

DIGITAL TECHNOLOGY FOR COMPARATIVE ANALYSIS OF PROTEIN ELECTROPHORETIC SPECTRA IN MAIZE BREEDING AND GENETIC RESEARCH

COMAROVA Galina, <https://orcid.org/0009-0001-0063-4586>

Technical University of Moldova, Faculty of Agricultural, Forestry and Environmental Sciences Chisinău, Republica Moldova
Corresponding e-mail: galina.comarova@am.utm.md

Successful interpretation of research results in biology depends largely on the design of the experimental scheme. A fundamental guiding principle in this context is the widely accepted “principle of the single difference.” Accordingly, testing of a working hypothesis is conducted by comparing the experimental variant with a control. In genetic and breeding studies, this experimental approach - regardless of the experimentation level - is considered standard. This is clearly illustrated by the long-term analysis of data from studies on plant protein polymorphism (specifically, for the endosperm storage protein zein in maize). According to literary data, in the methodology of interpreting electrophoretic (EP) spectra of zein from various maize genotypes, the primary tool for express assessment of the presence or absence of zein molecular forms (ZMFs) in the studied samples is their visual comparison, along with quantitative calculation of EP zone components and their relative electrophoretic mobility (rf).

In recent years, new methodological developments have emerged that expand the possibilities for interpreting zein polymorphism data. The use of an updated version of the “FOREZ-2” software has enabled the development of a digital technology for comparative analysis of protein EP spectra from contrasting maize genotypes.

The main idea of this technical approach is the automatic reciprocal synthesis of two EP spectra from the parental lines, followed by detection of the corresponding protein markers in the digital spectrum of the hybrid combination. The following procedure was tested to implement this concept:

- 1) inclusion in the FOREZ-2 database of the calculated formulas for the EP spectra of the two compared genotypes: the control line and the test line;
- 2) automatic synthesis of two versions of EP spectra for hybrid combinations of these genotypes - according to the principle of direct (D) and reverse (R) modeling;
- 3) as a result of the automatic reciprocal synthesis of the two parental line formulas, two hybrid EP matrices are displayed:

- the direct matrix (D), where markers indicating the elimination of ZMFs from the control line in the test line's EP spectrum are automatically highlighted, and
- the reverse matrix (R), where markers indicating enrichment of the zein protein profile in the test line are automatically displayed, i.e., the appearance of new ZMFs for the control line, reflecting the genetic differences of the test line from the control line.

The effectiveness of this digital EP spectrum processing technique was successfully demonstrated between 2020 and 2024 for *Zea mays L.* in studies involving gene and genome mutations, somaclonal lines, and self-pollinated lines from several heterotic groups of maize.

The range of obtained results allows for the recommendation of this digital technology as an optimal tool for interpreting zein EP spectra in maize breeding and genetic research.

Keywords: maize, polymorphism, zein, electrophoresis, reciprocal synthesis

Funding. This research was supported by the Ministry of Education and Research from the Republic of Moldova, institutional subprogram 020407- *GREEN*.