PROSPECTS OF ISOZYMES USAGE FOR SUGAR BEET GENETIC IMPROVEMENT

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INTRODUCTION

Genetic resources of cultivated plants consist of different lines, varieties, hybrids and wild populations. Determination of this genetic diversity is important for its preservations, usage and gathering. Taking into account the fact that morphological features of beet give little information and are subject to modification variability [1,2], the genetic marking using isozymes has been applied in our investigations.

The isozymes are rather precise in representing organismic specificity and determining genetic variability in morphologically homogeneous populations [3] have co-dominant character of exhibition, allow to estimate homo- and heterozygosity of plants by genes controlling the studied enzymes. The simplicity of the analysis carried and high level of information that give its results allow to use isozymes as genetic markers.

In this connection, using isozymes as markers in sugar beet breeding is topical and promising.

The aim of the investigation is to reveal possibilities of using isozymes for estimation of sugar beet breeding material.

MATERIALS AND METHODS

Inbred lines, forms with CMS, multi-germ pollinators developed in VNIISS, Belgium, USA and Sweden were used in the investigations.

The electrophoretic analysis of enzymes was conducted in starch gel [4]. Tris-citrate buffer system with pH=7.0 was used [5]. Histochemical staining of enzyme activity zones was performed according to standard metods [6]. Isozyme loci were labelled according to the commonly accepted rules [7J. Genetic distance between breeding materials was calculated with Nei procedure [8].

RESULTS AND DISCUSSION

The performed isozyme analyses have shown that breeding materials obtained with the inbreeding method have different ratios of homo- and beterozygotes in seven isozyme loci used by us, namely: Me-1, Idh-1, Idh-2, Mdh-1, Mdh-2, Gdh-l, Adh-l.

The true frequency of homo- and heterozygotes occurrence in the breeding material can be determined by their average characteristic that is the index of isozyme homozygosity Iiz [9], which is calculated on the formula: , where p is frequency of homozygotes occurrence in each of (n) isozyme loci.

The performed calculations have shown that the index of isozyme homozygosity in breeding materials is determined according to the way of their obtaining. In the populations of varieties it is 0,69 and close to Iiz value of materials after the first inbred crossing. Apparently, it is connected with the structure of the studied populations that have been represented mainly with closely-related materials (mixture of lines). Isozyme homozygosity index has exceeded theoretical value of F inbreeding rate for lines obtained as a result of the fist ($I1$) and second (I_2) inbreeding, being 0,67 for I1 and 0,84 for I_2. Breeding with the use of isozyme homozygosity index has allowed to increase this parameter of materials from sib crossings up to 0,81.

As a result of the carried out investigations, it has been noticed that the isozyme homozygosity index is higher in inbred lines than in the numbers obtained from sib crossings, in which, apparently, contamination by stranger pollen takes place due to poor isolation.

From the results of isozyme analysis, the matrix of genetic similarity index has been worked out and the dendrogram of genetic relationship between mate sterile shapes and MC-based sugar beet hybrids of different origin has been built (Fig.1).

Fig.1. Scheme of genetic relationships between different breeding materials developed on MC-basis. Comment: 1 - 87376,2 - 87388,3 - 88166,4 - 88115,5 - 88002,6-89530,7 - 89531,8 - 89332.
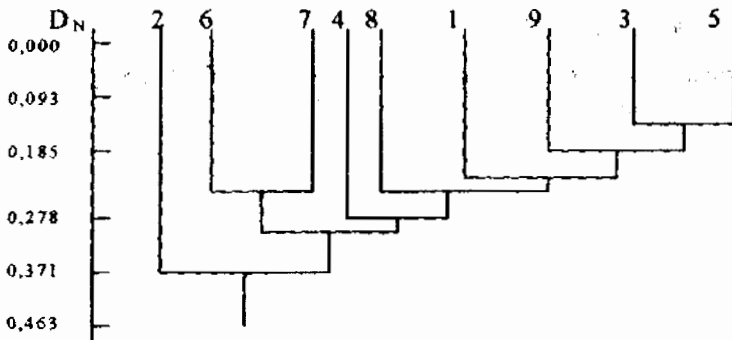
The study of genetic relationships between materials with cytoplasmic male sterility has shown that they are most distant from each other. The average value of genetic distances between MC-lines is $D_N=0.289$ that is probably connected with the techniques of the lines obtaining and weir different origin. The dendrogram built on the basis of the Nei genetic distance matrix allows to group close breeding numbers and to select lines that are extremely different from others genetically. So, numbers 87388 and 88115 are included in no one cluster, as the genetic distances between them and other breeding materials are rather big. Numbers 89530 and 89531 make one cluster in the dendrogram that suggests their closely related origin.

These materials have really been received from the "ICI" corporation (Belgium). They are at a large genetic distance from Ramon MC-lines, D_N being from 0,220 up to 0,528. And the average value of genetic distance between the presented foreign numbers and Ramon MC-lines is D_N=0,388. Breeding numbers 89331 and 89332 are F_1 hybrids from crossings between Ramon O-types and MC-lines from USA (89332) and Sweden (89331). And genetically, they are closer to Ramon materials, their D_N varies being from 0,087 up to 0,556. The average value of genetic distance, between these hybrids and Ramon MC-lines is D_N=0, 196. Studying the genetic distances of 19 sugar beet inbred lines and 5 populations have shown that genetic distance between most of them is small ranging from 0,020 up to 0,699 being 0,238 on the average.

The results obtained correspond to the origin of the studied sugar beet inbred lines, i.e. the genetic distance reflects the real relationships mat have developed in breeding materials historically. Thus, the use of isozyme analysis allows to identify sugar beet genotypes most exactly. Therefore, this method of estimation can be recommended for screening of initial material and genetic improvement at early stages of its development and selection of parent components for hybridization.

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