

The use of allelic variants of seed storage proteins in the production of sunflower parental lines

Igor Aksyonov

Tavria state agrotechnological university named after Dmytro Motornyi, Faculty of agricultural technologies and ecology, Department of crop production and horticulture named after V.Kalytka, 69011, Zaporozhie, Ukraine.

Abstract

The effectiveness of heterosis-based sunflower breeding is significantly enhanced when evaluating and developing lines and hybrids by selecting plants based on allelic variants of the electrophoretic spectra of seed storage proteins. The selection of plants based on allelic variants in the experiments was carried out using the method of electrophoresis of sunflower seed reserve proteins, as described by A. F. Popereya (Institute of Plant Breeding and Genetics, Ukraine). The studies conducted enabled the determination and identification of allelic variants in the electrophoretic patterns of the sunflower genotypes under investigation. During the study, the following loci were identified on electrophoregrams: HEL 1, HEL 2, HEL 3, HEL 4, HEL 5 and HEL 6. The creation of interspecific sunflower hybrids made it possible to expand genetic diversity and isolate genotypes with the new HEL 7, HEL 8, HEL 9 and nk loci. Based on the selection of plants according to protein spectra, new source material and new parental lines: inbred maternal lines and pollen fertility restorer lines with a high level of typicality (99.0–100.0%) were created. The use of new inbred lines in breeding combinations. The identification of sunflower genotypes based on allelic variants of the electrophoretic spectra of sunflower seed storage proteins addresses issues relating to improving the efficiency of plant evaluation and selection, expanding genetic diversity, improving the typicality of parental lines and hybrids, and obtaining parental lines that yield hybrids with high yield potential.

Keywords: Sunflower-1, Protein electrophoresis spectrum-2, Selection-3, Line-4, Typicality-5, Yield-6

The effectiveness of breeding work in the development of sunflower hybrids is based on the evaluation and selection of plants according to both morphological traits and allelic variants of the electrophoretic spectra of seed storage proteins. The use of protein spectra in hybrid breeding allows for the expansion of genetic diversity and the creation of new, identified parental lines.

The experiments identified allelic variants in the electrophoretic patterns of sunflower seed storage proteins, which enabled the identification, isolation and creation of new breeding material and new self-pollinated parental lines. The studies conducted demonstrated and confirmed that the genes encoding the synthesis of storage proteins are clustered as a single component or as a single group (block). Alleles of genes controlling polypeptide synthesis are represented on electrophoregrams as bands (components) within a block. A block of electrophoretic components serves as a phenotypic marker for the corresponding locus at the protein molecule level. The alleles on the electrophoregrams exhibited different mobility and intensity, which made it possible to identify different series of allelic variants for each cluster, to identify homozygotes for each allele (a characteristic of self-pollinated lines), and heterozygotes (a characteristic of hybridity). Alleles at each locus were arranged in order of increasing mobility and decreasing molecular weight from HEL1 to HEL 6.

Analysis of the electrophoregrams during the course of the study showed that the components of sunflower seed storage proteins (helianthins) are controlled by at least six loci: HEL1, HEL2, HEL3, HEL4, HEL5 and HEL6. The HEL1 and HEL6 genes are represented by one (homozygous) or two alleles (heterozygous). The HEL3 and HEL5 genes are always represented by a single allele. Differences in these genes can be observed in the intensity of the components of the electrophoretic spectra. The HEL2 gene is represented by two components. The HEL4 gene is represented on electrophoregrams by a series of components of varying mobility and intensity and controls the synthesis of the polypeptide block of the fourth electrophoretic spectrum. The group of sunflower seed storage proteins encoded by the HEL4 locus exhibits the greatest polymorphism of helianthins among all identified and described sunflower samples when subjected to electrophoretic separation.

An analysis of changes in the allelic variants of protein electrophoretic spectra during self-pollination and the hybridisation of the resulting parental lines established that the electrophoretic component cluster serves as a phenotypic marker for the corresponding polygenic locus at the protein molecule level and is equivalent to the concept of an 'allele' for a clustered locus.

The production of interspecific hybrids involving annual wild sunflower forms has enabled the isolation and creation of new breeding material with established and identified allelic variants of the Hel 7, Hel 8, HEL 9 and nk loci, which has significantly contributed to the expansion of genetic diversity in the breeding process.

The evaluation and selection of plants based on allelic variants of the electrophoretic spectra of helianthins, combined with an assessment of morphological traits, enabled the creation of the maternal sterile lines GE59A,





GE6A, GE195A, and nine sunflower pollen fertility restorer lines with a high level of genetic purity (99.0–100.0%), which are used in breeding to produce hybrid combinations. Using these sunflower lines, promising hybrids have been developed, which are currently undergoing competitive variety trials. The yield of the resulting sunflower hybrids ranges from 3.5 to 4.3 t/ha.

From a population of plants with identical and indistinguishable morphological traits of the hybrid combination of the interspecific hybrid Maxim $\times$ H. praecox, two pollen restorer lines, GE 106Rf and GE 3-38Rf, were isolated and established based on differences in the allelic variants of electrophoretic spectra. The sunflower line 106Rf, derived from line 3-38Rf, is characterised by a shorter growing season. In terms of growing season during, line 106Rf belongs to the third early maturity group. The growing season of plants from this line lasted 99 days, which is 15 days shorter than that of line 3-38Rf. The line 3-38Rf belongs to the 5th mid-season group, has a growing season of 114 days, and is characterised by a more higher level of yield potential in the hybrids combinations.

The lines obtained, when used in crossing combinations, yielded hybrids with varying levels of yield. Hybrid combinations produced using the pollen fertility restorer line GE 3-38Rf yield between 4.0 and 4.5 t/ha. Hybrid combinations produced using the pollen fertility restorer line GE 106Rf yielded between 3.10 and 3.54 t/ha.

When creating parental self-pollinated sunflower lines, analysis of allelic variants of the electrophoretic spectra of seed storage proteins demonstrates the necessity and effectiveness of evaluating and selecting plants based on protein spectra to improve genetic purity and bring the newly created breeding material to a homozygous state with a high level of typicality.

