

Search of Rare Alleles in the Gene pool of *Lathyrus sativus* L.

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The search of rare alleles in *Lathyrus sativus* L. had been first realized.

34 accessions from the collection of Vavilov Institute have been investigated using RAPD markers. The origin of the accessions was quite different: in accordance of the classification of F.Zalkind (1937) they belonged to 6 eco-geography groups. Construction of phylogenetic trees is satisfied by the method UPGMA.

After genotyping with RAPD markers investigated sample divided on two clear groups in compliance with two subspecies of *L.sativus* : ssp. asiaticus и ssp. europaeus. The most similar in the presence/absence and composition of RAPD-fragments were the accessions of the same origin.

Rare and widely occurring alleles have been calculated using the coefficient of genetic originality (CGO) (Potokina, 2008), based on the principle of "weighting" of the traits according to their frequency of occurrence (Smirnov, 1969). As a result the accessions with different levels of rare alleles and not having them as well as with the smallest and biggest number of rare alleles have been revealed. The occurrence of rare alleles had no correlation with eco-geography differentiation of the sample.

The determination of CGO is useful tool for searching unique accessions in germplasm collections.

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