

Electronic Supplementary Material

A clue to invasion success: genetic diversity quickly rebounds after introduction bottlenecks

Peter Kaňuch, Åsa Berggren, Anna Cassel-Lundhagen

Table S1 Characterisation of 9 microsatellite loci used in this study

Locus	Repeat motif	Allelic range	Reference
MR2-16	(GA)9GGGA	146–170	Holzhauer & Wolff 2005
MR2-42	(GA)14	95–165	Holzhauer & Wolff 2005
MR3-24	(CAT)7CAC(CAT)7	148–216	Holzhauer & Wolff 2005
MR3-34	(CAT)7(CGT)6CAG(AAG)3AAT(AAG)12	158–212	Holzhauer & Wolff 2005
Metroe08	(CA)14CG(CA)11	111–169	Kaňuch et al. 2010
Metroe19	(AG)19	79–109	Kaňuch et al. 2010
Metroe20	(AC)4(AG)17	109–141	Kaňuch et al. 2010
Metroe24	(AG)20	101–157	Kaňuch et al. 2010
Metroe27	(TC)14	121–165	Kaňuch et al. 2010

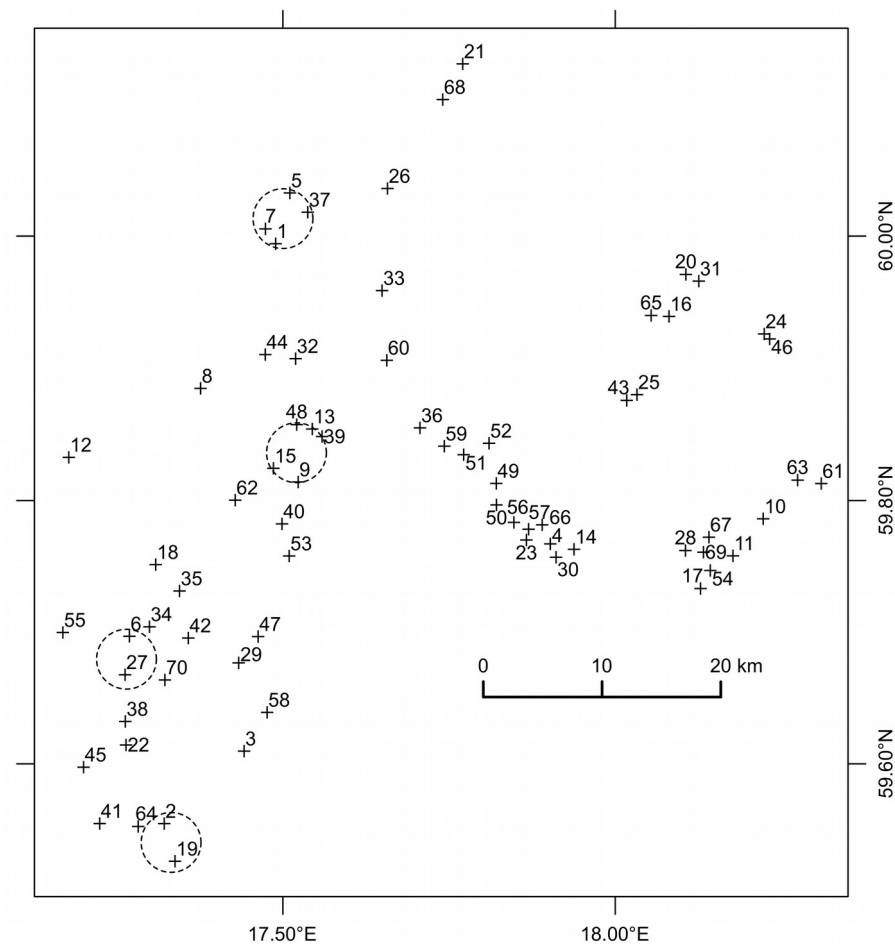


Fig. S1 ID labels of *M. roeselii* populations presented in Fig. 1

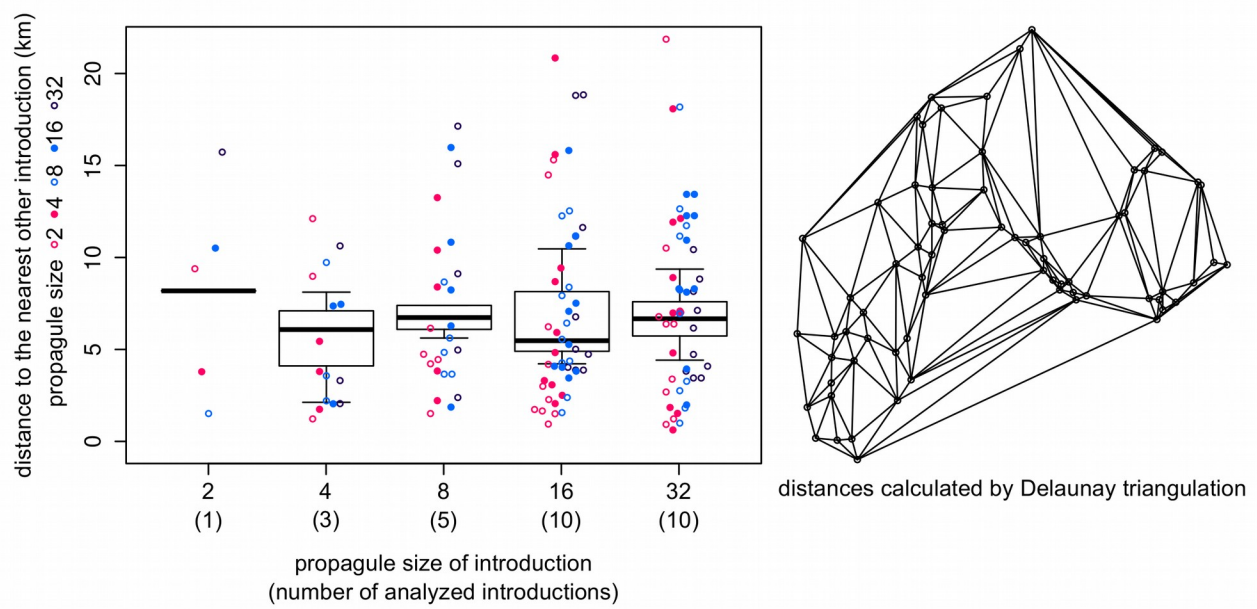


Fig. S2 Distances to the nearest other introductions of different propagule sizes

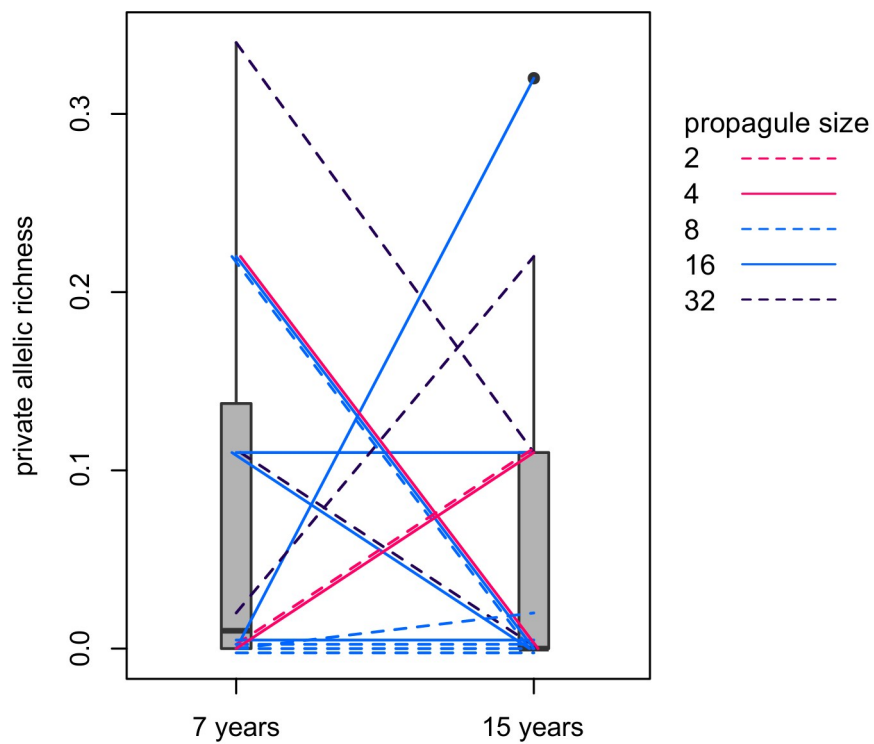


Fig. S3 Private allelic richness in introduced populations after 7 and 15 years since introductions

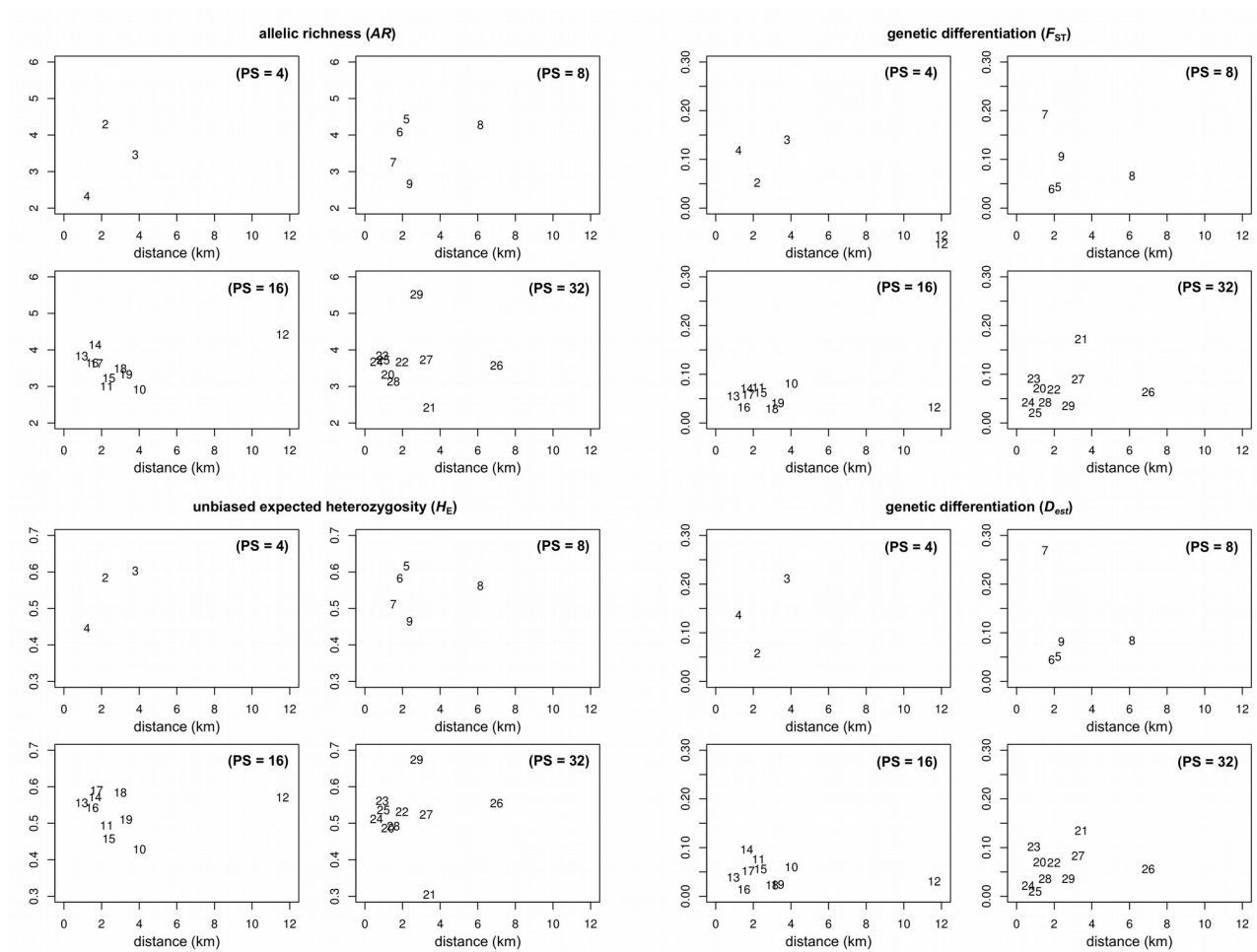


Fig. S4 Estimates of genetic diversity and differentiation of introductions (IDs substitute points in plots) founded by different propagule size (PS) plotted against geographical distance to the nearest other introductions