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First report of the smut fungus *Ustanciosporium appendiculatum* in Australia

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Abstract. *Ustanciosporium appendiculatum* was collected on *Rhynchospora exserta* from northern Western Australia in May 2009. The identification is based on morphological and sequence data which are presented for the first time. This is the first report of this smut fungus outside North America. *Rhynchospora exserta* is a new host species for this smut fungus.

Rhynchospora is a genus of sedges (Cyperaceae) with ~250–300 species worldwide with most diversity in tropical America (Thomas *et al*. 2009). In Australia there are ~17 species (~5 species endemic) (Wilson 2009). Vánky and Shivas (2008) list three species of smut fungus on *Rhynchospora* spp. in Australia, viz. *Cintractia amazonica* Syd. & P. Syd., *Leucocintractia scleriae* (DC) M. Piepenbr., Begerow & Oberw. and *Trichocintractia utriculicola* (Henn.) M. Piepenbr. During a survey of smut fungi in northern Western Australia in May 2009 a smut fungus was collected on *R. exserta* unlike any known from Australia. A specimen was deposited as BRIP 52556. At the same location plants of *R. exserta* were also infected with *Cintractia amazonica* Syd. & P. Syd. (deposited as BRIP 52535).

The smut was identified as a member of *Ustanciosporium* by morphological and molecular methods. Morphologically it matched the description of *U. appendiculatum* M. Piepenbr., which characteristically has spores with two conspicuous appendages, one on each flattened side as illustrated by light microscopy (Fischer 1953; as *Cintractia montagnei* (Tul.) Mag.) and by scanning electron microscopy (Piepenbring 2000).

Worldwide there are ~25 species of *Ustanciosporium*, of which ~17 occur on *Rhynchospora* (Vánky 2006). Vánky (2006) noted that mixed infections of *Ustanciosporium* spp. on *Rhynchospora* were frequently found and that this had caused numerous taxonomic and nomenclatural problems. Vánky (2006) raised the possibility that the *U. montagnei* complex, to which *U. appendiculatum* belongs, may comprise several morphologically similar species. Further molecular studies may help resolve this.

DNA was extracted following the protocol of the Qiagen Puregene Extraction Kit and the ribosomal internal transcribed spacer (ITS) region was amplified by polymerase chain reaction using conditions and primers described in White *et al*. (1990). A DNA specimen of *U. appendiculatum* has been stored in the Biosecurity Bank (http://www.biosecuritybank.com/), and the ITS sequence has been deposited in GenBank (GQ888733).

This is the first report of *U. appendiculatum* outside North America. A brief description of the Australian specimen (BRIP 52556) follows.

U. appendiculatum M. Piepenbr., *Nova Hedwigia* 70: 331 (2000).

Type on *Rhynchospora capitellata*, USA, Massachusetts, Plymouth Co., Plymouth, small pond near Fearing Pond, 7 Aug. 1936, F.C. Seymour 4857 (as *Cintractia montagnei*), M; isotype in NY.

Sori in all the spikelets of an inflorescence, black, powdery. Spores subglobose, ellipsoidal, or irregularly polygonal, flattened in lateral view, 13.0–18.5 × 10–15 µm, reddish brown, foveolate, smooth in profile, with sporogenous wall material (appendages) attached opposingly on the two flattened sides; wall even, 0.7–1.0 µm thick. Appendages attached to the spores or detached from them, globose to subglobose, 4–8 × 4–7 µm, pale yellowish brown.

Material examined: On *Rhynchospora exserta* C.B. Clarke, Western Australia, 35 km N of Drysdale River Station, alt. ~377 m, 17 May 2009, A.R. McTaggart, V.L. Challinor, M.J. Ryley, C.F. Gambley, T. Scharaschkin, M.D.E. and R.G. Shivas, BRIP 52556 (Fig. 1).

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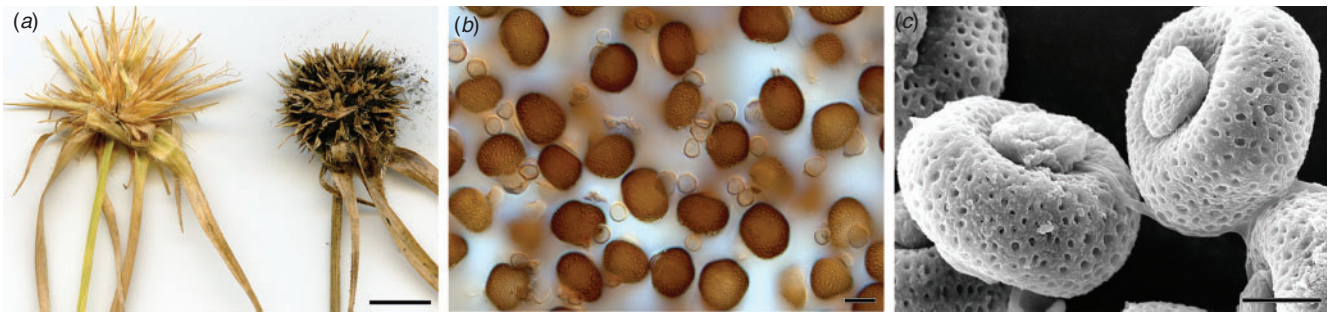

Fig. 1. *Ustanciosporium appendiculatum* (BRIP 52556). (*a*) Healthy inflorescence of *Rhynchospora exserta* (left), infected inflorescence (right). (*b*) Spores under light microscope and (*c*) scanning electron microscope. Bars = 1 cm (*a*), 10 µm (*b* and *c*).

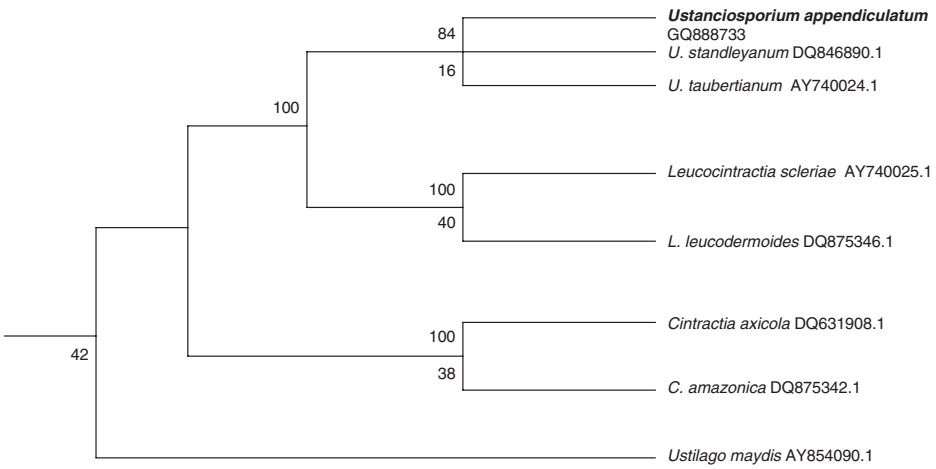

Fig. 2. Consensus tree obtained from a parsimony analysis on the ITS region. Bootstrap values from 1000 replicates shown above nodes and decay indices shown below nodes.

A Basic Local Alginment Search Tool (BLAST) search of the ITS DNA sequence data obtained for *Ustanciosporium appendiculatum* revealed an 89% sequence identity with *U. standleyanum* (Zundel) M. Piepenbr. (DQ846890.1) over 92% query coverage, and 81% similarity to *U. taubertianum* (Henn.) M. Piepenbr. & Begerow (AY740024.1) over 97% query coverage.

Analysis of the ITS region of *Ustanciosporium appendiculatum* and some closely related taxa from GenBank in an exhaustive maximum parsimony search using Phylogenetic Analysis Using Parsimony (PAUP)* v4.0b4 yielded two trees of equal length. The topologies of these trees were similar to a maximum likelihood analysis using PAUP* v4.0b4. A consensus tree of the parsimony analysis is shown in Fig. 2. *Ustanciosporium appendiculatum* is sister to two other *Ustanciosporium* species for which sequence data are available.

Acknowledgments

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