

Supplementary Figure S1

ITS1		
<i>R. delica</i>	ATCCAACCTCACCCCTTTGTGCATCACCGCGTGGGCCCCAC-----CC--TCTTGGGATCG	162
<i>R. mustelina</i>	GTCCATCTCACCCCTTTGTGCATCACCGCGTGGGCCCTCCC-----CCCATATTGGGAGGG	175
<i>R. sanguinea</i>	-TCCATTTACCCCTATGTGCACCAACCGGTGGGTCCCCTTTTCGGCTCGTCCCAGGGGG	95
B+	-----CACCCCTTTGTGCATCACCGCGTGGGTCCCCTTTTGGCTTGCTCGAGGGGG	52
RFR	-----CACCCCTTTGTGCATCACCGCGTGGGTCCCCT-----TCCTCGGAGGAGGG	46
SFR	----- <u>CACCCCTTTGTGCATCACCGCGTGGGTCCCCT</u> -----TCCTCGGAGGAGGG	46
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RusPrise 1F ->		
<i>R. delica</i>	-----GTTACGTTTTTC-----TACAAACACCTTTCTTTTAATGCATGTGTAGAATG	210
<i>R. mustelina</i>	-----GTTACGTTTTTA-----CACAGACACCTTT--TTTAATGCATGTGTAGAATG	221
<i>R. sanguinea</i>	-----GTCGCGTTTTTCA-----CACAAAC-----TCGATGCA-GTGTAGAATG	133
B+	-----GCTTGCCTTTTCA-----CACAAAC-----TCGATACC-GTGTAGAATG	90
RFR	AGGGGGGTGCTCAGTTTTTTAACATTATAAACACCCAT--TCAAACGTA-GTGTAGAATG	103
SFR	AGGGGGGTGCTCAGTTTTTTAACATTATAAACACCCAT--TCAAACGTA-GTGTAGAATG	103
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5.8s		
<i>R. delica</i>	TCTTCCTTTTTTGGCGATCACGCGCAATCAATACAACCTTTCAACAACGGATCTCTTGGCTC	270
<i>R. mustelina</i>	TCTTACTTTTTTGGCGATCACGCGCAATCAATACAACCTTTCAACAACGGATCTCTTGGCTC	280
<i>R. sanguinea</i>	TCT--CTTT---GCGATAACACGCAATTAATACAACCTTTCAACAACGGATCTCTTGGCTC	188
B+	TCT--CTT---GCGATAACACGCGATTAATACAACCTTTCAACAACGGATCTCTTGGCTC	144
RFR	TCT--TTGC--GCGATGACGCGGATCAATACAACCTTTCAACAACGGATCTCTTGGCTC	158
SFR	<u>TCT--TTGC--GCGATGACGCGGATCAATACAACCTTTCAACAACGGATCTCTTGGCTC</u>	158
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<i>R. delica</i>	TCGCATCGATGAAGAACGCGAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGA	330
<i>R. mustelina</i>	TCGCATCGATGAAGAACGCGAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGA	340
<i>R. sanguinea</i>	TCGCATCGATGAAGAACGCGAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGA	248
B+	TCGCATCGATGAAG-----	158
RFR	TCGCATCGATGAAG-----	172
SFR	<u>TCGCATCGATGAAG</u> -----	172
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<-RusPrise1R		

Alignment of the sequences of the genus *Russula* used and obtained in this study

Alignment sequence from *Russula delica* (GenBank accession no. AF345250), *Russula mustelina* (GenBank accession no. AY061693), *Russula sanguinea* (GenBank accession no. DQ65889), basidiocarp of *Russula sanguinea* DNA sample Limodorum roots and soil DNA samples Natural Park Roja Font. The shaded sequence correspond to part of the ribosomal intergenic spacer 1 (ITS1) and the unshaded sequence part of the 5.8s ribosomal gene, asterisks indicate identity of nucleotides and underlined sequences correspond to primers RusPrise1F/1R. The sequence positions correspond to the Genbank annotation for each sequence.