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**Forest Research and Cooperation
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Abstracts

Use of microsatellite markers for clonal identification in European larch seed orchard

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The Simple Sequence Repeats (SSR) method of DNA analyses was used to clonal identification in a model European larch (*Larix decidua* Mill.) seed orchard. Total genomic DNA was extracted by DNA Plant Mini Kit (QIAGEN) from needles taken from 170 sampled trees of seed orchard. Samples were screened using selected 13 polymorphic nuclear microsatellite markers. Measuring the size of amplification products was carried out using the genetic analyser Applied Biosystems 3500. The obtained data were analysed using the statistical programs CERVUS, GenAlEx 6.503 and Micro-Checker. There were detected 133 different alleles at 13 loci in the 170 European larch tree individuals from seed orchard. The most polymorphic in our set of samples was locus bcLK211. By applying the 13 suitable markers to the 42 clones from model seed orchard we obtained multilocus genotypes (MLG). Clone affiliation declared by its owner was confirmed in 71 % of sampled trees, but on the basis of obtained genotypes, it is possible to assign 98 % of sampled tree to clones from seed orchards. The obtained results illustrate the utility of the microsatellite loci for assessing spatial patterns of genetic diversity and for individual identification. This work was supported by the Ministry of Agriculture of the Czech Republic, institutional support MZE-RO0118.

Evaluation of the genetic diversity of selected Czech Norway spruce stands

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The genetic structure of selected Norway spruce stands from the Jeseníky Mts., Orlické hory Mts., and Krušné hory Mts. (Czech Republic) was studied to verify the genetic quality. The genetic variability of tree populations ensures the stability and sustainability of forest ecosystems. DNA polymorphism at twelve nuclear microsatellites of fourteen Norway spruce stands was investigated. The level of genetic diversity within 14 investigated Czech Norway spruce stands was relatively high. Mean values for number of different alleles ranged from 12.25 (stand SM J51) to 15.92 (stand SM T1). The values of observed heterozygosity (Ho) ranged from 0.65 to 0.81, and expected heterozygosity (He) from 0.81 to 0.86. Pairwise population FST values ranging from 0.007 to 0.030 indicated low genetic differentiation between units, and values of Nei's genetic distance among Norway spruce units ranged from 0.083 to 0.313. The structuring of investigated Norway spruce stands was also confirmed by different ratios of genetic profiles according to the Bayesian clustering method results. Closer genetic similarity was seen in the stands from the gene conservation unit in the Orlické hory than in other studied stands. The most genetically different stand was from the Krušné hory. Knowledge based on DNA analyses regarding the variability of genetic resources will contribute to the quality of the reproduction material and to creation of an optimal species composition in forests. This work was supported by the projects of the Ministry of Agriculture of the Czech Republic - institutional support MZE-RO0118 and no. NAZV QK1810129

Genetic structure of *Bertholletia excelsa* throughout the Brazilian Amazon region / Estrutura genética de *Bertholletia excelsa* ao longo da Amazônia brasileira

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A *Bertholletia excelsa* Bonpl. (Lecythidaceae) é uma espécie arbórea endêmica das matas de terra firme e com ampla distribuição ao longo de toda a Floresta Amazônica. De grande relevância econômica devido à extração das sementes realizada por populações locais, está entre os produtos mais exportados da Amazônia. Atualmente, faz parte da lista oficial das espécies em extinção, sendo classificada como vulnerável. Tendo em vista este contexto torna-se de suma importância o estabelecimento de estratégias para definição de áreas prioritárias para a conservação da espécie. Uma dessas ferramentas é a caracterização da diversidade e estrutura genética em populações naturais. Esse trabalho amostrou árvores em 22 populações naturais da *B. excelsa* ao longo da Amazônia brasileira, totalizando 140 amostras em todos os estados da região Norte. Foram construídas bibliotecas genômicas NextRAD, e o sequenciamento resultou na identificação de ~30.000 locos SNPs (*Single Nucleotide Polymorphism*). Com os genótipos SNPs foram estimados parâmetros de diversidade e estrutura genética. Observamos níveis elevados de diversidade genética e identificamos regiões da Amazônia brasileira com diversidade genética única. São apresentados resultados das estatísticas F de Wright, bem como a correlação entre distâncias genéticas e geográficas. Utilizamos o método Bayesiano de agrupamento implementado no pacote *geneland* para visualizar a estruturação genética na paisagem, que usamos para discutir propostas de áreas prioritárias para conservação. Apoio financeiro: Embrapa (Processo SEG: 02.13.05.017.00.00).

Lack of interaction between provenances and habitats of scots pine (*Pinus sylvestris* L.) in two experimental plots in Bosnia and Herzegovina

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The research studies interactions between provenances of Scots pine in two test planes (Romanija Glasinac, 1000 m and Gostović Zavidovići, 480 m above sea level) of different ecologic conditions in Bosnia and Herzegovina. The test includes 11 provenances with 10 families in each, and in five repetitions. All interactions are calculated on the basis of value of diameter at breast height and height of plants that are 21 years old. Šipovo was the best provenance in Glasinac plane, with average breast-height diameter amounting to 14.04 cm and 8.82 m height, while Olovo showed lowest results – 11.99 cm and 7.72 m. In Gostović plane, Bosanski Petrovac had the biggest average breast-height diameter – 12.28 cm while maximum height was recorded in Rogatica provenance – 10.96 m. Smallest average breast-height diameter (9.74 cm) and minimum height was recorded in Doboj seed orchard provenance. Variance analysis showed statistically significant differences between provenances in terms of diameter at breast height and height values. The obtained values of coefficient have shown that there