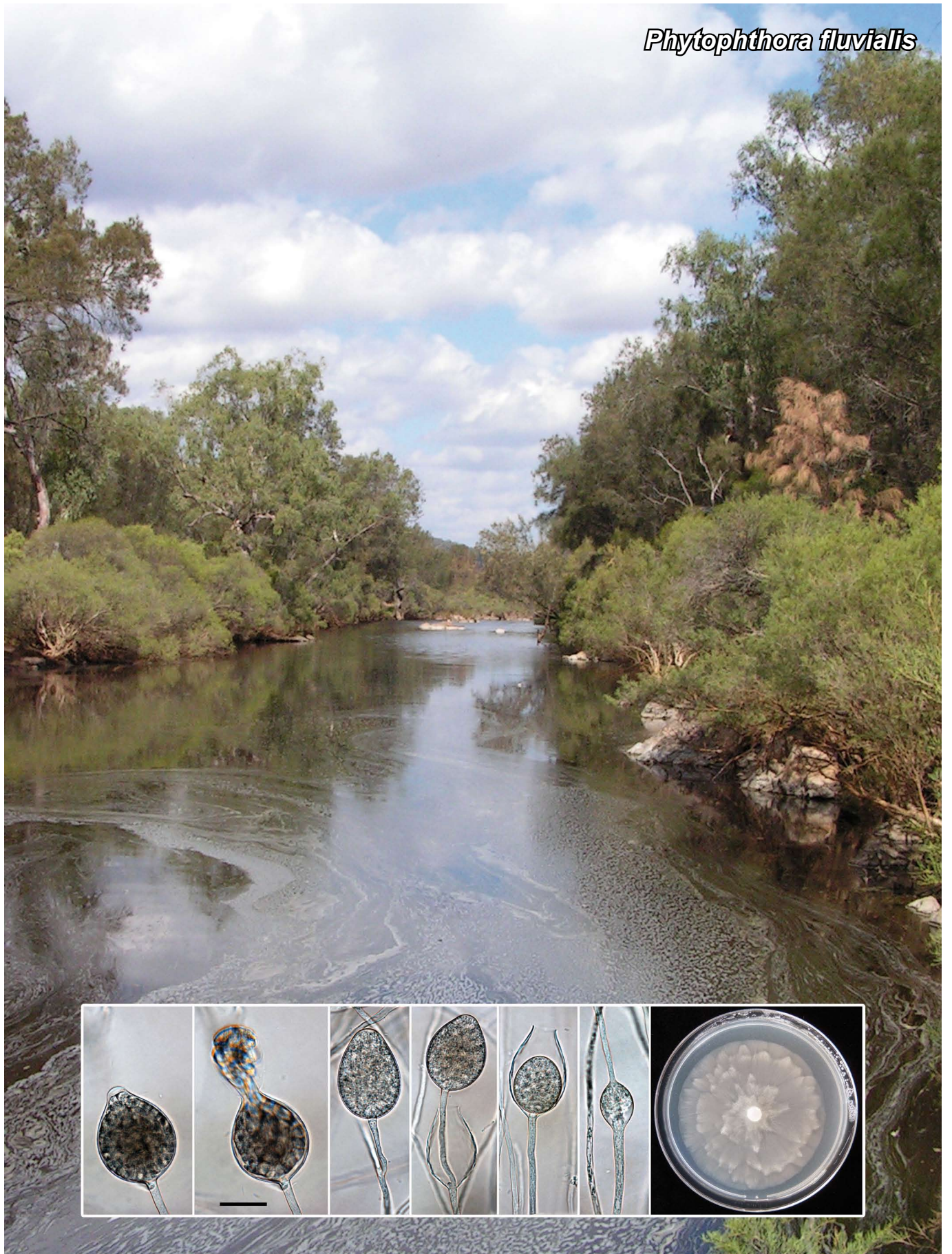


Phytophthora fluvialis



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Phytophthora fluvialis T. Jung & T.I. Burgess, *sp. nov.*

Phytophthorae litoralis similis, sed inflationibus hypharum non catenulatis et sine hyphis radiatis, sporangiis in medio maioribus ($53 \times 36.4 \mu\text{m}$), chlamydosporis nullis et caelis optimis (31.5°C) et maximis (37.5°C) altioribus. Regiones 'rDNA ITS', 'LSU', 'cox1' et 'HSP' cum sequentibus unicus (GenBank JF701436, JF951171, JF701442, JF701439).

Etymology. Named for the riparian ecosystems from which all isolates were recovered.

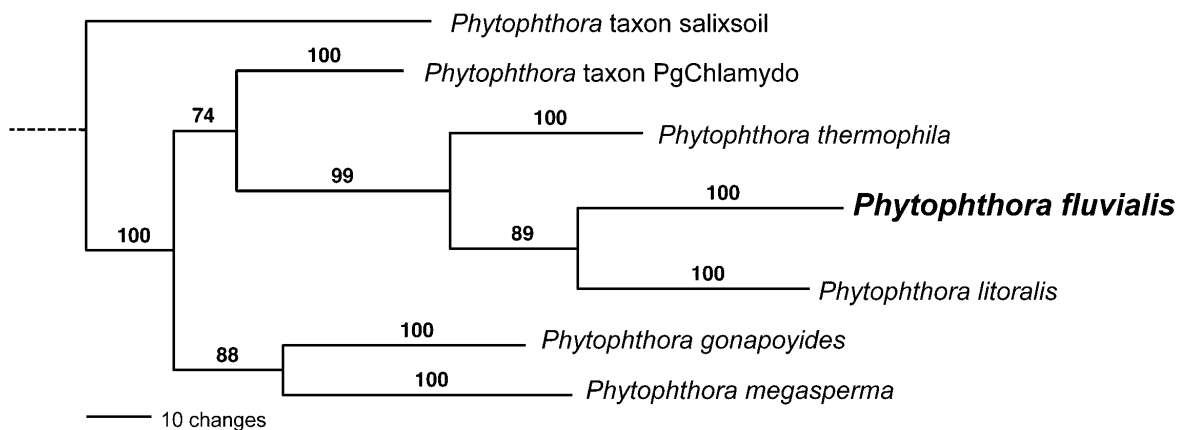
Sporangia produced abundantly in non-sterile soil extract, non-caducous, nonpapillate, broad-ovoid to elongated ovoid, limoniform or less frequently ellipsoid or obpyriform; $53 \pm 7.6 \times 36.4 \pm 6.1 \mu\text{m}$ (overall range $37\text{--}72 \times 21\text{--}54 \mu\text{m}$), length/breadth ratio 1.5 ± 0.2 . **Sporangial proliferation** external and in chains of internally proliferating sporangia in both a nested and extended way; secondary lateral sporangia regularly formed. Internally proliferating sporangiophores, sometimes branching inside or just outside of the empty sporangium. Diplanetism of zoospore cysts and the formation of microsporangia common in all isolates. Ellipsoid non-catenulate hyphal swellings ($12.1 \pm 4.7 \mu\text{m}$) without radiating hyphae infrequently formed. **Chlamydospores** not observed. **Gametangia** not produced in single culture or when paired with A1 and A2 tester strains of *P. cinnamomi*. Radial growth rates on V8 agar at optimum (31.5°C) and near the maximum (38°C) temperature $5.9 \pm 0.6 \text{ mm/d}$ and $1.2 \pm 0.2 \text{ mm/d}$, respectively.

Culture characteristics — Colonies on carrot agar (CA), V8A and potato-dextrose agar are stellate to rosaceous with limited aerial mycelium.

Typus. WESTERN AUSTRALIA, Moore River, baited from water in native bushland, Dec. 2009, *D. Hüberli*, holotype MURU 468; cultures ex-type CBS 129424 = MUCC 771, ITS sequence GenBank JF701436, *cox1* sequence JF701442, HSP90 sequence JF701439 and LSU sequence GenBank JF951171, MycoBank MB561042.

Additional specimens examined. WESTERN AUSTRALIA, Moore River, baited from water in native bushland, Dec. 2009, *D. Hüberli*, MUCC 772; Badgin-garra, baited from water in native bushland, 2007, collected by *Gjevan Consulting*, VHS17350.

Notes — Phylogenetically, *P. fluvialis* shares a common ancestor with *P. litoralis* and resides in a strongly supported cluster along with *P. thermophila*. In a multigene phylogeny of the ITS, HSP90 and *cox1* gene regions, *P. fluvialis* differs from *P. litoralis* by 77 steps (2.65%), *P. thermophila* by 91 steps (3.13%) and from the next closest relative, *P. taxon PgChlamydo*, by 116 steps (3.99%). *Phytophthora fluvialis*, *P. litoralis* and *P. thermophila* have all been isolated from waterways north of Perth in Western Australia (Jung et al. 2011). *Phytophthora fluvialis* has a similar life strategy to *P. litoralis*, being sterile and having abundant and continuous asexual multiplication in watercourses via chains of nested and extended internally proliferating sporangia, external proliferation, the production of secondary lateral sporangia and the frequent germination of cysts by releasing secondary zoospores (diplanetism) or by forming microsporangia. These two species can be separated by the absence of catenulate hyphal swellings and chlamydospores in *P. fluvialis*, the higher maximum temperature for growth of *P. fluvialis* (38°C) compared with *P. litoralis* (35°C) and the production of smaller sporangia in *P. litoralis* (av. $43.6 \pm 7.7 \times 29.4 \pm 5.4 \mu\text{m}$).



Colour illustrations. A typical river in Western Australia (T. Jung); ovoid sporangium just before and during release of zoospores; ovoid, secondary lateral sporangium; extended proliferation of nonpapillate sporangium; nested proliferation; ellipsoid hyphal swelling (T. Jung). Scale bar = 25 μm . Rosaceous colony on carrot agar (T.I. Burgess).

One of three most parsimonious trees (TL = 371; CI = 0.78; RI = 0.89; RC = 0.70) obtained from a heuristic search with 100 random taxon additions of a combined ITS, *cox1* and HSP90 sequence alignment using PAUP v4.0b10 (Swofford 2003). The scale bar shows 10 changes, and bootstrap support values from 1 000 replicates are shown at the nodes. Three isolates of each species were included in the analysis. The species described here is printed in **bold face**. The tree was rooted to *Phytophthora inundata* (not shown). The alignment and tree is available in TreeBASE (Accession SN11399).

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