Population structure and genetic diversity of Caucasian fir (*Abies nordmanniana*) in Georgia based on SSR marker analysis

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1 Table of Contents

2 List of Tables and Figures

3 List of Abbreviations

AMOVA:	Analysis of Molecular Variance
cpDNA:	Chloroplast DNA
CTAB:	Cetrimonium Bromide
EDTA:	Ethylenediaminetetraacetic Acid
F_{ST}:	The Fixation Index
IBD:	Isolation by Distance
LGM:	Last Glacial Maximum
PIC:	Polymorphic information content
mtDNA:	Mitochondrial DNA
s.d.:	Standard deviation
SSR:	Simple Sequence Repeats
UV:	Ultra-Violet
HO:	Observed Heterozygosity
HE:	Expected Heterozygosity
HWE:	Hardy-Weinberg Equilibrium

ACH:	Achara
ABA:	Abastumani
BAK:	Bakuriani
SMG:	Samegrelo
RCH:	Racha

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5 Abstract

SSR (simple sequence repeats) marker analysis on *Abies nordmanniana* indicates a correlation between geographic distance and pairwise differences in five tested populations in Georgia. The samples were collected from Achara, Abastumani, Bakuriani, Racha and Samegrelo. The isolation-by-distance model was confirmed by mantel test. Pairwise differences were very low in most pairs, indicating high gene flow and weak population substructuring. There was no strong genetic correlation between samples located on same mountain range (Lesser and Greater Caucasus), possibly indicating presence of land bridges, such as Likhi range, and/or strong capability of dispersing pollen on long distances. Admixture model with Structure analysis shows two possible population numbers (K = 2 and K = 7). Data indicates that Achara samples are most distinct from other populations.

Key words: *Abies nordmanniana*, SSR, Isolation by distance, gene flow