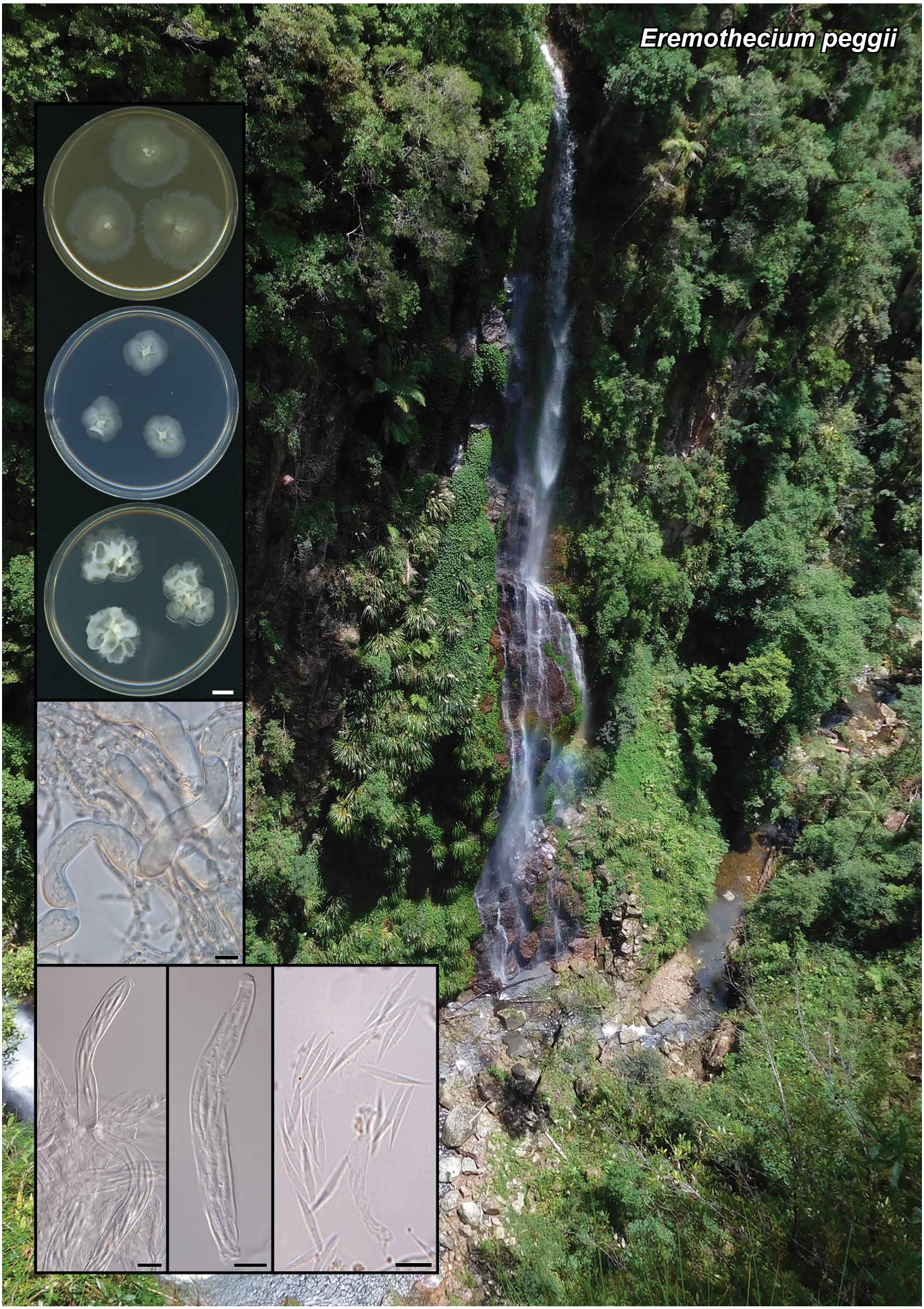

Eremothecium peggii

Fungal Planet 1248 – 13 July 2021

Eremothecium peggii R.G. Shivas, Marney, Cunningt. & Y.P. Tan, *sp. nov.*

Etymology. Named after Kenneth G. Pegg, an eminent Australian plant pathologist, from whose garden the fungus was first collected.

Classification — *Eremotheciaceae*, *Saccharomycetales*, *Saccharomycetes*.

Mycelium composed of filamentous hyphae, budding cells lacking. *Hyphae* coenocytic without true septa, undulate or straight walls, with abundant localized dense cytoplasmic regions, 2–9 µm wide, branches often at right angles, hyaline. *Asci* form directly from hyphae, mostly intercalary and aligned in chains, occasionally terminal or lateral, with a narrow base 3–5 µm wide, when immature cytoplasmic contents distinctively concave at base and separate from hyphal cytoplasm, irregularly sinuous to clavate-cylindrical, rounded at apex, hyaline, (20–)40–75(–120) × 8–18 µm, with 16 or 32 ascospores, splits irregularly. *Ascospores* acicular, straight or slightly curved, 15–21 × 1.5–2 µm, hyaline, widest at a narrow faint hyaline band near the middle, narrow to a truncate base less than 0.5 µm wide, arranged in the ascus in two (or four) opposed bundles of eight spores with apices pointed at the poles, germinate by a perpendicular or oblique germ tube at swollen mid-point.

Culture characteristics — On malt yeast extract peptone glucose agar after 4 wk in the dark at 25 °C, colonies 2–3.5 cm diam, flat, dull, dry, translucent, margin filamentous and irregular, raised, tenacious in their consistency.

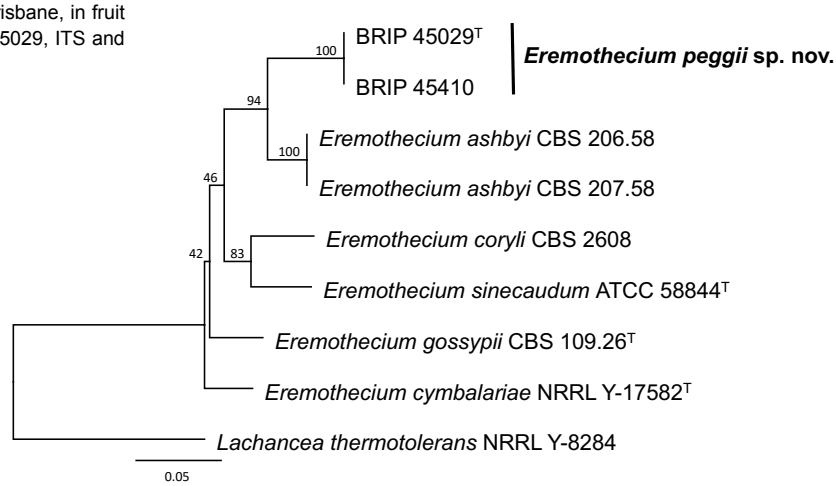
Typus. Australia, Queensland, Brisbane, in fruit of *Citrus australis*, 12 July 2004, *K.G. Pegg* (holotype BRIP 45029, culture ex-type BRIP 45029, ITS and LSU sequences GenBank MW442983 and MW442985, MycoBank MB 838410).

Additional material examined. Australia, Queensland, Brisbane, in fruit of *Citrus australis*, 26 July 2004, *K.G. Pegg* (culture BRIP 45029, ITS and LSU sequences GenBank MW442982 and MW442984).

Colour illustrations. Sub-tropical rainforest, Lamington National Park. Colonies of *E. peggii* on V8 agar (top), potato dextrose agar (middle) and malt yeast extract peptone glucose agar (bottom) after 4 wk in the dark at 25 °C; hyphae differentiating into asci, asci; ascus, ascospores. Scale bars = 1 cm (top), other = 10 µm.

Notes — The *Eremotheciaceae* is a monophyletic group of species that have needle-shaped ascospores (Kurtzman 1995). *Eremothecium* contains five species, *E. ashbyi*, *E. coryli*, *E. cymbalariae*, *E. gossypii* and *E. sinecaudum*, that are characterised by acicular ascospores (https://theyeasts.org, Kurtzman & Robnett 2003). One of these, *E. coryli*, has been associated with fruit dry rot in cultivated and indigenous *Citrus* in Australia (Shivas et al. 2005). During that study, *Eremothecium peggii* was isolated from fruit with dry rot of *Citrus australis* (Dooja, round lime), which is native to subtropical rainforest in New South Wales and Queensland, Australia. All species of *Eremothecium* are considered as plant pathogens, although the pathogenicity of *E. peggii* as the cause of fruit dry rot has not been demonstrated.

Based on a BLASTn search of NCBI GenBank nucleotide database, the closest hit against **LSU** sequences ex-type specimens were *E. cymbalariae* (strain NRRL Y-17582, GenBank NR_042628.1, Identities 854/884 (97 %), Gaps = 4 (0 %)); *E. sinecaudum* (strain ATCC 58844, GenBank XR_001930265.1, Identities 867/898 (97 %), Gaps = 5/898 (0 %)); and *E. gossypii* (strain CBS 109.26, GenBank NG_063967.1, Identities 863/899 (96 %), Gaps = 5/899 (0 %)). The closest hit against **ITS** sequences ex-type specimens was *Kluyveromyces aestuarii* (ex-type strain CBS 4438; GenBank NR_165976.1; Identities 208/218 (95 %), Gaps = 1 (0 %)).



Phylogenetic tree of *Eremothecium* species based on a maximum likelihood analysis of a combined multilocus alignment (ITS and LSU). Analyses were performed on the Geneious v. 11.1.2 platform (Biomatters Ltd.) using RAxML v. 8.2.11 (Stamatakis 2014) and MrBayes v. 3.2.6 (Ronquist & Huelsenbeck 2003), both based on the GTR substitution model with gamma-distribution rate variation. Branch lengths are proportional to distance. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). *Saccothecium rubi* and *S. sepincola* were used as outgroups. Novel taxa are indicated in **bold**. Ex-type strains are marked with T.

Roger G. Shivas, Centre for Crop Health, University of Southern Queensland, Toowoomba 4350, Queensland, Australia; e-mail: roger.shivas@usq.edu.au
Thomas S. Marney & Yu Pei Tan, Queensland Plant Pathology Herbarium, Department of Agriculture and Fisheries, Dutton Park 4102, Queensland, Australia; e-mail: thomas.marney@daf.qld.gov.au & yupei.tan@daf.qld.gov.au
James H. Cunnington, Department of Agriculture, Water and the Environment, Canberra 2600, Australian Capital Territory, Australia; e-mail: james.cunnington@awe.gov.au