Original article

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## Selection Evaluation and Genotyping of Clones of Plus Trees *Pinus sylvestris* L. Northern Kazakhstan

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**Abstract.** The article presents the results of selection and genetic evaluation and molecular passportization of 15 clones of plus trees Pinus sylvestris L. at the age of 37 years. The objects of research are located in the Akmola region of Northern Kazakhstan. The initial

placement of the ramets during their planting  $(3 \times 3 m)$  had an impact on the formation of the stand. The average preservation of 15 studied clones was 77,1 %. The proportion of ramets without signs of weakening was 41.1 %. During the examination, significant mechanical damage to the bark in the lower part of the trunks (no higher than 2 m in height) was found in 50 % of the ramets. At the initial stage, the main taxation indicators, crown parameters and genotyping of 15 clones were analyzed. The average height of all the studied clones is 18.9±0.3 m, the average diameter of the trunk at a height of 1.3 m is 20.3±0.4 cm, the average diameter of the crown is 3.7±0.2 m. The assessment of qualitative features allowed us to identify clones with high trunk quality (straightness), with dense crowns: 6, 17, 25, 30, 22, 34, 38. In the study of clones, weak fruiting was found (from 20 to 80–100 cones for rameta), which is due to the small size of the crowns and the fruiting tier. On the basis of isoenzyme and microsatellite analysis, the genotypes of clones of plus trees were determined, as well as the frequency of occurrence of the identified alleles. As a result of the conducted studies, diagnostic allelic combinations of individual loci were identified for 73.3 % of clones. Genetic identification made it possible to establish that 98.7 % of the trees correspond to the studied clones. The discrepancy between the clonal affiliation of two trees was confirmed by both isoenzyme and microsatellite analyses.

*Keywords:* Pinus sylvestris L., clones of plus trees, height of tree, diameter of trunk, crown size, genotype.

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