Appendix C – *introgress* analysis

In order to examine the rate of introgression at each microsatellite loci, we performed this analysis in the *R*-package 'introgress' (Gompert and Buerkle 2009; 2010). All known offspring were used in this analysis, not just the recruits included in each cohort. Parentage of each offspring was determined from a reconstructed pedigree.

The results show that individuals introgressed among most loci. Output figures from *introgress* can be found below, one showing the mosaic of microsatellites per individuals and the predicted origin of the allele (Fig.1). The high rate of introgression may have been affected by a high rate of similar alleles present in both populations, although genetically differentiated (F_{ST}=0.0172). The other shows each microsatellite locus, and the result of introgression compared to a null model (Fig. 2).

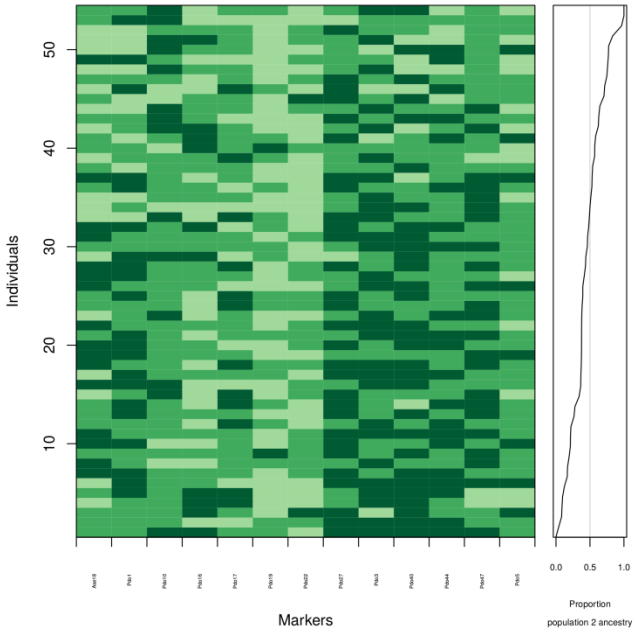
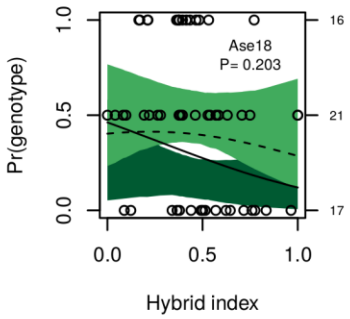
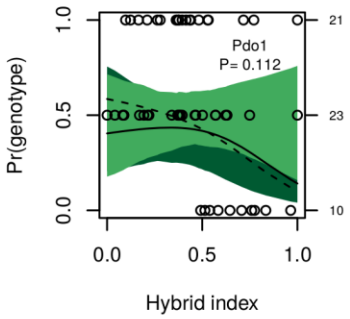
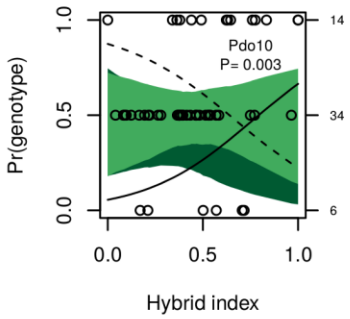
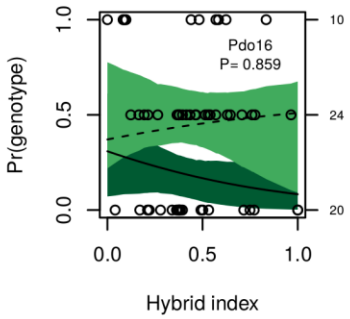


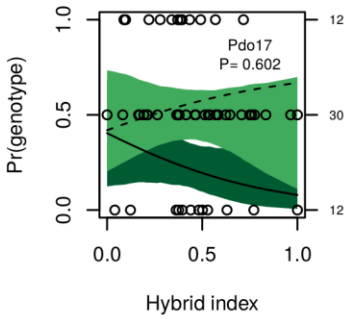
Figure 1. All known offspring (n = 54) from parents either translocated or residents in 2002. Dark green colour represents contribution from the source population, mid-green represents intermixed contribution and light green represents contribution from the resident population.

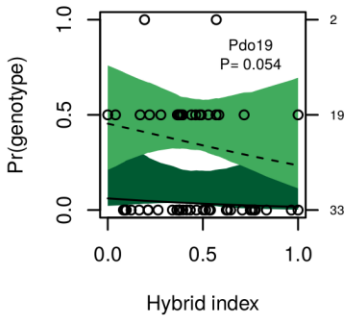

Ase18
P= 0.203
Pr(genotype)
Hybrid index

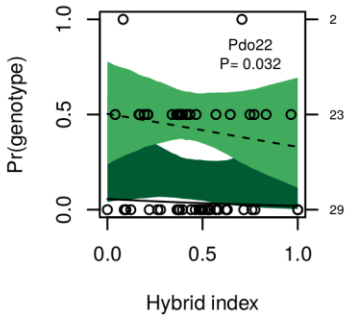

Pdo1
P= 0.112
Pr(genotype)
Hybrid index

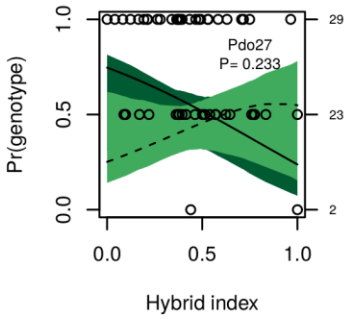

Pdo10
P= 0.003
Pr(genotype)
Hybrid index

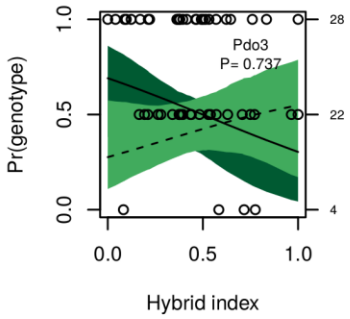

Pdo16
P= 0.859
Pr(genotype)
Hybrid index


Pdo17
P= 0.602
Pr(genotype)
Hybrid index


Pdo19
P= 0.054
Pr(genotype)
Hybrid index


Pdo22
P= 0.032
Pr(genotype)
Hybrid index


Pdo27
P= 0.233
Pr(genotype)
Hybrid index


Pdo3
P= 0.737
Pr(genotype)
Hybrid index

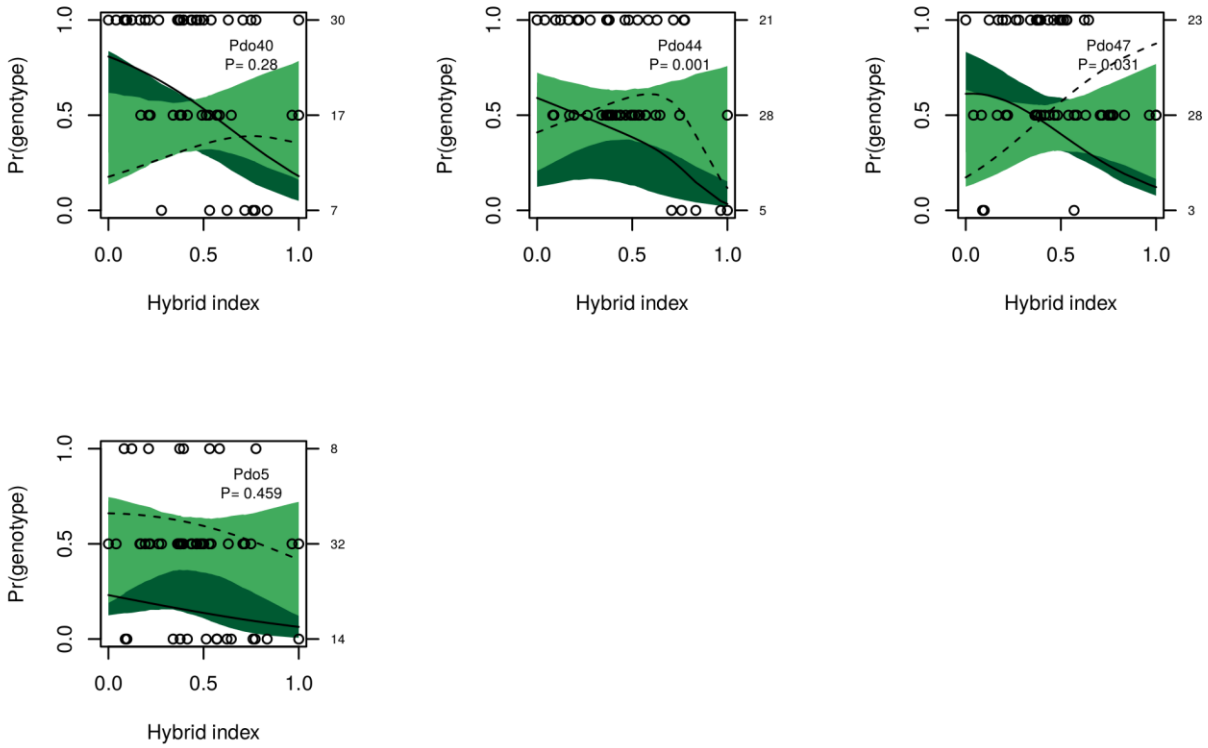


Figure 2. Clines for each microsatellite loci (n = 13).

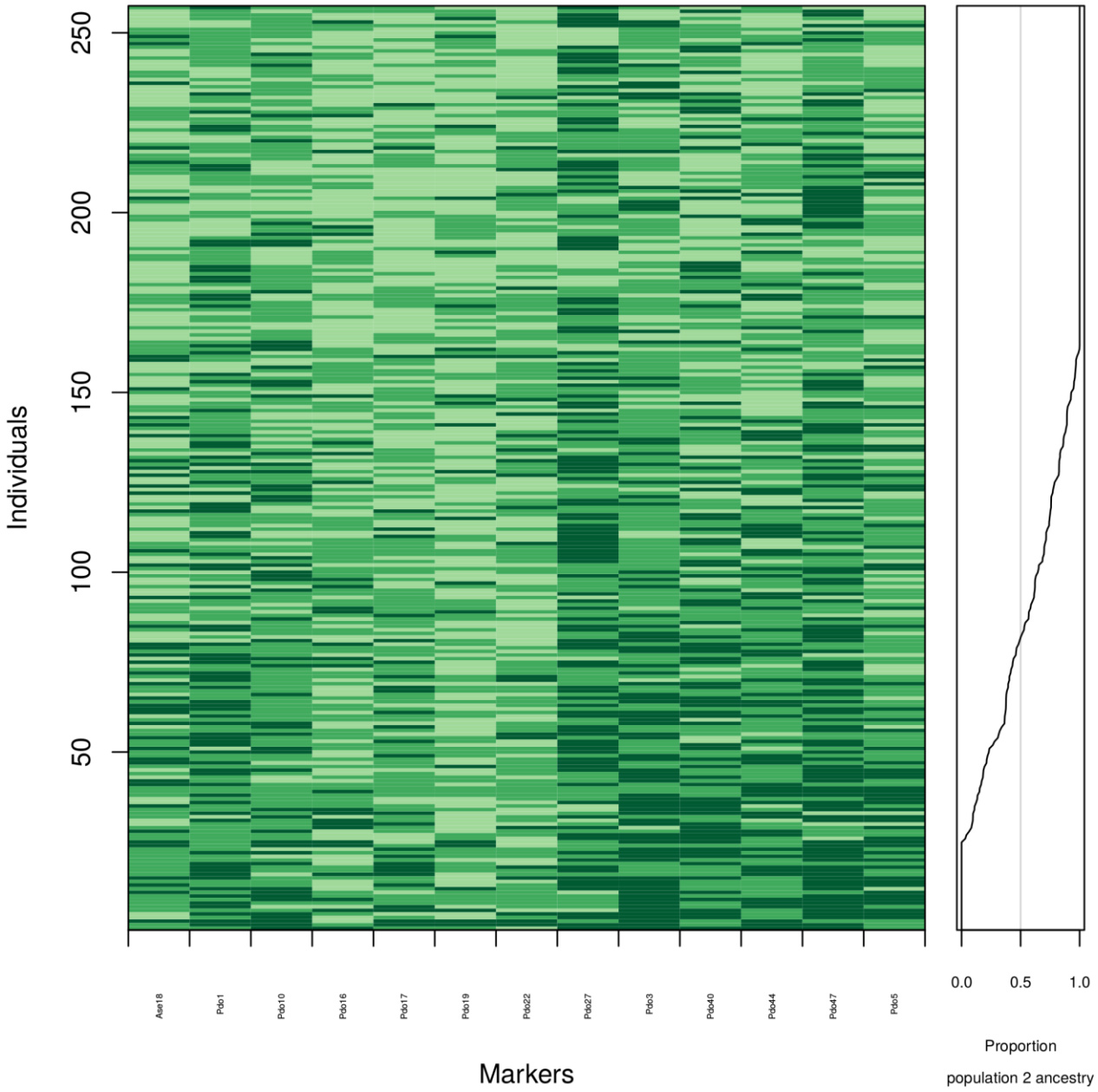
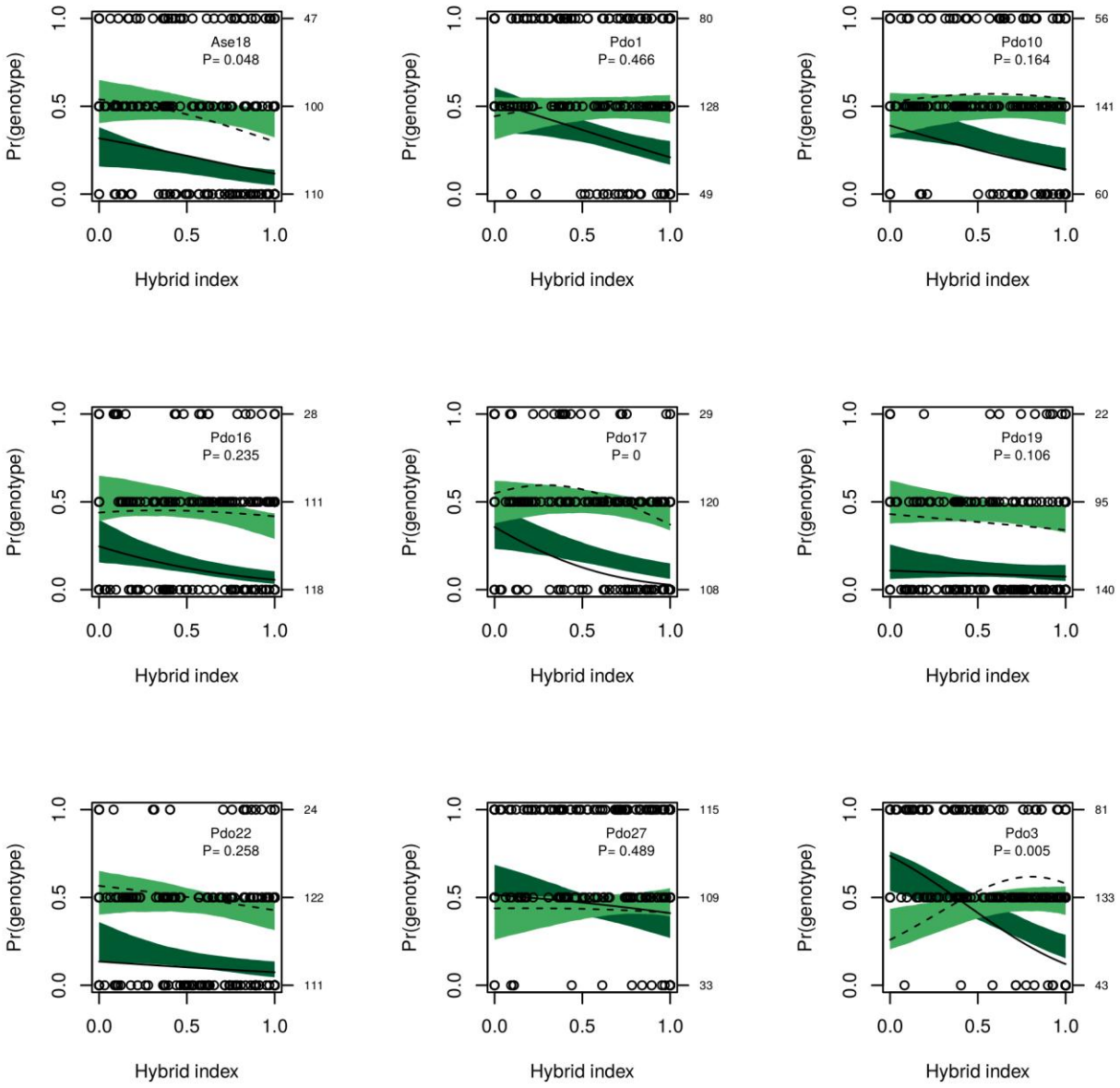


Figure 3. All known offspring (n = 257) from parents from 2002.
Dark green colour represents contribution from the source population, mid-green represents intermixed contribution and light green represents contribution from the resident population.


Ase18
P= 0.048
Pdo1
P= 0.466
Pdo10
P= 0.164
Pdo16
P= 0.235
Pdo17
P= 0
Pdo19
P= 0.106
Pdo22
P= 0.258
Pdo27
P= 0.489
Pdo3
P= 0.005
Pr(genotype)
Hybrid index
0.0
0.5
1.0
47
100
110
80
128
49
56
141
60
28
111
118
29
120
108
22
95
140
24
122
111
115
109
33
81
133
43

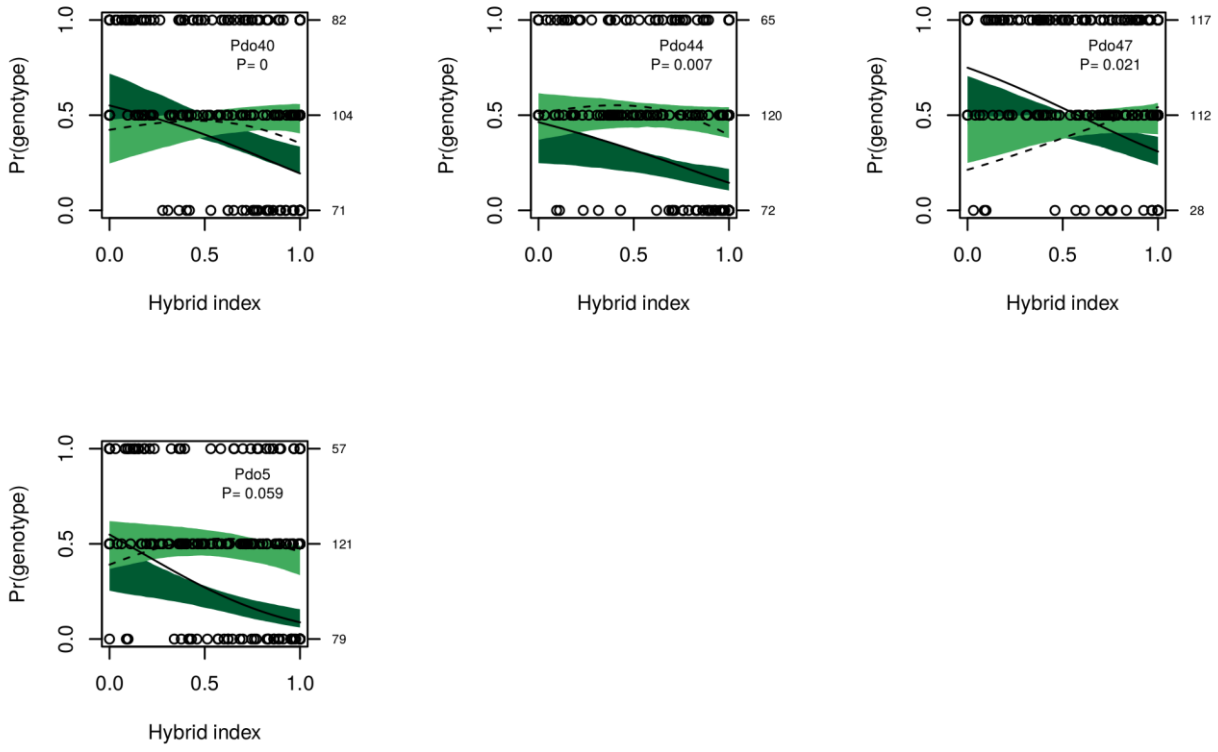


Figure 4. Clines for each microsatellite loci (n = 13).

References

Gompert Z, Buerkle CA (2009) A powerful regression-based method for admixture mapping of isolation across the genome of hybrids. Mol. Ecol. 18, 1207–1224.

Gompert Z, Buerkle CA (2010) INTROGRESS: a software package for mapping components of isolation in hybrids. Mol. Ecol. Res. 10, 378–384