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ФЫЛЫМ КОМИТЕТИ  
БИОЛОГИЯ ЖӘНЕ ӨСІМДІКТЕР БИОТЕХНОЛОГИЯСЫ ИНСТИТУТЫ

МИНИСТЕРСТВО НАУКИ И ВЫСШЕГО ОБРАЗОВАНИЯ РЕСПУБЛИКИ КАЗАХСТАН  
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ИНСТИТУТ БИОЛОГИИ И БИОТЕХНОЛОГИИ РАСТЕНИЙ

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## **Session 1.**

# **Genetic Resources and Biodiversity**

**GENETIC ADAPTATION STRATEGIES OF RHODIOLA LINEARIFOLIA PLANTS FROM VARIOUS ECOLOGICAL AND GEOGRAPHICAL POPULATIONS**

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Representatives of the Crassulaceae family's genus Rhodiola are succulents and have a great capacity for adaptation to unfavorable environmental influences. We studied the individual specimens from three different natural populations of nature reserves in various mountainous regions of Kazakhstan.

One of the most significant tools for analyzing plant resources, including numerous genetic processes in wild populations, is the analysis of molecular genetic polymorphism. This work aimed to look at the polymorphisms of allelic variations of the superoxide dismutase (SOD) and auxin response factor (ARF) gene families, as well as the genetic diversity of from three different natural populations of *R. linearifolia*, using the retrotransposons-based fingerprinting approach. The multi-locus exon-primed intron-crossing (EPIC-PCR) profiling approach was used to examine allelic variations in the SOD and ARF gene families. We implemented the inter-primer binding site (iPBS) PCR amplification technique for genome profiling, which demonstrated a significant level of polymorphism in the Rhodiola samples studied. The results obtained in this study show a high level of molecular genetic polymorphism in the coding part of the genome in the studied samples.

Both SOD family genes and ARF genes had a great variety of EPIC-PCR amplicons in populations studied. Yes, the analyzed populations of *R. linearifolia*, respond mainly similarly to stress. But the results indicate the presence of genetic differences or structural features between these populations, which may be associated with adaptation to different environmental conditions or allelic drift.

The iPBS profiling analysis for the studied samples of analyzed populations also revealed the level of genetic differentiation of the studied populations and demonstrated Genetic profiles contained both common amplicons and unique one's characteristic of each specific population of *R. linearifolia*. Based on the results of genetic analysis of populations based on DNA profiling data, we can conclude that about 64% of genetic diversity is due to intrapopulation variability.

The variability in the regulatory regions of the ARFs and SOD genes may be associated with different plant responses to stress factors, while PBS polymorphism may be due to the geographic remoteness of populations and the influence of environmental conditions.

So, the genetic variety of wild populations of *R. linearifolia* leads to their improved tolerance of opposing environmental circumstances and evolutionary divergence.