

Supplementary Information 2

Materials and Methods

The following taxa were removed to resolve conflicts among the *rps4* and *nad5* loci: *Acroporium pungens*, *Aloina rigida*, *Bellibarbula recurva*, *Bruchia drummondii*, *Bryohumbertia filifolia*, *Bryomanginia saintpierrei*, *Calymperes lonchophyllum*, *Campylopodium euphorocladium*, *Clastobryophilum bogoricum*, *Clastobryum tenuirameum*, *Dicnemon seriatum*, *Ephemeropsis trentepohlioides*, *Hondaella brachytheciella*, *Hookeria lucens*, *Hymenodontopsis stressmannii*, *Hymenolomopsis toluensis*, *Hyophila involuta*, *Mesotus celatus*, *Osculatia globosum*, *Polymerodon andinus*, *Reimersia inconspicua*, *Syntrichia ruralis*, *Timmia megapolitana*, and *Tortella humilis*, *Warburgiella leucocytus*.

Taxa removed to resolve conflicts among the *rps4/nad5* and *nuc26S* data sets: *Dendroligotrichum dendroides*, *Notoligotrichum australe*, *Dicranoweisia crispula*, *Hygrodicranum boliviana*, *Hypnodontopsis spathulatus*, *Cheilothela chloropus*, *Weisiopsis anomala*, *Ganguleea angulosa*, *Triquetrella californica*, *Holomitrium arboreum*, *Blindia acuta*, *Schistidium apocarpum*, *Pseudobraunia californica*, *Pseudocrossidium aureum*, *Campylostelium augustifolium*, *Pulchrinodus inflatus*, *Mniomalia semilimbata*, *Phyllocladon falcifolium*, *Aulacomnium androgynum*, *Cladomnion ericoides*, *Cladomniopsis crenatoobtusa*, *Euptychium robustum*, *Glyphothecium sciuroides*, *Hampeella pallens*, *Orthorrhynchium elegans*, *Ptychomnion aciculare*, *Tetraphidopsis pusilla*, *Garovaglia elegans*, *Amblyodon dealbatus*, *Aplodon wormskioldii*, *Meesia triquetra*, *Neomeesia paludella*, *Paludella squarrosa*, *Tetraplodon mnioides*, *Cardotiella subappendiculata*, *Cyrtopus setosus*, *Hypnodendron microstictum*, *Racopilum tomentosum*, *Cyathophorum bulbosum*, *Aulacopilum hodgkinsoniae*, *Rhamphidium dicranoides*, *Trematodon longicollis*, *Venturiella sinensis*, *Wilsoniella karsteniana*, *Dicranella heteromalla*, *Stenodesmus tenuicuspis*, *Habrodon perpusillus*, *Leucodon sciuroides*, *Dimorphocladon borneense*, *Hamatocaulis vernicosus*, *Sanionia orthothecioides*, *Scorpidium scorpioides*, *Achrophyllum quadrifarium*, *Adelothecium bogotense*, *Beeveria distichophylloides*, *Benitotania wakatentakii*, *Bryobrothera crenulata*, *Crosbya straminea*, *Daltonia gracilis*, *Distichophyllidium nymanianum*, *Distichophyllum pulchellum*, and *Leskeodon auratus*.

Results

Table S.2.1: Optimal substitution models for individual data partitions. Notation as used by the “lset” command of PAUP* (Swofford, 1998).

<i>partition</i>	<i>model</i>
<i>rps4</i> first codon positions	Base=(0.4843 0.1207 0.1224) Nst=6 Rmat=(1.5969 5.9936 0.1215 1.8581 5.9936) Rates=gamma Shape=0.8309 Pinvar=0.1675
<i>rps4</i> second codon positions	Base=(0.4020 0.1956 0.1035) Nst=6 Rmat=(1.8473 7.0500 0.2536 2.1525 7.0500) Rates=gamma Shape=0.6945 Pinvar=0.3175
<i>rps4</i> third codon position	Base=(0.4756 0.0536 0.0674) Nst=6 Rmat=(1.1211 5.8781 0.0678 2.6019 5.8781) Rates=gamma Shape=2.6872 Pinvar=0.0053
<i>rps4</i> all codon positions	Base=(0.4723 0.0761 0.0617) Nst=6 Rmat=(1.2503 7.5482 0.0728 2.8877 4.8559) Rates=gamma Shape=0.8586 Pinvar=0.1685
<i>nad5</i>	Base=(0.2659 0.2044 0.1683) Nst=6 Rmat=(1.5359 5.5597 0.1962 0.7724 5.5597) Rates=gamma Shape=1.1012 Pinvar=0.1768
<i>nuc26S</i>	Base=(0.1680 0.2693 0.3972) Nst=6 Rmat=(1.0000 3.5922 0.6574 0.6574 5.5687) Rates=gamma Shape=0.4742 Pinvar=0.5381
<i>rps4/nad5</i>	Base=(0.3936 0.1163 0.1019) Nst=6 Rmat=(1.4062 6.1748 0.1160 1.6461 5.7529) Rates=gamma Shape=0.6845 Pinvar=0.1682;
<i>rps4/nad5/nuc26s</i>	Base=(0.3362 0.1784 0.1780) Nst=6 Rmat=(1.1575 5.0187 0.2177 1.1201 5.7560) Rates=gamma Shape=0.5773 Pinvar=0.3455;

Supplemental Data Figures:

Figure S.2.1: Rps4 - 50% majority-rule consensus tree of 32,000 trees from the MCMC analysis. * the accessions *Hymenostylium recurvirostre* and *Pottia truncata* were later identified as *Ceratodon* sp.

Figure S.2.2: Nad5 - 50% majority-rule consensus tree of 32,000 trees from the MCMC analysis.

Figure S.2.3: Nuc26S - 50% majority-rule consensus tree of 32,000 trees from the MCMC analysis.

Figure S.2.4: Optimal ML tree for the Rps4 dataset under the GTR+I+G model (-ln likelihood = 28427.90907; optimal parameters: A/C = 1.63485, A/G = 7.22664, A/T = 0.09404, C/G = 2.96553, C/T = 6.75490, G/T = 1(fixed); f(A) = 0.46702, f(C) = 0.07167, f(G) = 0.07637, f(T) = 0.38495; gamma shape = 0.960; proportion invariant = 0.170).

Figure S.2.5: Optimal ML tree for the Nad5 dataset under the GTR+I+G model (-ln likelihood = 25890.93262; optimal parameters: A/C = 1.80485, A/G = 4.72086, A/T = 0.20628, C/G = 0.84334, C/T = 7.76839, G/T = 1(fixed); f(A) = 0.28617, f(C) = 0.17771, f(G) = 0.19301, f(T) = 0.3431; gamma shape = 0.954; proportion invariant = 0.160).

Figure S.2.6: Optimal ML tree for the Nuc26S dataset under the GTR+I+G model (-ln likelihood = 14134.69801; optimal parameters: A/C = 0.83110, A/G = 3.69358, A/T = 0.70300, C/G = 0.52717, C/T = 5.09783, G/T = 1(fixed); f(A) = 0.16477, f(C) = 0.28592, f(G) = 0.39013, f(T) = 0.15918; gamma shape = 0.583; proportion invariant = 0.615).

Figure S.2.7: Rps4/Nad5 - 50% majority-rule consensus tree of 24,000 trees from the MCMC analysis.

Figure S.2.8: Optimal ML tree for the combined Rps4/Nad5 dataset under the GTR+I+G model (-ln likelihood = 53220.04681; optimal parameters: A/C = 1.23669, A/G = 6.30676, A/T = 0.11699, C/G = 1.45839, C/T = 5.01781, G/T = 1(fixed); f(A) = 0.38569, f(C) = 0.12827, f(G) = 0.09952, f(T) = 0.38653; gamma shape = 0.662; proportion invariant = 0.156).

Figure S.2.9: Rps4/Nad5/nuc26S - 50% majority-rule consensus tree of 32,000 trees from the MCMC analysis.

Figure S.2.10: Optimal ML tree for the combined model Rps4/Nad5/nuc26S (-ln likelihood = 54575.69502; optimal parameters: A/C = 1.11660, A/G = 5.05961, A/T = 0.21653, C/G = 1.06108, C/T = 5.64569, G/T = 1(fixed); f(A) = 0.33561, f(C) = 0.18362, f(G) = 0.17805, f(T) = 0.30272; gamma shape = 0.573; proportion invariant = 0.341).