Phylogenomic reassessment of *Cyttaria* Berk.

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Introduction

Cyttaria Berk., is an enigmatic genus of *Ascomycota*, the species of which are obligately associated with southern beech trees (*Nothofagceae*)[1].These fungi have been a biological wonder since Charles Darwin first brought back a specimen collected from Tierra del Fuego during the expedition of the Beagle. *Cyttaria* exhibit a Gondwanan distribution, limited to *Nothofagaceae* hosts in the temperate forests of southern South America, Australia, and New Zealand. It has been thought their symbiosis represents long-term coevolution with their hosts[2]. Here we sequenced the genomes of 26 specimens representing 11 species and investigate cophylogenetic paterns between *Cyttaria* and their *Nothofagacae* hosts to revaluate past studies, and to enable future work In the ecology and evolution of *Cyttaria*.

Methodology

Phylogenetic analysis

3173 single copy BUSCO[3] genes conserved across *Leotiomycetes* were used for phylogenomic analysis. Tree topology was determined using weighted-hybrid ASTRAL[4] analysis of individual ML gene trees, branch lengths were then estimated using IQ-TREE 2 with automatic model finder[5,6].

Cophylogenetic analysis

Quantitative cophylogenetic analysis was performed using our *Cyttaria* species tree and an existing phylogeny of *Nothofagus*[7].A procrustean approached implemented through the R package paco[8] was used under the "quasiswap" model algorithm and the parameters symmetric =T and nperm = 1000.

BUSCO and Genome Assessment
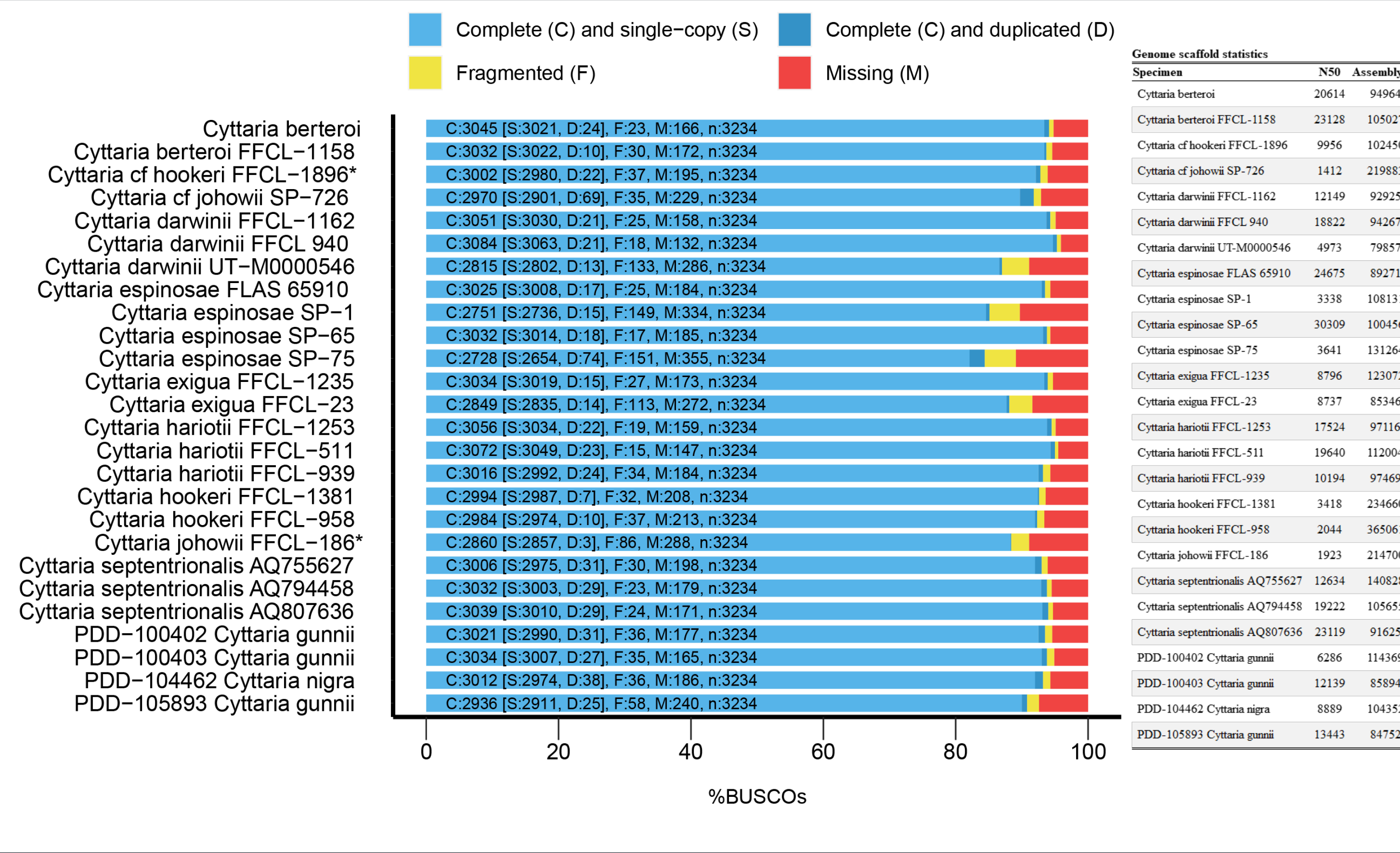
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# *Cyttaria* Berk. exhibits significant cophylogenetic relationships with their *Nothofagus* hosts

3173 single copy BUSCO genes

PACo results:

$m^2_{xy} = 0.82$
p-value = 0.009
nperm = 1000

Derived from:
[7]Sauquet H, et al., 2012. Testing the Impact of Calibration on Molecular Divergence Times Using a Fossil-Rich Group: The Case of *Nothofagus* (Fagales). Systematic Biology 61:289–313.

Australia (AU)   New Zealand (NZ)   Southern South America (SSA)
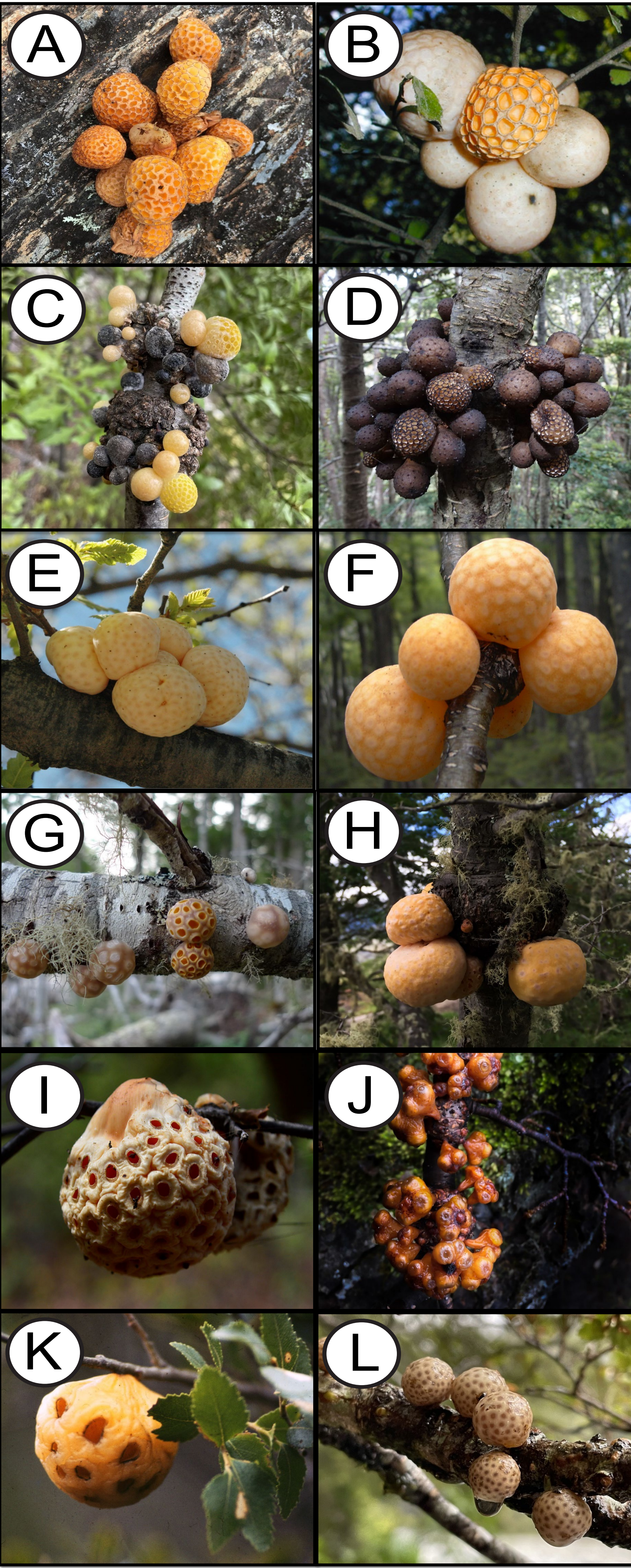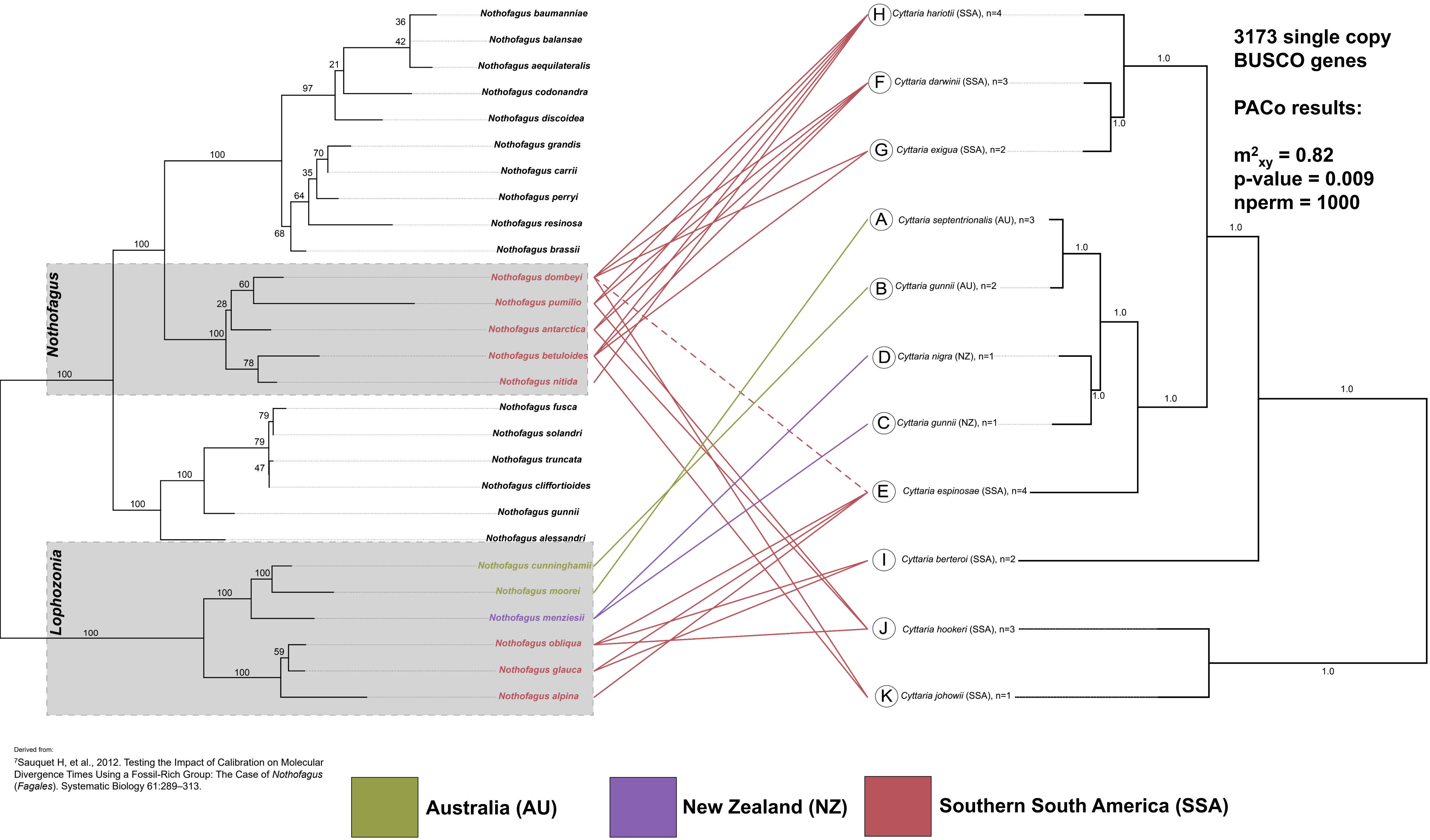
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