiveness of selection. Genetic advance as a percentage of the mean was also used to compare the expected selection response among characteristics expressed in different measurement units.

Traits combining relatively high heritability with substantial genetic advance were considered particularly promising for phenotypic selection.

Trait relationships and selection efficiency

Relationships among quantitative traits were evaluated to determine the contribution of individual characteristics to productivity. Particular attention was given to relationships between seed cotton yield and its major components, including boll number, boll weight, fruiting branch number, and fiber characteristics.

The overall selection value of individual traits was assessed by integrating their variability, heritability, expected genetic response, and association with economically important characteristics. Genotypes possessing favorable combinations of productivity and fiber traits were regarded as promising breeding material.

Results

The comparative evaluation of *G. hirsutum* genotypes revealed noticeable variation in the expression of the studied quantitative characteristics. Differences were observed in plant architecture, reproductive development, yield components,

and fiber-related traits, demonstrating the presence of potentially useful variability within the breeding material.

Plant height and fruiting branch number reflected differences in plant architecture among genotypes. These characteristics are important because the spatial distribution of fruiting structures influences boll formation and ultimately affects productivity. However, increased vegetative growth alone should not be regarded as an indicator of superior yield performance because excessive vegetative development may alter the balance between vegetative and reproductive growth.

Variation in boll number and boll weight was particularly important from a breeding perspective. Both characteristics represent major components of seed cotton yield. Genotypes capable of maintaining a favorable combination of boll number and boll weight are potentially valuable sources for increasing productivity.

The comparison of genotypic and phenotypic variation indicated that environmental influence differed among the studied characteristics. Traits with comparatively close genotypic and phenotypic variation can be regarded as more genetically stable, whereas greater differences indicate a stronger contribution of environmental conditions to observed phenotypic variability.

Heritability assessment further demonstrated that quantitative characteristics differ in the extent to which their phenotypic variation reflects genetic differences. Characteristics with a substantial heritable component provide greater opportunities for effective phenotypic selection. Nevertheless, the breeding value of high heritability becomes more informative when considered together with expected genetic advance.

Traits combining high heritability with substantial genetic advance are particularly valuable because this combination suggests that a meaningful proportion of phenotypic variation can be transferred to subsequent generations. Such characteristics can respond more efficiently to directional selection and can therefore serve as practical criteria for distinguishing superior breeding material. Seed cotton yield exhibited a complex relationship with its component traits. Yield formation cannot be explained by a single morphological characteristic because it results from the combined effects of plant architecture, fruiting capacity, boll retention, boll size, and other physiological and environmental factors. Consequently, simultaneous evaluation of several yield components provides a more reliable strategy than selection based exclusively on final yield.

Fiber percentage and fiber length represent important technological characteristics that should be considered simultaneously with productivity. Selection focused exclusively on high seed cotton yield may not necessarily result in genotypes possessing desirable fiber characteristics. Therefore, breeding material should be evaluated for the balance between agronomic productivity and technological quality.

The integrated evaluation of quantitative traits allowed the identification of characteristics that may be particularly informative for selection. Genotypes combining favorable productivity components, relatively stable phenotypic expression, and desirable fiber characteristics represent the most valuable material for subsequent breeding cycles and the development of new cotton varieties.

Discussion

Quantitative traits in cotton are characterized by complex genetic control and considerable environmental sensitivity. Consequently, determining the genetic component of phenotypic variability is fundamental for designing effective selection programs.

The presence of substantial variation among genotypes creates opportunities for genetic improvement. However, phenotypic variability itself does not guarantee successful selection. When a trait is strongly influenced by environmental conditions, phenotypically superior plants may not necessarily transmit the same performance to subsequent generations. This emphasizes the importance of considering heritability together with the magnitude of variability.

The joint interpretation of heritability and genetic advance is especially useful for determining the potential response to selection. High heritability associated with high genetic advance generally suggests that selection based on phenotypic performance may result in meaningful genetic improvement. In contrast, high heritability accompanied by limited genetic advance may indicate more complex genetic control and reduce the efficiency of straightforward phenotypic selection. Yield improvement represents a particularly challenging objective because seed cotton yield is determined by several interdependent characteristics. Boll number and boll weight are among the most direct yield components, whereas fruiting branch number and plant architecture influence the formation and distribution of reproductive structures. The contribution of these traits may vary among genetic backgrounds and environmental conditions.

Therefore, selection based on several complementary characteristics is likely to be more reliable than selection for yield alone. Genotypes combining favorable boll characteristics with suitable plant architecture and acceptable fiber properties should receive priority in breeding programs.

Another important aspect is the simultaneous improvement of productivity and fiber quality. Modern cotton breeding requires varieties capable of providing high yield without deterioration in fiber characteristics. Genetic relationships between yield and fiber traits can complicate simultaneous improvement when unfavorable associations occur. The use of diverse parental material and careful evaluation across breeding generations can help obtain desirable recombinations. The assessment of quantitative trait inheritance also has direct implications for parental selection. Genotypes displaying desirable values for highly heritable traits

can serve as valuable sources of favorable alleles. Crossing genetically differentiated parents with complementary characteristics may broaden variability in segregating generations and increase opportunities for obtaining superior recombinants.

The present approach demonstrates that breeding efficiency should be evaluated through an integrated framework rather than on the basis of a single parameter. Genetic variability indicates the available diversity, heritability reflects the genetic contribution to phenotypic expression, genetic advance predicts potential response to selection, and trait relationships provide information on the consequences of simultaneous selection.

Together, these parameters provide a scientific basis for identifying promising genotypes and improving the efficiency of breeding programs aimed at developing new *G. hirsutum* varieties.

Conclusion

The inheritance and selection value of quantitative traits represent fundamental components of genetic improvement in cotton. The evaluation of *Gossypium hirsutum* L. breeding material demonstrated that economically important characteristics differ in their variability, genetic determination, and potential response to selection.

The combined consideration of genotypic and phenotypic variability, heritability, genetic advance, and relationships among traits provides a more reliable basis for selection than the use of phenotypic performance alone. Traits combining substantial genetic variability, relatively high heritability, and favorable expected genetic response are particularly valuable as selection criteria.

Yield improvement should be based on the simultaneous evaluation of major productivity components, particularly boll number and boll weight, while maintaining desirable fiber percentage and fiber length. Such an integrated selection strategy can increase the probability of identifying genetically valuable forms with a favorable balance between productivity and fiber quality.

Promising genotypes identified through comprehensive quantitative trait evaluation can be used both as direct selection material and as parental forms in hybridization programs. The integration of genetic parameters with conventional phenotypic selection can therefore improve breeding efficiency and contribute to the development of new high-yielding and agronomically valuable cotton varieties.

References

1. Allard R.W. *Principles of Plant Breeding*. 2nd ed. New York: John Wiley & Sons; 1999.

2. Burton G.W., DeVane E.H. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*. 1953;45:478–481.
3. Falconer D.S., Mackay T.F.C. *Introduction to Quantitative Genetics*. 4th ed. Harlow: Longman; 1996.
4. Johnson H.W., Robinson H.F., Comstock R.E. Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*. 1955;47:314–318.
5. Khan N.U., Hassan G., Marwat K.B., Batool S., Makhdoom K., Khan I., et al. Genetic variability and heritability in upland cotton. *Pakistan Journal of Botany*. 2009;41(4):1695–1705.
6. Ulloa M., Meredith W.R. Genetic linkage map and QTL analysis of agronomic and fiber quality traits in an intraspecific population. *Journal of Cotton Science*. 2000;4:161–170.
7. Zeng L., Meredith W.R., Gutierrez O.A., Boykin D.L. Identification of associations between SSR markers and fiber traits in an exotic germplasm derived from multiple crosses among *Gossypium tetraploid* species. *Theoretical and Applied Genetics*. 2009;119:93–103.
8. Abdurakhmonov I.Y., Kohel R.J., Yu J.Z., Pepper A.E., Abdullaev A.A., Kushanov F.N., et al. Molecular diversity and association mapping of fiber quality traits in exotic *G. hirsutum* L. germplasm. *Genomics*. 2008;92:478–487.
9. Fang D.D., Percy R.G., editors. *Cotton*. 2nd ed. Madison, WI: American Society of Agronomy, Crop Science Society of America, Soil Science Society of America; 2015.
10. Zhang T., Hu Y., Jiang W., Fang L., Guan X., Chen J., et al. Sequencing of allotetraploid cotton (*Gossypium hirsutum* L. acc. TM-1) provides a resource for fiber improvement. *Nature Biotechnology*. 2015;33:531–537.
11. Huang G., Huang J.Q., Chen X.Y., Zhu Y.X. Recent advances and future perspectives in cotton research. *Annual Review of Plant Biology*. 2021;72:437–462.
12. Li F., Fan G., Lu C., Xiao G., Zou C., Kohel R.J., et al. Genome sequence of cultivated upland cotton (*Gossypium hirsutum* TM-1) provides insights into genome evolution. *Nature Biotechnology*. 2015;33:524–530.