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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

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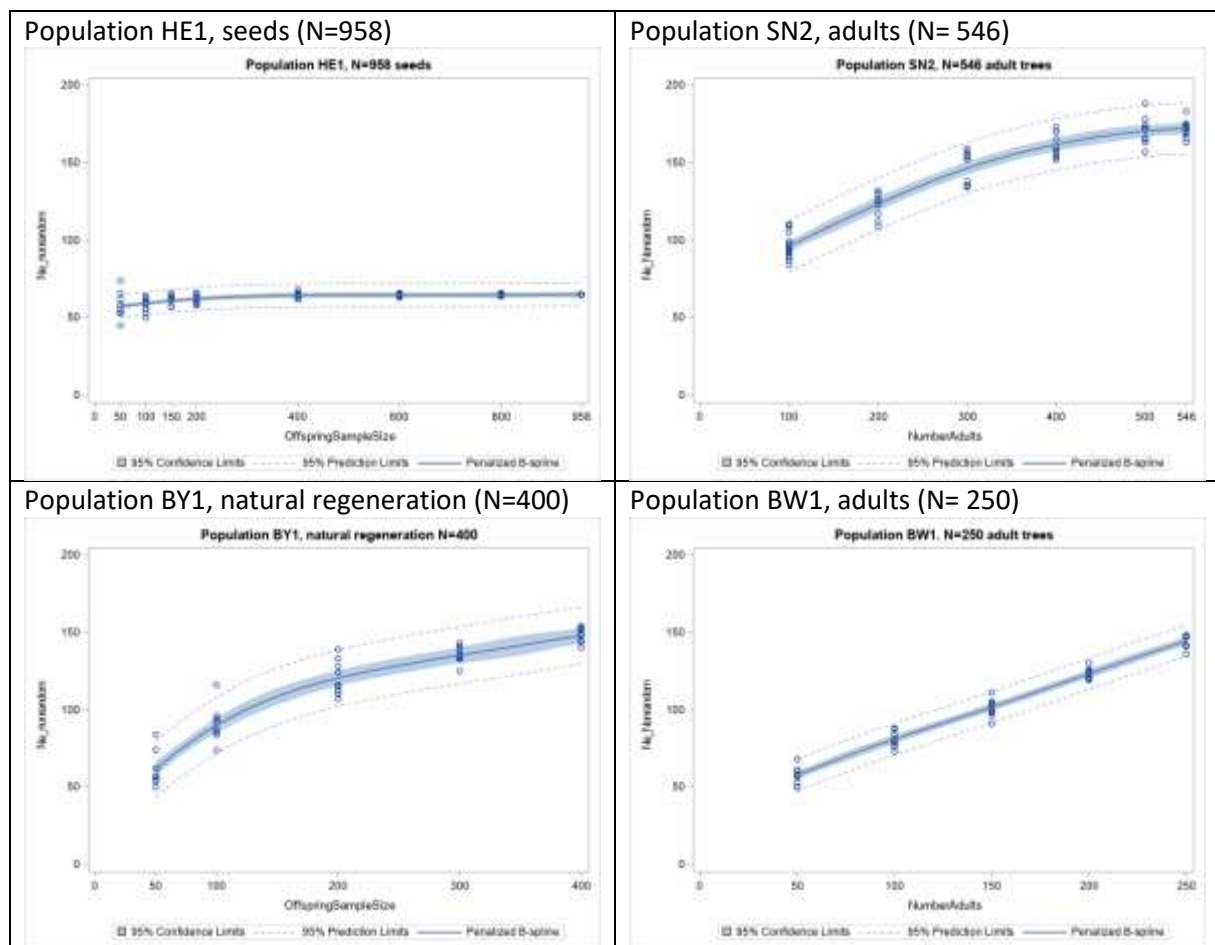
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Online Resource 8: Sample size effects: Dependency of N_e estimates from SF model (nonrandom mating) from samples drawn from random subsets, 10 replicates each (replicates for the total sample size were derived from COLONY runs with different random seeds).

Since experimentally achieved sample sizes for genotyping may have affected N_e estimates, we attempt to get an idea of the dependence of these measures on the genotyped sample sizes. As cases studies, four examples were selected: the largest adult population (SN2 with $N=546$ trees), a typical adult population (BW1 with $N=250$ trees) a typical sample of natural regeneration (BY1 with $N=400$) and the largest seed sample (HE1 with $N=958$). Random subsets with increasing sample sizes and 10 replicates each were created using SAS (proc surveyselect, method simple random sampling). In addition, the total samples for all four cases were run 10 times with different random seed numbers for replication. The prepared COLONY input files for random subsets of SN2 and BW1 were run as single sample analyses. Runs for random subsets of offspring samples of populations BY1 and HE1 included candidate parents but were performed without known mothers. All other parameter settings are the same as for the parentage analyses, except for precision, which was set to medium. The results of the random subsamples were compared with the respective total sample (10 replicates each) using Dunnett's t test (SAS proc glm).

In the seed cohort of the HE1 beech population ($N=958$), a plateau is reached at $N=150$. From $N=150$ or greater, there was no longer a significant difference in N_e values from the total sample size. The largest adult population (SN2 with $N=546$ trees) reached its plateau at $N=500$. The typical sample of natural regeneration (BY1 with $N=400$) approaches but does not quite reach a plateau as subsample size increases, whereas the adult population with the targeted size (BW1 with $N=250$) did not yet reach a plateau.



Dunnett's t Tests: This test controls the Type I experimentwise error for comparisons of all treatments against a control.

	Sample Size Comparison	Difference Between Means	Simultaneous 95% Confidence Limits		Comparisons significant at the 0.05 level ***
Population HE1, seeds (N=958)	800 - 958	-0.300	-4.644	4.044	
	600 - 958	-0.500	-4.844	3.844	
	400 - 958	-0.700	-5.044	3.644	
	200 - 958	-2.800	-7.144	1.544	
	150 - 958	-3.300	-7.644	1.044	
	100 - 958	-6.900	-11.244	-2.556	***
	50 - 958	-7.300	-11.644	-2.956	***

	Sample Size Comparison	Difference Between Means	Simultaneous 95% Confidence Limits		Comparisons significant at the 0.05 level ***
Population SN2, adults (N= 546)	500 - 546	-1.218	-10.324	7.887	
	400 - 546	-10.818	-19.924	-1.713	***
	300 - 546	-24.718	-33.824	-15.613	***
	200 - 546	-49.018	-58.124	-39.913	***
	100 - 546	-75.642	-83.706	-67.578	***
Population BY1, natural regeneration (N=400)	300 - 400	-12.800	-22.712	-2.888	***
	200 - 400	-28.100	-38.012	-18.188	***
	100 - 400	-57.300	-67.212	-47.388	***
	50 - 400	-86.800	-96.712	-76.888	***
Population BW1, adults (N= 250)	200 - 250	-20.900	-26.392	-15.408	***
	150 - 250	-43.200	-48.692	-37.708	***
	100 - 250	-63.100	-68.592	-57.608	***
	50 - 250	-86.800	-92.292	-81.308	***