Porodiplodia livstonae
Porodiplodiaceae Crous, fam. nov.

Classification — *Porodiplodiaceae*, Helotiales, Leotiomycetes.

*Conidiomata* eumastigous, uni- to multiocular, brown, globose, aggregated on agar, ostiolate, or hypomycetous, forming clusters of conidiophores. *Conidiophores* lining inner cavity of conidioma, subcylindrical, hyaline, smooth, branched, septate, proliferating percurrently near apex, or occurring in clusters on hyphae, septate, subcylindrical, with upper cells pigmented; conidigenous cells proliferating percurrently, or phialidic, with prominent collarettes. *Conidia* in chains, fusoid-ellipsoidal to subcylindrical, hyaline to medium brown, smooth to finely verruculose, guttulate, 0–1-septate.


Notes — The family *Porodiplodiaceae* presently contains two genera, namely *Porodiplodia* and a chalara-like fungus, *Chalara clidemiae* (see Crous et al. 2016b), as well as a strain identified as *Chalara africana* (OC0018).

Porodiplodia Crous, gen. nov.

Etymology. Name refers to a morphological similarity to the genus *Diplodia*, but with conidia having a minute basal pore in the hilum.

*Conidiomata* eumastigous, uni- to multiocular, brown, globose, aggregated on agar, ostiolate. *Conidiophores* lining inner cavity, subcylindrical, hyaline, smooth, branched, septate, proliferating percurrently near apex. *Paraphyses* intermingled among conidiophores, hyaline, smooth, septate, subcylindrical with obtuse ends. *Conidia* in short chains (–3), fusoid-ellipsoidal to subcylindrical, medium brown, finely verruculose, guttulate, thick-walled, 1-septate, apex obtuse (at times with central pore), base truncate with central pore, 2 µm diam.

Type species. *Porodiplodia livistonae* Crous. MycoBank MB825420.

Porodiplodia livistonae Crous, sp. nov.

Etymology. Name refers to the host genus *Livistona* from which it was isolated.


Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 17 mm diam after 2 wk at 25 °C. On MEA surface saffron, reverse cinnamon. On OA surface cinnamon, with diffuse cinnamon pigment.

**Type. Australia.** New South Wales, Murramarang National Park, on leaves of *Livistona australis* (Arecaceae), 27 Nov. 2016, P.W. Crous (holotype CBS H-23574, culture ex-type CPC 32154 = CBS 144428, ITS and LSU sequences GenBank MH327809.1 and MH327845.1, MycoBank MB825421).

Notes — A genus that should be compared to *Porodiplodia* is the monotypic genus *Hendersonina*, based on *H. sacchari*. *Hendersonina sacchari* is a fungus that has been implicated with collar rot of sugarcane, though it is accepted to be of minor importance (Nyyväl 2013). The morphology of the monotypic genus *Hendersonina* has remained somewhat confused. Sutton (1980) described the conidioma as eumastigous, but showed conidia as being fusoid to somewhat cylindrical, 1-septate, with a dark, thickened scar at each end (conidia from different specimens given as 21–28 × 5.5–9.5 µm, 19–29 × 4–5 µm, 17–24 × 4–5 µm). The conidiogenesis was described and illustrated as (not observed in original material) enteroblastic, phialidic, with prominent periclinal thickening. The matter was further confused in that Butler & Khan (1913) also referred to hyaline, asceptate secondary conidia.

The two species of *Porodiplodia* studied here in culture are characterised by eumastigonic conidiomata, and conidia occurring in short chains. Although a pore was observed at both ends in several conidia, this was rather uncommon. They were never thickened and darkened, and were found only in secondary and tertiary conidia. *Porodiplodia* differs from *Hendersonina* due to its branched conidiophores, conidia lacking scars, and being conspicuously 1-septate (septa in *Hendersonina* are thin-walled). It differs from other genera allied to *Diplodia* (Phillips et al. 2013, Yang et al. 2017) in having conidia occurring in short chains, with visible central pores in their hila.

Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Chalara clidemiae* (GenBank NR_145313.1; Identities = 521/540 (96 %), 1 gap (0 %)), *Mollisia caespiticia* (GenBank KY965813.1; Identities = 496/531 (93 %), 2 gaps (0 %)) and *Pezizella discreta* (GenBank JF908571.1; Identities = 509/550 (93 %), 3 gaps (0 %)). Closest hits using the LSU sequence are *Chalara clidemiae* (GenBank KX228321.1; Identities = 864/871 (99 %), no gaps), *Chalara africana* (GenBank FJ176249.1; Identities = 840/885 (98 %), 2 gaps (0 %)) and *Urceolella crispula* (GenBank JNO86682.1; Identities = 859/892 (96 %), 1 gap (0 %)).