

I. Jimenez Luna, X. Besoain, S. Saa, E. Peach-Fine, F. Cadiz Morales, N. Riquelme, A. Larach, J. Morales, E. Ezcurra, V.E.T.M. Ashworth, P.E. Rolshausen (2022). Identity and pathogenicity of *Botryosphaeriaceae* and *Diaporthaceae* from *Juglans regia* in Chile. *Phytopathologia Mediterranea* 61(1): 79-94. doi: 10.36253/phyto-12832

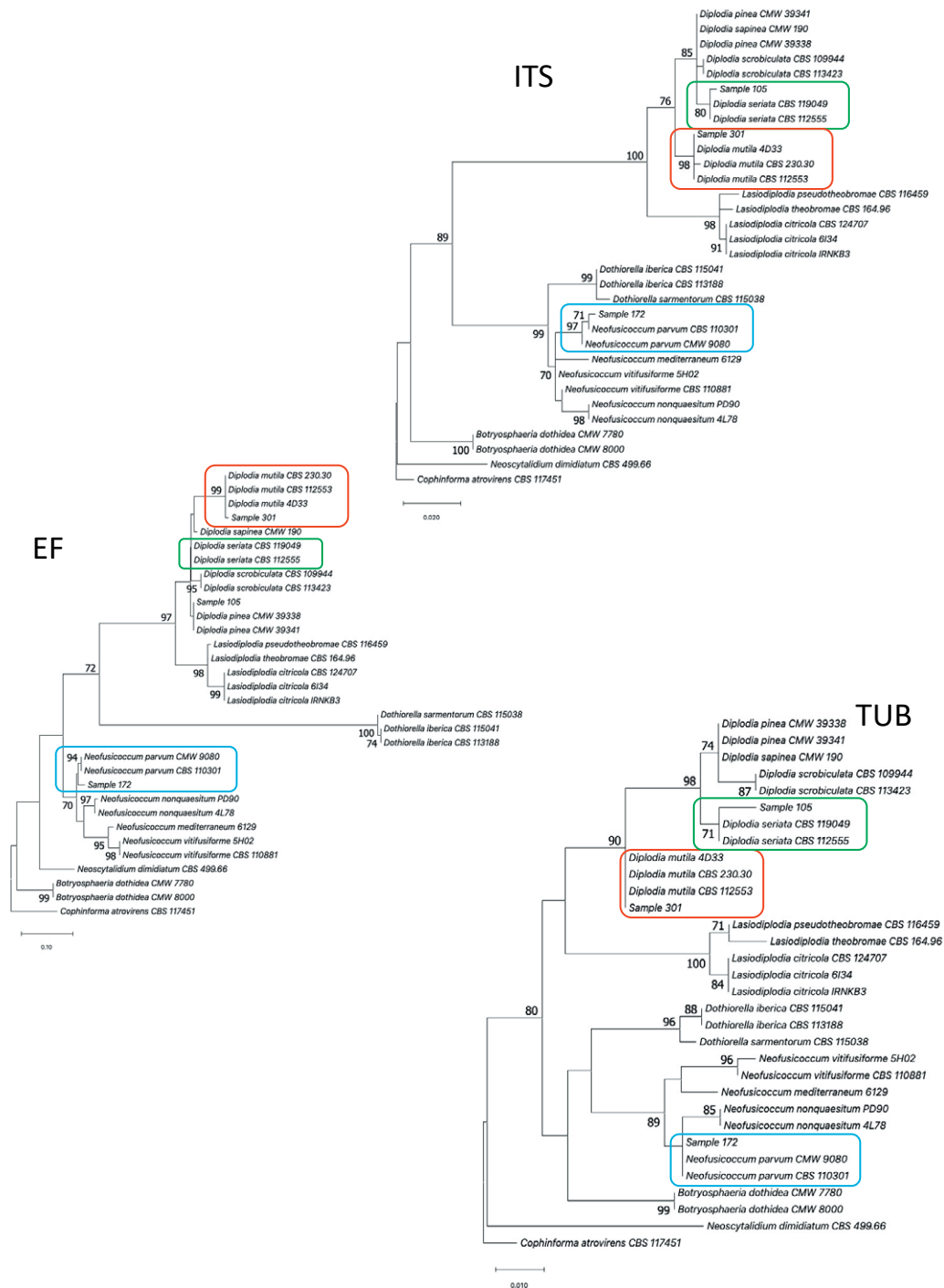


Figure S1. Best Maximum Likelihood trees for separate partitions of *Botryosphaeriaceae*.

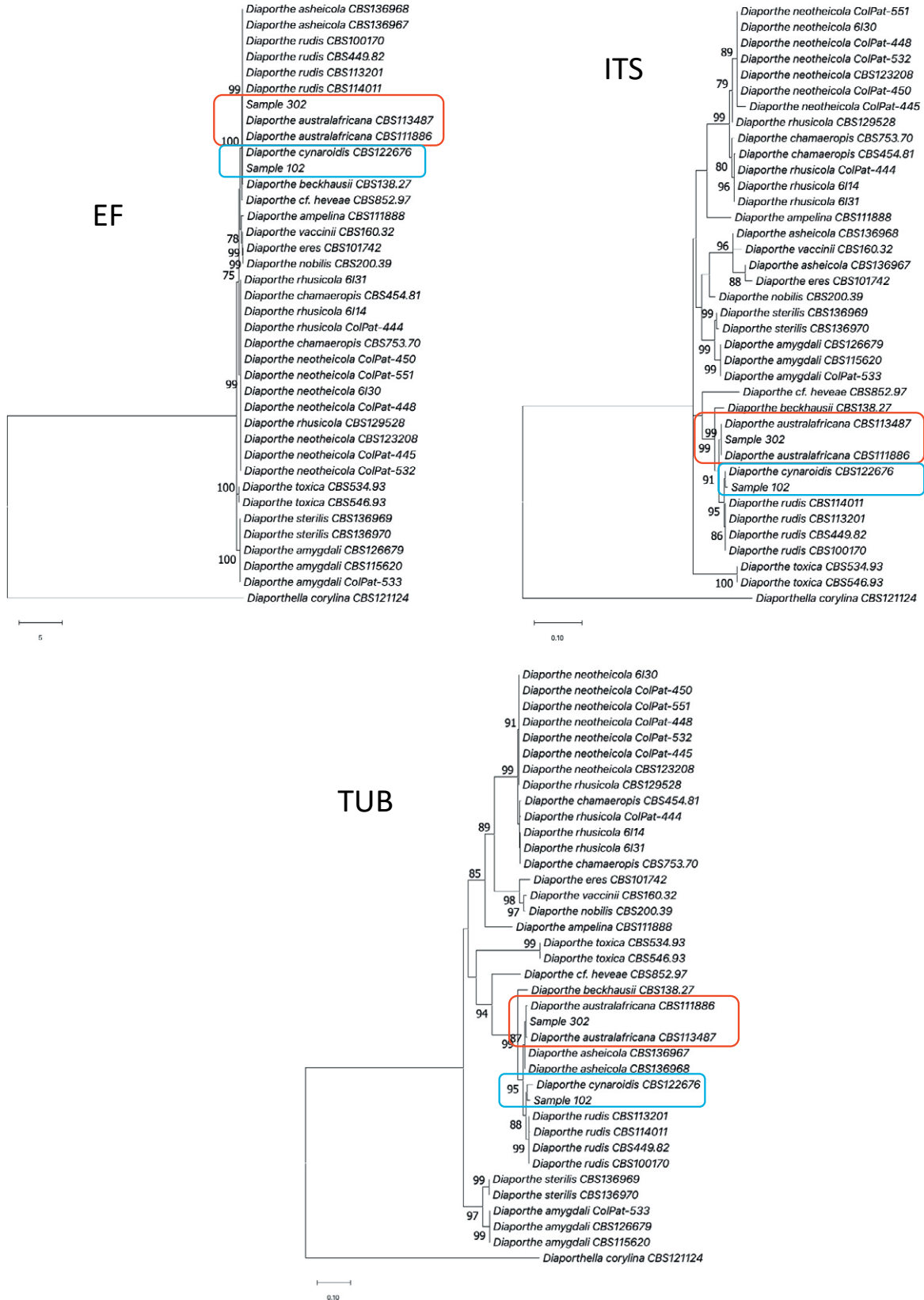


Figure S2. Best Maximum Likelihood trees for separate partitions of *Diaporthaceae*.

**Table S1.** Bootstrap support values for respective species clades containing our fungal samples in the best trees inferred using Maximum Likelihood. Support values are given for clades in each gene partition separately (ITS, EF and TUB) and for the entire concatenated region. The concatenated region provided strong bootstrap support for the taxonomic identity of all five fungal isolates. Although individual gene regions often showed lower bootstrap support, their topologies did not conflict with the that of the concatenated phylogeny.

Family	Isolate	Closest species	Bootstrap support [%]			
			ITS	EF	TUB	Concatenated
<i>Diaporthaceae</i>	Sample 102	<i>Diaporthe cynaroidis</i>	<70	100	<70	95
<i>Diaporthaceae</i>	Sample 302	<i>Diaporthe australafricana</i>	99	<70	<70	95
<i>Botryosphaeriaceae</i>	Sample 105	<i>Diplodia seriata</i>	80	<70	71	91
<i>Botryosphaeriaceae</i>	Sample 172	<i>Neofusicoccum parvum</i>	97	<70	<70	99
<i>Botryosphaeriaceae</i>	Sample 301	<i>Diplodia mutila</i>	98	99	<70	100