**S1 Text. The DNA extraction and sequencing procedures for modern specimens.**

The modern specimens used in molecular analyses are listed in S1 Table. Total DNA was extracted from field-collected specimens dried by silica gel using the DNeasy Plant Mini Kit (QIAGEN, Tokyo, Japan) following the instructions of the manufacturer. The total DNA was used as a template for polymerase chain reaction (PCR) amplification using a TOYOBO KOD FX Neo (TOYOBO CO. LTD., Oosaka, Japan). Primers used for PCR amplification were: 28S *r*RNA gene: T01 (5’-TAAGCATATCAGTAAGCGGAG-3’) – V (5’-CGTATCGCCAGTTCTGCTTACC-3’), F449 (5’-CCCGAAGATGGTGAACTATG-3’) – G (5’-CACCACGTCCTCCTACTC-3’), T04 (5’-GCAGGACGGTGGCCATGGAAGT-3’) - 28F (5’-CAGAGCACTGGGCAGAAAATCAC-3’), and T05 (5’-GCAACGGKCAAAGGGAATCCG-3’) - T15 (5’-TGATAGGAAGAGCCGACATCGA-3’) [1, 2]; 18S rRNA gene: SR1 (5’-CCTGGTTGATCCTGCCAG-3’) - SR9 (5’-AACTAAGAACGGCCATGCAC-3’), and SR4 (5’-AGCCGCGGTAATTCCAGCT-3’) - SR12 (5’-CCTTCYGCAGGTTCACCTAC-3’) [3]; *rbc*L: F8 (5’-GGYGTAATTCCATATGCWAAAATG-3’) - R1150 (5’-GCATTTGWCCACARTGAATACC-3’) and F645 (5’-ATGMGHTGGAAAGAAAGATT-3’) - R1381 (5’- ATCTTTCCATAAATCTARAGC-3’) [4]; COI: GazF1 (5’-TCAACAAATCATAAAGATATTGG-3’) - GazR1 (5’-ACTTCTGGATGTCCAAAAAAYCA-3’) [5]. The temperature-cycling protocol was: 28S *r*RNA gene: 2 min at 94°C for an initial denaturation step, followed by 35 cycles of 15 sec denaturation at 94°C, 30 sec primer annealing at 55°C, and 1 min extension at 68°C, with a final 7 min extension at 72°C, and then a hold at 4°C; *rbc*L and COI: 2 min at 94°C for an initial denaturation step, followed by 35 cycles of 15 sec denaturation at 94°C, 30 sec primer annealing at 46°C and 1 min extension at 68°C, with a final 7 min extension at 72°C, and then a hold at 4°C. The amplified DNA fragments were purified using QIAquick PCR Purification Kit (QIAGEN, Tokyo, Japan). Cycle-sequencing with BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems, Tokyo, Japan) was carried out in a 7.5 μl volume of reaction: 2 μl of BigDye Terminator v3.1 Reaction Mix, 10-30 ng/ml of PCR product, 10 pmol of primer, and dH2O to 7.5 μl. The cycle-sequencing program consisted of an initial step at 97°C for 2 min, 25 sequencing cycles (97°C for 10 s, 50°C for 25 s, 60°C for 2 min). The BigDye-labeled PCR products were ethanol-precipitated following the manufacturer's protocol and completely sequenced using ABI PRISM 310 Genetic Analyzer (Applied Biosystems, Tokyo, Japan). Reverse and direct chromatograms were assembled using the program GeneStudioTM Professional Ver. 2.2. (GeneStudio, Inc.).

**Additional References**

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