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ANALYSIS OF GENETIC DIVERSITY AMONG SOME BARLEY (HORDEUM VULGARE L.) CULTIVARS USING MOLECULAR MARKERS (SSR-SIMPLE SEQUENCE REPEAT)

ANALIZA DIVERSITATII GENETICE PRIN UTILIZAREA DE MARKERI MOLECULARI (SSR-SIMPLE SEQUENCE REPEAT) IN CULTURA DE ORZ (HORDEUM VULGARE L.)

D. P. SIMIONIUC - USAMV Iasi
Jutta AHLEMEYER, W. FRIEDT, F. ORDON - University Justus von Liebig Giessen
Violeta SIMIONIUC - USAMV Iasi

Barley is and will remain a very important crop for the European countries. The interest for this cereal is obvious if we look at the number of research grants regarding this species and the number of scientists involved. This paper is based on researches which are included in a very large project financed by German Research Foundation (DFG) and are still in progress.

For the study, a set of 65 six-rowed and 52 two-rowed winter barley cultivars was selected. The existing pedigree information was analysed and a dendrogram based on coancestry estimates was generated for many of the analysed cultivars.

Also, the whole set of 117 cultivars was genotyped by means of SSR (Simple Sequence Repeats) markers. For most of the 20 SSRs analysed up to now we found a high number of alleles per locus. For many (13 of the 20 SSRs) of them the distribution of these alleles differs significantly between six-rowed and two-rowed types for. Due to these differences, six-rowed and two-rowed varieties are clearly separated in a dendrogram based on genetic similarities between varieties (with some exceptions). The grouping of varieties in this dendrogram corresponds in many cases with known pedigree data.