Supplementary Table S2 – Loci tested in the present study, annealing temperature, primers used, length of the aligned sequences, note about the detected sequence polymorphisms and reference for the source of the primers. n.a. – not analysed due to unsuccessful amplification; SNP – single nucleotide polymorphism.

Locus	TA [°C]	Primers	Length [bp]	Polymorphism
Nuclear				
ITS1-5.8S-ITS2[8]	56	ITS1, ITS4	617	1 ambiguous position
ppc[1]	55	*PPCX4F*, *PPCX5R*	n.a.	unspecific amplification
*topo*6[2]	59	*top6_2F_305*, *Top6_3F_464*, *Top6_8R_1680*	n.a.	n.a.
isi[3]	55	*isi-ex3F*, *isi-ex5R*	n.a.	unspecific amplification
Chloroplast				
*psb*M-*ycf*6[4]	54	*ycf6F*, *psbMR*	917	1SNP (A/G)
*trn*C-*ycf*6[4]	54	*trnC*^{GCA}*F*, *ycf6R*	795	2 SNP (T/G; polyT)
*trn*Q-*rps*16[5]	54	*trnQ*^{UUG}, *rpS16x1*	448	7 bp insert + 1SNP (polyT)
*rps*16[4]	52	*rpS16F*, *rpS16R*	738	1 SNP (polyT)
*trn*T-*trn*F[9]	52	*a*, *f*	1581	2 SNP (A/T; polyA)
*trn*K-*mat*K[10]	52	*3914F*, *2R*, *trnK 3R*	1082	1 SNP (polyT)
*trn*D-*trn*T[4]	54	*trnD*^{GUC}*F*, *trnT*^{GGU}	827	0
*trn*D-*psb*M[4]	54	trn*D*^{GUC}*R*, *psbMF*	590	0
*trn*S-*trnf*M[4]	55	*trnS*^{UGA}, *trnfM*^{CAU}	978	0
*trn*H-*psb*A[6]	54	*psbA*, *trnH*:	300	0
*ndh*F[7]	50	*ndhF-913_F*, *ndhF_R*	913	0
*rpo*B-*trn*C[4]	54	*rpoB*, *trnC*^{GCA}*R*	n.a.	n.a.
*trn*S-*trn*L[4]	50	*trnS*^{GGA}, *trnL*^{UAA}*R*	n.a.	n.a.
*rpl*16[4]	50	*rpL16F71*, *rpL16R1516*	n.a.	n.a.
*pet*L-*psb*E[5]	54	*petL*, *psbE*	n.a.	n.a.

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