

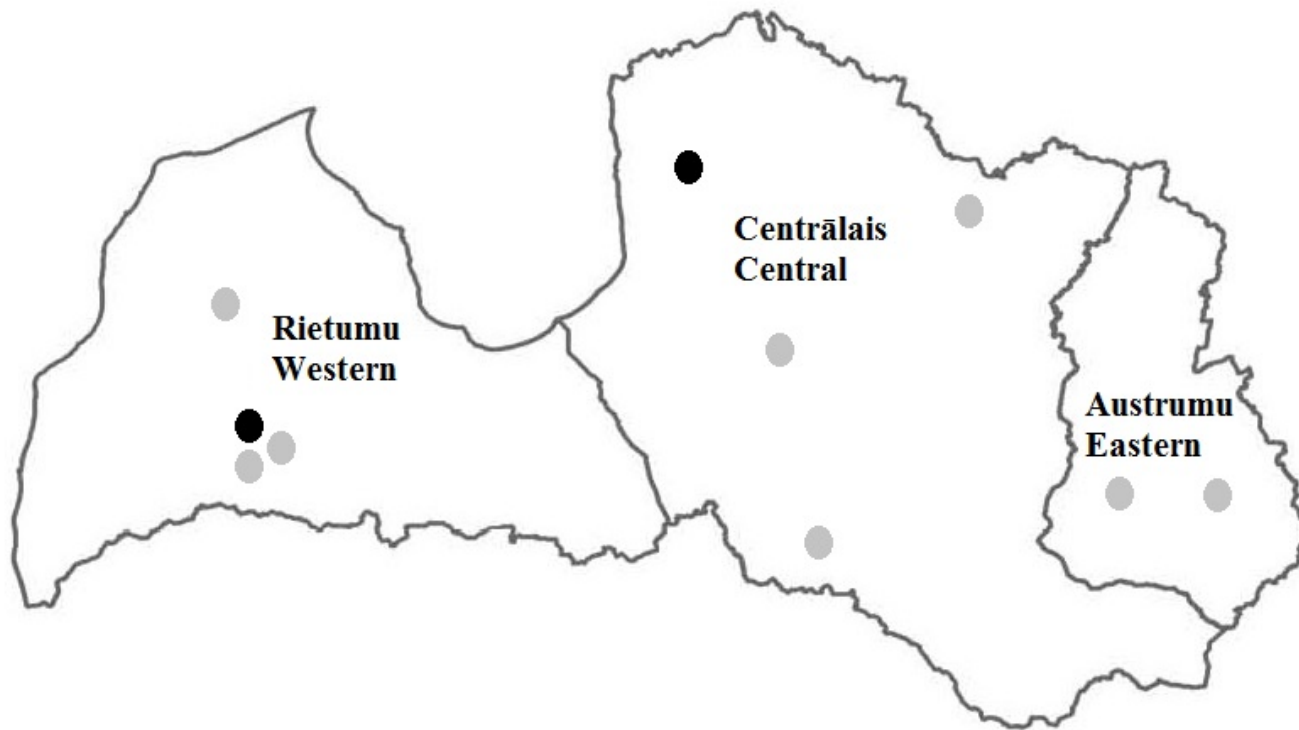
Influence of seed year on genetic diversity of progenies of Norway spruce seed orchard

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- Material for the study was collected from progenies of two Norway spruce seed orchards: Remte – located in south-western part of Latvia, consisting of 50 clones, and Katvari – located in north-eastern part of Latvia, consisting of 20 clones.
- Random selection of 217 (for Remte) and 274 (for Katvari) progenies was done in progeny trials, where average sample of both seed orchards were represented, located in Forest research stations Auce (central part of Latvia) and Kalsnava (eastern part of Latvia) forest districts.
- Mature forest stands were represented by samples from randomly selected trees (with distance of 100m) or seedlings from average seed sample of the stand.
- Stands were randomly chosen to represent western (3 stands, 139 trees in total), central (3 stands, 144 trees) and eastern (2 stands, 96 trees) provenance regions.
- DNA, extracted from the needles, was analysed with 6 nuclear SSR markers.

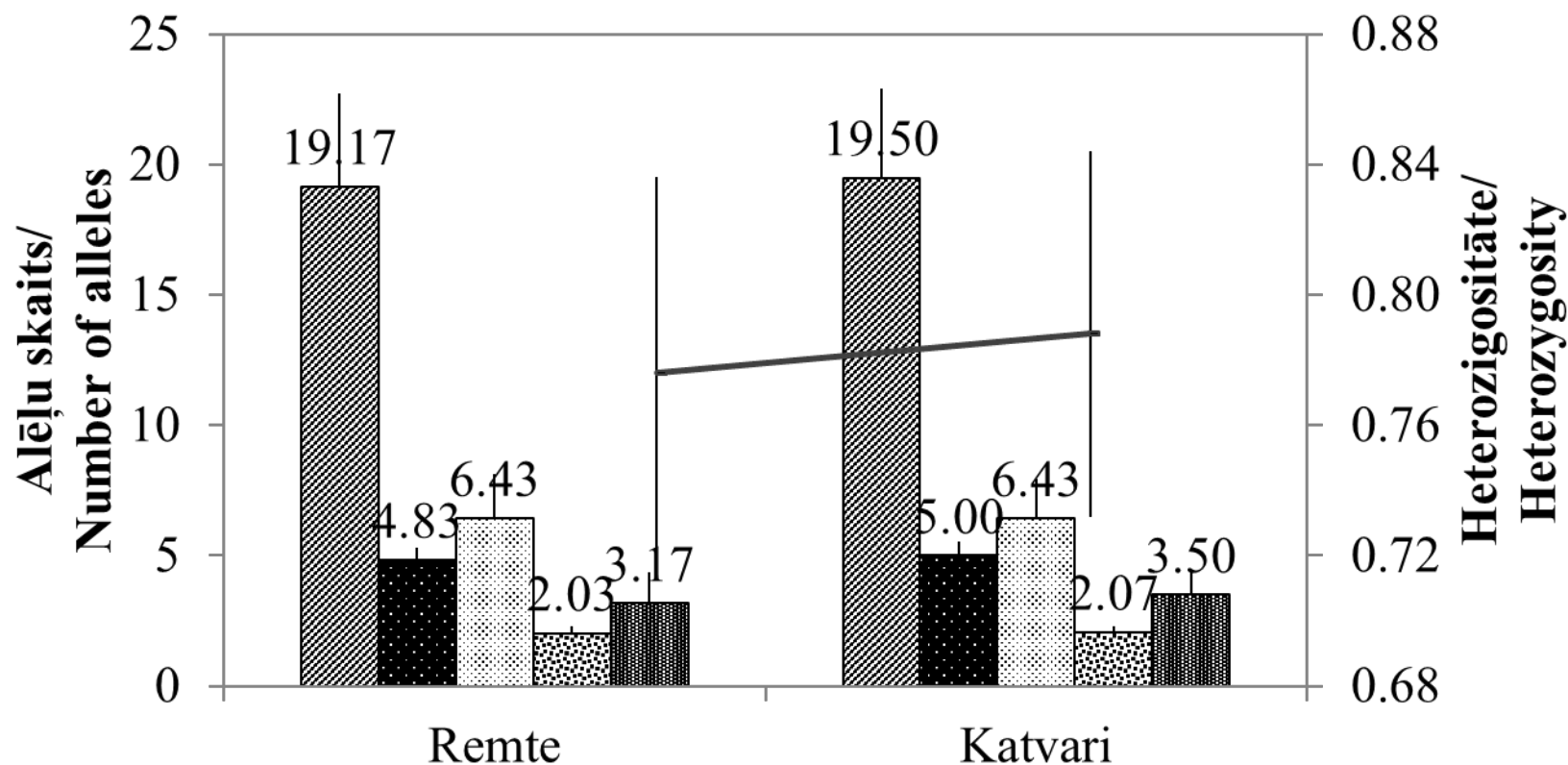


Materials and methods





Results: seed orchards



Na	Na = No. of Different Alleles
Na Freq. >= 5%	Na (Freq >= 5%) = No. of Different Alleles with a Frequency >= 5%
Ne	Ne = No. of Effective Alleles = 1 / (Sum pi^2)
I	I = Shannon's Information Index = -1* Sum (pi * Ln (pi))
No.	No. Private Alleles = No. of Alleles Unique to a Single Population
He	He = Expected Heterozygosity = 1 - Sum pi^2



Results



Population	SO1	SO2	Reg1	Reg2	Reg3
Na	19.2	19.5	16.5	17.2	17.5
Na Freq. $\geq 5\%$	4.8	5.0	5.0	4.8	4.0
Ne	6.43	6.43	6.68	6.72	5.70
I	2.03	2.07	1.93	1.93	1.91
He	0.78	0.79	0.74	0.73	0.72

Na = No. of Different Alleles
Na (Freq $\geq 5\%$) = No. of Different Alleles with a Frequency $\geq 5\%$
Ne = No. of Effective Alleles = $1 / (\sum p_i^2)$
I = Shannon's Information Index = $-1 * \sum (p_i * \ln(p_i))$
He = Expected Heterozygosity = $1 - \sum p_i^2$

Use of selected (bread) seed material – plants from seed orchards – does not threaten genetic diversity

Izmantojot sēklu plantāciju materiālu meža atjaunošanā ģenētiskā daudzveidība nav apdraudēta



Thank You!

Paldies !