# ASSESSMENT OF GENETIC DIVERSITY OF MAIZE (Zea mays L.) VARIETIES AND SAMPLES: THEORETICAL AND METHODOLOGICAL FOUNDATIONS

**Jangirova Nafisa Abdumannonovna**
*O'simliklar genetik resurslari*
*ilmiy-tadqiqot instituti, O'zbekiston*
*Stajor tadqiqotchi*

**Abstract:** *This article analyzes the theoretical and methodological foundations for assessing the genetic diversity of maize (Zea mays L.) varieties and samples. The importance of morpho-biological traits, biometric-statistical methods, and molecular marker technologies (SSR, SNP) in identifying genetic polymorphism is highlighted. An integrated assessment approach is proposed for predicting heterosis and identifying promising donor genotypes.*

**Keywords:** *genetic diversity, polymorphism, molecular markers, selection index, heterosis, phenotypic variation, biometric analysis.*

## Introduction

Maize (Zea mays L.) is one of the leading cereal crops globally. It is widely used for food, feed, and industrial purposes. Climate change, water scarcity, and soil degradation make the development of high-yielding and stress-resistant varieties a pressing scientific problem. The efficiency of breeding programs directly depends on the level of genetic diversity. Genetic variation allows the creation of new gene combinations, enhances adaptive traits, and maximizes heterosis effect.

2. Literature Review

Previous studies have emphasized the importance of assessing genetic diversity in maize using morphological and molecular approaches. SSR and SNP markers provide high-resolution detection of genetic polymorphism, while phenotypic traits serve as practical initial selection criteria in breeding programs. Integrated approaches combining phenotypic and molecular data improve prediction accuracy for promising genotypes.

3. Methodology

3.1 Phenotypic Evaluation

Key traits for assessment include plant height, cob length, number of kernels per cob, 1000-kernel weight, vegetative period duration, and yield.

3.2 Statistical Analysis

- Analysis of variance (ANOVA)
- Coefficient of variation (CV%)
- Correlation and regression analysis
- Cluster analysis and PCA

3.3 Molecular Analysis

- SSR and SNP markers
- Polymorphism percentage
- Genetic distance (Nei coefficient)
- UPGMA dendrogram

Integrated analysis of phenotypic and molecular data provides a robust framework for selection and prediction of heterosis.

4. Expected Results and Scientific Novelty

- Determination of genetic diversity levels in maize genotypes.
- Assessment of correlations between phenotypic and molecular traits.
- Identification of parental lines with high genetic distances for heterosis prediction.
- Proposal of an integrated model for predicting promising donor genotypes.
- Scientific novelty: A comprehensive integrative model for genetic diversity assessment in maize is proposed.

5. Discussion

An integrated approach combining phenotypic and molecular evaluation accelerates the breeding process and enhances its accuracy. Molecular markers allow selection independent of environmental influence, while phenotypic traits provide direct evaluation of agronomic importance.

**Conclusion**

1. Genetic diversity is a key factor for successful maize breeding.
2. Combined phenotypic and molecular approaches offer the most effective selection strategy.
3. Genetic distance is a crucial parameter for heterosis prediction.
4. The proposed integrated assessment model facilitates the development of high-yielding and stress-resistant varieties.

**References:**

1. Hallauer A.R., Carena M.J., Miranda Filho J.B. Quantitative Genetics in Maize Breeding. Springer.
2. Mohammadi S.A., Prasanna B.M. Analysis of genetic diversity in crop plants. Crop Science.
3. Xu Y. Molecular Plant Breeding. CAB International.
4. FAO Statistical Database.
5. Smith J.S.C. Genetic diversity in maize. Crop Science.