

The habitat traits drive genetic diversity of a widespread epiphytic lichen *Usnea subfloridana* in hemiboreal forests

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INTRODUCTION

- ◉ The genetic diversity, which enables evolutionary processes, provides the raw material for adaptation to changing environment, and ensures healthy populations, is an important part of overall biodiversity (Helm et al. 2009; Frankham et al. 2010). It could be influenced by exogenous factors of habitats.
- ◉ The genetic diversity of lichens and its spatial distribution could be shaped by e.g. habitat quality (host tree age) or by different types of habitat disturbances (Werth et al. 2006; Otalora et al. 2011; Degtjarenko et al. 2016).
- ◉ The genetic variation of populations of common and widely distributed epiphytic lichens is imperfectly studied aspect, especially in hemiboreal forests.
- ◉ We aimed to study the genetic variation of vegetatively reproducing epiphytic lichen *Usnea subfloridana* Stirt. (**Fig. 1**) populations from two geographical regions in Estonia, Northern Europe.



Fig. 1. The target species – *Usnea subfloridana* (lichenized Ascomycota, fam. Parmeliaceae), grows mainly on *Picea abies*, *Pinus sylvestris* & *Betula pendula*.

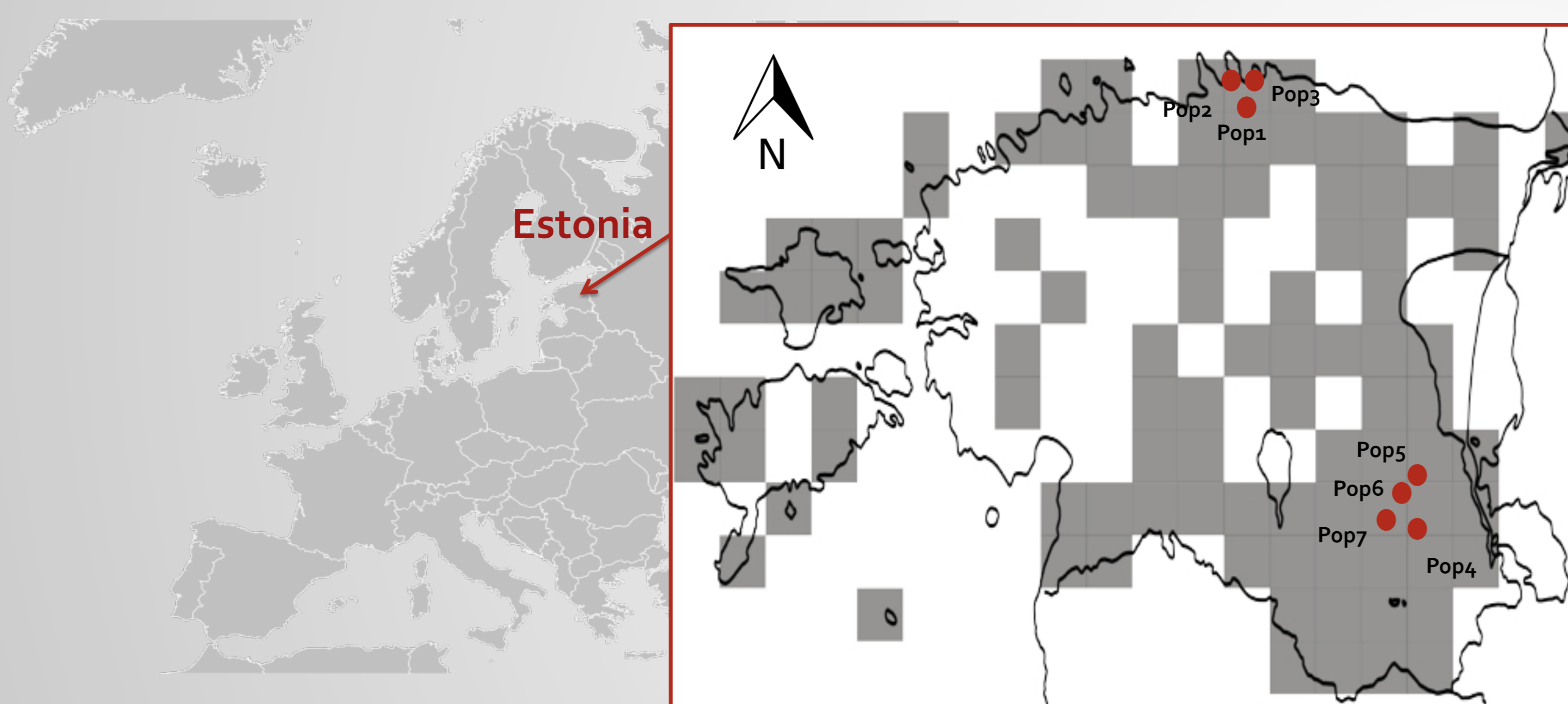


Fig. 2. The distribution map of *Usnea subfloridana* in Estonia (marked with gray), and the locality of studied *Usnea subfloridana* populations in Estonia. Each red circle represents the central coordinates of studied *U. subfloridana* populations.

MATERIAL & METHODS

- ◉ We studied seven lichen populations from two different regions (located in ca. 210 km from each other) of Estonia using recently developed nine fungus specific microsatellite markers (Tõrra et al. 2014).
- ◉ A total of 314 shrubby *Usnea* thalli were randomly sampled from Norway spruce in forest stands between 84-143 years.
- ◉ We used the GenAlex & Microsatellite Analyzer softwares for calculations of different genetic variables, and then applied GRM analyses to study the relationships between different genetic variables and characteristics of forest stands.

RESULTS

- ◉ AMOVA results revealed low but significant genetic differentiation between regions ($\Phi_{IRT}=0.015$; $P=0.003$) as well as among the populations ($\Phi_{IPT}=0.021$; $P=0.002$). Those results are clearly illustrated by Principal Coordinate Analysis (**Fig. 3**).
- ◉ The percentage of multilocus genotypes or clonal diversity (M) was significantly positively correlated with forest stand age in both regions (**Fig. 4**).
- ◉ The genetic diversity (H) was also positively correlated with forest mean stand age in both regions, but relationship appears insignificant.
- ◉ The number of private alleles (P) was significantly depending on the mean DBH of spruces and varies also among regions.
- ◉ The mean stand age and forest structure (percentage of *Pinus sylvestris*, *Picea abies*, *Betula pendula* in the first tree layer) revealed significant effect on the minimum number of colonization events per population (C).

Principal Coordinate Analysis (PCoA)

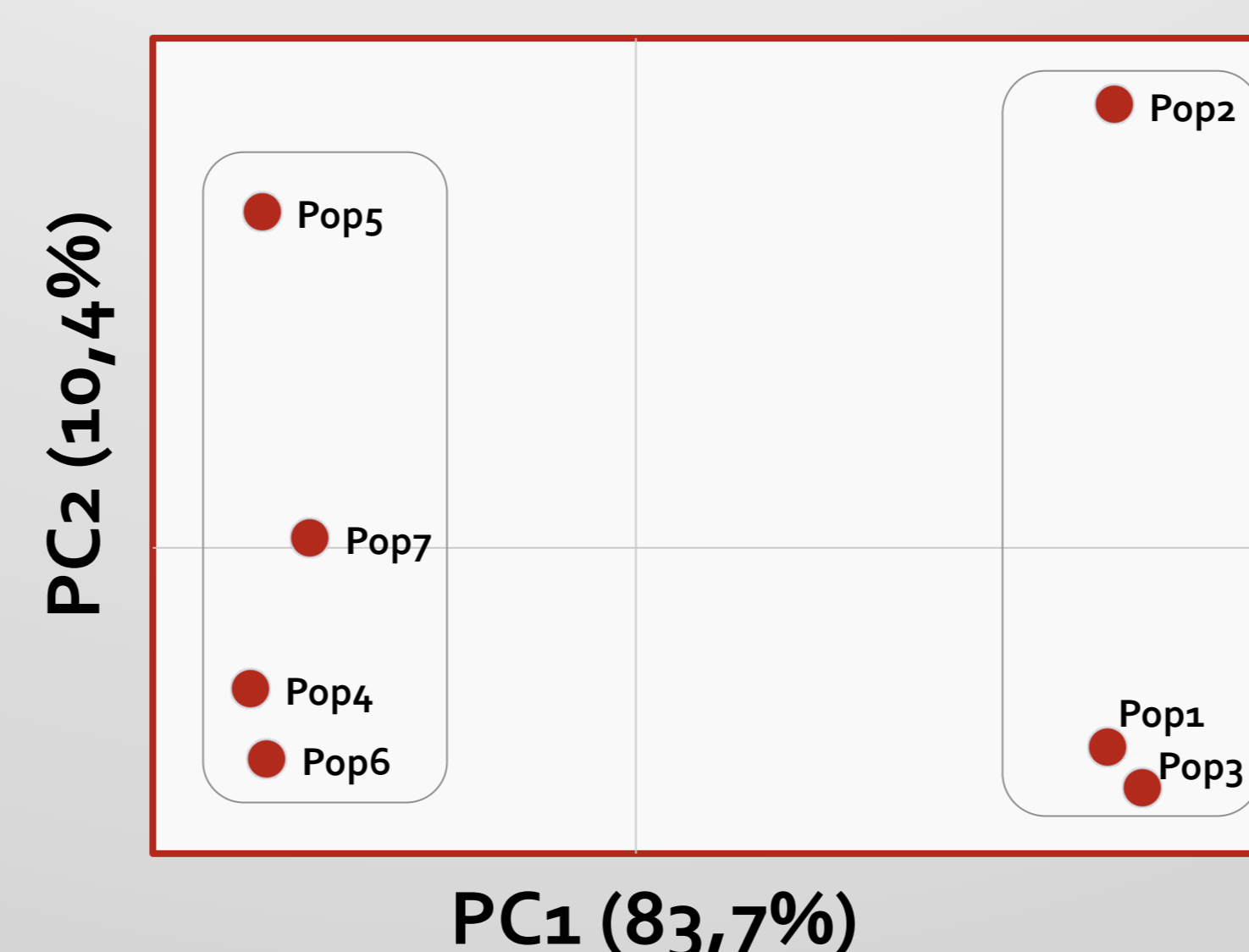


Fig. 3. The results of Principal Coordinate Analysis (PCoA). Each red circle represents the population of *Usnea subfloridana*. **Pop1-3** from Northern region, and **Pop4-7** from Southern region.

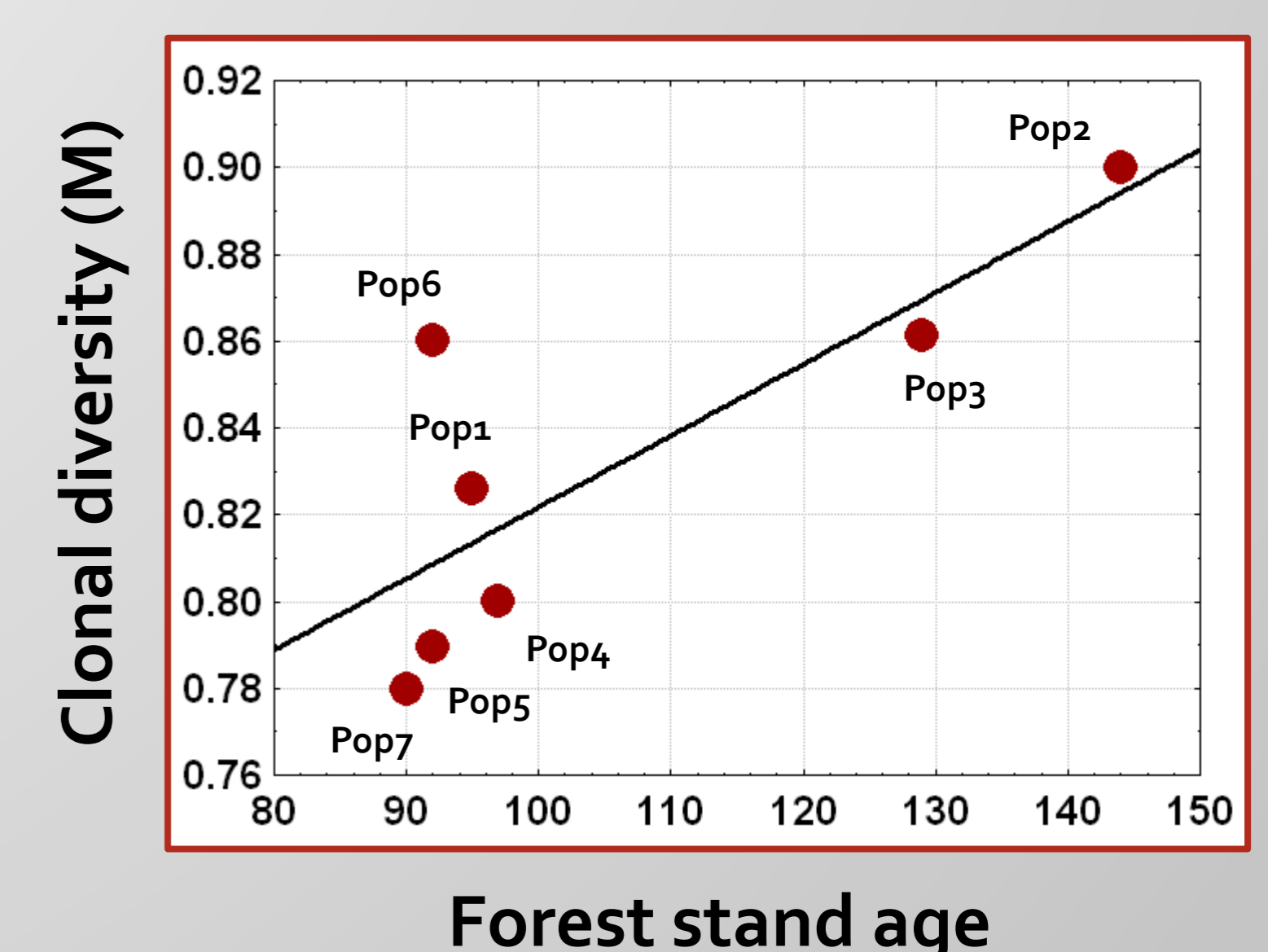


Fig. 4. The clonal diversity of *Usnea subfloridana* populations according to result of GRM analysis.

CONCLUSIONS

- ◉ Our results indicate that in hemiboreal forests the genetic diversity of lichen populations is shaped by forest stand age and forest structure, but also varies among geographical regions (North vs South).
- ◉ More research is needed to better understand population dynamics of asexually reproducing *U. subfloridana*.

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