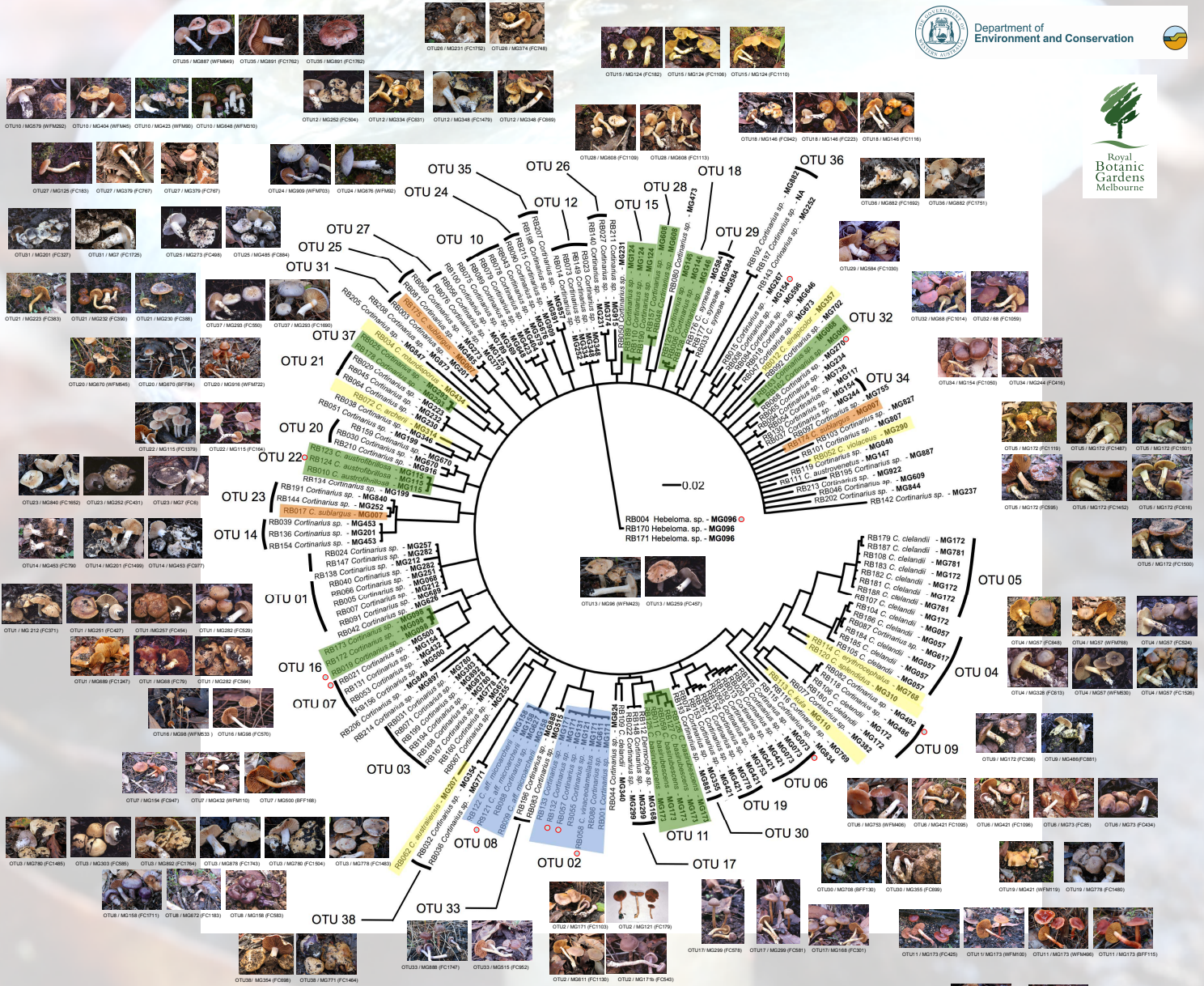


Comparing morphological species as used in ecological surveys against molecular barcoding with the ITS region: a case study of *Cortinarius* in the south-west of Western Australia. II. An illustrated phylogenetic tree.

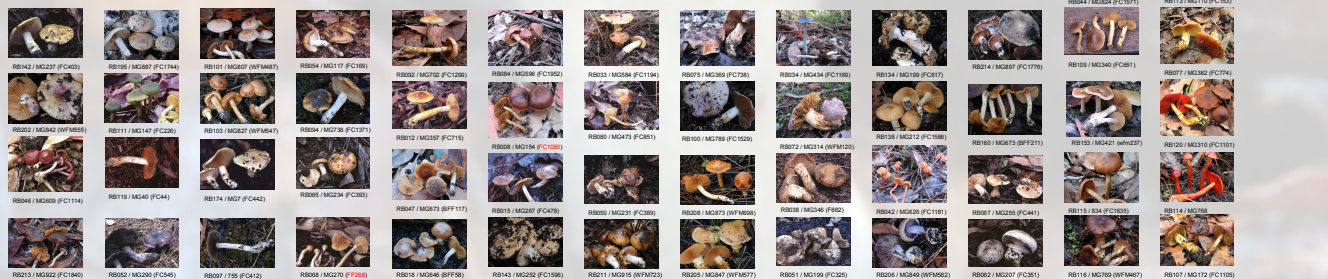
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Molecular species represented by single collections:



Tree based on phylogenetic analysis of ITS sequences of 178 collections of *Cortinarius* (including outgroup, *Hebeloma* sp. MG96). Each collection has collection (RB) number followed by morpho-species group (MG) designation. Eight of the multi-collection morpho-species formed an exclusive clade (OTU- operational taxonomic unit), such as *C. austrofibriolus*, *C. basirubescens* and *C. sp.* including MG98, MG124 and MG293 [green highlight]; 10 multi-collection morpho-species were mixed with other species or singletons, as in clade 2 (which consisted of the four collections of *C. vinaceolamellatus*, along with the single collections of each of *C. sp.* MG121, MG131 and MG611) and clade 8 (which consisted of the three collections of *C. microarcheri* along with the single collection of *C. sp.* MG627) [blue highlight]; and the remaining 13 multi-collection morpho-species were split across more than one clade (as in *C. sublargus* and *C. sp.* MG421) or formed several singletons (as in *C. sp.* MG199) [orange highlight]. About half of the original 86 singleton morpho-species remained as singletons in the molecular analysis, such as *C. archeri*, *C. australensis*, *C. erythrocephalus*, *C. kula*, *C. splendidus*, *C. rotundisporus*, *C. sinapicolor*, *C. violaceus* [yellow highlight]. No photo for collection (○).