The genetic diversity of *Usnea subfloridana* in hemiboreal forests

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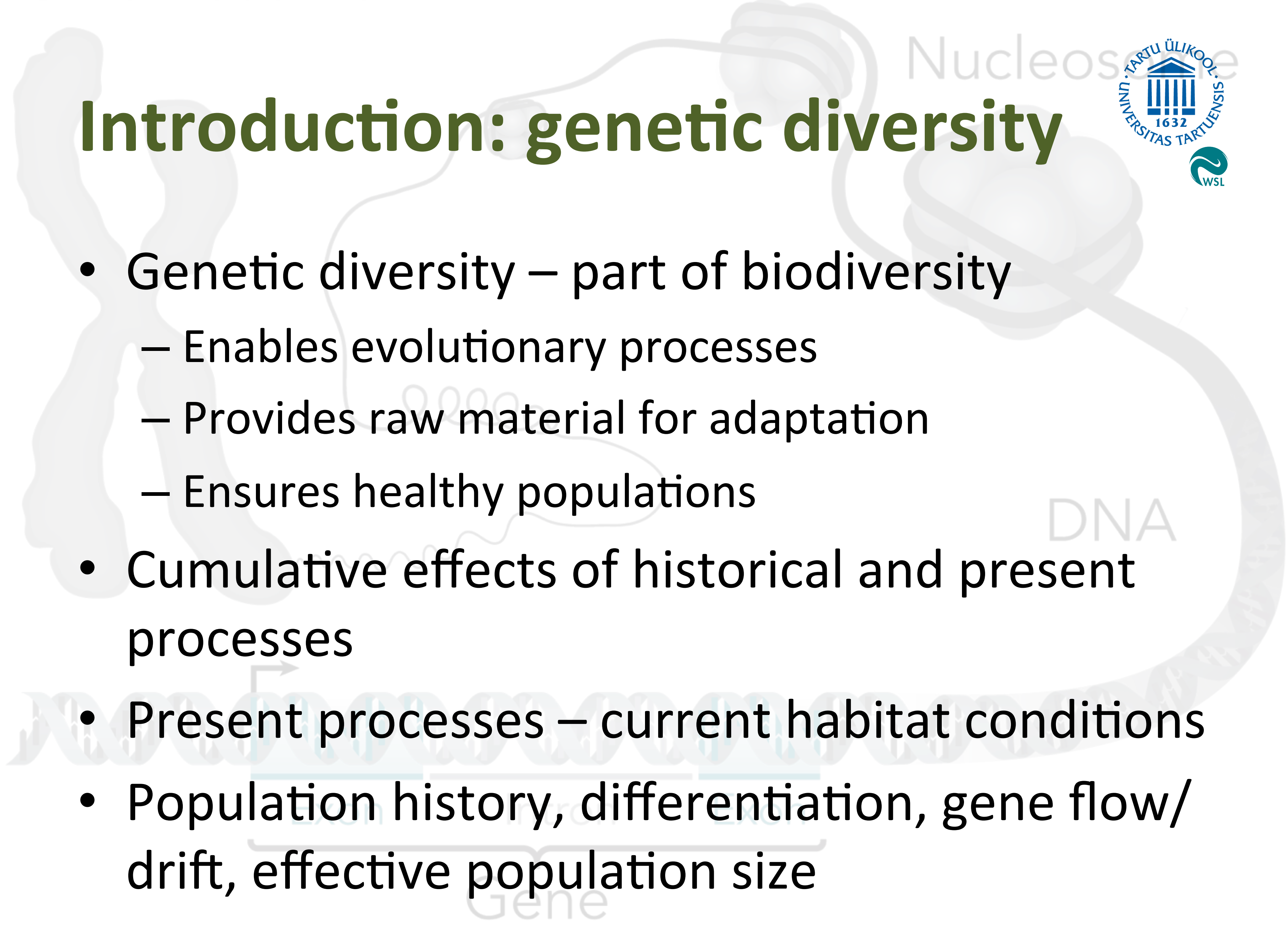
Introduction: genetic diversity



- Genetic diversity – part of biodiversity
  - Enables evolutionary processes
  - Provides raw material for adaptation
  - Ensures healthy populations
- Cumulative effects of historical and present processes
- Present processes – current habitat conditions
- Population history, differentiation, gene flow/drift, effective population size

Introduction: influencing factors

- Different results:
  - Study species
  - Its distribution and status
  - Geographical scale
- Habitat quality (host tree age)
- Different type of disturbance (e.g. fires, logging, air pollution), microclimatic factors (e.g. altitude above sea level, sample height on host tree, distance from rivers)

Image: http://igz.ilmeny.ac.ru/RED_BOOK/rast_lishainiki_lobarievie_lobariya_legochnaya_01.html

Introduction: methods

- Fungal secondary metabolites
- Universal fingerprinting techniques – ISSR, RAPD, RFLP
- PCR-based markers – rDNA markers (ITS, IGS, SSU, LSU)
- Microsatellites

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CAAGGCGTTGACAGTGTGTGTGTGTCTTATCACTGCGTC
GTTCCGCAACTGTCACACACACACAGAATAGTGACGCAG
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  1. Highly polymorphic
  2. Species-specific
  3. Selectively neutral
  4. High mutation rate
- 14 lichen-forming fungi

Aims of research

Population genetics of lichen-forming fungus at regional scale

- Genetic variation at **7 microsatellite loci** in mycobiont of epiphytic lichen *Usnea subfloridana*
  - Genetic differentiation of *U. subfloridana* populations
  - Relationships between habitat characteristics & measurements of genetic diversity

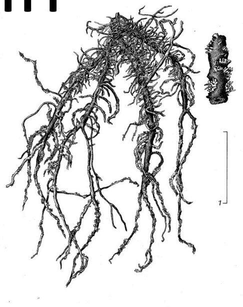

Image: http://lichenportal.org/portal/imagelib/imgdetails.php?imgid=359985

Target-species

- ***Usnea subfloridana*** (lichenized Ascomycota, fam. Parmeliaceae)
- Widely distributed across Eurasia, Macaronesia, North America
- Grows mainly on coniferous (*Picea abies, Pinus sylvestris*) & deciduous trees (*Betula pendula*)
- Asexually by soredia

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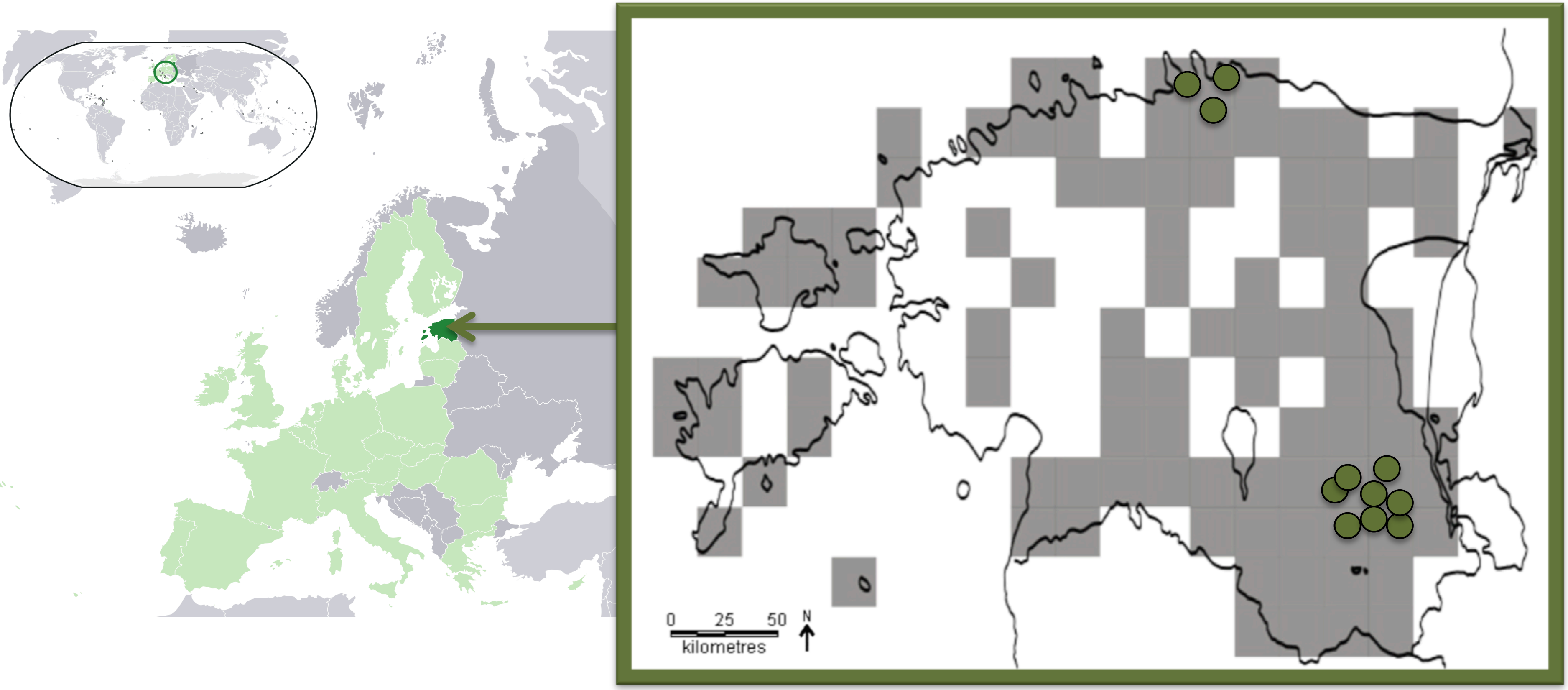
Study area

- *Pinus sylvestris*-dominated hemiboreal forests (*Oxalis – Vaccinium myrtillus* site type, *Vaccinium myrtillus* site type, *Vaccinium vitis-idaea* site types)



The distribution map of *Usnea subfloridana* in Estonia, and the locality of study area (marked with green circle)

Sampling

- **11** lichen populations – **9** from SE & **3** from N
- 30-62 specimens per populations from Norway spruces (up to 6 m)
- BHC of host tree at 1.3 m
- Stand or habitat age
- Tree species composition
- Size of forest site
- Sample size as additional

Molecular & Statistical analyses

Microscopy

Thin layer chromatography (TLC)

DNA isolation

Multiplex-PCR

Fragment lengths

Electropherograms (GeneMapper)

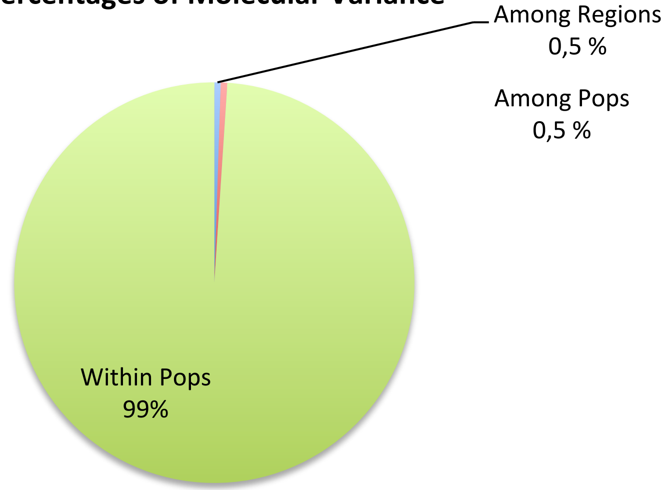
H, A, I, M, G, P, C → Genetic variables by GenAlex, MSA, HP-Rare, Arlequin, R software, AMOVA, statistics (GRM) in Statictica 7

Results: AMOVA

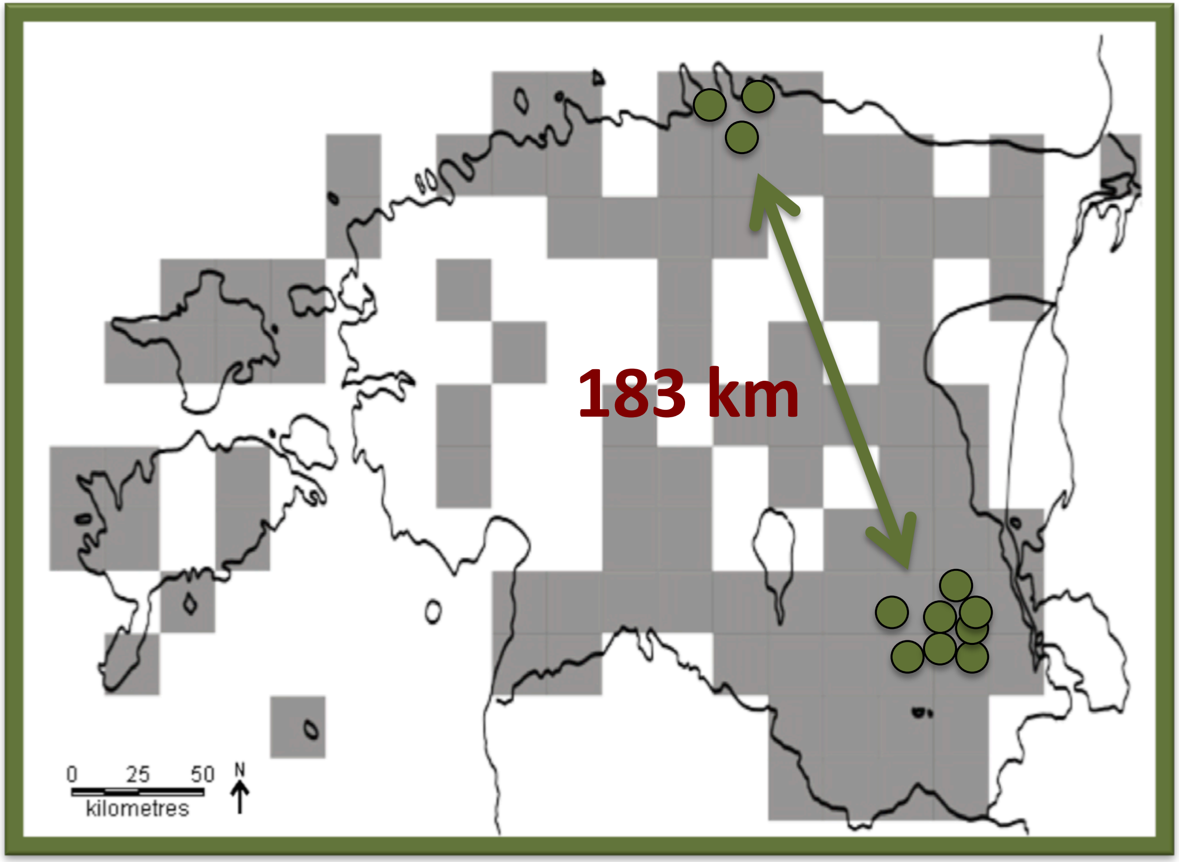
- **66** alleles at **7** microsatellite loci in **578** specimens
- **AMOVA:**
  - Within populations or among individuals (99 %)

Negligible, but significant genetic differentiation among populations and regions

Percentages of Molecular Variance



Results: shared multilocus genotypes



Identical multilocus genotypes between populations and between geographical regions

Results: shared multilocus genotypes & AMOVA

- Negligible genetic differentiation & shared multilocus genotypes between regions

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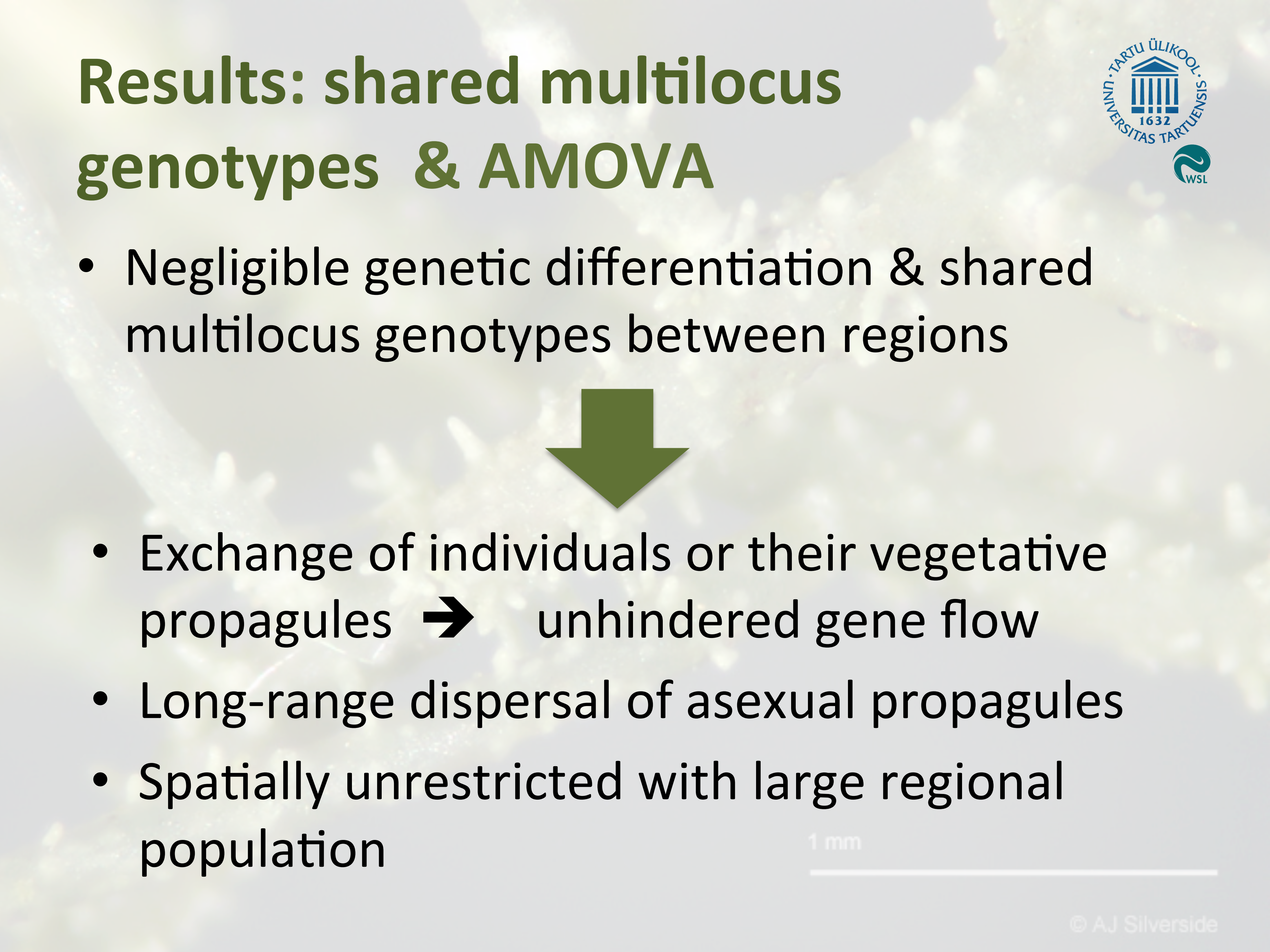
- Exchange of individuals or their vegetative propagules ➔ unhindered gene flow
- Long-range dispersal of asexual propagules
- Spatially unrestricted with large regional population



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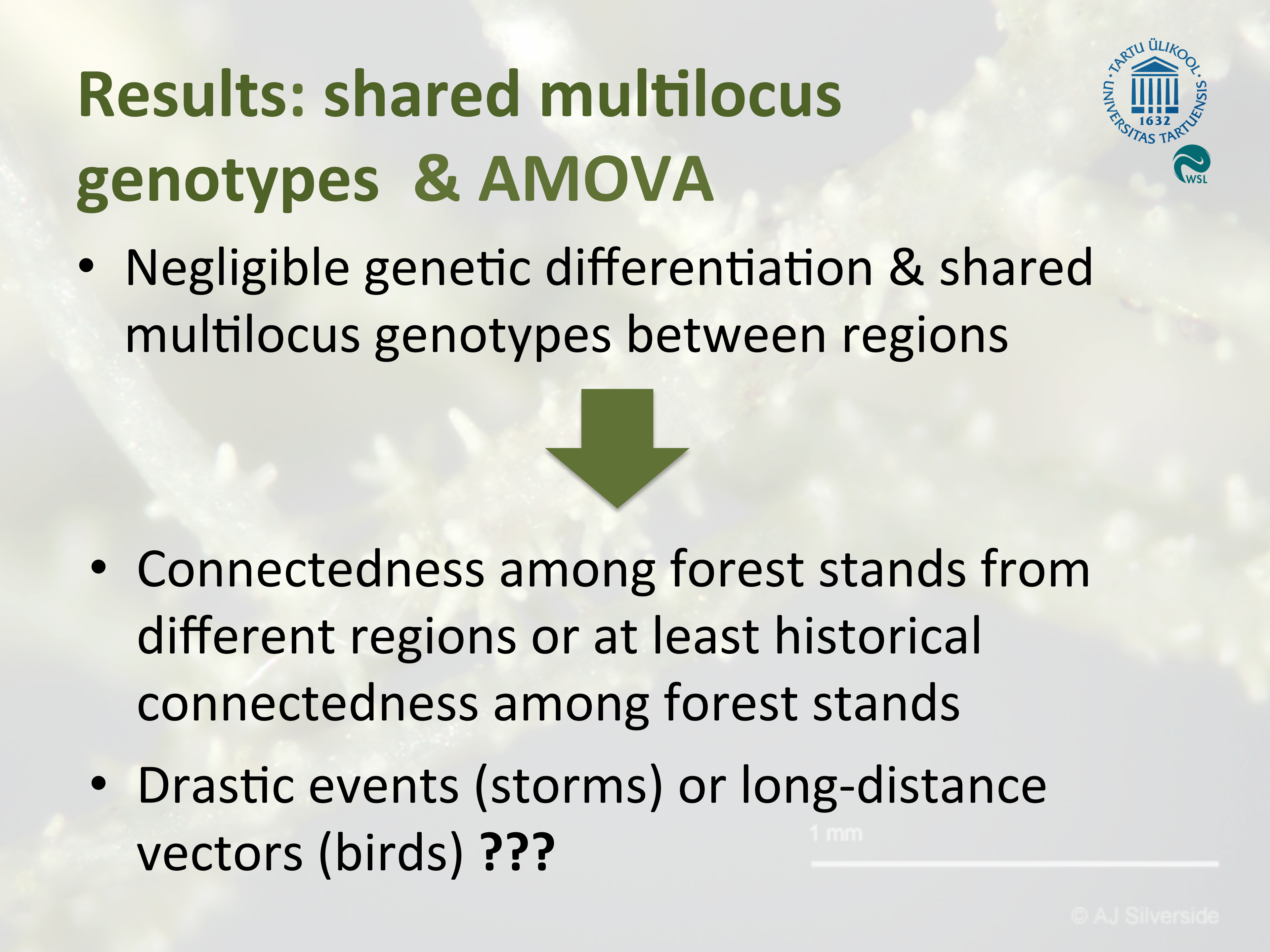
Results: shared multilocus genotypes & AMOVA

- Negligible genetic differentiation & shared multilocus genotypes between regions

- Connectedness among forest stands from different regions or at least historical connectedness among forest stands
- Drastic events (storms) or long-distance vectors (birds) **???**



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Results: colonization events (C) & number of private alleles (P)

- No significant effect of tree species composition and forest age on C & P

↓

- *Usnea* populations developed from multiple independent immigration events from large, genetically diverse source populations

Results: clonal diversity (M)

- Clonal diversity (0,77–0,90; SD=0,04)
- No significant effect of tree species composition and forest age on M

⬇

- No differences in population dynamics – same demographic stage **?**

Results: genetic diversity (H) & allelic richness (A)

- No significant effect of tree species composition and forest age on H & A

↓

- Variation in forest stand age (92–174 years) was not sufficient to reveal a difference between young and old-growth forests

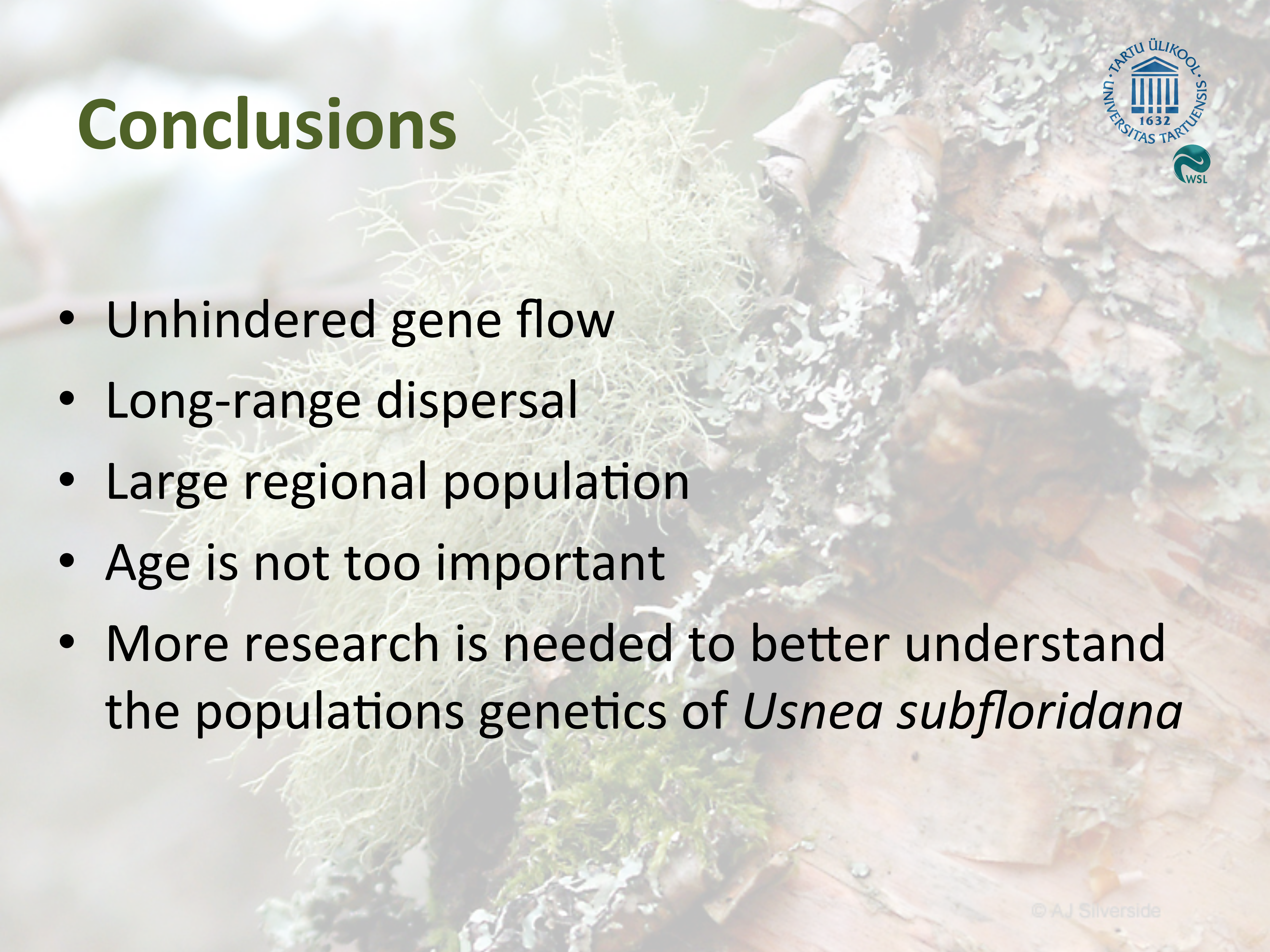
Results: genetic diversity (H) & allelic richness (A)

- No significant effect of tree species composition and forest age on H & A

- Habitat age is not too important in explaining of genetic patterns of *U. subfloridana*
- Relationships between tree age and epiphytic biomass of *Usnea* species was not linear in boreal forest (Boudreault et al. 2009)
- Microclimatic heterogeneity **???**

Conclusions

- Unhindered gene flow
- Long-range dispersal
- Large regional population
- Age is not too important
- More research is needed to better understand the populations genetics of *Usnea subfloridana*



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Thank you for your attention!

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Photo by Tiiu Tõrra