

Appendix 3.0 Maximum parsimony tree (MP) of the ITS region

Heuristic search settings:

Optimality criterion = parsimony

Character-status summary:

Of 520 total characters:

All characters are of type 'unord'

All characters have equal weight

344 characters are constant

174 variable characters are parsimony-uninformative

Number of parsimony-informative characters = 2

Gaps are treated as "missing"

Starting tree(s) obtained via stepwise addition

Addition sequence: random

Number of replicates = 10000

Starting seed = 550032745

Number of trees held at each step during stepwise addition = 1

Branch-swapping algorithm: tree-bisection-reconnection (TBR)

Steepest descent option not in effect

Initial 'MaxTrees' setting = 100

Branches collapsed (creating polytomies) if maximum branch length is zero

'MulTrees' option in effect

Topological constraints not enforced

Trees are unrooted

Heuristic search completed

Total number of rearrangements tried = 2492

Score of best tree(s) found = 178

Number of trees retained = 2

Time used = 4.25 sec

Tree-island profile:

Island	Size	First tree	Last tree	Score	First replicate	Times hit
1	2	1	2	178	1	10000

Tree description:

Unrooted tree(s) rooted using outgroup method

Optimality criterion = parsimony

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Character-state optimization: Accelerated transformation (ACCTRAN)

Tree number 1 (rooted using default outgroup)

Tree length = 178

Consistency index (CI) = 1.0000

Homoplasy index (HI) = 0.0000

CI excluding uninformative characters = 1.0000
HI excluding uninformative characters = 0.0000
Retention index (RI) = 1.0000
Rescaled consistency index (RC) = 1.0000

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/ 2954
+ 2953
+ 2952
+ 0362
+ 0361
+ 5059
/--+ 1350
| + 3533
| + 3532
| + 1349
/-----+
+ 0301
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| + 0201
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| \-- GQ203796
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--- Phoma sp. HQ608114

/----- 2954
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