

Supplementary material

Appendix 1. The microsatellite markers (10 loci) and primers. All markers were amplified in three multiplex sets.

Locus	Primer sequences and fluoro-label (5'-3')	Size (bp)	Repeat	# alleles	Ho	He	Ref.
PCR multiplex set A							
Remiz-01	F: [VIC]TGCCTTCTATCAAGCATGAGC R: TGTGCATGTAAGATTCCATCTATC	167 171 175 179 183 187	4	6	0.736	0.640	Meszaros et al. 2008
Remiz-07	F: [NED]GGTAAAGCTGGTGCACAAAATG R: GGTCTATGAAAGATGATAGATGATGG	163 167 171 175 179	4	5	0.731	0.669	Meszaros et al. 2008
Remiz-09	F: [6-FAM]AATTACTGAAGAACAACACATCTGG R: GGACAGCTGGAGAGCAACTC	109 113 117 121 125 129 133	4	7	0.360	0.646	Meszaros et al. 2008
PCR multiplex set B							
Remiz-10	F: [NED]ATCACTCCCAGTGATAGCC R: CCTCAGCACTGAGAATAGGG	196 200 202 204 208 212 216	4	7	0.779	0.680	Meszaros et al. 2008
Remiz-18	F: [VIC]CATTAAATGATTGGATATGGCAAG R: GTCCTCTGCCTGTCGTTC	85 89 93 97 101 105 109	4	7	0.856	0.711	Meszaros et al. 2008
CAM10	F: [6-FAM]TATCCMGAGAATGGGCATC R: KGCTCTCATTGTCATGCTG	179 183 185 187 189	2	5	0.237	0.223	Dawson et al. 2013
PCR multiplex set C							
TG04-061	F: [PET]GACAATGGCTATGAAATAAATTAGGC R: AGAAGGGCATTGAAGCACAC	191 193 195	2	3	0.190	0.160	Dawson et al. 2010
TG13-009	F: [VIC]TGTGGTGGGATAGTGGACTG R: CTGTAAAATGTGCAAGTAACAGAGC	194 196 198	2	3	0.108	0.141	Dawson et al. 2010
TG05-053	F: [NED]GCATCATCTGGTTGAACTCTC R: ACCCTGTTTACAGTGAGGTGTT	231 233 235 237 239 241	2	6	0.691	0.607	Dawson et al. 2010
TG13-017	F: [6-FAM]GCTTTGCATCTTGCCTTAAA R: GGTAACATAACATTCCAACCTCCT	308 310 312	2	3	0.315	0.279	Dawson et al. 20

Appendix 2. Haplotypes (16) and variable sites in the mtDNA cytochrome-*b* in 64 individuals of the genus *Remiz*.

#Haplotype	Composite haplotyp	Frequency	Taxon codes
1	ATCCCGAAATACGATGGCTCACCCGGCCCAGATTACTATACACTA	2	[R_cons1 R_cons3]
2	ATCCCGAAATACAATGGCTCACCCGGCCCAGATTACTGTACACTA	2	[R_cons2 Rcons_108]
3	ATCCCGAAATACAATGGCTCACCCAGCCCAGTTACTATACACTA	1	[Rcons_109]
4	GTCCCGGAGCGTAACAACCTATCCACCTTGAACGTGCACGCGTCA	6	[Rcoro_cor1 Rcoro_cor2 Rcoro_KA46263 Rcoro_KA46264*
5	GTACCCGGGGCGCAGCAATCCATCTACCCCGAACCGCCACGTATCA	1	[Rmac_neg1]
6	GTCCCGGGGCGCAGCAATCCATCTACCCCGAACCGCCACGTATCA	40	[Rmac_neg10 Rmac_neg11 Rmac_neg12 Rmac_neg13**
7	GACCCGGGGCGCAGCAATCCATCTACCCCGAACCGCCACGTATCA	1	[Rmac_neg14]
8	GTCCCGGGGCGCAGCAATCCATCTACCCCGAACCGCCACGTATCT	1	[Rmac_neg18]
9	GTCTCGGGGCGCAGCAATCCATTTACCCCGAACCGCCACGTATCA	1	[Rpen_menz10]
10	AACCCGGGGCGCAGCAATCCATCTACCCCGAACCGCCACATATCA	1	[Rpen_menz15]
11	AACCCGGGGCGCAGCAATCCATCTACCCCGAACCGCCACGTATCA	1	[Rpen_menz16]
12	ATCCCGGGGCGCAGCAATCCATCTACCCCGAACCGCCACGTATCA	3	[Rpen_menz19 Rpen_menz23 Rpen_menz3]
13	ATCCCGGGGCGCAGCAATCCTTCTACCCCGAACCGCCACGTATCA	1	[Rpen_menz22]
14	GTCCAGGGGCGCAGCAATCCATCTACCCCGAACCGCCACGTATCA	1	[Rpen_menz5]
15	ATCCCGGGGCGCAGCAATCCATCTACTCCGAACCGCCACGTATCA	1	[Rpen_menz6]
16	GTCCAGGGGCGCAGCAATCCATTTACCCCGAACCGCCACGTATCA	1	[Rpen_menz7]
Taxon codes continue...			
*Rcor_stol_7901 Rcor_stol_7990]			
** Rmac_neg15 Rmac_neg16 Rmac_neg17 Rmac_neg2 Rmac_neg3 Rmac_neg5			
Rmac_neg6 Rmac_neg7 Rmac_neg8 Rmac_neg9 Rm_macro_1901 Rm_macro_1907			
Rm_ssapo_KA46261 Rpen_menz1 Rpen_menz11 Rpen_menz12 Rpen_menz13			
Rpen_menz14 Rpen_menz17 Rpen_menz18 Rpen_menz2 Rpen_menz20			
Rpen_menz21 Rpen_menz24 Rpen_menz25 Rpen_menz26 Rpen_menz27			
Rpen_menz4 Rpen_menz8 Rpen_menz9 Rp_caspius_1930 Rpen_pend_186			
RppendSic_AV30408 RppendSic_AV30410]			

Appendix 3. Standard diversity indices of *R. pendulinus* and *R. macronyx* based on ten microsatellite loci. Loci with significant P-values are indicated in bold letter.

Locus	<i>R. pendulinus</i>						<i>R. macronyx</i>					
	alleles	Obs. Het.	Exp. Het.	P-value	s. d.	range	alleles	Obs. Het.	Exp. Het.	P-value	s. d.	range
Rem-01	7	0.731	0.733	0.248	0.0004	24	5	0.833	0.756	0.132	0.0003	16
Rem-07	5	0.808	0.756	0.967	0.0002	16	3	0.500	0.527	1.000	0.0000	8
Rem-09	5	0.231	0.518	0.000	0.0000	20	5	0.278	0.603	0.000	0.0000	20
Rem-10	6	0.769	0.757	0.968	0.0002	20	5	0.556	0.646	0.809	0.0004	12
Rem-18	7	0.731	0.809	0.401	0.0004	24	4	0.722	0.722	0.947	0.0002	16
TG-061	3	0.269	0.245	1.000	0.0000	4	2	0.056	0.056	1.000	0.0000	2
TG-009	2	0.038	0.038	1.000	0.0000	2	3	0.111	0.160	0.086	0.0003	4
CAM-10	3	0.154	0.147	1.000	0.0000	10	2	0.111	0.108	1.000	0.0000	8
TG-053	6	0.577	0.810	0.010	0.0001	10	6	0.941	0.797	0.018	0.0001	10
TG-017	3	0.154	0.147	1.000	0.0000	4	3	0.333	0.341	0.513	0.0005	4