Thekopsora minima causes blueberry rust in south-eastern Queensland and northern New South Wales

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Received: 12 March 2013 / Accepted: 28 April 2013 / Published online: 21 June 2013
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Abstract The cause of blueberry rust in eastern Australia was determined by molecular and morphological analysis as *Thekopsora minima*.

Keywords Large Subunit region · *Naohidemyces* · Pucciniales · *Vaccinium*

Vaccinium (Ericaceae) is host to three rust fungi, *Naohidemyces vaccinii*, *N. fujisanensis* and *Thekopsora minima*, which are morphologically distinguished by aecial and telial characteristics (Sato et al. 1993). The uredinial stage of blueberry rust was first recorded from Australia in 2003.

In September 2012, a specimen of rust on blueberry (*Vaccinium corymbosum*) from Bundaberg, Queensland, was forwarded to Biosecurity Queensland and lodged as BRIP 57654 with the DAFF Plant Pathology Herbarium. The specimen was examined microscopically. Uredinia were present on lower leaf surfaces in groups up to 5 mm diameter, confluent, vein limited, on necrotic spots with the corresponding upper leaf surface dark brown with a bright red diffuse border, subepidermal, erumpent, round, 100–200 µm diameter, yellow (Fig. 1a). A peridium was present with a central pore. Urediniospores were subglobose, ellipsoidal to obovoid, yellow, 15–27×13–19 µm, with a wall that was 1–2 µm thick and echinulate (Fig. 1b).

DNA was extracted from this specimen according to the protocol outlined by Aime (2006) using the UltraClean

Plant DNA Isolation Kit (MoBio Laboratories, Solana Beach, CA, USA). The ITS2-LSU region was amplified with Rust2INV (Aime 2006)/LR7 (Vilgalys and Hester 1990) and nested with LROR/LR6 (Vilgalys and Hester 1990). The 28S sequence of blueberry rust (GenBank KC763340) had high identity to *Thekopsora minima* (HM439777 and GU355675; 99 % identical over 100 % query coverage) in a BLAST search. A match to *Naohidemyces vaccinii* was also returned with a lower sequence identity (DQ354561; 95 % identical over 99 % query coverage). Based on a phylogenetic reconstruction of closely related taxa from GenBank (Fig. 2), the pathogen was identified as *T. minima*.

The blueberry rusts in *Thekopsora* and *Naohidemyces* are heteroecious. The aecial stage of each occurs on the conifer *Tsuga* in the northern hemisphere. Aecial morphology is a reliable character to distinguish the two genera. *Naohidemyces* has aecia that are *Uredo*-type, with aeciospores borne singly on pedicels (Sato et al. 1993). *Thekopsora* differs by having aecia that are *Peridermium*-type, with aeciospores in chains (Sato et al. 1993). Telial morphology also differentiates the genera. The germ pores of *Naohidemyces* occur in the centre of the teliospores, whereas germ pores of *Thekopsora* are situated in the corner of each cell (Sato et al. 1993). Uredinial differentiation of *Thekopsora* and *Naohidemyces* is more subtle. Uredinia of *Naohidemyces* are enclosed by a peridium with conspicuous ostiolar cells, which are not present in *Thekopsora* (Sato et al. 1993). The size of urediniospores of species of *Thekopsora* and *Naohidemyces* on *Vaccinium* is not a useful taxonomic character.

Thekopsora minima was recently reported from South Africa (Mostert et al. 2010) and Mexico (Rebollar-Alviter et al. 2011) based on inoculation studies and molecular data. Australian specimens of blueberry rust held in BRIP were identified as *T. minima* by morphology, and in some cases by LSU sequence data, which is indicated by GenBank numbers as follows. Specimens examined: on *Vaccinium corymbosum* L., Brooklet, Byron Bay, New South Wales,

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Fig. 1 *Thekopsora minima* on *Vaccinium corymbosum*. **a** Abaxial and adaxial leaf symptoms; **b** Urediniospores. Scale A=1 cm; B=10 μ m

Australia, 19 February 2003, J.M. Anderson, BRIP 39896; Redlands Research Station, Cleveland, Queensland, Australia, 22 August 2008, J. Moisander, BRIP 52162, GenBank# KC763341; Nambour, Queensland,

Australia, 15 September 2009, J. Nagle, BRIP 52832, GenBank# KC763342.

Naohidemycetes vaccinii and *N. fujisanensis* were not regarded as pathogens of blueberry by Sato et al. (1993),

Fig. 2 Phylogram recovered from a maximum likelihood search and SPR tree improvement in PhyML with an alignment of the LSU region. aRLT values >90 % shown above nodes

although they infected other *Vaccinium* species. *Naohidemycetes* is not recorded in Australia.

Acknowledgments This work was partly funded by the Australian Biological Resources Study, grant number RFL212-33.

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