

The mean value of F_{ST} for analyzed spruce populations was 0.146.

Genetic distance between tested spruce provenances from the Beskidy Mts. was equal to 0.027. Most of the populations were divided into several small clusters, separated by small distances both between and inside formed units. Only in the case of Region 73 Jasina, a significant distinction from remaining provenances was noted which was indicated by large genetic distance equal to 0.23 (fig. 2).

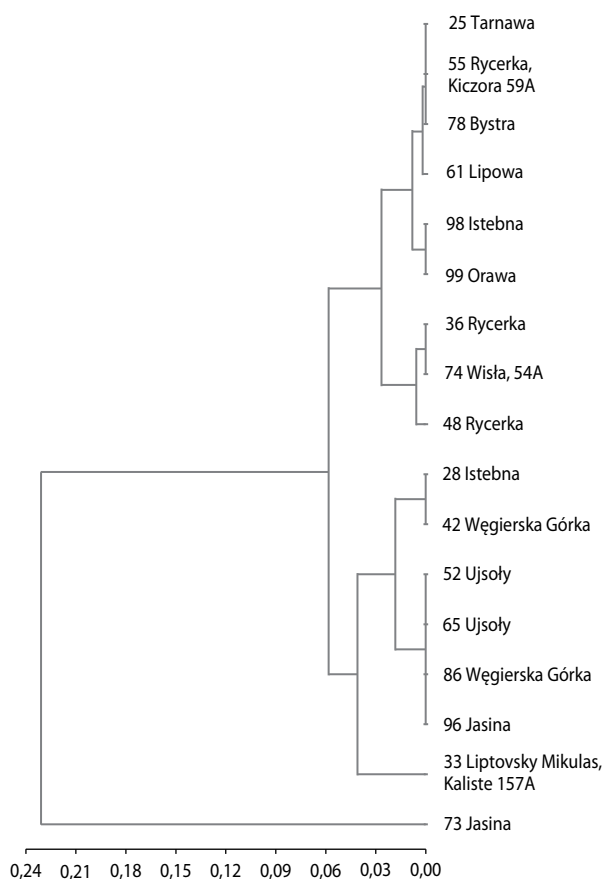


Fig. 2. Dendrogram constructed for Norway spruce populations from the Beskidy Mts. based on Nei's genetic identity (1978) by unweighted pair-group method using arithmetic averages (UPGMA)

No significant correlations were found between genetic diversity measures and altitude of parent stands as well as the type of seed source used to set up the experiment.

DISCUSSION

Genetic diversity of spruce population from the Beskidy Mts., expressed as mean number of allele per locus ($N_a = 1.42$) and observed heterozygosity ($H_o = 0.12$), is significantly lower from spruce polymorphism based on 7 loci, noted by Bergmann and Gregorius (1979) ($N_a = 2.14-3.14$, $H_o = 0.36-0.45$). Differences in the estimated values of genetic diversity can result from the number of analyzed loci and a level of polymorphism as well as from the type of the object used in the study. The highest consistency of results was obtained when compared with studies on selected spruce provenances tested in IPTNS-IUFRO 1964/68 experiment, where mean number of alleles per locus was 1.41 and observed heterozygosity – 0.11 (Masternak et al. 2011).

High values of the parameters tested were calculated for Istebna spruces (provenance 28), which confirms data previously presented by Polak-Berecka and Perchlicka (2007). Comparable results were found in the study conducted by Modrzyński and Prus-Głowacki (1998) which indicated high polymorphism (80%) and genetic diversity expressed as mean number of alleles (2.40) and observed heterozygosity (0.228) for Istebna provenance. Breeding characteristics of spruces from Istebna region have been proven in numerous provenance experiments (Giertych 1984). The analysis of the values of selection parameters tested on IUFRO 1964/68 conservation area in Krynica, revealed very high quality of spruces from the Beskid Śląski Mts. which was expressed by high survival rate, tree height corresponding to the 1st site class and, in most cases, late flushing and resistance to spring frosts. Spruce forests from the Beskid Śląski Mts. are assigned to a group of provenances for which growth characteristics improve with age (Sabor 1996). The value of F_{ST} coefficient calculated for 17 spruce provenances from the Beskidy Mts. was equal to 0.146 indicating that almost 15% of variability was explained by interpopulation differentiation. The obtained value is significantly higher that previously described in other works on coniferous species of wide distribution in which 90% of variability was attributed to variation within population (Ledig 1986). The high value of F_{ST} coefficient can result from low gene flow between analyzed populations according to the rule saying that the lower level of gene flow the smaller intrapopulation variation is observed being

accompanied by higher variation between populations (Burczyk 1998).

Genetic distance between spruces from the Beskidy Mts. was equal to 0.027 and similar to the value obtained by Lewandowski and Burczyk (2002) for spruce populations from the southern region of north-east Poland. The results presented in our work also confirm those obtained by Lewandowski et al. (1997). In the latter work, the highest individuality (0.008) was found between a group of populations from the Sudety Mts. and north-east Poland, while the lowest – between populations from the Beskidy Mts. and the north-eastern part of Poland (0.005). Obtained values of genetic distances for spruce populations from the Beskidy Mts. are lower than those for Swedish (0.084), Belarusian (0.081), Russian (0.073) and Ukrainian (0.077) provenances (Krutovskii and Bergmann 1995). At the same time, they exceed values noted for provenances from the entire range of distribution (0.007) (Langercrantz and Ryman 1990) as well as for Slovakian (0.016) (Paule et al. 1990) and Italian spruces (0.019) (Giannini et al. 1991).

In this study no differences in spruce genetic structure dependent on the type of seed source used to set up the experiment were documented. Studies conducted by Giertych (2002) and Skrøppa (1994) further indicate that phenotypic selection does not affect a level of genetic variation in spruces. Evaluation of the influence of selection on genetic structure of forest trees requires additional research with the greatest possible number of individuals as well as applying various biochemical and molecular markers.

Provenance experiments are important objects of research that allow not only for gaining knowledge about phenotypic and genetic value of progeny tested stands, but they also constitute *in vivo* genetic banks. This is especially important in the face of disaster and the loss of valuable parent's stands when tested material can be used for reconstituting the population (Chałupka et al. 2008). History of the spruce provenances, tested in IPTNS-IUFRO 1964/68 experiment in Krynica showed, however, that sometimes valuable material may be irretrievably lost.

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