New Disease Reports

First record of the fungus *Blumeriella kerriae* in the UK

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In September 2014, a sample of Japanese rose, *Kerria japonica*, exhibiting severe defoliation and stem lesions was submitted to RHS Gardening Advice from a garden in West Yorkshire, England (Fig. 1). Further samples were subsequently received from 12 locations across England (Fig. 2). Leaves of infected samples exhibited numerous small red-brown spots (1-5 mm diameter) with dark purple borders (Fig. 1). Spots were visible on both leaf surfaces and sometimes numbered in the hundreds on a single leaf. In humid conditions clusters of white spores were visible in the centre of the spots. As the infection progressed the spots coalesced and the leaves turned yellow through to brown and fell from the stems. Stem lesions appeared as purple-brown, slightly-sunken elliptical cankers which remained visible on the stems throughout the year. Cankers which girdled the stem resulted in extensive stem die-back.

Upon microscopic examination it was determined that the symptoms were caused by the fungus *Blumeriella kerriae* (Stewart, 1917). *Blumeriella kerriae* is widespread on *K. japonica* in America causing twig and leaf blight, but has not previously been recorded on any host plant in the UK. Acervuli were scattered across each spot/lesion. Conidia were filiform, curved, hyaline, 45-94 x 1.4-5.6 µm (mean 69 x 3.5 µm) (n = 60) (Fig. 3). Observations differed to Stewart's original description which described 1-septate conidia; observed conidia were mainly 2-3 septate, with occasional 1-septate conidia.

A single spore isolate on potato dextrose agar was obtained and deposited in the RHS Wisley culture collection (JS20160615). The internal transcribed spacer (ITS) region of rDNA was amplified (White *et al*., 1990) and sequenced (GenBank Accession No. KY929501). There were no previous DNA sequences for *B. kerriae* available in GenBank. Fungal ITS sequences for species within the family *Dermateaceae*, including *Blumeriella jappii* (Pederson *et al*., 2010), were obtained to place KY929501 within a phylogenetic tree. Sequences were aligned with the MUSCLE v3.8.31 algorithm (Edgar, 2004). The beginning and end of the alignment, where base callings were ambiguous, were excluded from the analysis. Phylogenetic trees were constructed through Bayesian inference analysis performed in MrBayes v3.2.6 (Ronquist *et al*., 2012) with the GTR + I + G model identified by MrModeltest v2.3 (Nylander, 2004). The analyses were run for 1,000,000 generations, sampling every 1000 generations. Trees from the first 25% of the sampled generations were discarded. Phylogenetic analysis placed *B. kerriae* (KY929501) in a cluster with the closely related cherry leaf pathogen *B. jappii* (Fig. 4).

To confirm pathogenicity, a conidial suspension (~10^5 conidia/ml, sterile distilled water, 0.2% Tween-20) was prepared by harvesting fresh conidia from stem lesions. All observed spores were consistent with *B. kerriae*. The spore suspension was sprayed onto newly emerged leaves of *K. japonica* plants. Inoculated plants were held in a humidity chamber for 48 h and thereafter placed in a glasshouse. After 13 days, typical leaf spot symptoms developed on the leaves of inoculated plants. *Blumeriella kerria* conidia were produced from acervuli in the leaf spots, fulfilling Koch's postulates. A control plant treated with sterilised water and Tween-20 remained symptomless.

Kerria japonica is a valuable garden and hedging plant with high tolerance for poor environmental conditions. Until now it has had no serious pest or disease problems in the UK. The spread of *Blumeriella kerriae* in the UK will change how *K. japonica* is used in UK horticulture and may result in gradual loss of the plant from retail.

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Figure 1

Figure 2

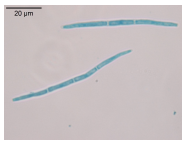

Figure 3

Figure 4

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