

Table of Contents

In Press

Article Archive

- JFS (64) 2018
- JFS (63) 2017
- JFS (62) 2016
- JFS (61) 2015

- Issue No. 1 (1-44)
- Issue No. 2 (45-88)
- Issue No. 3 (89-139)
- Issue No. 4 (141-187)
- Issue No. 5 (189-234)
- Issue No. 6 (235-276)
- Issue No. 7 (277-324)
- Issue No. 8 (325-368)
- Issue No. 9 (369-415)
- Issue No. 10 (417-464)
- Issue No. 11 (465-514)
- Issue No. 12 (515-561)

- JFS (60) 2014
- JFS (59) 2013
- JFS (58) 2012
- JFS (57) 2011
- JFS (56) 2010
- JFS (55) 2009
- JFS (54) 2008
- JFS (53) 2007
- JFS (52) 2006
- JFS (51) 2005
- JFS (50) 2004
- JFS (49) 2003

Editorial Board

Ethical Standards

Peer Review Process

Reviewers 2017

For Authors

Author Declaration

Instruction for Authors

Submission Templates

Guide for Authors

Copyright Statement

Submission/Login

## Use of nuclear microsatellite loci for evaluating genetic diversity among selected populations of *Abies alba* Mill. in the Czech Republic

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The simple sequence repeats (SSR) method of DNA analysis was used to determine genetic diversity within and among silver fir (*Abies alba* Mill.) populations. Total genomic DNA was extracted from 250 *Abies alba* adult individuals collected from 8 important populations growing in different parts of the Czech Republic. Samples were screened using eight selected polymorphic nuclear microsatellite markers. PCR products were separated by capillary electrophoresis. Identified genetic loci were verified as reliable and polymorphic and were used for comparative genetic analyses of silver fir populations. The genotypic data from the adult trees implies genetic differences among the studied populations. The populations' genetic diversity expressed as Shannon's information index values was highest in the JD06 population from Hochwald. The lowest genetic diversity was in the JD02 population from Velké Polčané, Morávka. The longest genetic distance appeared between the JD02 (Velké Polčané, Morávka) and JD07 (Hojsova Stráž) populations. The closest genetic distance was between the JD01 (Babín) and JD03 (Vodslivý) populations.

### Keywords:

simple sequence repeats; silver fir populations; genetic variability and differentiation; genetic distance; gene reserves; DNA analysis

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(p1-p7).

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