

Phylogenomic reassessment of *Cyttaria* Berk.

Alexander J. Bradshaw^{1,2}, Guiliana Faruici³, Donald H. Pfister⁴, Bryn T.M. Dentinger^{1,2}

¹Natural History Museum of Utah, ²University of Utah-School of Biological Sciences, ³Fungi Foundation, ⁴Harvard University

Introduction

Cyttaria Berk., is an enigmatic genus of *Ascomycota*, the species of which are obligately associated with southern beech trees (*Nothofagaceae*)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 hosts². Here we sequenced the genomes of 26 specimens representing 11 species and investigate cophylogenetic between *Cyttaria* and their *Nothofagaceae* hosts to reevaluate past studies, and to enable future work In the ecology and evolution of *Cyttaria*.

Methodology

DNA sequencing

Samples were sequenced with 2x150bp Illumina Novoseq provided through the University of Utah high-throughput genomics core.

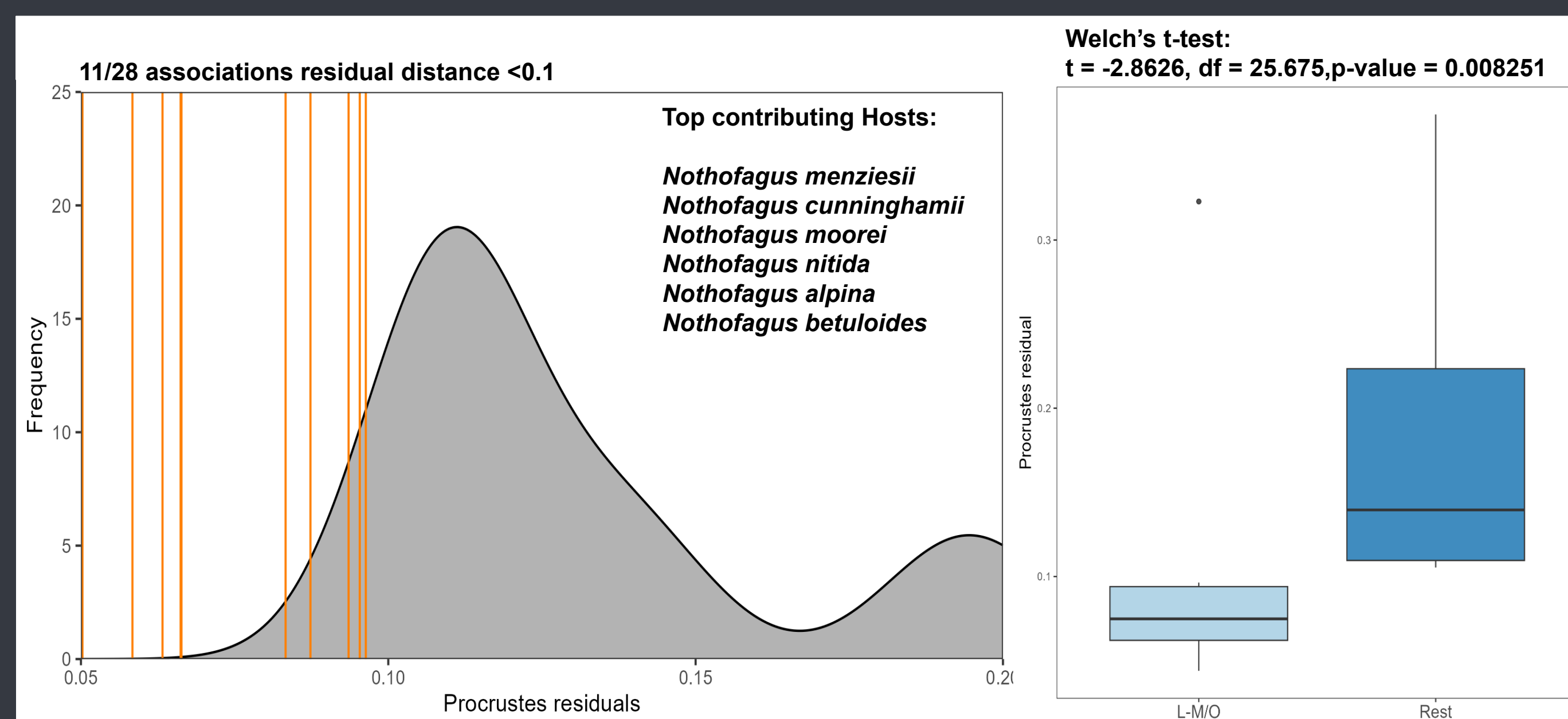
Phylogenetic analysis

3173 single copy BUSCO³ genes conserved across *Leotiomycetes* were used for phylogenomic analysis. Tree topology was determined using weighted-hybrid ASTRAL⁴ Branch Lengths were then estimated using IQ-TREE 2 with model finder^{5,6}.

Cophylogenetic analysis

Quantitative Cophylogenetic analysis was performed using a on our *Cyttaria* species tree and a previous studies *Nothofagus* species tree⁷ Procrustean approached implemented through the R package paco⁸ under using the “quasiswap” model algorithm and the parameters symmetric =T and nperm = 1000.

Cophylogenetic contribution

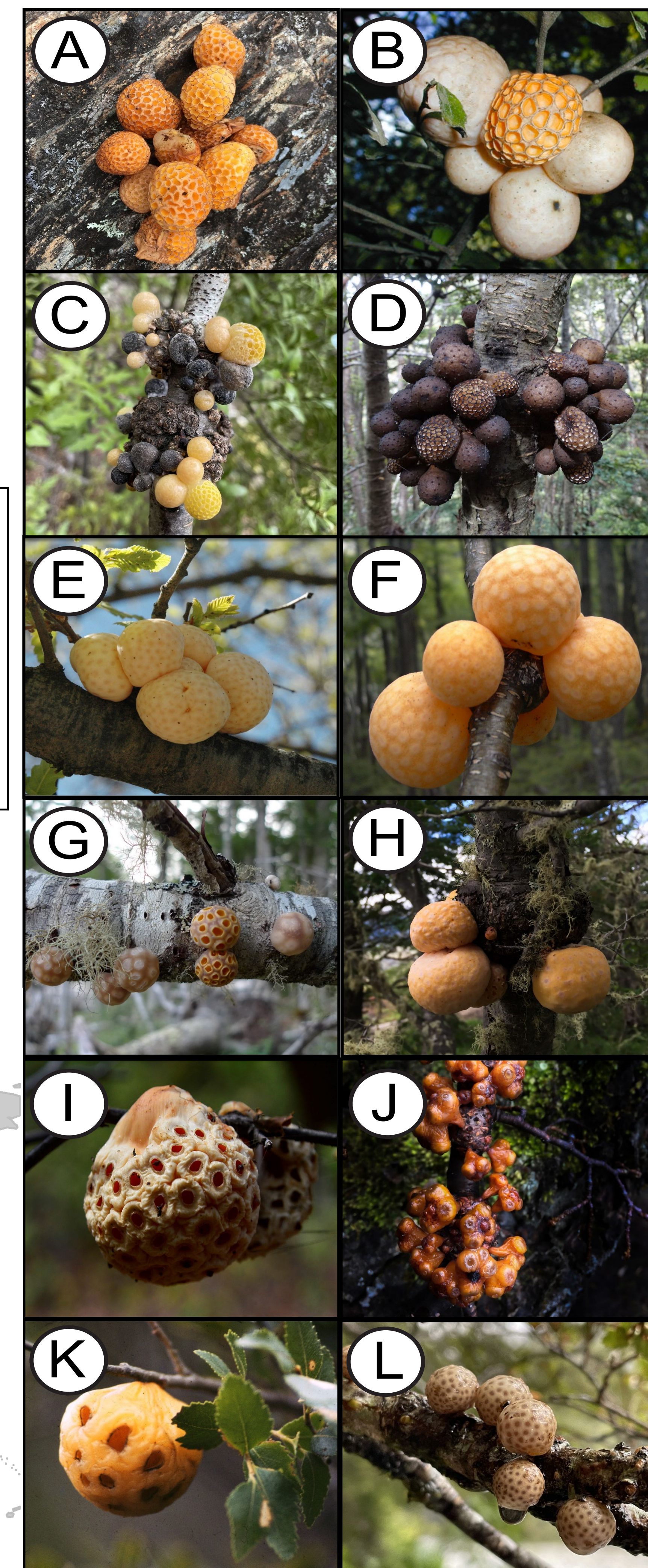
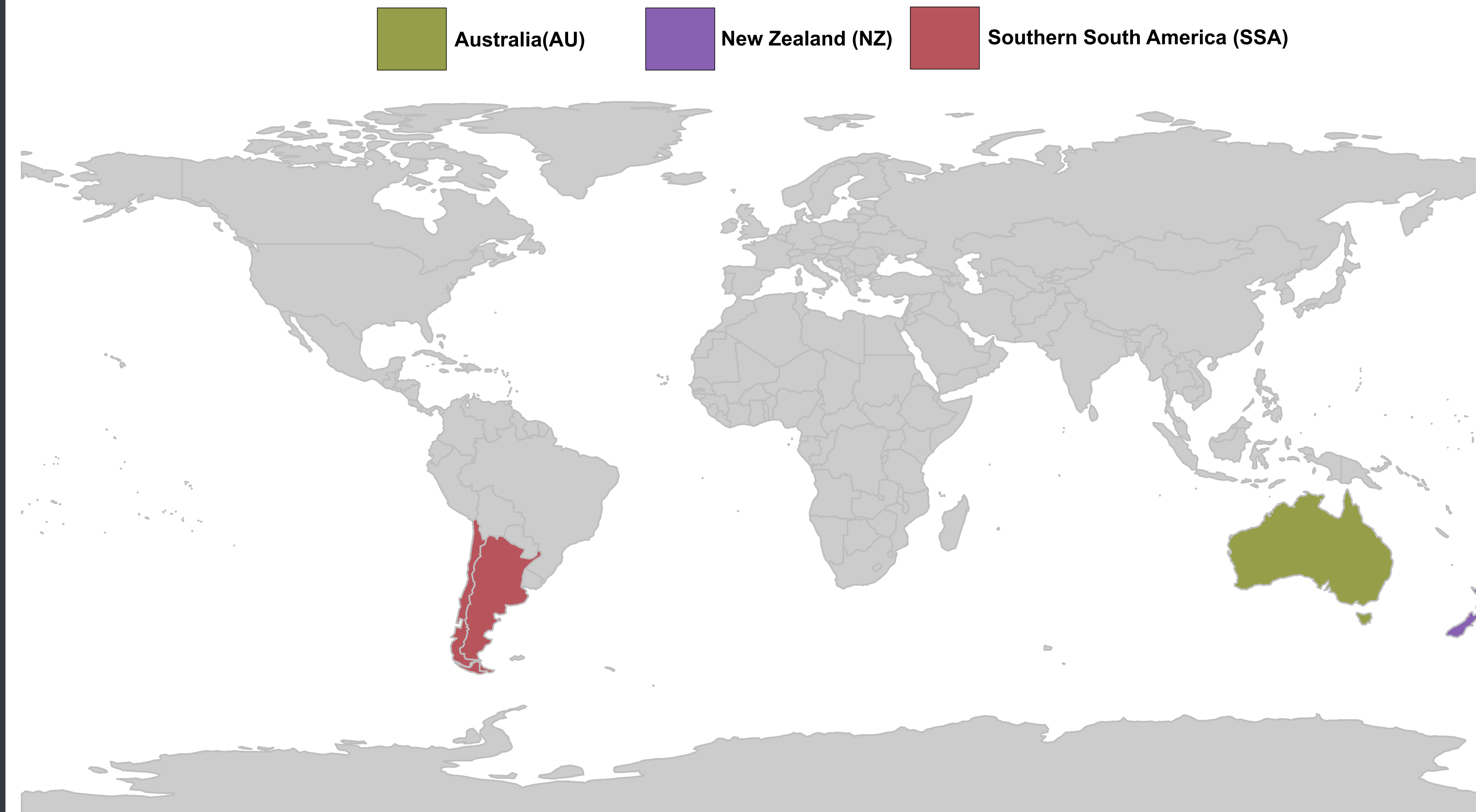
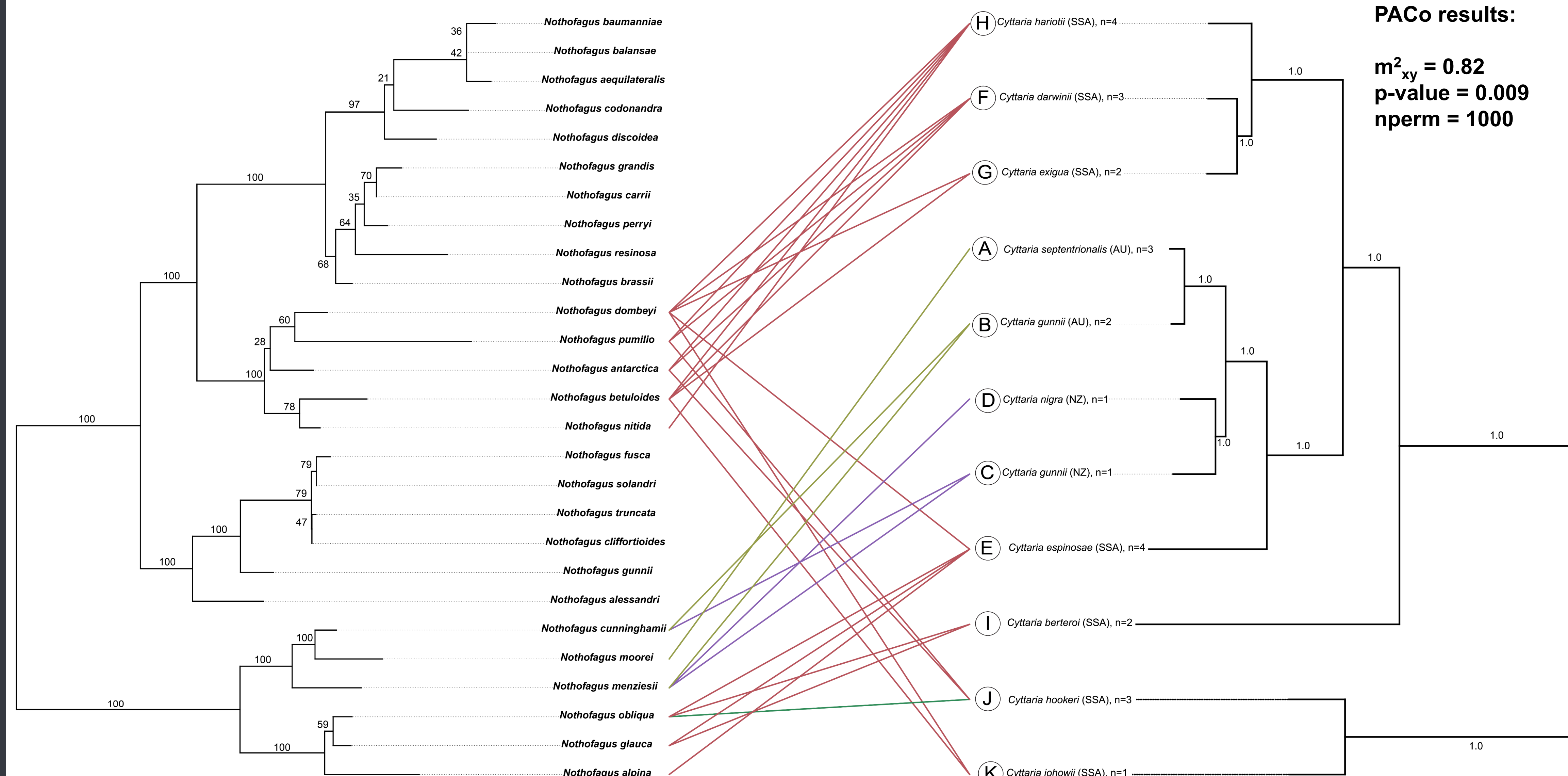


Works cited

- ¹Peterson KR, Pfister DH. Phylogeny of *Cyttaria* inferred from nuclear and mitochondrial sequence and morphological data. 19.
- ²Peterson KR, Pfister DH, Bell CD. 2010. Cophylogeny and biogeography of the fungal parasite *Cyttaria* and its host *Nothofagus*, southern beech. *Mycologia* 102:1417–1425.
- ³Simão FA, Waterhouse RM, Ioannidis P, Kriventseva EV, Zdobnov EM. 2015. BUSCO: assessing genome assembly and annotation completeness with single-copy orthologs. *Bioinformatics* 31:3210–3212.
- ⁴Zhang C, Mirarab S. 2022. Weighting by Gene Tree Uncertainty Improves Accuracy of Quartet-based Species Trees. *Molecular Biology and Evolution* 39:msac215.
- ⁵Minh BQ, Schmidt HA, Chernomor O, Schrempf D, Woodhams MD, Haeseler A von, Lanfear R. 2020. IQ-TREE 2: New Models and Efficient Methods for Phylogenetic Inference in the Genomic Era. *Molecular Biology and Evolution* 37:1530–1534.
- ⁶Kalyaanamoorthy S, Minh BQ, Wong TKF, Haeseler A von, Jermini LS. 2017. ModelFinder: fast model selection for accurate phylogenetic estimates. *Nature Methods* 14:587–589.
- ⁷Sauquet H, Ho SYW, Gandolfo MA, Jordan GJ, Wilf P, Cantrill DJ, Bayly MJ, Bromham L, Brown GK, Carpenter RJ, Lee DM, Murphy DJ, Sniderman JMK, Udovicic F. 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.
- ⁸Hutchinson MC, Cagua EF, Balbuena JA, Stouffer DB, Poisot T. 2017. paco: implementing Procrustean Approach to Cophylogeny in R. *Methods in Ecology and Evolution* 8:932–940.

The genus *Cyttaria* shows significant cophylogenetic relationships with *Nothofagus* hosts

Cophylogeny and Global Distribution of *Cyttaria*



Acknowledgments

Matt Smith (University of Florida Herbarium), Maj Padamsee (New Zealand Fungarium, Andrew Franks (Queensland Herbarium), **need person we got *Cyttaria espinosae* from, anyone else co-authors would like, funding???**

