

Phytophthora moyotij



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***Phytophthora moyootj* T.I. Burgess, sp. nov.**

Etymology. Named for the swamp or wetlands from which isolates were recovered (moyootj = swamp country in the local Aboriginal Nyoongar language).

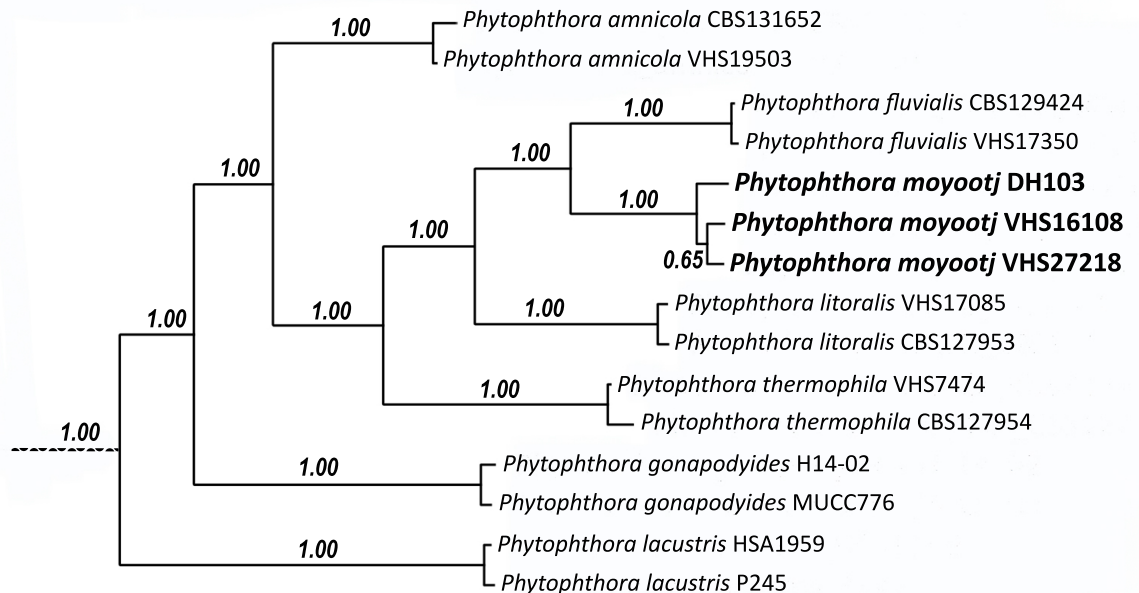
Sporangia produced abundantly in non-sterile soil extract; non-caducous, non-papillate with long unbranched sporangiophores, most commonly ovoid (63 %), with broad ovoid (11.5 %), limoni-form (9 %), elongated ovoid (8.5 %), globose (5 %) and mouse shapes (3 %) also found; $39.6 \pm 10.8 \times 26.5 \pm 4.2 \mu\text{m}$ (overall range $18\text{--}73.3 \times 18.3\text{--}38.4 \mu\text{m}$), length/breadth ratio 1.5 ± 0.4 . **Sporangial proliferation** in chains of internally proliferating sporangia, both nested and extended. **Hyphal swellings** absent although rarely sporangia failed to produce septa and these then continued to grow from the apex to produce 'sporangia shaped' swellings. **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 temperature (25–30 °C) and near the maximum temperature (32.5 °C), $5.5 \pm 0.5 \text{ mm/d}$ and $0.8 \pm 0.1 \text{ mm/d}$, respectively.

Culture characteristics — Colonies have a stellate pattern on carrot agar and V8 agar and a fluffy irregular pattern on potato dextrose agar.

Typus. AUSTRALIA, Western Australia, Walpole, mud from vehicle, 2012, collected by Department of Parks and Wildlife (holotype MURU 469, cultures ex-type CBS 138759 = VHS27218; ITS sequence GenBank KJ372256, β -tubulin sequence GenBank KJ372303, HSP90 sequence GenBank KJ396730, *cox1* sequence GenBank KJ396702, NADH sequence GenBank KJ396681, LSU sequence GenBank KP004501, MycoBank MB809152).

Additional specimens examined. AUSTRALIA, Western Australia, Fitzgerald River National Park, baited from soil in native heathland, 2006, collected by Department of Parks and Wildlife, VHS16108; Jarrahdale, isolated from water from restored pit at mine site, 2012, *D. Hüberli*, DH103.

Notes — Phylogenetically, *P. moyootj* resides in a strongly supported terminal clade and shares a common ancestor with *P. fluvialis*, *P. litoralis* and *P. thermophila* (Jung et al. 2011, Crous et al. 2011, 2012a). In a multigene phylogeny of the ITS, HSP90, BT, NADH and *cox1* gene regions, *P. moyootj* differs from *P. fluvialis* by 87 bp (1.8 %), *P. litoralis* by 107 bp (2.3 %) and *P. thermophila* by 118 bp (2.6 %). These four species have all been isolated from waterways and wetlands in the south-west of Western Australia. *Phytophthora moyootj* has a life strategy similar to *P. litoralis* and *P. fluvialis*, being sterile in culture and having abundant and continuous asexual multiplication chains of nested and extended internally proliferating sporangia. *Phytophthora moyootj* can be separated from these species because it lacks external proliferation of sporangia and hyphal swellings and it has lower optimum and maximum temperatures for growth.



Colour illustrations. Typical niche for recovery of *P. moyootj*; mature sporangia, ovoid, broad ovoid, ovoid just before release of zoospores, nested proliferation, empty sporangia with trapped encysted zoospores, internal nested and extended proliferation. Scale bar = 25 μm . Stellate colony on V8 agar (T.I. Burgess).

Bayesian inference tree based on concatenated ITS, BT, HSP90, *cox1* and NADH sequence alignment generated in MrBayes using the GTR substitution model. The posterior probability is shown at the nodes. The species described here is printed in bold face. The tree was rooted to *P. humicola* (not shown). The alignment and tree are available in TreeBASE (Submission ID 15985).

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