Two new species of *Ustilaginomycetes* on *Chrysopogon fallax* from Australia

Roger G. Shivas^{1*}, James H. Cunnington² and Kálmán Vánky³

¹Plant Pathology Herbarium, Queensland Department of Primary Industries and Fisheries, 80 Meiers Road, Indooroopilly, Queensland 4068, Australia

²Department of Primary Industries, Research and Development Division, Knoxfield, Private Bag 15, Ferntree Gully Delivery Centre, Victoria 3156, Australia

³Herbarium Ustilaginales Vánky (HUV), Gabriel-Biel-Str. 5, D-72076 Tübingen, Germany

Shivas, R.G., Cunnington, J.H. and Vánky, K. (2004). Two new species of *Ustilaginomycetes* on *Chrysopogon fallax* from Australia. Fungal Diversity 16: 147-156.

Sporisorium fallax sp. nov. (Ustilaginaceae, Ustilaginomycetes) is described and illustrated from inflorescences of Chrysopogon fallax collected in the Northern Territory, Australia. Ribosomal DNA Internal Transcribed Spacer sequences confirmed S. fallax to be distinct from two morphologically similar species, S. tumefaciens and S. tumiforme, on C. fallax. Macalpinomyces tubiformis sp. nov. (Ustilaginaceae, Ustilaginomycetes) is described and illustrated from ovaries of Chrysopogon fallax collected in Queensland, Australia.

Key words: *Macalpinomyces tubiformis, Sporisorium fallax, Sporisorium tumefaciens, Sporisorium tumiforme*, taxonomy, *Ustilaginaceae*.

Introduction

Recent studies have lead to the discovery and classification of several new species of smut fungi in Australia (Shivas and Vánky, 2001, 2002, 2003a,b; Vánky and Shivas, 2001a,b). Vánky (2004) recognised and designed a key for eight known species (two in *Macalpinomyces* and six in *Sporisorium*) of smut fungi (*Ustilaginomycetes*) on *Chrysopogon* (tribe *Andropogoneae*, subfamily *Panicoideae*, *Poaceae*). Three of these species, *Sporisorium andropogonis-aciculati* (Petch) Vánky, *Sporisorium tumefaciens* (McAlpine) Vánky and *Sporisorium tumiforme* Vánky, occur in Australia. The latter two species produce elongated, cylindrical sori that destroy the entire inflorescence of their hosts. Examination of specimens of *Sporisorium* on *Chrysopogon* spp. with similar sori held in Herbarium BRIP revealed another species that could not be ascribed to any of the species known to occur on *Chrysopogon*.

^{*} Corresponding author: Roger G. Shivas; e-mail: roger.shivas@dpi.qld.gov.au

Ribosomal DNA Internal Transcribed Spacer (ITS) region sequences have been previously used in the taxonomy and classification of *Ustilaginomycetes* (Boyd and Carris, 1997; Boyd *et al.*, 1998; Cunnington and Shivas, 2004). To confirm that this new species of *Sporisorium* was distinct from others occurring on *Chrysopogon fallax* in Australia, ITS sequences were obtained for this species and compared with those for *Sporisorium tumefaciens* and *S. tumiforme*. A new species of *Macalpinomyces* on *Chrysopogon fallax* S.T. Blake is also described and illustrated.

Materials and Methods

Pressed and dried specimens were used for studies of sorus structure and spore morphology. For light microscopy (LM) studies and spore measurements, dried spores were rehydrated in lactic acid by gently heating to boiling point. For scanning electron microscopy (SEM) studies, dried spores were dusted on double-sided adhesive tape, mounted on a specimen stub, sputter-coated with gold-palladium, *ca.* 20 nm, and examined in a SEM at 10 kV.

Six specimens of *Sporisorium*, all from *Chrysopogon fallax*, were used for molecular analysis (Table 1). DNA was extracted by grinding a small amount of spores (1 mm^3) in 50 µL of 5% Chelex-100 (Biorad). The material was spun down briefly in a microcentrifuge.

The initial PCR was performed in 25 µL containing 1 µL DNA extract, 200 µM of each dNTP, 1.5 mM MgCl₂, 2.5 µL 10× buffer, 4 ng each of primers ITSF1 (Gardes and Bruns, 1993) and **ITSUR** (TGTTCGCTATCGGTCTCTCC) (Cunnington and Shivas, 2004), and 0.5 units of Hotstar Taq (Qiagen). Reaction cycles were 15 minutes at 95°C, 35 cycles of: 30 second at 94°C, 30 seconds at 50°C, 1 minute at 72°C. A nested PCR was performed in 25 µL as outlined above, but using primers ITS5 (White et al., 1990) and ITSUR using 1 µL of the first round PCR product as template. PCR products were detected by running 4 μ L on a 1.4% agarose gel in TBE buffer. Nested PCR products were purified using a QIAquick PCR Purification Kit (Qiagen) and sequenced directly using primers ITS5 (White et al., 1990) and ITS4, with an ABI PRISM[®] BIGDYE[™] Terminator Cycle Sequencing Kit (Perkin-Elmer) according to the manufacturers instructions.

These sequences were aligned using ClustalX (Thompson *et al.*, 1997) and the ITS sequence for *Sporisorium reilianum* (GenBank accession AF135432) was included as an outgroup. A neighbour-joining tree was created using the Kimura-2-paramater method and a complete deletion of gaps using MEGA (Kumar *et al.*, 2001). 1000 bootstrap replicates were performed.

Species	Herbarium	Location in Northern	Date of	GenBank
	accession	Territory, Australia	collection	accession
S. fallax	BRIP 27687	268 km SE Katherine	15 Mar 2000	AY333940
S. fallax	BRIP 27690	350 km N Devil's	15 Mar 2000	AY333941
-		Marbles		
S. fallax	BRIP 27031	Todd's Monument	16 Mar 2000	AY333942
S. tumefaciens	BRIP 27688	Helen Springs	16 Mar 2000	AY333943
S. tumefaciens	BRIP 27689	Stuart Highway between	15 Mar 2000	AY333944
-		Tennant Creek and		
		Katherine		
S. tumiforme	BRIP 26919	Newcastle Creek	16 Mar 2000	AY333945

Table 1. Sporisorium specimens with collection details including GenBank accession numbers for ITS sequences used in this study.

Taxonomy

<i>Sporisorium fallax</i> R.G. Shivas & J.H. Cunnington, sp. nov.	(Figs. 2	2-7)
Etymology: from Latin fallax (deceptive). Refers to its close resemblar	nce to and	other
species on the same host, as well as to the host plant species.		

Typus in matrice *Chrysopogon fallax* S.T. Blake, Australia, Northern Territory, 268 km SE urbe Katherine, 16°38'29" S, 133°22'45" E, alt. 250 m.s.m., 15.III.2000, leg. R.G. Shivas, I.T. Riley, C. Vánky et K. Vánky [Holotypus in BRIP 27687; isotypi in HUV 18119 et VPRI 31661; paratypi in matrice *C. fallax*, Stuart Highway, prope "Todd's Monument", 16°55'23" S, 133°25'22" E, 16.III.2000, leg. R.G. Shivas, I.T. Riley, C. Vánky et K. Vánky, BRIP 27031, HUV 20374 et VPRI 31526; 349 km N urbe Alice Springs, prope "Devil's Marbles", 20°33'59" S, 134°15'34" E, alt. 460 m.s.m., 15.III.2000, leg. R.G. Shivas, I.T. Riley, C. Vánky, BRIP 27690, HUV 20375; in matrice *C. latifolius* S.T. Blake, Northern Territory, Litchfield National Park, prope Lake Rum Jungle, 13°01'29" S, 130°59'04" E, alt. 140 m.s.m., 13.III.2000, leg. R.G. Shivas, I.T. Riley, C. Vánky et K. Vánky, BRIP 27685, HUV 20376].

Sori flores recentes omnes destruentes, vagina foliorum primo celati, elongati cylindrati, 50×5 mm, peridio denso, cinerascenti tecti, postea protrudenti. Peridium, ubi maturavit, paulatim decidit, patefaciens massam laxarum sporarum glomerum atram, pulveream et columellas plurimas, longas, simplices, flagelliformes. *Glomera sporarum* globosa, subglobosa vel ovata, atrobrunnea, $30-65 \times 30-85 \mu$ m diam., semi-permanentia, secedentia in doe genera *sporarum* (exteriores et interiores). Exteriores sporae globosae, subglobosae usque ad subpolyedriciter inaequales, atrorubrobrunneae, $6-8 \times 6-10 \mu$ m, leves usque ad dense verruculosae, pariete 1-3 μ m crasso. Interiores sporae globosae, subglobosae, usque ad subpolyedriciter inaequales, saepe angulares, pallide flavidobrunneae usque mediocriter rubrobrunneae, $7-10 \times 8-12 \mu$ m, dense punctatae-verruculosae, paries 0,5-1,0 μ m. *Cellulae steriles* non conspectae.

Sori (Fig. 2) destroying the entire inflorescence, at first concealed by the leaf sheath, elongated cylindrical, 50×5 mm, covered by a thick, greyish peridium, later protruding, at maturity the perdium flakes away exposing the black, powdery mass of loose spore balls and several, long, simple, flagelliform columella. *Spore balls* (Figs. 3, 5) globose, subglobose to ovoid, dark brown, 30-65 × 30-85 µm diam., semi-permanent, separating into two



Figs. 2-5. Sporisorium fallax (from BRIP 27031, holotype). **2.** Sorus in an infected inflorescence of *Chrysopogon fallax* showing flagelliform columellae. **3.** Spore ball and loose spores. **4.** Spores in LM (some dark outer spores arrowed). **5.** Spore ball in SEM. Bars: 2 = 1 cm; $3-5 = 20 \mu$ m.

types of *spores* (outer and inner) (Figs. 4, 6-7). Outer spores globose, subglobose to subpolyhedrally irregular, dark reddish-brown, 6-8 × 6-10 μ m, smooth to densely verruculose, wall 1-3 μ m thick. Inner spores globose, subglobose to subpolyhedrally irregular, often angular, pale yellowish-brown to medium reddish-brown, 7-10 × 8-12 μ m, densely punctate-verruculose, wall 0.5-1.0 μ m. *Sterile cells* not seen.

Fungal Diversity



Figs. 6-11. Spores. **6-7.** *Sporisorium fallax* (from BRIP 27031, holotype). **8-9.** *Sporisorium tumiforme* (from BRIP 26919). **10-11.** *Sporisorium tumefaciens* (from BRIP 27689). Bars: 6, 8, $10 = 3 \mu m$; 7, 9, $11 = 2 \mu m$.

On Poaceae: Chrysopogon fallax S.T. Blake, C. latifolius S.T. Blake, Australia.

Sporisorium fallax is macroscopically similar to S. tumefaciens and S. tumiforme, in that each of these smut fungi produces long (5 cm), cylindrical sori that are partly hidden by the uppermost leaf sheath. Furthermore, the sori of these three species destroy the entire inflorescence and have thick peridia

and numerous filiform columellae. Microscopically the three species can be separated on the morphology of spores and spore balls. *Sporisorium fallax* has rather permanent spore balls and two types (dimorphic) of spores that are often angular. *Sporisorium tumefaciens* (Figs. 10-11) and *S. tumiforme* (Figs. 8-9) have spore balls that easily separate by pressure and spores of one type that are mostly rounded rather than angular. Vánky (2004) discusses the differences between *S. tumefaciens* and *S. tumiforme*.



Fig. 1. Phylogenetic relationships of *Sporisorium fallax, S. tumefaciens* and *S. tumiforme* based on ITS sequences.

The neighbour-joining tree based on ITS sequences (Fig. 1) clearly showed *S. fallax* to be distinct from both *S. tumiforme* and *S. tumefaciens*. The latter two species were found to have very similar ITS sequences. Although only three specimens were examined, the sequence differences between *S. tumiforme* and *S. tumefaciens* were comparable to the difference found between different specimens of *S. fallax*. This agrees with the large number of morphological similarities shared by the two species and indicates that they have only recently diverged from a common ancestor.

Macalpinomyces tubiformis R.G. Shivas & Vánky, **sp. nov.** (Figs. 12-17)

Etymology: from Latin *tubus* (pipe) and *-formis* (forming). Refers to the shape of the sorus.

Typus in matrice *Chrysopogon fallax* S.T. Blake, Australia, Queensland, cca. 20 km N oppid. Gingin, 24°54'13" S, 151°54'12" E, alt. cca. 108 m.s.m., 25.IV.2003, leg. M.D.E. Shivas & R.G. Shivas [Holotypus in BRIP 39858; isotypus in HUV 20303].

Sori in spiculis et sessilibus et pedicellati nonnullis inflorescentiae eiusdem, organa floralia intima destruentes, longe tubiformes, saepe inclinati vel torti, $2-3 \times 25-50$ mm, peridio cinereo origine plantae nutrientis et fungali cooperti, quo longitudinaliter rupto massam atrobrunneam, pulveream sporarum, catervis cellularum sterilium intermixtam ostendentes. *Sporae* globosae, subglobosae, plerumque ellipsoidales, $8-11 \times 9-13,5 \mu$ m, olivaceobrunneae; pariete aequali, simul cum verrucis dense dispositis, acutis, pyramidalibus inclusis 1,5-2,5 μ m ceasso. *Cellulae steriles* in catervis irregularibus, cellulae singulae globosae, subglobosae, ellipsoidales, $5-8(-10) \times 5-9,5(-12) \mu$ m, hyalinae; pariete tenui, cca. 0,5 μ m, levi.



Figs. 12-16. *Macalpinomyces tubiformis* (from BRIP 39858, holotype). **12.** Sori in ovaries of *Chrysopogon fallax.* **13.** Spores and sterile cells in LM. **14-15.** Spores in SEM. **16.** Surface warts on spore. Bars: 12 = 1 cm; $13 = 10 \text{ }\mu\text{m}$; $14 = 5 \text{ }\mu\text{m}$; $15 = 2 \text{ }\mu\text{m}$; $16 = 1 \text{ }\mu\text{m}$.



Fig. 17. *Macalpinomyces tubiformis* (from BRIP 39858, holotype). Sori in some sessile and pedicelled spikelets of an inflorescence of *Chrysopogon fallax* (left). A triplet of spikelets with a sorus protruding from the sessile, hermaphrodite spikelet and a sorus from one of the pedicelled, male spikelets (right). Bars: (left) = 1 cm; (right) = 2.5 mm.

Sori (Figs. 12, 17) in some sessile and pedicelled spikelets of an inflorescence, destroying the innermost floral organs, long tubiform, often bent or twisted, $2-3 \times 25-50$ mm, covered by a grey peridium of host and fungal origin which ruptures longitudinally disclosing the dark brown, powdery mass of spores intermixed with groups of sterile cells. *Spores* (Figs. 13-15) globose, subglobose, usually ellipsoidal, $8-11 \times 9-13.5 \mu m$, olivaceous-brown; wall even, $1.5-2.5 \mu m$ thick including the densely situated, acute, pyramidal warts (Fig. 16). Sterile cells (Fig. 13) in irregular groups, single cells globose, subglobose, ellipsoidal, $5-8(-10) \times 5-9.5(-12) \mu m$, hyaline; wall thin, *ca*. 0.5 μm , smooth.

On *Poaceae: Chrysopogon fallax* S.T. Blake, Australia. Known only from the type collection.

Macalpinomyces tubiformis has spores ornamented with acute, pyramidal warts and is thereby distinct from all known smut fungi on *Chrysopogon*. SEM showed that the acute tips of the spore ornamentations were hooked (Fig. 16).

Acknowledgements

We are grateful to Desley Tree (Herbarium BRIP) who prepared the SEM photographs and to Don Barrett (University of Queensland) for the Latin diagnosis of *Sporisorium fallax* and Dr S. Tóth (Gödöllő, Hungary) for the Latin diagnosis of *Macalpinomyces tubiformis*.

References

- Boyd, M.L. and Carris, L.M. (1997). Molecular relationships among varieties of the *Tilletia fusca* (*T. bromi*) complex and related species. Mycological Research 101: 269-277.
- Boyd, M.L., Carris, L.M. and Gray, P.M. (1998). Characterisation of *Tilletia goloskokovii* and allied species. Mycologia 90: 310-322.
- Cunnington, J.H. and Shivas, R.G. (2004). The phylogenetic position of *Tilletia nigrifaciens*. Australasian Mycologist 22: 53-56.
- Gardes, M. and Bruns, T.D. (1993). ITS primers with enhanced specificity for basidiomycetes applications to the identification of mycorrhizae and rusts. Molecular Ecology 2: 113-118.
- Kumar, S., Tamura, K., Jakobsen, I.B. and Nei, M. (2001). MEGA2: molecular evolutionary genetics analysis software. Bioinformatics 17: 1244-1245.
- Shivas, R.G. and Vánky, K. (2001). The smut fungi on *Cynodon*, including *Sporisorium normanensis*, a new species from Australia. Fungal Diversity 8: 339-353.
- Shivas, R.G. and Vánky, K. (2002). A new smut fungus, *Sporisorium centrale* sp. nov. on *Themeda* from Australia. Fungal Diversity 11: 141-144.
- Shivas, R.G. and Vánky, K. (2003a). First record of a smut fungus on *Byblidaceae: Yelsemia lowrieana*, a new species from Australia. Fungal Diversity 13: 131-135.
- Shivas, R.G. and Vánky, K. (2003b). Biodiversity of Australian Ustilaginomycetes. Fungal Diversity 13: 137-152.

- Thompson, J.D., Gibson, T.J., Plewniak, F., Jeanmougin, F. and Higgins, D.G. (1997). The ClustalX windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Research 24: 4876-4882.
- Vánky, K. (2004). The smut fungi of Chrysopogon (Gramineae). Fungal Diversity (in press).
- Vánky, K. and Shivas, R.G. (2001a). New smut fungi (Ustilaginomycetes) from Australia. Fungal Diversity 7: 147-176.
- Vánky, K. and Shivas, R.G. (2001b). Smut fungi (Ustilaginomycetes) of *Sorghum* (Gramineae) with special regard to Australasia. Mycotaxon 80: 339-353.
- White, T.J., Bruns, T., Lee, S. and Taylor, J. (1990). Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics, In: *PCR Protocols: A Guide to Methods and Applications* (eds. M.A Innis, D.H. Gelfand, J.J. Sninsky and T.J. White). Academic Press, New York: 315-322.

(Received 1 November 2003; accepted 26 January 2004)