



RAPD ANALYSIS OF GENETIC STRUCTURE IN FOUR NATURAL POPULATIONS OF *TAXUS BACCATA* FROM SOUTHERN POLAND

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This work assessed genetic diversity and genetic structure using random amplified polymorphic DNA (RAPD) variation in 120 individuals of four natural populations of *Taxus baccata* growing in southern Poland (3 in mountains and one in lowland) to obtain basic information on this natural resource. With 9 primers, 185 highly reproducible and clear RAPD bands were obtained. Genetic diversity within populations was relatively high, with percentages of polymorphic bands ranging from 48.65% to 77.30%, averaging 69.59% (Shannon index 0.311). Global AMOVA showed that genetic variation between populations accounted for 26% of total variation, with the remainder (74%) occurring within population. Pairwise Φ_{PT} values were not correlated with geographic distance. Two groups of populations were distinguished by ANOVA and principal coordinate analysis (PCO) based on a Euclidean metric: those growing in mountains (Nowa Wieś, Ciszowa Góra, Zadni Gaj), with higher internal diversity, and those growing in lowlands (Liswarta), with lower internal diversity. The results are typical for an outcrossing, wind-pollinated and long-lived woody species.

Key words: DNA markers, genetic diversity, RAPD, *Taxus baccata* L., yew.

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