New Disease Reports

First report of *Colletotrichum acutatum sensu lato* (*Colletotrichum godetiae*) causing anthracnose on grapevine (*Vitis vinifera*) in the United Kingdom

R. Baroncelli [1,2]*, S. Sreenivasaprasad [1,3], C.R. Lane [4], M.R. Thon [2] and S.A. Sukno [2]

[1] *Warwick HRI, University of Warwick, Coventry, CV4 7AL. United Kingdom*; [2] *Centro Hispano-Luso de Investigaciones Agrarias (CIALE), Departamento de Microbiología y Genética, Universidad de Salamanca, C/ Río Duero 12, Villamayor, 37185 Salamanca, Spain*; [3] *University of Bedfordshire, Park Square, Luton, Bedfordshire LU1 3JU, United Kingdom (current address)*; [4] *The Food and Environment Research Agency, Sand Hutton, York, YO41 1LZ, UK*

*E-mail: riccardobaroncelli@gmail.com

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In November 2009, twelve specimens of grapevine (*Vitis vinifera*) cv. Brant in the area of Penrith, Cumbria in the United Kingdom were showing necrotic black leaf spotting and abundant orange sporulation on the upper leaf surface. Infected plant material was submitted to the FERA (Food and Environment Research Agency) Plant Clinic for diagnosis. The tissue samples were surface sterilised for one minute in 20% sodium hypochlorite and cultured on potato dextrose agar. Monoconidial isolates grown at 25°C with a 12 hour light period had light grey cottony aerial mycelium with colour ranging from whitish to dark grey on the reverse side of the colony. The cultures had orange spores organised in small masses and dark melanised structures similar to acervuli. Disease symptoms and morphology suggested that a member of the genus *Colletotrichum* caused the disease. Given the fact that strains of *Colletotrichum* often belong to aggregates of species that can be difficult or impossible to distinguish morphologically, a representative isolate was sent to the University of Warwick for further analysis.

Total DNA was extracted using a modified Chelex100 protocol (Baroncelli, 2012). The internal transcribed spacer region (ITS) of the nuclear ribosomal DNA repeat region was amplified and sequenced using the universal primers ITS4 and ITS5. The resulting sequence was 100% identical to *C. acutatum* species sequences obtained by a BLAST search in GenBank. Due to the low resolution of this locus in the *C. acutatum* species complex, two other loci were used to further characterise the isolate: primers TB5 and TB6 were used for the amplification and sequencing of the variable region 1, spanning the exons 3, 4, 5, and part of 6 of the β-tubulin (TUB) gene (Baroncelli, 2012). Primers GDF1 and GDR1 were used to amplify a 200-bp intron region of the glyceraldehyde 3-phosphate dehydrogenase (GAPDH) gene (Baroncelli, 2012). Sequences were deposited in GenBank (Accession No. KF834203 for ITS, KF834204 for TUB and KF834205 for GAPDH). Using BLAST searches the sequences obtained in this study were 100% identical to some sequences deposited in GenBank as *C. clavatum* and as *C. godetiae. C. clavatum* was described by Faedda *et al.* (2011), but is synonymous to *C. godetiae* , the latter name having priority (see Damm *et al.*, 2012). The phylogenetic analysis carried out with the sequences obtained from GenBank revealed that the isolate clustered within the *C. godetiae* clade (Damm *et al.*, 2012), as suggested by the BLAST results.

Previous studies have demonstrated that the pathogen is present on *Vitis* spp. in different countries worldwide such as the USA, Australia and Japan (Whitelaw-Weckert *et al.*, 1990; Yamamoto *et al.*, 1990). To our knowledge, this is the first report of anthracnose on *V. vinifera* by *Colletotrichum* in the UK, where *V. vinifera* is a popular ornamental plant and is also grown commercially for dessert and wine grapes. Wine grapes are a small but economically important crop in southern England and with climate change, grape production is an expanding industry there. Reports of *Colletotrichum* spp. on new hosts and in new geographic locations are essential for the study and for control of these often polyphagous and flexible pathogens. *C. godetiae* is frequently found on *Fragaria* spp. and other hosts and it is likely that *Fragaria* may act as a reservoir of inoculum for *Vitis* and vice versa. The isolate has been deposited in the CBS culture collection Utrecht, The Netherlands (CBS 129951).

References

Baroncelli R, 2012. *Colletotrichum acutatum sensu lato: from diversity study to genome analysis.* Coventry, United Kingdom: University of Warwick, PhD thesis.

Damm U, Cannon PF, Woudenberg JHC, Crous PW, 2012. The *Colletotrichum acutatum* species complex. *Studies in Mycology* **73**, 37-113. http://dx.doi.org/10.3114/sim0010

Faedda R, Agosteo GE, Schena L, Mosca S, Frisullo S, Magnano di San Lio G, Cacciola SO, 2011. *Colletotrichum clavatum sp. nov*. identified as the causal agent of olive anthracnose in Italy. *Phytopathologia Mediterranea* **50**, 283-302.

Whitelaw-Weckert MA, Curtin SJ, Huang R, Steel CC, Blanchard CL, Roffey PE. 2007. Phylogenetic relationships and pathogenicity of *Colletotrichum acutatum*isolates from grape in subtropical Australia. *Plant Pathology* **56**, 448-463. http://dx.doi.org/10.1111/j.1365-3059.2007.01569.x

Yamamoto J, Sato T, Tomioka K, 1999. [Occurrence of ripe rot of grapes (*Vitis vinifera* L.) caused by *Colletotrichum acutatum* Simmonds ex Simmonds.] *Annals of the Phytopathological Society of Japan* **65**, 83-86. http://dx.doi.org/10.3186/jjphytopath.65.83

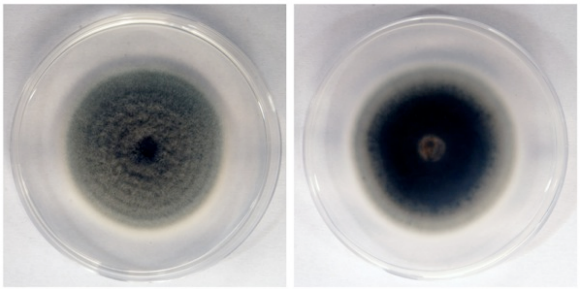

Figure 1

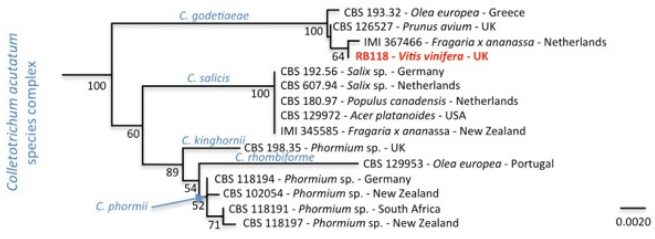

Figure 2

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