

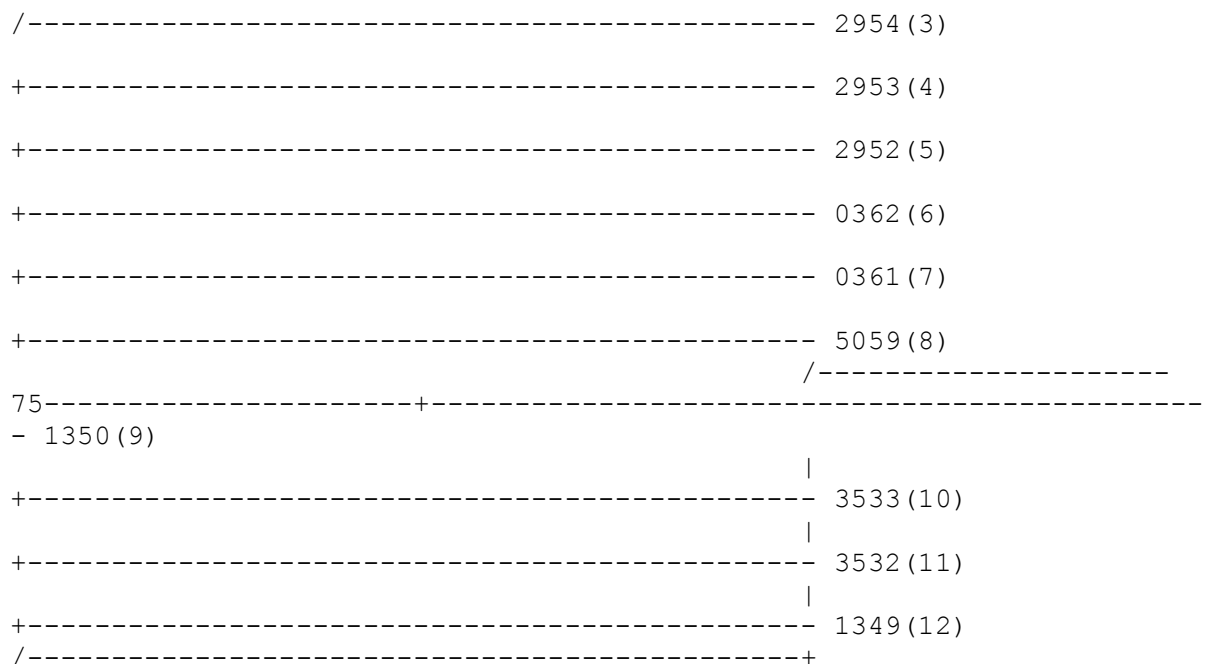
**Appendix 5.0** ITS region majority rule consensus tree of 60,001 post-burning trees sampled by the Bayesian search algorithm

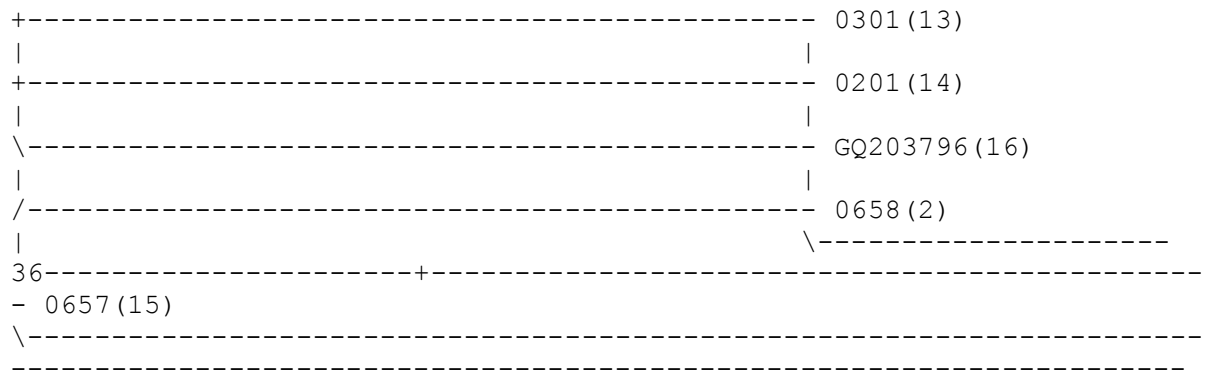
```

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)





Phoma sp. HQ608114 (1)

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

(none)