Appendix S3: Null allele frequencies, microsatellite characteristics, Hardy-Weinberg equilibrium and genetic diversity.

The analysis conducted with MICROCHECKER v2.2.3 (Van Oosterhout *et al.* 2004) confirmed the absence of large allele dropout and scoring errors due stuttering in our dataset. We estimated the frequencies of null alleles (*r*) for each locus by the expectation maximization algorithm (Dempster *et al.* 1977) implemented in FREENA (Chapuis and Estoup 2007). Null allele frequencies ranged from 0 for *Mic26*, *Mic24* and *COR46bis* to 0.62 for *COR58*, with a mean value equal to 0.24 ± 0.21. To avoid bias due to null alleles, the genetic analyses were performed with seven loci (*Mic13*, *Mic20*, *Mic22*, *Mic24*, *Mic26*, *Mic27*, *COR46bis*), for which the mean *r* was < 0.1 (see Chapuis *et al.* 2008). Based on these seven microsatellites, we looked for the occurrence of null alleles in each sample using MICROCHECKER v2.2.3. Null alleles were present in all the samples except PZ-20.

Departure from panmixia was tested for each sample using the score test for heterozygote deficiency. Significance was addressed using a Markov-chain algorithm (Guo and Thompson 1992; Raymond and Rousset 1995) with default parameters. The *f* estimator of F_{IS} (Weir and Cockerham 1984) was computed for each sample. Computations were done using GENEPOP v.4.0 (Rousset 2008). We tested the null hypothesis of linkage equilibrium for each pair of loci in each sample using the permutation procedure (n = 1000) implemented in GENETIX v.4.05 (Belkhir *et al.* 2004). Observed heterozygosity (H_o) and gene diversity (H_e; Nei 1973) were computed for each sample using GENETIX. We used ADZE (Szpiech *et al.* 2008) to compute the allelic richness ($Ar_{(g)}$) for each sample with a rarefaction method (Petit *et al.* 1998) and *g*, the minimum number of genes at one locus in one of the samples, set to 64.

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