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EVALUATION OF GENETIC DIVERSITY AND STUDY OF GENETIC RELATIONSHIP BETWEEN ISSR MARKERS AND LOCAL WINEGRAPE SAMPLES

Winegrape genotypes of Azerbaijan are characterized by a wide range of polymorphisms, their population being the heritages of valuable plant and selective significance by forming different biotypes, clones, shapes and variations. Therefore, in the gene pool each winegrape genotype should be identified and collected, delivered to future generations safely and efficiently, and should be achieved the providing the demand for vine-growing and wine making products and continued development of this area through the achievement of the maximum potential. The rich genetic material of the Azerbaijan winegrape is an integral part of the world's grape genetic resources.

One of the most pressing issues in todays is to properly preserve the diversity of these genetic material, represented by wild and cultural aboriginal vinegrapes and passing on to future generations. For this purpose, winegrape samples collected from different regions should be categorized by complex use of molecular-genetic, populations-statistics methods, their genetic diversity should be studied, relationship should be investigated, and the genetic distance between cultural and wild winegrape samples should be determined.

The genetic diversity, in other words, genotypic heterozygosis of the importance of adaptation in heterozygosis, polymorphism and natural populations is expressed by the genetic interpopulation and intrapopulationdiversity and specifies the probability of evolution.

Genetic diversity is the basis of breeding and provides useful utilization of breeding programs by breeders more effectively. As the level of genetic diversity increases within the population, the range of natural and artificial selection increases.

The rich genetic material of the Azerbaijani vine grape is an inherent part of the world's grape genetic resources. Conservation of the diversity of these genetic materials, represented by wild and cultural aboriginal grape sam-

ples, properly preserving and transmitting to future generations is one of the most pressing issues in today's world. For this purpose, grape samples collected from different regions and included in collections should be pasportizated by molecular-genetic, populations-statistics, etc. the methods completely, their genetic diversity should be studied, relative relationships should be investigated, and genetic distance between cultural and wild vine grape samples should be determined.

One of the types of PZR-based molecular markers is the ISSR markers. In this method, one or more primers of 15-24 nucleotides were used. ISSR is a dominant marker, relatively fast and cheap. Through the ISSR markers, many research works have been done in the grape. In the current research, 29 grape genotypes were evaluated by ISSR markers and genetic relationship degree were identified among the samples.

As it is known, unlike the specific primers designated for a plant, the nonspecific ISSR marker is able to amplify DNA fragments in different plants. However, the in formativeness, polymorphism, and profiles of these markers vary depending on the plant and the studied collection. Initially, the selected 10 ISSR primers were originally tested over 5 varieties. Analyzes continued with 4 ISSR primers, giving polymorph and clear clauses.

Such diversity observed at the level of DNA is very important in breeding programs. Thus, based on the existence of a cross-pollination system in most grape samples, it is possible to increase the amount of heterozygote's in the population, and realize the target breeding for this plant by achieving maximum heterosis by potential hybridization methods observed in the current samples.

Identifying of genetic relationships in plants during experiments is one of the major lines of molecular-genetic research. Thus, in order to determine the genetic relationships, genotypes are grouped into clusters based on genetic similarity or genetic distance index calculated on the basis of different formulas.

In the studied winegrape collection, most of the genotypes were identical, but selected samples with different profiles, differed from others. The fact that many of the studied samples located in the same clusters is related to the small number of analyzed loci, rather than their identity. Selection of genetically different forms in separate clusters in the cluster analysis allows for practical guidance on winegrape selection, prediction, and use in future hybridization processes. In breeding, the value of such genetically different samples is very important.