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GENETIC ANALYSIS OF SWEET CORN LINES BASED ON SH$_2$ ENDOSPERM STRUCTURE GENE

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Abstract. *One of the three genes of the endosperm structure is used in the selection of sweet corn; its recessive mutation sh$_2$ activates the accumulation of sucrose in the structural complex of sugars and represses the starch synthesis. Hybrids of "super-sweet" corn have improved grain taste and slower conversion of sugars into starch. Therefore, it is important to use different genetic sources of breeding features in the creation of a new linear material that meets the requirements of modern heterosis selection of sweet corn.*

The ***aim*** *of the work was to study the lines of sweet corn and to identify among them new sources of selectively valuable economic features.*

Materials and methods of research. *A working collection of sweet corn seed material was created. It includes more than 100 genetic samples, 22 of which are lines of super-sweet corn. Based on the analysis of adaptive and phenotypic sings, we selected the 10 best lines for research. A comprehensive assessment and analysis of samples for economically valuable traits – productivity per plant, maturity group, etc. was carried out according to the "Methodical recommendations for field and laboratory study of genetic resources of corn". The assessment of morphological features was carried out according to the "Classifier-handbook of Zea mays L.".*

Statistical analyses of data were carried out using the Microsoft Excel software ($p > 0.05$).

Research results and discussion*. A complex assessment of morphological characteristics and productivity of sweet corn lines was carried out.*

To expand the genetic diversity of sweet corn in the selection process, it is necessary to use samples that are characterized by a wide range of signs. Therefore, the evaluation of the lines of "super-sweet" corn was carried out according to the complex of morpho-biological features: the vegetation period; the number of leaves on the plant; the presence of stepsons and stipules; the plant height; the panicle shape; the height of attachment of a cob; the size of the cob and its shape; the cob diameter; the number of grain rows and the number of grains in one row; the seed size and seed color; the productivity of one cob.

Significant variability of physiological functions of plants, in particular, the extension of the duration of the vegetation period was shown in the study of sweet corn lines. According to the level of manifestation of economically valuable features of "super-sweet" forms of corn and morpho-biological features, their diversity was established.

Significant differences between the studied lines were observed for the following characteristics: the number of seeds in one row (coefficient of variation was 27.66%) and the number of grain rows (V = 18.9%).

The study of samples on the basis of "duration of the vegetation period" by counting the number of days from germination to wax ripeness and the number of leaves on the main stem was carried out. Based on the study of this feature, the samples were divided into two groups of maturity: early – four lines (18.2%) with a duration of 70-75 days and six medium ripe lines (27.3%) with a vegetation period of 76-81 days.

The plant height and the height of attachment of the cobs characterize the suitability of the samples for mechanized harvesting and are important for sweet corn. In addition, tall forms provide higher yields. As a result of studying the plant height in different samples, it was found that the plant height varied from 125 to 184 cm. The sweet corn is characterized by a fairly low attachment of the first cob, which was formed on average at a height of 10 – 30 cm from the soil surface. Attachment of economically valuable cob was observed at a height of 30 – 50 cm.

In terms of cob length, five lines of sweet corn formed short cobs (14 to 16 cm), four lines were of medium length and one was characterized by the largest cob size – more than 20 cm.

The sign "the number of grains from the cob" is one of the main, as it provides individual grain productivity of plants. This feature is formed on the basis of two indicators: the number of grain rows and the number of grains from one row. According to this feature, five lines had an average productivity of one cob (351-450 pcs.), three lines – the low one (260 - 350 pcs.) and two lines – the high one (451-580 pcs.).

Conclusions and prospects. *According to the results of study the main morpho-biological signs of sweet corn lines with the mutant* sh_2 *gene, the sources of individual selection valuable peculiarities were identified. Lines SH-234 and SH-936 were marked as donors of sign of plant height. Lines SH-621, SH-234 and SH-936 were the best in terms of seed productivity of cobs. According to the growing season, all lines are divided into early (4 lines) and medium ripe (6 lines). The lines SH-234, SH-113 (number of grain rows) and SH-621 (number of seeds in a row) were the best in terms of productivity, and lines SH-318 and SH-936 – in terms of the cob length (14.45 cm and 13.26 cm, respectively). Only one line SH-477 had strongly wrinkled seeds. Thus, the studied sweet corn lines were characterized by high genotypic diversity; the SH-936 and SH-621 lines were the best in terms of the sign complex.*

Key words: *sweet corn,* sh_2 *mutant gene, vegetation period, morpho-biological signs, productivity*