ASSESSMENT OF THE STRUCTURE AND DIVERSITY OF LATVIAN *ACER PLATANOIDES* POPULATIONS USING CROSS-SPECIES NUCLEAR MICROSATELLITE MARKERS

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Acer platanoides L. (Norway maple) is the most widespread native maple species in Europe, with a distribution from south and central Europe to northern Europe and Scandinavia. *Acer platanoides* is widespread throughout the territory of Latvia, and is mainly found in mixed broadleaf and conifer stands. The genetic diversity and differentiation of Latvian *A. platanoides* populations was analysed. Sampled populations were located throughout the territory of Latvia, and were selected to represent a range of ecological conditions, with differing levels of anthropogenic impact. A total of 496 individuals from 21 populations were analysed with eight microsatellite markers, which were developed from related *Acer* species. The obtained molecular data revealed a moderate level of polymorphism, and the analysed Latvian *A. platanoides* populations were moderately differentiated. This study provides an initial assessment of the genetic diversity and differentiation of Latvian *A. platanoides* populations, and is also one of the first reports of the analysis of *A. platanoides* populations using microsatellite markers. The results can be utilised to define *A. platanoides* genetic resource stands to ensure conservation of a wide range of germplasm.

Keywords: Norway maple, genetic resources, population genetics.

INTRODUCTION

Acer platanoides L. (Norway maple) is the most widespread native maple species in Europe, with its natural distribution ranging from Greece, Balkans, Northern Italy and the Pyrenees to southern Fennoscandia, and toward the East up to the Ural Mountains. It is not native to western France, the UK, the Netherlands and Denmark. This species can grow in a wide range of soils and habitat conditions, from sea level up to 1400 m elevation (Caudullo and de Rigo, 2016).

A. platanoides is monoecious, with individuals bearing both male and female flowers, which are mainly insect pollinated. Seeds are medium-sized, with double samaras, and are wind-dispersed. There is little evidence of vegetative reproduction. A study of characteristics of *A. platanoides* and *A. pseudoplatanus* seeds collected along a 2200 km long latitudinal gradient from Italy to Norway indicated that the seed mass of *A. platanoides* was negatively influenced by increasing temperatures, and that seed viability was related to seed mass, with larger seeds having higher viability

(Carón *et al.*, 2014). Seeds of *A. pseudoplatanus* were less influenced by climatic factors. This indicates that seeds of northern *A. platanoides* populations are currently of higher quality than those of southern and central origin; however, climate change can potentially have a relatively negative effect on seed quality.

Acer platanoides is widespread throughout the territory of Latvia. The largest areas are found in eastern regions, with the largest proportion of the total stand area found in the Latgale Highlands (364.8 ha, 16.3%) and Augšzeme (235.6 ha, 10.5%). A substantial proportion also grows in the coastal lowlands (222.7 ha, 10.0%), but in this region stands are typical of urban (Rīga, Jūrmala, Ventspils) and suburban forests. *A. platanoides* forest stands are characteristic in nutrient-rich mineral soil sites — Oxalidos, Hylocomiosa, Aegopodiosa forest types (88.9% of total area). *A. platanoides* is mainly found in mixed broadleaf and conifer stands. Currently, *A. platanoides* reproduces very intensively in extensively managed broadleaf and coniferous forests, especially in pine stands, as well as in urban and suburban environments (urban forests), which indicates the ruderal or

pioneer species strategy of *A. platanoides*. Under current changing environmental conditions, maple is a typical colonising species of broad-leaved forest stands in Latvia. *A. platanoides* individuals in forest stands are of different ages, and are not characterised by the formation of multi-story stands, renewal is gradual and stands contain a continuum of individuals by age.

Currently, there are very few studies of the genetic diversity and population structure of *A. platanoides*. Two studies utilised isozyme markers to analyse *A. platanoides* in Finland (Rusanen *et al.*, 2000), and *A. platanoides* populations in northern Europe (Rusanen *et al.*, 2003). The latter study compared genetic diversity and population differentiation between central and marginal populations of *A. platanoides*. Contrary to expectations, there was no difference in the genetic diversity between central and marginal populations, and the marginal populations were less differentiated than the central populations. This result was related to post-glacial climate changes and the vegetation history in northern Europe, and the current marginal population distribution is a result of the contraction of a previously continuously distributed population rather than an expansion from the distribution centre. Therefore, fragmentation of northern marginal populations occurred too recently for genetic drift to have an impact on the diversity and differentiation of these populations. In addition, anthropogenic impacts have been more prolonged and extensive in central European populations (Rusanen *et al.*, 2003).

DNA markers can provide valuable additional information about the diversity and structure of populations. They are often more informative than phenotypic parameters, as they are not influenced by environmental conditions, and can be assessed at any stage of the growing season or life cycle. Microsatellites or simple sequence repeat (SSR) markers are widely utilised for population genetic studies, as they are highly polymorphic, and are codominant, which enable direct quantification of heterozygosity. One major drawback is that they need to be developed for each locus, by characterising DNA sequences surrounding the repeat regions, which entails considerable time and effort. Microsatellite markers are predominantly species specific, but can be transferred to related species. However, transfer to other species can result in amplification of non-specific PCR products or null alleles. Null alleles occur when there is a mutation in the primer binding sites in some alleles, leading to a lack of PCR amplification of these alleles. The presence of null alleles can be inferred by comparison of observed and expected heterozygosities, assuming the analysed populations are in Hardy-Weinberg equilibrium. In addition, often lower levels of diversity are revealed by microsatellite markers in species other than those from which they were developed. No microsatellite markers have been developed for *A. platanoides* so far, but microsatellite markers have been developed for *A. pseudoplatanus* (Pandey *et al.*, 2004), *A. miyabei* and *A. saccharum* (Harmon *et al.*, 2017). Both sets of markers were tested in a range of *Acer* species, and a proportion of these markers were reported to amplify PCR products from *A. platanoides*.

The aim of this study was to analyse the genetic diversity and differentiation of Latvian *A. platanoides* populations. The analysed populations were located throughout the territory of Latvia, and were selected to represent a range of ecological conditions, with mixed stands consisting of different species, both broadleaf and coniferous, as well as differing levels of anthropogenic impact. The results can be utilised to define *A. platanoides* genetic resource stands to ensure conservation of a wide range of germplasm.

MATERIALS AND METHODS

Analysed populations and sample collection. Samples for DNA extraction were collected from 21 *A. platanoides* plots located throughout the territory of Latvia. Leaf or twig samples were collected from 24 individuals from each plot. A total of 504 individuals were collected from 21 populations (Fig. 1, Table 1).

DNA was extracted using a modified CTAB method (Doyle and Doyle, 1990). A total of 15 microsatellite markers were used to genotype the sampled individuals: As_di1, As_di9, As_di15, As_di21, As_di49, As_tetra1 (Harmon *et al.*, 2017); MAP2, MAP9, MAP10, MAP12, MAP33, MAP40, MAP46 (Pandey *et al.*, 2004); Acmi11, Acmi33 (Saeki *et al.*, 2015). None of these markers were developed specifically for *A. platanoides*, but were derived from sugar maple (*Acer saccharum* Marsh.) (Harmon *et al.*, 2017), sycamore (*Acer pseudoplatanus* L.) (Pandey *et al.*, 2004) and *Acer miyabei* Maxim. (Saeki *et al.*, 2015).

PCR reactions were performed in a volume of 10 µl containing approximately 50 ng DNA, 2 µl HOT FIREPol® Blend Master Mix (Solis BioDyne) (containing 10 mM MgCl₂), 0.3 µM forward and reverse primers. PCR was carried out in a thermocycler (Eppendorf Mastercycler epgradient) using the following protocol: initial predenaturation step at 95 °C for 15 min, followed by 35 cycles of 95 °C for 30 s, 60 °C for 30 s, and 72 °C for 40 s and a final extension step of 72 °C for 10 min for all markers with the exception of Map2, Map10, Map33: Map9, Map40, Map46: AsTetra, Acmi33, Map12, where the annealing temperature was 55 °C. All PCR reaction products were diluted 1 : 10 with

Fig. 1. Analysed *A. platanoides* population in Latvia (black dots – site numbering as in Table 1)

Table 1. Details of analysed *A. platanoides* populations

No.	Name	Stand species composition/description	Anthropogenic impact	Region	Coordinates
1	Limbaži	<i>A. platanoides</i> (with <i>Fraxinus excelsior</i>)	Low	Eastern	57.517, 24.528
2	Madona	<i>Pinus sylvestris</i> with <i>A. platanoides</i> in 2nd storey	Medium	Eastern	56.826, 26.306
3	Taurene	<i>Picea abies</i>	Low	Eastern	57.166, 25.692
4	Rundāle	<i>A. platanoides</i> (with <i>Fraxinus excelsior</i>)	Low	Western	56.422, 24.043
5	Ventspils	<i>Pinus sylvestris</i> with <i>A. platanoides</i>	High	Western	57.405, 21.573
6	Smiltene	Undergrowth beneath <i>Betula</i> and other broadleaf species	Low	Eastern	57.433, 25.785
7	Priekule	<i>Pinus sylvestris</i> with <i>A. platanoides</i> in 2nd storey	Low	Eastern	57.364, 25.402
8	Šķēde	Roadside	Medium	Western	57.256, 22.734
9	Glāzšķūnis	Clearing, rejuvenation with broadleaf species	Medium	Eastern	56.796, 24.869
10	Ērgļi	Mixed <i>Pinus sylvestris</i> , <i>Picea abies</i> , <i>Quercus robur</i>	Medium	Eastern	56.906, 25.632
11	Kuprava	<i>Tilia cordata</i>	Low	Eastern	57.276, 27.500
12	Gaujiena	<i>Pinus sylvestris</i>	High	Eastern	57.519, 26.399
13	Laidi	Mixed broadleaf forest by cemetery	High	Western	56.742, 21.872
14	Saldus	<i>A. platanoides</i> , <i>Picea abies</i> , <i>Quercus robur</i>	Low	Western	56.641, 22.541
15	Ogre	<i>Pinus sylvestris</i> with <i>A. platanoides</i> in 2nd storey	High	Eastern	56.812, 24.615
16	Rauda	<i>A. platanoides</i> juvenile stand	Low	Eastern	55.873, 26.279
17	Klauce	<i>A. platanoides</i> (with <i>Fraxinus excelsior</i>)	Low	Eastern	56.287, 25.583
18	Kurmene	<i>A. platanoides</i> along the River Mēmele	Medium	Eastern	56.419, 24.828
19	Jēkabpils	<i>A. platanoides</i> and <i>Tilia cordata</i> , old park	High	Eastern	57.744, 25.171
20	Tukums	Abandoned settlement, <i>A. platanoides</i> and <i>Tilia cordata</i>	High	Western	56.997, 23.033
21	Dagda	Shrubbery by cemetery	High	Eastern	56.102, 27.521

deionised water, and visualised on an Applied Biosystems ABI Prism 3100xl Genetic Analyser. Genotyping was performed using GeneMapper 4.0. (Applied Biosystems). All the MAP markers were monomorphic in the analysed samples, and therefore were not analysed. Individuals with missing data at more than three loci were also removed prior to analysis. As a result, a total of 496 individuals from 21 populations were retained for further analysis.

Micro-Checker 2.2 (Van Oosterhout *et al.*, 2004) was used to identify potential null alleles. GenAIEx 6.501 (Peakall and Smouse, 2012) was used to calculate genetic diversity indices, and AMOVA and pairwise population differentiation (F_{ST}) (using 999 permutations) as well as the probability of identity, which is the probability that two individuals have the same genotype by chance. This can also be calculated taking into account sibling relationships. STRUCTURE 2.3.4 was used to determine clustering of the populations using a 100 000 burning period, followed by 150 000 MCMC steps, K was determined for 1 to 21 with 15 runs for each value of K. The LOCPRIOR model was used, using the sampling location as default information to assist clustering, which is recommended for use with datasets with a weak structure signal (Pritchard *et al.*, 2000). The optimal value of K was determined using the ΔK method (Evanno *et al.*, 2005) using STRUCTURE HARVESTER (Earl, 2012) and the probability by K using median values of Ln(Pr Data) implemented via the CLUMPAK server (Kopelman *et al.*, 2015). Coefficients of membership to the most likely K cluster number were visualised using Distruct via the CLUMPAK server.

RESULTS

The presence of potential null alleles was assessed using Micro-Checker 2.2, and the number of potential null alleles was not high. While loci with potential null alleles were identified in 10 of the 21 analysed populations, most had only one locus with potential null alleles, and the remaining two populations each had two loci with potential null alleles. In addition, only two loci had potential null alleles in more than two populations — As_di2 and As_di49 (in five and three populations, respectively). Therefore, all loci were retained for further analyses.

The genetic diversity parameters of the analysed loci are summarised in Table 2. The total number of alleles at each locus ranged from 4 (As_di15 and As_tetra1) to 15 (As_di49), while the average number of alleles (over all populations) at each locus ranged from 2.14 (As_di15) to 6.48 (As_di49). The fixation index or inbreeding coefficient (F) was negative for most loci, with the exception of As_di1, As_di9 and As_di49. However, as mentioned previously, this heterozygote excess (indicating the potential presence of null alleles) at these loci was not detected in all populations, and so all loci were retained for analyses.

The genetic diversity parameters of the analysed populations are summarised in Table 3. The average number of alleles (over all loci) ranged from 3.63 (Tukums) to 5.50 (Kurmene). The Madona population also had the lowest values for number of effective alleles (N_e) and information index (I). However, the Šķēde population had the highest N_e

Table 2. Genetic diversity parameters of the analysed loci

	Acml1	As_di1	As_di9	As_di15	As_di21	As_di49	As_tetral	Acml33
Natot	12	9	12	4	11	15	4	13
Na (SE)	3.52 (0.18)	3.29 (0.20)	4.95 (0.19)	2.14 (0.10)	5.29 (0.24)	6.48 (0.24)	3.05 (0.05)	6.33 (0.31)
Ne (SE)	1.69 (0.13)	2.19 (0.07)	3.09 (0.16)	1.61 (0.08)	2.91 (0.13)	3.48 (0.19)	2.17 (0.06)	3.84 (0.20)
I (SE)	0.68 (0.06)	0.87 (0.03)	1.26 (0.05)	0.54 (0.04)	1.26 (0.05)	1.45 (0.05)	0.87 (0.02)	1.49 (0.04)
Ho (SE)	0.36 (0.03)	0.44 (0.03)	0.63 (0.02)	0.36 (0.04)	0.67 (0.03)	0.60 (0.04)	0.60 (0.03)	0.76 (0.03)
uHe (SE)	0.37 (0.04)	0.55 (0.01)	0.67 (0.02)	0.36 (0.03)	0.65 (0.02)	0.71 (0.02)	0.55 (0.01)	0.74 (0.02)
F (SE)	-0.01 (0.04)	0.17 (0.05)	0.03 (0.03)	-0.02 (0.05)	-0.06 (0.04)	0.13 (0.04)	-0.12 (0.05)	-0.05 (0.03)

Natot; total number of alleles; Na, average number of alleles over all loci; Ne, average number of effective alleles over all loci; I, average information index over all loci; Ho, average observed heterozygosity over all loci; uHe, average unbiased expected heterozygosity over all loci; F, average inbreeding coefficient over all loci; SE, standard error

Table 3. Genetic diversity parameters of the analysed populations (average values over all analysed loci)

	Na (SE)	Ne (SE)	I (SE)	Ho (SE)	uHe (SE)	F (SE)
Limbaži	4.00 (0.53)	2.33 (0.37)	0.93 (0.15)	0.48 (0.06)	0.51 (0.08)	-0.02 (0.05)
Ventspils	4.00 (0.57)	2.51 (0.27)	1.02 (0.12)	0.50 (0.04)	0.58 (0.04)	0.10 (0.07)
Madona	4.25 (0.77)	2.09 (0.40)	0.85 (0.15)	0.48 (0.07)	0.45 (0.07)	-0.11 (0.04)
Rundāle	4.00 (0.65)	2.80 (0.38)	1.08 (0.15)	0.62 (0.07)	0.61 (0.05)	-0.04 (0.07)
Taurene	4.13 (0.55)	2.40 (0.24)	1.01 (0.10)	0.58 (0.05)	0.57 (0.04)	-0.04 (0.06)
Priekule	3.88 (0.61)	2.32 (0.33)	0.90 (0.15)	0.54 (0.10)	0.52 (0.07)	-0.06 (0.10)
Smiltene	4.25 (0.49)	2.88 (0.37)	1.15 (0.12)	0.57 (0.10)	0.63 (0.05)	0.06 (0.15)
Šķēde	4.88 (0.72)	3.02 (0.47)	1.17 (0.17)	0.49 (0.06)	0.61 (0.07)	0.15 (0.07)
Glāzšķūnis	4.00 (0.73)	2.43 (0.30)	0.99 (0.15)	0.64 (0.07)	0.55 (0.06)	-0.19 (0.05)
Kuprava	4.63 (0.65)	2.83 (0.44)	1.11 (0.17)	0.57 (0.09)	0.58 (0.08)	-0.01 (0.04)
Gaujiena	4.63 (0.71)	2.91 (0.43)	1.14 (0.17)	0.52 (0.08)	0.60 (0.08)	0.14 (0.08)
Ērgļi	4.38 (0.68)	2.53 (0.30)	1.05 (0.13)	0.50 (0.05)	0.57 (0.06)	0.09 (0.05)
Ogre	4.63 (0.68)	2.60 (0.35)	1.08 (0.14)	0.57 (0.06)	0.58 (0.06)	0.00 (0.04)
Laidi	4.25 (0.59)	2.75 (0.41)	1.06 (0.17)	0.53 (0.08)	0.57 (0.08)	0.03 (0.06)
Saldus	4.38 (0.56)	2.61 (0.32)	1.07 (0.14)	0.56 (0.08)	0.58 (0.06)	0.01 (0.10)
Tukums	3.63 (0.42)	2.37 (0.29)	0.93 (0.14)	0.55 (0.10)	0.53 (0.07)	-0.06 (0.08)
Rauda	4.75 (0.70)	2.75 (0.41)	1.12 (0.14)	0.58 (0.08)	0.60 (0.05)	0.04 (0.06)
Dagda	4.75 (0.73)	2.60 (0.33)	1.09 (0.15)	0.54 (0.07)	0.57 (0.06)	0.04 (0.04)
Klaucē	4.50 (0.82)	2.80 (0.45)	1.08 (0.15)	0.60 (0.08)	0.60 (0.05)	-0.02 (0.11)
Kurmene	5.50 (0.78)	2.81 (0.34)	1.19 (0.13)	0.55 (0.06)	0.62 (0.05)	0.08 (0.05)
Jēkabpils	4.63 (0.38)	2.74 (0.30)	1.13 (0.10)	0.61 (0.07)	0.61 (0.05)	-0.01 (0.09)

Na, number of alleles; Ne, number of effective alleles; I, information index; Ho, observed heterozygosity; uHe, unbiased expected heterozygosity; F, inbreeding coefficient; SE, standard error

value, indicating that allele frequencies were more evenly distributed in this population compared to Kurmene. The fixation index (F) ranged from -0.19 (Glāzšķūnis) to 0.15 (Šķēde).

The probability of identity, which is the probability that two individuals of a population or sample have the same genotype by chance, over all loci and all populations, was 6.4×10^{-7} , and for siblings it was 2.8×10^{-3} . Analysing the probability of identity in each population separately, these values ranged from 1.5×10^{-6} in Smiltene (3.3×10^{-3} for siblings) to 1.3×10^{-4} in Madona (1.9×10^{-2} for siblings). A total of ten pairs of individuals were identified with identical multilocus genotypes. Each matching pair was within one population, and these matching genotypes were found

in seven populations (Rundāle, Tukums, Glāzšķūnis, Madona, Limbaži, Klaucē, Kurmene).

Unique alleles were found in seven populations (Limbaži, Madona, Kuprava, Ērgļi, Klaucē, Kurmene, Jēkabpils), with frequencies ranging from 0.021 to 0.364 (average 0.076). The majority of unique alleles were found in the Jēkabpils population (18 of a total of 27). In addition, almost all unique alleles with a frequency over 0.05 were found in the Jēkabpils population, with 10 of the 18 unique alleles in this population having a frequency above 0.05. Analysis of molecular variance (AMOVA) indicated that 9% of genetic variation was between populations, and 91% within populations ($F_{st} = 0.088$, $p < 0.001$). Pairwise F_{st} values ranged from 0.009 (Kuprava-Gaujiena) to 0.215 (Madona-Jēkabpils). Pairwise Nei genetic distances were

Fig. 2. PCoA of pairwise Nei genetic distances between analysed *A. platanooides* populations. Percentage of variation explained by axis 1 – 87.52, axis 2 – 4.62.

calculated, and were used to generate a PCoA plot (Fig. 2). Most of the analysed populations were clustered together, with Jēkabkalns being the most distinct, followed by Madona and Klaucē. The Saldus, Tukums, and Ogre populations were slightly differentiated from the remaining populations. There was no evidence of higher order structure, either by region (Eastern and Western), or anthropogenic impact (high, medium, low), with AMOVA indicating that differentiation between these groups was low – $F_{st} = 0.01$ ($p < 0.001$) in both cases. Mantel analysis of the pairwise genetic and geographic distance matrices indicated that there was no significant relationship between genetic and geographical distances.

Bayesian clustering was done, taking into account the population of origin of the analysed individuals. This assists clustering in sample sets with low differentiation. Based on the ΔK method (Evanno *et al.*, 2005), the most likely number of clusters was two. Assessing the probability by K using median values of $\ln(\text{Pr Data})$, the K for which

$K=2$

$K=11$

Fig. 3. Plots of coefficients of membership for $K = 2$ the most likely number of clusters as determined by the ΔK method and $K = 11$, the most likely number of clusters as determined by the median values of $\ln(\text{Pr Data})$.

$\text{Pr}(K = k)$ was highest and equal to 11. Graphical display of population structure based on ΔK and K calculated using median values of $\ln(\text{Pr Data})$ revealed the probability of each individual to be attributed to one of the studied *A. platanooides* populations in Latvia (Fig. 3). In both cases, the Jēkabkalns population was clearly differentiated from other populations studied. In the case where $K = 11$, the differentiation of other populations was less clear, with individuals having mixed cluster assignment, but Madona population was also differentiated and to a lesser extent the Klaucē and Priekule populations. This corresponds to the PCoA analysis, showing most pronouncedly the differentiation of the Jēkabkalns and Madona populations.

DISCUSSION

This is the first report of the population genetic analysis of *A. platanooides* using microsatellite markers. Microsatellite markers have not been developed specifically for *A. pla-*

atanoides, but can be transferred from related *Acer* species (Pandey *et al.*, 2004; Saeki *et al.*, 2015; Harmon *et al.*, 2017). In this study, the microsatellite markers developed for sycamore (*Acer pseudoplatanus* L.) (Pandey *et al.*, 2004) were monomorphic, but the markers derived from sugar maple (*Acer saccharum* Marsh.) (Harmon *et al.*, 2017) and *Acer miyabei* Maxim. (Saeki *et al.*, 2015) were polymorphic. These markers revealed a moderate level of polymorphism, the average number of alleles over all loci and populations was 4.38, and the expected heterozygosity (gene diversity) was 0.58. There was no convincing evidence for the widespread presence of null alleles, which can occur with the cross-species transfer of microsatellite markers.

The analysed Latvian *A. platanoides* populations were moderately differentiated ($F_{st} = 0.088$, $p < 0.001$), similar to results reported for the isozyme analysis of northern European population ($F_{st} = 0.099$) (Rusanen *et al.*, 2003). This level of differentiation could be related with insect pollination and wind dispersal of medium sized seeds. The Jēkabpils population was highly differentiated from all other populations, and had the largest number of unique alleles, the majority of which were of high frequency. The factors causing the higher differentiation of this population is not immediately clear. This population is located in the territory of an old park, with high human impact, and planting of highly differentiated imported germplasm could influence the differentiation of this population. However, there was no direct evidence of former introduction of diversified plant material, and other populations also had a high anthropogenic impact.

Based on the comparison of molecular data, several pairs of individuals with identical multilocus genotypes were found, and each of these pairs were distributed within one population. This indicates that *A. platanoides* can reproduce vegetatively, or that the utilised microsatellite markers do not have sufficient resolution to distinguish genetically distinct individuals. The probability of identity values for siblings was 2.8×10^{-3} over all analysed loci and populations, which is not extremely low, so the analysis of additional loci might distinguish these individuals. There are no reports in the scientific literature about the vegetative reproduction of *A. platanoides* in natural conditions, although rooting of cuttings in glasshouse conditions has been reported (Tomov, 2017). The possibility of vegetative reproduction in natural conditions should be further investigated by detailed spatial analysis of *A. platanoides* stands, and possibly the use of additional genetic markers.

This study provides an initial assessment of the genetic diversity and differentiation of Latvian *A. platanoides* populations, and is also one of the first reports of the analysis of *A. platanoides* populations using microsatellite markers. Several directions for future investigation were revealed, particularly the investigation of vegetative reproduction in *A. platanoides*, as well as the basis of the high differentiation of the Jēkabpils population. The results of the current study will enable efficient designation of genetic resource

stands, conservation of the genetic diversity of *A. platanoides*, as well as identification of more differentiated populations.

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LATVIJAS ACER PLATANOIDES POPULĀCIJU STRUKTŪRAS UN DAUDZVEIDĪBAS NOVĒRTĒJUMS, IZMANTOJOT KODOLA MIKROSATELĪTU MARĶIERUS

Acer platanoides L. (parastā kļava) ir visizplatītākā kļavu suga Eiropā, kura sastopama no Dienvideiropas un Centrāleiropas līdz Ziemeļeiropai un Skandināvijai. *A. platanoides* ir plaši izplatīta visā Latvijas teritorijā, galvenokārt sastopama jauktās platlapju un skuju koku audzēs. Pētījumā analizēta Latvijas *A. platanoides* populāciju ģenētiskā daudzveidība un diferenciācija. Populācijas atlasītas visā Latvijas teritorijā un aug dažādos ekoloģiskos apstākļos ar atšķirīgu antropogēnas ietekmes līmeni. Kopumā 496 indivīdi no 21 populācijas tika analizēti ar astoņiem mikrosatelītu marķieriem. Marķieri atklāja mērenu polimorfisma līmeni, un analizētās Latvijas *A. platanoides* populācijas bija mēreni diferencētas. Šis pētījums sniedz sākotnēju Latvijas *A. platanoides* populāciju ģenētiskās daudzveidības un diferenciācijas novērtējumu, kā arī ir viens no pirmajiem ziņojumiem par *A. platanoides* populāciju analīzi, izmantojot mikrosatelītu marķierus. Rezultātus var izmantot, lai definētu *A. platanoides* ģenētisko resursu audzes, lai nodrošinātu efektīvu ģenētiskās daudzveidības saglabāšanu.