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# Genetic Parameters in Horticulture and Arboriculture

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## Abstract

Genetic parameters are values that describe the influence of genes on various phenotypic traits. The most important parameters include: heritability (a measure indicating what portion of the variability of a given trait is due to the action of genes in a population), genetic correlation (a measure that describes the interdependence between two traits at the genetic level), and breeding value (an assessment of an individual's genetic potential in transmitting traits to offspring). The most crucial parameters that can facilitate the breeding process are those related to the effects of additive gene action and dominance gene action, as well as their interactions. Estimating genetic parameters is a key element in the fields of population genetics and breeding. These parameters allow for understanding how genes affect phenotypic traits and how these traits can be controlled and improved through selection. Modern methods of estimating genetic parameters rely on both classical statistical methods and advanced molecular genetics techniques.

**Keywords:** Horticulture; Arboriculture; Genetic-mathematical models; Molecular genetics; Genomic selection

## Introduction

The inheritance of quantitative traits is a very important aspect of scientific and breeding research in horticulture and arboriculture [1]. The selection process, especially in the latter discipline, is very time-consuming and can be complicated. Traditional selection methods, based solely on phenotypic observations, have been developed using genetic-mathematical models [2]. One of the greatest achievements of traditional selective breeding was the proposal of genetic parameters related to the effects of gene action [3]. These include main effects and interaction effects. The former include parameters related to the effects of additive gene action and dominance gene action. Interaction effects, on the other hand, include additive-additive interaction, dominance-dominance interaction, and additive-dominance interaction [4].

In classical genetics, these parameters are estimated based solely on phenotypic observations [5]. One of the oldest and most frequently used methods for estimating genetic parameters is pedigree analysis. This method uses information about the relationships between individuals in a population to estimate heritability and breeding values. Pedigree data are analyzed using mixed models, which allow for the separation of the effects of genotype from environmental influences. Despite the fact that the exact number of genes determining a trait is not known, the estimation concerns the total value of gene action or their interactions. Since quantitative traits are determined by many genes, even over 100, obtaining a population of individuals with all possible sets of alleles is unlikely. For example, if a trait is determined by only ten genes, each with only two alleles, the total number of possible genotypes is $2^{10}=1024$. Obtaining such a large population is possible only theoretically, and the fact that each genotype would have a different set of alleles is almost impossible. In practice, a population consisting of 100-200 individuals is considered very large. Such population size results in the estimators of genetic parameters related to the effects of gene action being underestimated.

Molecular genetics is a field of science that studies the structure and function of genes at the molecular level. In recent decades, achievements in this field have had a significant impact on many aspects of biology, medicine, and agriculture. One of the most important applications of molecular genetics is the estimation of genetic parameters, which is crucial for breeding selection, the diagnosis of genetic diseases, and evolutionary research [6]. Achievements in molecular genetics have revolutionized many scientific disciplines. Its impact on the breeding process is also very significant. Molecular genetics focuses on the analysis of DNA, RNA, and proteins, which are the fundamental carriers of genetic information in living organisms. Tools such as DNA sequencing, PCR (polymerase chain reaction), and gene-editing technologies (e.g., CRISPR-Cas9) allow scientists to precisely study and modify genes [7]. It has become possible to evaluate the effects of individual genes determining quantitative traits. This has also influenced the estimation of genetic parameters. Methods for selecting markers linked to genes affecting trait expression have been developed, and patterns of genetic parameter estimators have been determined. Although molecular genetics enables the identification of individual genes, the assessment of genetic parameters concerns only selected genes that have the greatest impact on trait expression [8-13]. This is due to the limitations of methods regarding the selection of markers for final models and linkages between genes.

Genome sequencing has enabled the complete understanding of the DNA sequence of organisms, which is crucial for identifying the genes responsible for specific traits [14]. This allows for more accurate estimation of genetic parameters. Marker-assisted selection (MAS) techniques use genetic markers linked to desirable traits, allowing for more precise breeding selection. Molecular markers make it possible to quickly and efficiently select individuals with the best genotypes, reducing the time needed to improve breeding traits in agriculture and animal husbandry. Genomic selection (GS) is a technique that uses genotypic data from the entire genome to estimate breeding values. GS allows for predicting the breeding value of individuals based on their genetic profile, significantly increasing selection efficiency. This is particularly important in plant and animal breeding, where traditional selection methods are time-consuming and costly. Gene editing with CRISPR-Cas9 technology enables precise modification of DNA to introduce desired genetic changes. This technology allows not only the study of gene functions but also the direct modification of genotypes, opening new possibilities in gene therapy and genetic engineering.

Mathematical models and statistical methods play a significant role in the precision of genetic parameter estimation [15]. Mixed models are widely used in the estimation of genetic parameters. They allow for the inclusion of both fixed and random effects. These models are particularly useful in pedigree data analysis and genomic selection, where various sources of variability must be accurately accounted for. Bayesian estimation methods use a probabilistic approach to estimate genetic parameters. These methods are especially effective in genomic selection, where the large amount of genotypic data requires advanced computational techniques. Bayesian models allow for the consideration of uncertainty associated with estimates and better utilization of available genetic information.

Although methods for estimating genetic parameters are highly advanced, challenges remain in their application [16]. High sequencing costs, complex data analyses, and the need for large study populations are just a few of these challenges. The future of genetic parameter estimation lies in the continued development of sequencing technologies, bioinformatics, and machine learning algorithms, which will enable even more precise and efficient use of genetic information. Recent research has focused on the impact of triple QTL-QTL-QTL gene interactions on the expression of quantitative traits [17-21]. The results have shown that ignoring this interaction in genetic-mathematical models leads to incorrect assessment of the epistasis effect (additive-additive interaction).

## Conclusion

The estimation of genetic parameters is crucial in animal and plant breeding. Modern methods allow breeders to select individuals with the best genotypes, leading to improvements in traits such as yield, product quality, and resistance to diseases and environmental stresses. Achievements in molecular genetics have wide applications. In agriculture, breeding, horticulture, and arboriculture, molecular genetics enables more efficient breeding selection, improvement of qualitative and quantitative crop traits, and the creation of disease and pest-resistant varieties. The advancements in molecular genetics have a significant impact on the estimation of genetic parameters, revolutionizing many fields of science and industry. Modern molecular techniques allow for more precise examination, selection, and modification of genes, leading to significant progress in medicine, agriculture, and basic research. The future of molecular genetics promises further development of tools and methods that will be even more precise and efficient, opening new possibilities in understanding and utilizing genetic potential.

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