

Online Resource 3

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Effective population size of adult and offspring cohorts as a genetic monitoring tool in two stand-forming and wind-pollinated tree species: *Fagus sylvatica* L. and *Picea abies* (L.) Karst.

Conservation Genetics SPRINGER

Heike Liesebach, Pascal Eusemann, Aki M. Höltnen, Ute Tröber, Oleksandra Kuchma, Manuel Karopka, Frank Becker, Ralf Kätzel, Barbara Fussi

Corresponding author: Heike Liesebach

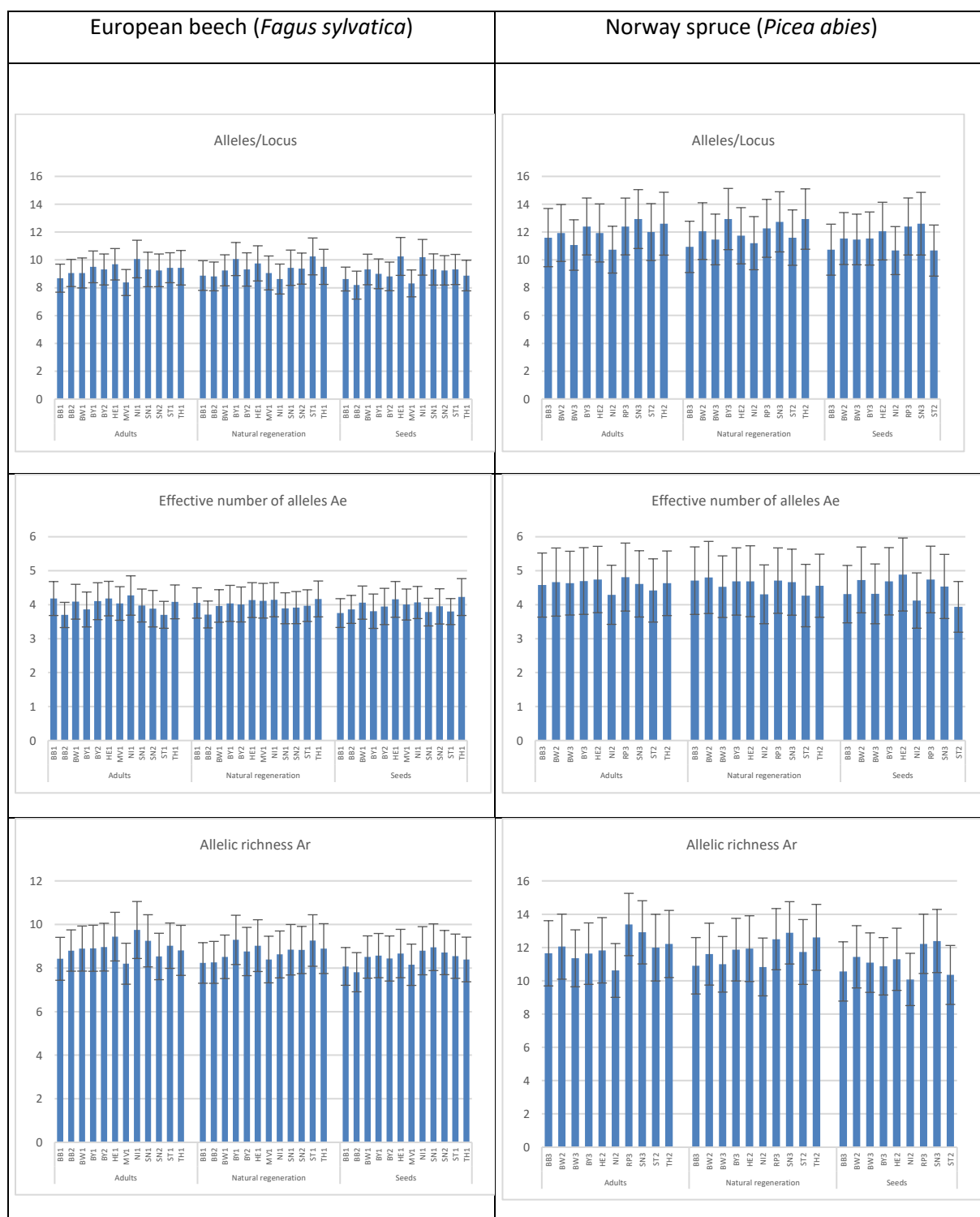
heike.liesebach@thuenen.de

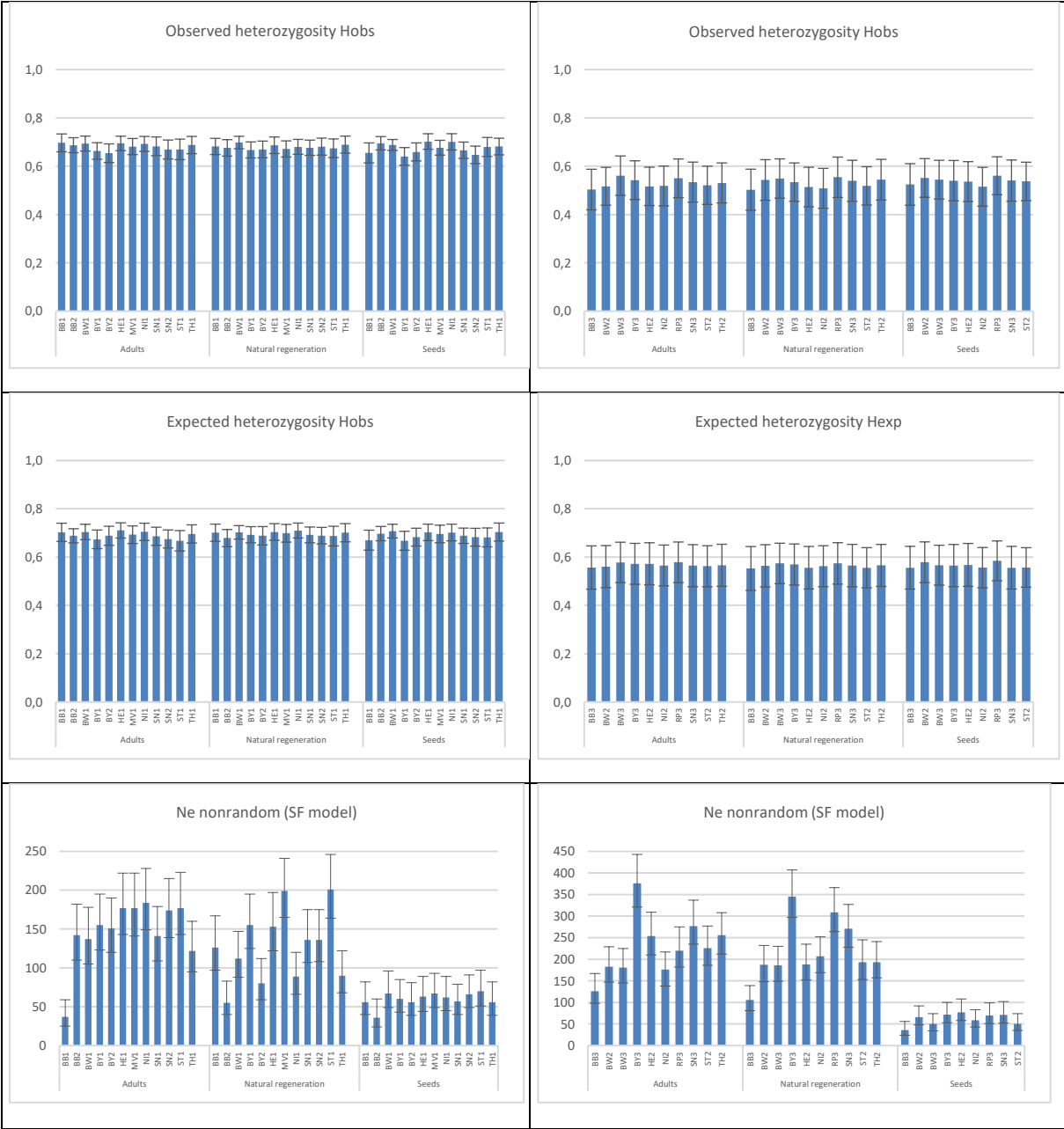
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Online Resource 3 Part A: Graphics for genetic diversity parameters of 12 beech and 10 spruce monitoring plots in the age cohorts Adults, Natural Regeneration, Seeds (for population abbreviations see Table 1)

Online Resource 3 Part B: Comparison of mean values of genetic diversity parameters between age cohorts (Adults, Natural Regeneration, Seeds), performed as t-test (proc glm in SAS). Norway spruce without TH2 because of missing seed sample

Graphics for genetic diversity parameters of 12 beech and 10 spruce monitoring plots in the age cohorts Adults, Natural Regeneration, Seeds (for population abbreviations see Table 1)

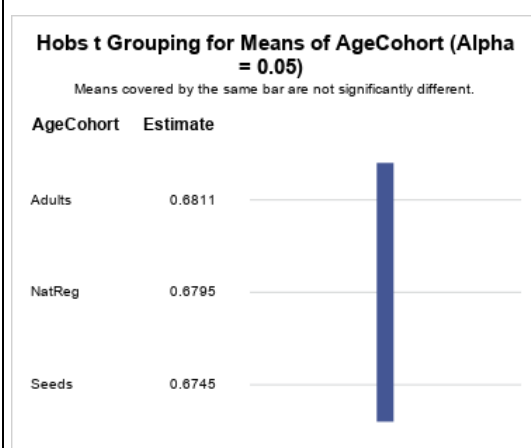




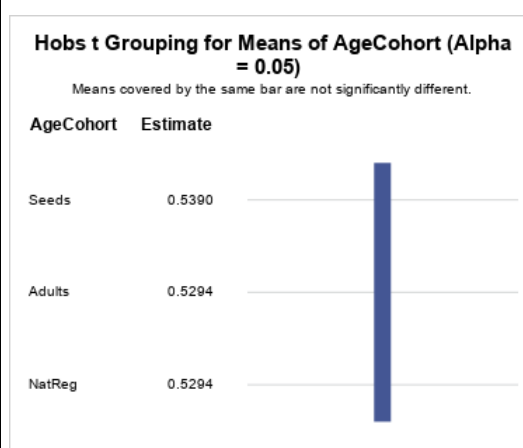
Comparison of mean values of genetic diversity parameters between age cohorts (Adults, Natural Regeneration, Seeds), performed as t-test (proc glm in SAS). Norway spruce without TH2 because of missing seed sample

European beech (<i>Fagus sylvatica</i>)	Norway spruce (<i>Picea abies</i>)																
Alleles/Locus: $p = 0.5426$ AL t Grouping for Means of AgeCohort (Alpha = 0.05) Means covered by the same bar are not significantly different. <table> <thead> <tr> <th>AgeCohort</th><th>Estimate</th></tr> </thead> <tbody> <tr> <td>NatReg</td><td>9.3596</td></tr> <tr> <td>Adults</td><td>9.2660</td></tr> <tr> <td>Seeds</td><td>9.1201</td></tr> </tbody> </table>	AgeCohort	Estimate	NatReg	9.3596	Adults	9.2660	Seeds	9.1201	Alleles/Locus: $p = 0.4492$ AL t Grouping for Means of AgeCohort (Alpha = 0.05) Means covered by the same bar are not significantly different. <table> <thead> <tr> <th>AgeCohort</th><th>Estimate</th></tr> </thead> <tbody> <tr> <td>Adults</td><td>11.8888</td></tr> <tr> <td>NatReg</td><td>11.8814</td></tr> <tr> <td>Seeds</td><td>11.5186</td></tr> </tbody> </table>	AgeCohort	Estimate	Adults	11.8888	NatReg	11.8814	Seeds	11.5186
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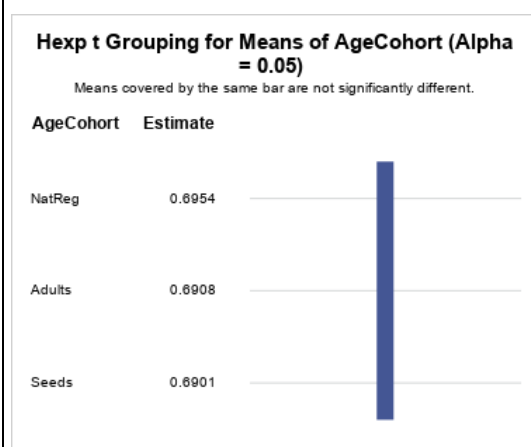
Observed heterozygosity: $p = 0.5478$



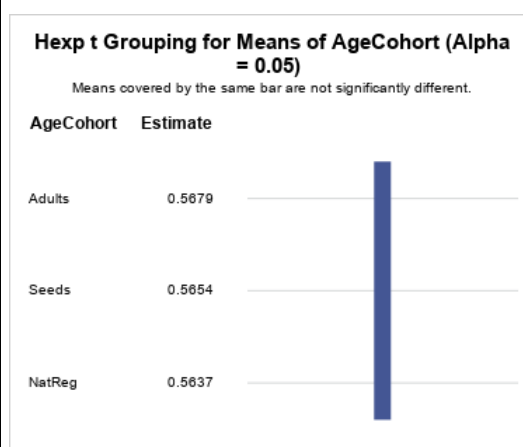
Observed heterozygosity: $p = 0.4065$



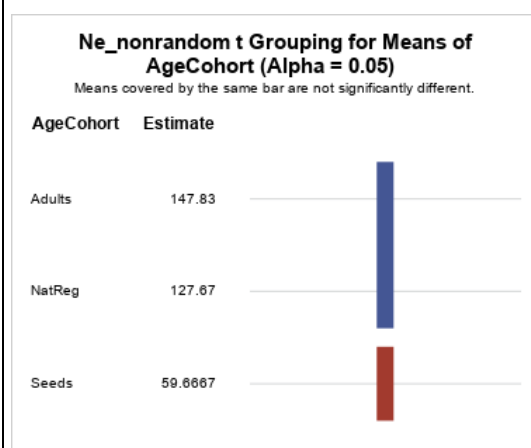
Expected heterozygosity: $p = 0.5202$



Expected heterozygosity: $p = 0.6029$



Ne_nonrandom (SF model): $p < .0001$



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