

# Genetic signature of the natural gene pool of *Tilia cordata* Mill. in Lithuania: compound evolutionary and anthropogenic effects

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## Abstract

*Tilia cordata* Mill. is a valuable tree species enriching the ecological values of the coniferous dominated boreal forests in northerly Europe. Following the historical decline, spreading of *Tilia* sp. is challenged by the elevated inbreeding and habitat fragmentation. We aimed to identify the main factors affecting the genetic potential of *Tilia cordata* for natural expansion by studying the geographical distribution of genetic diversity of *Tilia cordata* in semi-boreal forests of Lithuania. We used 14 genomic microsatellite markers to genotype 543 individuals from 23 wild growing populations of *Tilia cordata* in Lithuania. We found that *Tilia cordata* retained high levels of genetic diversity (population  $F_{is} = 0$  to 0.15,  $H_o = 0.53$  to 0.69,  $H_e = 0.56$  to 0.75). AMOVA, Bayesian clustering and Monmonier's barrier detection indicate weak but significant differentiation among the populations ( $F_{st} = 0.037^{***}$ ) into geographically interpretable clusters of (a) western Lithuania with high genetic heterogeneity but low genetic diversity, bottleneck effects, (b) peaking values of genetic diversity of *Tilia cordata* on rich and most soils of midland lowland, and (c) the most differentiated populations on poor soils of the coolest north-eastern highland possessing the highest rare allele frequency but elevated inbreeding and bottleneck effects, presumably, due to sub-structuring. We conclude that the genepool of *Tilia cordata* in Lithuania contains (a) the autochthonous populations of high genetic diversity representing the pre-historical genepools, that can be promoted, and (b) the escapes from urban sources of low diversity, that must be contained.

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