Appendix 5.0 ITS region majority rule consensus tree of 60,001 post-burning trees sampled by the Bayesian search algorithm

```
Bootstrap method with heuristic search:
  Number of bootstrap replicates = 1000
  Starting seed = 1809504208
  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 = 100
    Starting seed = 2080338920
  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

   1000 bootstrap replicates completed
   Time used = 48.95 sec

Bootstrap 50% majority-rule consensus tree
   (plus other groups compatible with this tree)


/----------------------------------------------- 2954(3)

+----------------------------------------------- 2953(4)

+----------------------------------------------- 2952(5)

+----------------------------------------------- 0362(6)

+----------------------------------------------- 0361(7)

+----------------------------------------------- 5059(8)
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75----------------------+-----------------------------------------------
- 1350(9)
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+----------------------------------------------- 3533(10)
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+----------------------------------------------- 3532(11)
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+----------------------------------------------- 1349(12)
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+----------------------------------------------- 0301(13)
|                                              |
+----------------------------------------------- 0201(14)
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\----------------------------------------------- GQ203796(16)
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/----------------------------------------------- 0658(2)
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36----------------------+----------------------------------------------
- 0657(15)
\----------------------------------------------------------------------
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Phoma sp. HQ608114(1)

Bipartitions found in one or more trees and frequency of occurrence
(bootstrap support values):

  (none)
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