Evaluation of leek (*Allium porrum*) genomic polymorphism using the AFLP method

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Leek (*Allium porrum* L.) is an important green vegetable crop in Europe and Asia. In Russia, the popularity of leek increases every year due to its valuable taste and nutrition/dietary properties, which are a consequence of the high content of secondary metabolites. Despite the importance of this vegetable, data on the biochemical composition and phenotypic polymorphism of leek accessions, as well as molecular-genetic characteristics of *A. porrum* genome variability and individual genes polymorphism are extremely limited. In this study, the AFLP method was applied to determine the genomic variability of 65 leek accessions from the collection of the Federal Scientific Center of Vegetable Growing (FSCVG). As an outgroup, species *A. ampeloprasum*, *A. commutatum* and *A. pyrenaicum* were used, because together with the leek they are included into the *A. ampeloprasum* complex. Using two selected primer combinations (with six selective nucleotides at the 3′-end), for each sample analyzed, a unique AFLP spectrum was obtained. A total of 721 fragments were identified, of which 675 (93.6 %) were polymorphic for leek accessions, and 103 were accession-specific. The calculated genetic distances ranged from 0.32 to 0.75 (GDcp 0.58). According to PCO-analysis, the accessions of leek form two unequal groups (16 and 49 accessions), equally distanced from the outgroup. Four accessions, cultivars (Florena (Netherlands), Good fellow (Russia)) and breeding lines (2017, 2038), were distanced from the rest of the analyzed leek accessions, which reflects the difference in their genomes.Thus, an AFLP analysis revealed a high genomic polymorphism level of leek accessions from the FSCVG collection. *A. porrum* accessions formed an isolated sub-cluster that validates *A. porrum* as a separate species other than *A. ampeloprasum*.