**Table S2:**

**Genetic regions and sequence primers used for testing DNA quality through both Qiagen and CTAB extraction tests. All indicated lengths of target genetic regions are evaluated based on gel electrophoresis.**

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| --- |
| **Nuclear genome markers** |
| **region** | **name** | **sequence (5’-3’)** | **target DNA region length [bp]** | **reference** |
| *ITS* | *5,8SR* | TCGATGAAGAACGCAGCG | 450 | Hopple and Vilgalys, 1999 |
| *ITS2* | GCTGCGTTCTTCATCGATGC | White et al, 1990  |
| *ITS5-*bryo | GGAAGGAGAAGTCGTAACAAGG | 380 | Sabovljević and Frahm, 2011  |
| *ITSC-*bryo | GCAATTCACACTACGTATCGC | ― |
| *ITSD-*bryo | CTCTCAGCAACGGATATCTTG | 450 | ― |
| *ITS4-*bryo | TCCTCCGCTTAGTGATATGC | ― |
| *18S* rRNA | *NS1* | GTAGTCATATGCTTGTCTC | 1000 | Cox et al, 2000 |
| *PCRB* | TGATCCTTCCGCAGGTT | ― |
| *adk* gene | *adk* forward | GAAGAAGCCAGAAAACTGGGC | 1000 | McDaniel and Shaw, 2005 |
| *adk* reverse | GTCACCCCATCTTCAGCAAC | ― |
| *phy2* gene | *phy2* forward | GGCATGGAAATGATGTGTTG | 1000 | ― |
| *phy2* reverse | CATCACTGTACCCATCTCG | ― |
| **Plastid genome markers** |
| **region** | **name** | **sequence (5’-3’)** | **target DNA region length [bp]** | **reference** |
| *psbAF*-*trnHR2* | *psbAF* | GTTATGCATGAACGTAATGCTC | 250 | Stech and Frey, 2008 |
| *trnHR-2* | CGCGCATGGTGGATTCACAATCC | ― |
| *atpI*-*atpH* | *atpI* | TATTTACAAGYGGTATTCAAGCT | 550 | Shaw et al, 2007 |
| *atpH* | CCAAYCCAGCAGCAATAAC | — |
| *trnL*-*trnF* | *trnL* (UAA) 5’exon  | CGAAATTGGTAGACGCTGCG | 450 | Quandt and Stech, 2004 (primer C)  |
| *trnF* (GAA)  | ATTTGAACTGGTGACACGAG | ― (primer F) |
| *trnT-trnF* | *trnT* (UGU) | CATTACAAGTGCGACGCTCT | 1500 | ― (primer A) |
| *trnF* (GAA) | see above | ― (primer F) |
| *rps5’-trnS* | *rps5’* | ATGTCCCGTTATCGAGGACCT | 650 | Souza-Chies et al, 1997 |
| *trnS* | TACCGAGGGTTCGAATC | ― |
| *atpB1*-*rbcL1* | *atpB1* | ACATCKARTACKGGACCAATAA | 650 | Chiang et al, 1998 |
| *rbcL1* | AACACCAGCTTTRAATCCAA | — |
| *psbB*-*clpP* | *Bry\_psbB* | ATGAACACGATACCTAGGYAAACC | 1000 | Piñeiro et al, 2012 |
| *Bry\_clpP1,2* | CATTGAAGCAGCTAATCCC | — |
| **selected fragments of *trnS*-*trnF* region**  |
| *rpsM’-trnS*  | *rpsM’* | TAGACATATTTTAGTTAATGG | 500 | Souza-Chies et al, 1997 |
| *trnS* | see above | — |
| *rpsM’-rps3’*  | *rpsM’* | see above  | 250 | — |
| *rps3’* | ATATTCTACAACTAACAACTC | — |
| *rpsM2-rpsM*  | *rpsM2* | TTTTACTACAACTACTTGAGA | 100 | — |
| *rpsM* | CCATTAACTAAAATATGTGT | — |
| *rpsM1-rpsM*  | *rpsM1* | CAATATCGTATTCGTCTAGAA | 200 | — |
| *rpsM* | see above | — |
| *rps5’-rpsM*  | *rps5’* | see above | 300 | — |
| *rpsM* | see above | — |
| *trnT-trnL* | *trnT* (UGU)  | see above  | 400 | Quandt and Stech, 2004 (primer A) |
| *trnL* (UAA) 5’Exon  | TCTACCAATTTCGCCATACC  | — (primer B) |
| *trnL* intron | *trnL* (UAA) 5’Exon  | as above  | 500 | ― (primer C) |
| *trnL* (UAA) 3’Exon  | GGGGGTAGAGGGACTTGAAC  | ― (primer D) |
| *trnL-trnF* | *trnL* (UAA) 3’Exon  | GGTTCAAGTCCCTCTATCCC  | 200 | ― (primer E) |
| *trnF* (GAA)  | as above  | ― (primer F) |
| *trnL* intron | trnL (UAA) 5’Exon  | as above | 200 | ― (primer C) |
| trnL (UAA) intron  | GTTTCCTTTGAGTCTCTGCAC | ― (primer Dx) |
| *trnL* intron | trnL (UAA) 5’Exon  | as above | 200 | ― (primer C) |
| trnL (UAA) intron  | CTTCCATTGAGTCTCTGCACC | ― (primer Di) |
| *P6*  loop | *P6* loop-g | GGGCAATCCTGAGCCAA | 100 | Taberlet et al, 2007  |
| *P6* loop-h | CCATTGAGTCTCTGCACCTATC | — |