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Genetic Diversity of Natural Populations of Scotch Pine in the Northern Part of the Republic of Karelia

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Abstract. In this study, we assessed the genetic diversity and population structure of Scotch pine (Pinus sylvestris L.) using 13 microsatellite loci in 5 populations from the northern part of the Republic of Karelia. Our analysis showed a high allelic diversity of the Scots pine population in the studied areas. Although, in terms of the degree of uniformity of the distribution of allelic variants within the samples, all the studied populations are quite homogeneous. The result of the AMOVA analysis showed a relatively low level of interpopulation differentiation, within the population the variability is 93 %, and the interpopulation share of variability is 7 %. According to the results of cluster analysis carried out on the basis of the matrix of genetic distances by M. Nei, we revealed the population structure of P. sylvestris in the northern part of Karelia. All studied populations were divided into two large groups.

Key words: Scotch pine, natural populations, genetic structure, PCR, microsatellites, genetic diversity, EST-SSR.

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