

Phylogenetic analysis of South American *Berberis* species and their related rust fungi

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Introduction: New races of both *Puccinia graminis* and *P. striiformis* are frequently reported throughout the world. Sexual recombination on a susceptible *Berberis* species host may have produced some of these new reported races, or could generate future new races. The two centers of diversity of simple-leaved *Berberis* are South American and Asia. In 2016 and 2017, we sampled and sequenced both *Berberis* and *Berberis* infected with rust fungi in South America from a) the *Aequinoctiales Berberis* subgroup¹ in Ecuador and b) the *Euaustales Berberis* subgroup¹ in Argentina, Brazil, Chile, and Uruguay.

Methods: *Berberis* leaves and rust pustules (when available) were collected and sent to Ag Canada for sequencing. Ecuadorian samples were also sequenced in Ecuador. Phylogenetic analysis was done in Ecuador. ITS sequence data is presented.

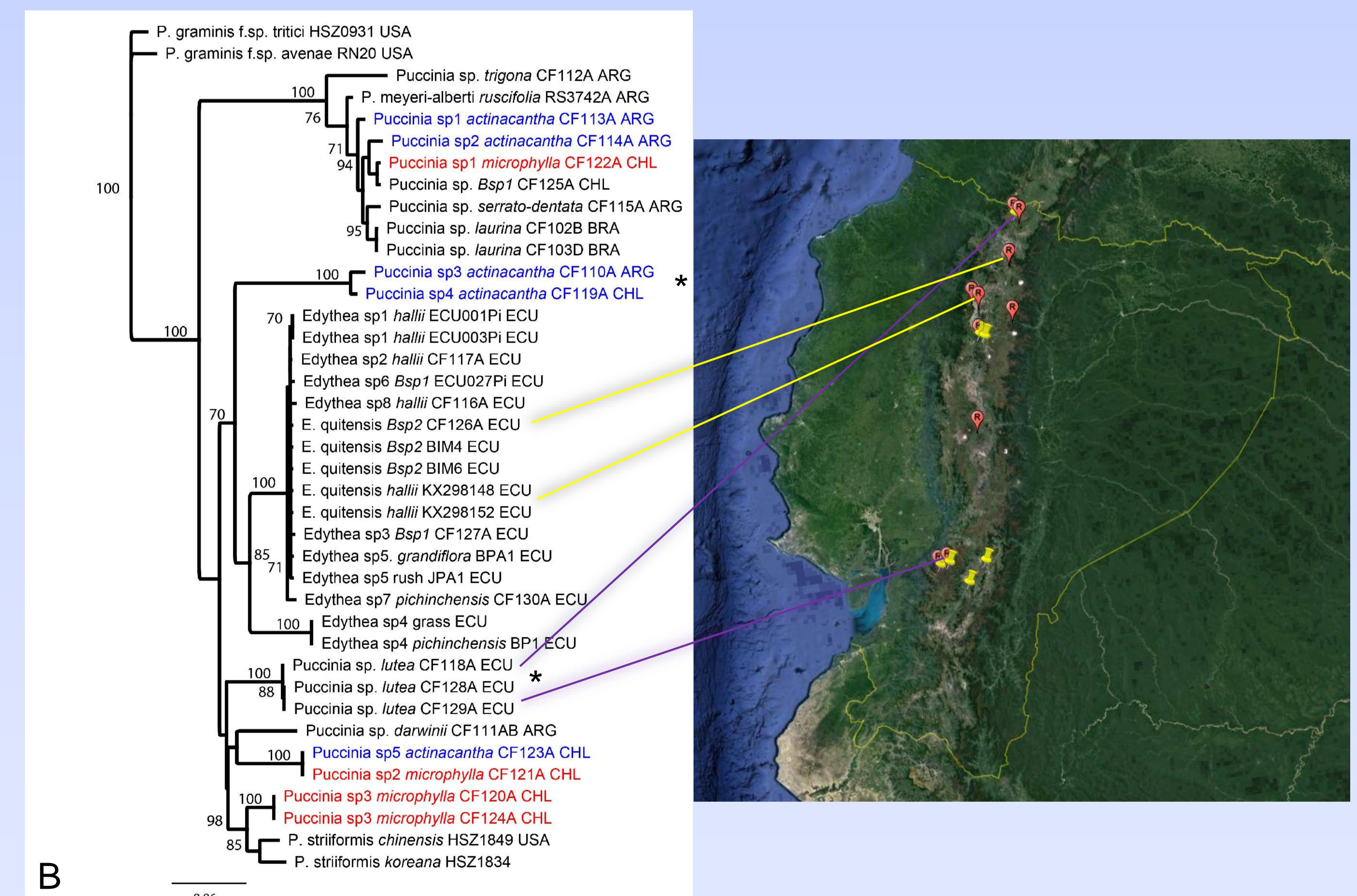
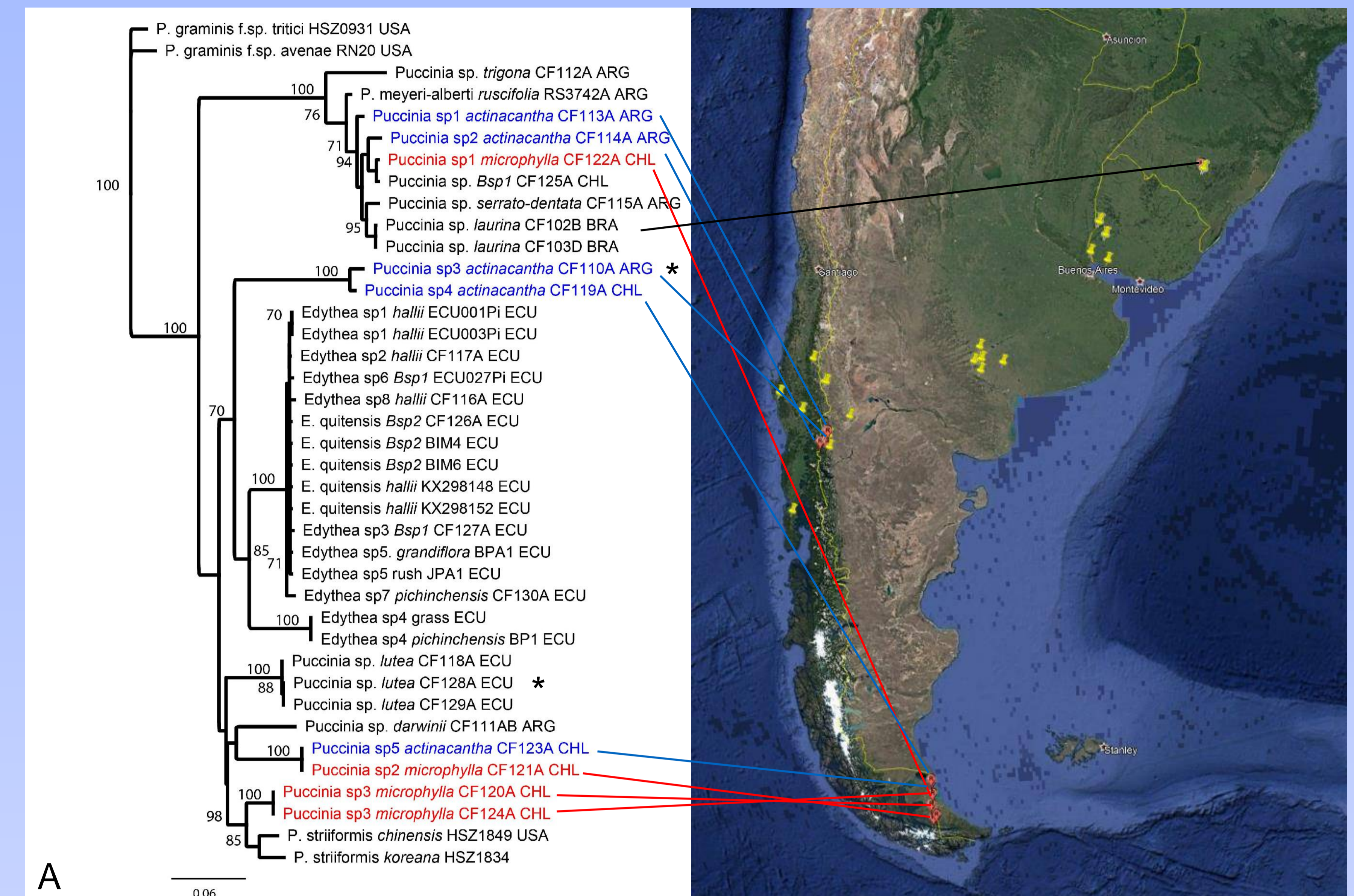
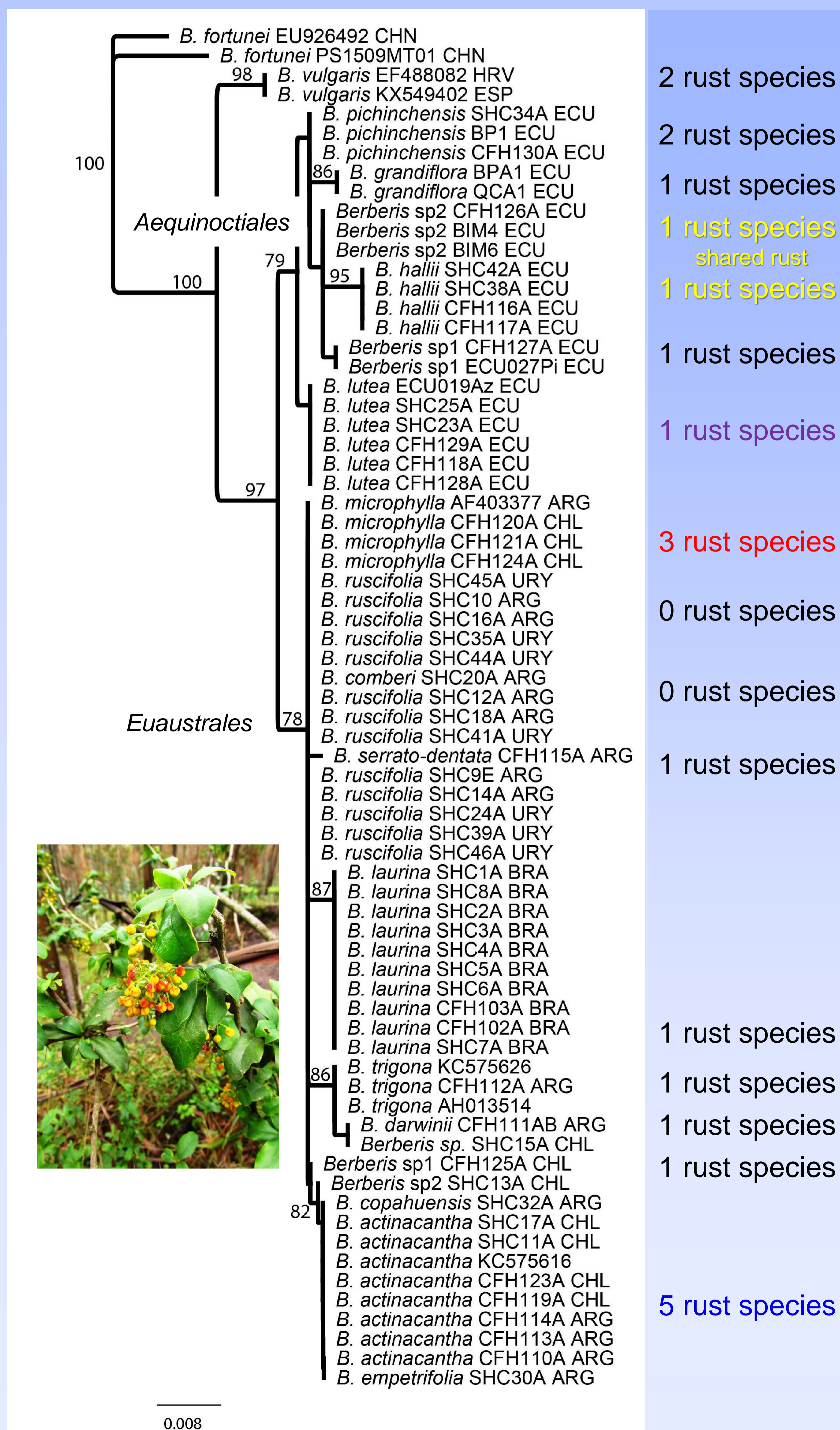


Fig. 2. Phylogenetic analysis of the rust collected on *Berberis* species in South America. Sample names are: the rust name, *Berberis* species, collection #, 3-letter country code. A) rusts from the *Euaustales Berberis*, B) from the *Aequinoctiales Berberis*. 📍 represent CFH samples 📍 represent SCH samples from Fig. 1. Rust species on most widely distributed *Berberis* do not fit the *Aequinoctiales/Euaustales* plant subgroup pattern (* in Fig 2 A and B).

Results To date we have sequence for 14 named and 4 un-named *Berberis* species, and 22 rust species, with none of the rusts identified as *P. graminis* or *P. striiformis*. Most *Berberis* species have one rust pathogen, one *Berberis* species has 5 rust pathogens, and one rust pathogen was found on 2 *Berberis* species. The rust fungi generally mimic the phylogenetic clades of the host, except in the case of rust species on *B. actinacantha* and *B. lutea*.

Acknowledgments 1) Kim, Y.-D., Kim, S.-H., & Landrum, L. (2004). Funding from AAFC Project #J-001312 and Pontificia Universidad Católica del Ecuador. We thank Quinn Eggertson (AAFC-Ottawa), and Diana Flores (Universidad Católica) for technical assistance.