USE MOLECULAR MARKERS FOR DIFFERENTIATION POPULATIONS OF STIPA CAPILLATA GROWING IN THE REGIONS WITH HIGH CHRONICAL DOSES OF $\gamma$-RADIATION

Sarsenbaev K.N.
Institute of radiation safety and ecology, Kurchatov, Kazakhstan
e-mail: kanatsarsenbaev@hotmail.com

The aim of our study is to detect genetical diversity of 36 populations of Stipa capillata, based on their individual RAPD, MGH, $\alpha$- and $\beta$-amylase, phosphatase, peroxidase, nonspecific esterase, polypeptides, soluble proteins. This patterns have been use to provide more objective analysis genotype and genetic relationships between radiated and non-radiated by $\gamma$-radiation population.

DNA from investigated populations was analyzed by RAPD-method with 10-15 nucleotide primers. Dendograms was constructed based on the similarity matrix data by applying the unweighted pair group method with arithmetic averages (UPGMA) cluster analysis. Proteins and enzymes by PAG-electrophoresis.

Among the examined 15 primers only four showed polymorphic pattern. The number of amplicons obtained by primers varied from 9 to 39. High level of radiation change compound complex of studied enzymes and proteins, but deference between populations growing on uncontaminated areas on the level of used markers very low. It was proposed that growing Stipa plants during 40 years on the contaminated areas leads to appearance new genotypes.