IOSR Journal of Biotechnology and Biochemistry (IOSR-JBB)
ISSN: 2455-264X, Volume 5, Issue 2 (Mar. – Apr. 2019), PP 53-58
www.iosrjournals.org

Studies on Genetic Variability and Heritability in Okra (*Abelmoschus esculentus* L.)

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Abstract
Okra (Abelmoschus esculentus L.) is one of the most economically and nutritionally significant vegetable crops grown across tropical and subtropical regions of the world. Improving its yield, quality, and stress tolerance through systematic breeding depends critically on understanding the genetic architecture of key traits — and that is precisely where studies on genetic variability and heritability become indispensable. This article reviews the current body of research on genetic variability, heritability, and genetic advance in okra, examining how these parameters behave across traits like fruit yield, plant height, days to first flowering, number of branches, and pod characteristics. The review draws on decades of field trials, germplasm evaluations, and quantitative genetic analyses to show that most economically important traits in okra display considerable genotypic variation, moderate to high heritability, and, in many cases, high genetic advance — a combination that breeders regard as the most favorable scenario for effective selection. The article also discusses the statistical tools used to partition variance, the implications of genotype-environment interaction, and the practical consequences of these findings for okra improvement programs in South Asia, Africa, and beyond.

Keywords: *genetic variability, genetic advance, plant breeding, okra, heritability, quantitative traits*

I. Introduction

Okra is one of those crops that rarely gets the headline attention of rice or wheat, but try telling that to a farmer in Bihar, a smallholder in West Africa, or a home cook in the American South. This warm-season vegetable — technically a fruit — is consumed in extraordinary quantities across more than 80 countries. Its tender pods are rich in dietary fiber, folate, vitamins C and K, and various antioxidants. The plant itself is remarkably heat-tolerant and drought-hardy, which makes it particularly valuable in regions where other vegetables struggle to survive the summer months.

Despite its importance, average okra yields remain frustratingly low in most producing countries. In India, for instance, national average yields hover around 8–10 tones per hectare, well below the crop's genetic potential, which experimental plots have demonstrated can exceed 20 tones per hectare under optimal conditions (Reddy *et al.,* 2013). Closing that gap requires sustained breeding effort — and sustained breeding effort requires a clear understanding of the genetic variability present within available germplasm, as well as the heritability of the traits breeders most want to improve.

Genetic variability is the raw material of breeding. Without it, selection has nothing to work with. A population where all individuals are genetically identical for a given trait will not respond to selection no matter how intense the selection pressure applied. Heritability, on the other hand, tells breeders how much of the observed variation between plants is actually due to their genetic differences, as opposed to environmental fluctuations in soil, rainfall, temperature, or agronomic management. High heritability means that superior-performing plants are likely to pass that superiority on to their offspring. Low heritability means that today's best performer might simply have gotten lucky with a favorable microenvironment — and its seeds will disappoint you next season.

Together, genetic variability and heritability estimates form the foundation for predicting genetic advance — the actual gain in mean performance that a breeding program can expect from one cycle of selection. This trio of parameters has been studied extensively in okra since the 1970s, with research accelerating sharply in the 2000s as more germplasm collections became available for evaluation and statistical methods for analyzing quantitative traits became more accessible.

This article reviews what that body of research has established, where the gaps and disagreements remain, and what the collective findings mean for practical okra improvement.

II. Understanding the Parameters: Variability, Heritability, and Genetic Advance

2.1 What Genetic Variability Really Means in Practice

The research work of plant breeders who study genetic diversity in crops focuses on two main questions: which plant characteristics show the most genetic variation and which specific traits depend on their inherited genetic material? The standard way to quantify this involves partitioning the total phenotypic variance observed in a population into its genetic and environmental components. The analysis produces two main statistical results. The first measurement, genotypic coefficient of variation (GCV), lets scientists determine genetic diversity in traits by calculating the genetic variation to trait mean ratio because it enables them to compare different traits that have different unit measurements. The second measurement, phenotypic coefficient of variation (PCV), needs to be used because it measures all existing variations including the natural environmental variations that happen in the study. When GCV and PCV values approach each other, the result shows which environmental factors caused plant differences because breeders can trust that all visible traits arise from plant genetics.

The existence of high GCV values for a trait indicates that scientists have sufficient genetic diversity available for research purposes. Selection becomes challenging because of low GCV values, which require breeders to examine extensive germplasm collections and use induced mutagenesis and interspecific hybridization methods to create new genetic diversity. The analysis of multiple okra experiments shows that plant height and fruit yield per plant and number of fruits per plant display moderate to high GCV values, whereas days to first flowering shows a more restricted distribution (Adeniji *et al.,* 2007; Akinyele and Osekita, 2006).

2.2 Heritability: The Signal-to-Noise Ratio of Genetics

Heritability as a broad concept measures how much total phenotypic variance scientific study finds between different human beings because of their genetic differences. A heritability of 0.8 for a trait means that 80% of the observed variation between plants reflects genuine genetic differences — the remaining 20% is environmental noise. A heritability of 0.3 means the opposite: most of what you observe reflects circumstance, not inheritance.

The common method used to assess heritability in crop breeding studies shows broad-sense heritability (H^2) because it provides easy calculations from field trial data that researchers replicate. Narrow-sense heritability (h^2) enables genetic variance partitioning into two parts which include additive and non-additive components; this method predicts selection response better than other methods but needs advanced testing setups for proper estimation.

The combination of heritability estimates with genetic advance shows practical breeding value for estimation purposes. A trait can show high heritability but low genetic advance if the genetic variance is primarily non-additive — meaning that gene interactions (dominance and epistasis) drive most of the genetic differences rather than the straightforward additive effects that selection actually captures. A trait can achieve high genetic advancement with moderate heritability when it possesses high additive genetic variance. The combination that breeders most want to see — and that appears frequently in okra research — is high heritability paired with high genetic advance expressed as a percentage of the mean (Falconer and Mackay, 1996; Singh and Chaudhary, 2004).

III. Genetic Variability Studies in Okra: What the Research Shows

3.1 Variation Across Yield and Yield-Related Traits

The most critical research area for farmers and breeders focuses on fruit yield per plant which serves as their primary breeding objective. Studies consistently report wide genotypic variation for this trait in okra. The research conducted by Mulukenet *al.* (2015) assessed 50 okra genotypes through a large-scale evaluation which produced GCV values that ranged between 18% and 32% across different environments while the corresponding PCV values showed only slight increases. Indian germplasm evaluations have shown similar results according to the research conducted by Patel *et al.* (2012) and Sharma *et al.* (2011). The three main elements that determine okra yield are number of fruits per plant, average fruit weight, and fruit length, which display significant genetic differences. The number of fruits per plant shows the greatest differences between plant varieties because this measurement responds better to management methods while it depends on branching behavior and the length oftime fruits develop. Fruit weight shows somewhat lower variability but is particularly important for market acceptability — consumers in most markets strongly prefer pods within specific size ranges. Okra demonstrates various genetic differences in plant height measurements. Consumers need this information because taller plants usually produce higher crop yields but plant height affects various factors including harvest efficiency and lodging resistance and canopy architecture. The species includes genotypes that range from compact 60 cm types to sprawling 200 cm plants which enables breeders to choose growth habits that match various production systems (Reddy *et al.* 2013).

3.2 Days to Flowering and Maturity

Days to first flowering is an essential trait for okra breeders who need to establish their breeding programs according to different growing seasons and market availability periods. Early-flowering genotypes enable rainfed systems to avoid terminal drought stress while developing marketable pods before peak-season price collapse and their use in intensive agricultural systems that require constant land availability. Late-flowering types may suit environments with long, reliable rainy seasons where extended vegetative growth translates into higher total biomass and yield.

The genetic variation of okra days to first flowering shows moderate levels because it permits meaningful selection despite being lower than yield traits. The research conducted in West Africa and South Asia discovered GCV values for this particular characteristic that range between 8 and 15 percent (Adeniji *et al.,* 2007; Patel *et al.,* 2012). The narrow range exists because okra flowering time depends on photoperiod responses which restrict the environmental range that produces adaptive variation. The existing constraints allow enough variation to modify mean flowering time by one to two weeks through a single selection cycle which has significant practical implications.

Days to first pod harvest shows a similar pattern because it demonstrates moderate variability while GCV values exceed flowering results by several percentage points due to increased pod development rate differences among genotypes.

Figure 1 illustrates how genetic and phenotypic coefficients of variation compare across major okra traits, drawing on pooled estimates from multiple published studies, and highlights the traits where genetic variation is richest relative to environmental noise.

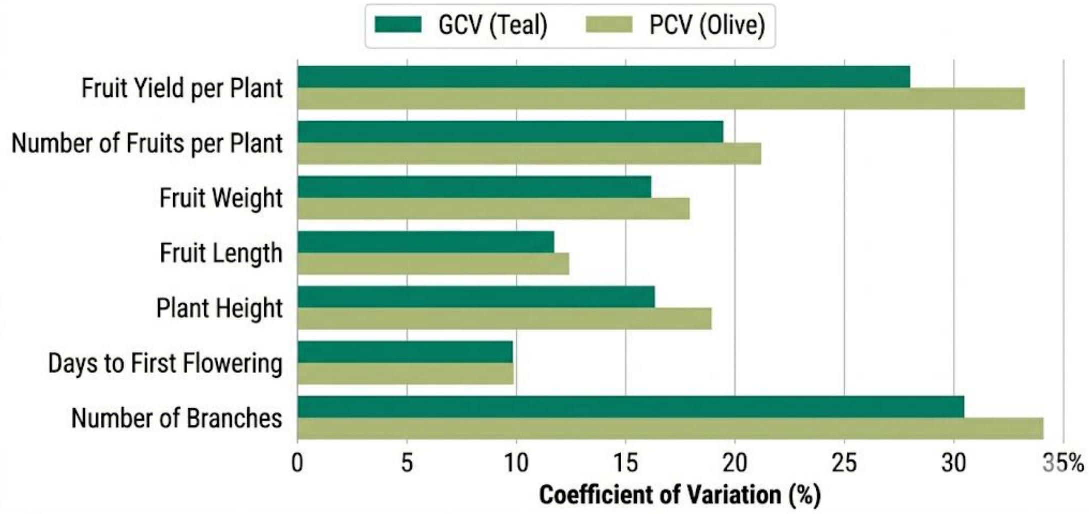

Figure 1: Comparison of Genotypic and Phenotypic Coefficients of Variation Across Key Okra Traits — Pooled Estimates from Multi-Environment Trials

This horizontal paired bar chart displays genotypic coefficient of variation (GCV, shown in dark bars) and phenotypic coefficient of variation (PCV, shown in lighter bars) for seven key okra traits: fruit yield per plant, number of fruits per plant, fruit weight, fruit length, plant height, days to first flowering, and number of branches. The horizontal axis represents coefficient of variation as a percentage, ranging from 0% to 35%. The GCV values for yield and branching traits reach their maximum between 18% and 32% while days to flowering and fruit length measurements show GCV values between 8% and 15%. The gap between GCV and PCV bars is narrowest for days to first flowering, indicating low environmental influence on that trait, while fruit yield per plant shows a somewhat larger PCV-GCV gap, reflecting greater sensitivity to environmental conditions. The primary insight shows that yield-related traits contain the most usable genetic variation, which businesses can use to improve their products yet these traits also show the strongest response to environmental changes.

3.3 Variability in Quality Traits

Okra breeders now focus on quality traits which include pod fiber content and pod color and pod mucilage content and their protection against yellowing after harvest. The specified traits hold great importance because they determine how okra will be used in fresh markets and processing facilities while customer preferences for these traits continue to develop as okra enters high-end urban markets and international export networks.

Researchers have studied yield traits more extensively than they have examined quality traits because the process of measuring quality traits needs more resources to achieve precise results. Research studies found that these traits show significant genetic variation for pod color which ranges from pale green through deep green to red-podded genotypes and for mucilage content which determines cooking quality and perceived palatability and for fiber content at harvest (Salehuzzaman*et al.,* 2008). Red-podded okra genotypes display higher anthocyanin concentrations together with more potent antioxidant properties which have gained popularity among health-conscious consumers although breeding programs traditionally neglected these traits in favor of yield optimization.

IV. Heritability Estimates Across Okra Traits

4.1 High-Heritability Traits and Their Implications

The reviewed studies show that plant height and days to first flowering and fruit length and number of branches have broad-sense heritability estimates which range from 70 to 90 percent (Akinyele and Osekita, 2006; Benchasri, 2012; Sharma *et al.,* 2011). The developmental nature of days to first flowering makes it easy to understand because the trait depends on a few major genes which control the process and thus show less response to environmental changes that impact yield measurements.

Breeders can use plant height heritability to choose between compact and tall growth habits because selected plants will produce offspring with the same traits. This is practically important because plant architecture influences everything from irrigation efficiency to labor costs at harvest. When a breeder selects short-statured plants in one generation, she can be reasonably confident her next generation will be shorter on average — and that is exactly the kind of predictability that makes a breeding program efficient.

4.2 Yield Traits: Moderate Heritability, High Genetic Advance

Heritability estimates for fruit yield per plant and number of fruits per plant display greater variability between research studies, which typically report moderate heritability values that range from 50 to 75 percent. The reported estimates show variability because natural environmental differences and distinct germplasm sets exist, while the studies differ in their measurement methods by some studies using single-season data and other studies using multi-season or multi-location means, which results in higher heritability estimates through location-specific environmental effect averaging.

The research findings demonstrate that okra yield traits show strong genetic progress, which occurs even when heritability levels remain at intermediate values. Breeders use the mean fruit yield genetic advance percentage, which exceeds 20-30 percent in published studies, as a selection effectiveness indicator that shows positive breeding value for selection (Patel *et al.* 2012; Reddy *et al.* 2013). The additive genetic variance pattern shows that it accounts for a significant portion of okra yield variation, which benefits traditional pedigree and mass selection methods.

The relationship between heritability and genetic advance in okra traits follows a pattern that shows two distinct improvement paths because traits in the high-heritability high-genetic-advance quadrant can be improved through direct selection while high-heritability traits with low-genetic-advance require other breeding methods.

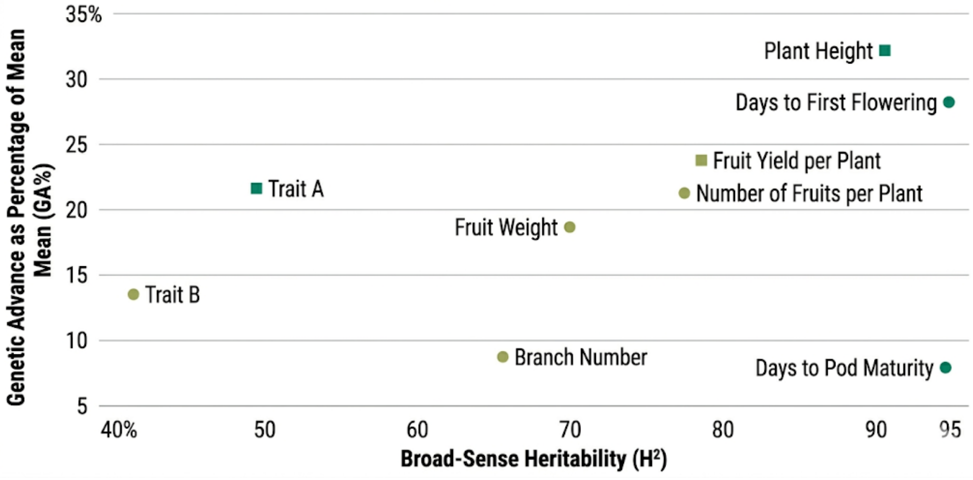

Figure 2: Scatter Plot of Broad-Sense Heritability vs Genetic Advance as Percentage of Mean for Key Okra Traits

The scatter plot shows seven okra traits which are plotted onto two axes which show broad-sense heritability measurements known as H² on the x-axis which extends from 40% to 95% and genetic advance measurements known as GA% on the y-axis which extends from 5% to 35%. Data points represent each trait which comes with a corresponding label. The upper-right quadrant shows plant height together with days to first flowering which exhibit both high H^2 and high GA% values which confirm their suitability for direct selection. The middle-right zone shows fruit yield per plant together with number of fruits per plant which display moderate-to-high H^2 and high GA% values that produce effective selection results although environmental conditions affect their performance. The lower-right quadrant of the graph displays days to pod maturity which shows high H^2 values and low GA% values because non-additive genetic effects control this trait. The visual pattern clearly identifies which traits breeders should prioritize for direct phenotypic selection versus which traits they should use marker-assisted selection or population improvement methods to develop.

4.3 Genotype-Environment Interaction and Its Consequences

The practical value of variability research extends to its ability to show how different genotypes respond to testing in various environmental conditions. The genotype which achieves the highest yield in Patna performs at an average level in Varanasi and shows poor results in Dhaka. The phenomenon known as genotype-environment interaction (GEI) creates major difficulties for researchers who need to understand both variability and heritability measurement results. Heritability estimates become invalid when GEI effects exceed the genetic variation present in the studied population. The GCV value derived from one specific trial will create an excessive prediction of genetic variation which breeders can use across all environmental testing situations. Modern okra breeding programs now assess potential genotypes through testing at three to five different locations which represent all possible environmental conditions before they select specific varieties for release (Muluken*et al*., 2015).

Research identifies certain okra traits which maintain their genotypic rankings between different environmental conditions because plant height and days to flowering show greater consistency than fruit yield per plant which experiences major rank fluctuations between locations. Researchers have utilized stability analysis methods such as AMMI (Additive Main Effects and Multiplicative Interaction) and GGE biplot approaches to examine okra data in recent years for identifying genotypes that achieve high average yield while maintaining stability across different environments (Benchasri, 2012 and Sharma *et al.,* 2011). The most valuable outcomes of a study about variability and heritability research create multiple genotypes which produce superior results throughout all locations where farmers cultivate okra.

V. Genetic Diversity and Its Sources

5.1 Landraces, Wild Relatives, and Introduced Germplasm

Three main sources provide genetic diversity for the purpose of okra breeding development. Farmers who protect their landraces through time across multiple agricultural regions provide the primary base of genetic diversity which can be used for breeding purposes. The wild relatives of cultivated plants especially the other Abelmoschus species contain valuable genetic traits which provide protections against diseases and enable drought survival and other essential characteristics which do not exist in the cultivated gene pool. The breeding programs at local institutions can access different plant varieties which come from international collections and especially from AVRDC (now the World Vegetable Center) and Indian and Nigerian and Ethiopian national genebanks.

Research studies show that landraces together with germplasm accessions from multiple geographic regions have greater genetic variations than the improved crop varieties which breeding programs developed through their official methods according to the findings of Salehuzzaman and his colleagues in 2008. The finding occurs because the majority of improved variety programs which use intense selection methods and choose their starting plants from a limited selection have created decreased genetic diversity within their developed varieties but achieved higher crop yield results. The practical implication is that breeding programs should prioritize landrace and wild relative germplasm diversity because climate change creates new challenges for breeding programs which need heat tolerance and water-use efficiency and disease resistance traits.

5.2 Molecular Markers and Genetic Diversity Assessment

The researchers developed a new method to investigate okra genetic diversity through their molecular marker research. The researchers used SSR and SNP markers to study genetic diversity across collection sites which contained accessions ranging between 50 and 500 samples (Nwangburuka*et al.,* 2011 and Zhao *et al.,* 2016).

The research shows that okra genetic diversity changes according to geographic location because South Asian and Southeast Asian accessions display different diversity patterns than African and Middle Eastern accessions. The research demonstrates that accessions with different morphological characteristics maintain close genetic ties while accessions that look alike in the field show hidden genetic variations in their molecular marker alleles. Breeders use this information to create crosses which will produce maximum heterosis while preventing unintentional inbreeding from occurring in their breeding populations.

VI. Conclusion

Genetic variability and heritability studies have collectively painted a reasonably clear picture of okra's quantitative genetic landscape. Most traits of importance to breeders — fruit yield, number of fruits, plant height, days to flowering, and various pod quality characteristics — show meaningful genetic variation within available germplasm. Heritability estimates for many traits are moderate to high, and genetic advance calculations suggest that selection will produce substantial gains across multiple trait categories.

The most practically useful finding is the combination of high heritability and high genetic advance seen for several traits, which validates the effectiveness of conventional phenotypic selection in okra breeding programs. For yield improvement specifically, selection through component traits offers a more reliable path than direct selection on total yield, given the latter's higher sensitivity to environmental fluctuation.

What the field needs now is broader geographic coverage of variability studies, deeper characterization of quality traits, and better integration of molecular tools with conventional phenotypic approaches. Okra deserves more systematic breeding investment than it has historically received — and the genetic variability to support that investment clearly exists. The raw material is there. What matters now is how intelligently and consistently breeders choose to exploit it.

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