

## GENETIC DIVERSITY OF LINSEED ACCESSION

**SIRINE MAHJOUB<sup>1</sup>, ISTVÁN KRISTÓ<sup>2</sup>, MELINDA TAR<sup>2\*</sup>**

<sup>1</sup>University of Szeged Faculty of Agriculture

Andrássy u. 15., H-6800 Hódmezővásárhely, Hungary

<sup>2</sup>National Agricultural Research and Innovation Centre, Department of Field  
Crops Research

Alsó Kikötő sor 9., H-6726 Szeged, Hungary

[tar.melinda@noko.naik.hu](mailto:tar.melinda@noko.naik.hu)

Flax (*Linum usitatissimum* L) is the third largest natural fiber crop and one of the major oil crops in the world. In this study genetic diversity of 33 flax cultivars were assessed. Fifteen polymorphic microsatellite markers (SSRs) were used. A total of 117 alleles were detected with an average of 7.93 alleles per locus ranging from 3 (LU6 and LU22) to 13 (LU8 and LU27). The polymorphic information content (PIC) value of each SSR primer pairs ranged from 0.34 to 0.80 with an average of 0.62. Cluster analysis based on Jaccard's similarity coefficient using UPGMA grouped the 33 flax varieties into three clusters. The Jaccard's similarity ranged between 0.42 to 0.96. The genotype Lidgate showed the least similarity with Norman. These two genotypes could be well used as parents in breeding program for developing improved varieties.