



# Stem rust (*Puccinia graminis*) identified on spring barley in the UK adjacent to infected *Berberis vulgaris*

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Received: 19 Aug 2019. Published: 22 Sep 2019. Keywords: *Berberis vulgaris*, pathogen surveillance, wheat stem rust

Wheat stem rust caused by the fungus *Puccinia graminis* f.sp. *tritici* is a notorious disease of wheat and barley (Leonard & Szabo, 2005). In western Europe, following many decades of absence the disease started to re-emerge in 2013 with sporadic wheat stem rust outbreaks reported in Germany, Sweden and Denmark (Hovmøller, 2019). In the same year a single wheat plant infected with stem rust was discovered in the UK, which marked the first record of the disease in over 60 years (Lewis *et al.*, 2018). These initial outbreaks were seen as an early warning of the potential resurgence of a forgotten foe (Saunders *et al.*, 2019). Accordingly, a much larger outbreak was recorded in Sicily in 2016 (Hovmøller, 2019).

The wheat stem rust pathogen is heteroecious undertaking asexual reproduction on cereals and grasses and completing its sexual cycle through infection of an alternate host, common barberry (*Berberis vulgaris*) and many other species in the *Berberis* genus (Leonard & Szabo, 2005). The importance of the alternate host as a source of genetically diverse inoculum historically led to legislation and exclusion campaigns to limit its presence particularly in western Europe, USA and Canada. However, due to the absence of the disease for many decades in western Europe, *B. vulgaris* has been increasing in prevalence. Accordingly, a wheat stem rust outbreak in Sweden in 2017 occurred in an area where *B. vulgaris* was located (Berlin, 2017).

In mid-July to early August 2019, we identified symptoms typical of stem rust on approximately 20 late-sown spring barley plants in Suffolk in the UK (Figs. 1-2). These infected barley plants were recorded on the edge of a field within metres of an established *B. vulgaris* hedgerow that was also heavily infected in the spring with orange, tube-like aecial structures typical of stem rust (Figs. 3-4). DNA was extracted from infected barley stems and aecia identified on *B. vulgaris* leaves using the DNeasy Plant mini kit (Qiagen, UK) and the internal transcribed spacer (ITS) region amplified using primers 5ITS (5'-GGAAGTAAAAGTCGTAACAAGGT-3') and 3ITS (5'-ACTCCTTGGTCCGTGTTCA-3'). PCR products were sequenced (Genewiz, USA) and sequences deposited in Genbank (MN385566-7). A sequence alignment was then performed including 27 additional ITS sequences from various *P. graminis* formae *speciales*. Phylogenetic analysis was performed using a neighbour-joining approach with 1,000 bootstrap replicates (Fig. 5). This analysis confirmed (i) the presence of *P. graminis*, and (ii) that the *P. graminis* ITS sequences from barley and *B. vulgaris* infections clustered in a clade with other *P. graminis* formae *speciales* that predominantly infect wheat (*Triticum aestivum*) and barley (*Hordeum vulgare*), wild rye (*Secale strictum*) and couch grass (*Elymus* spp.), which are too similar to differentiate using gene sequence analysis.

This report illustrates that stem rust can be identified late in the season on barley in the UK, most likely caused by inoculum originating on neighbouring *B. vulgaris* plants. The early maturation of UK wheat and barley varieties may currently act as an effective control mechanism for stem rust infection. However, as the climate continues to shift, earlier summer temperatures could encourage wheat stem rust re-emergence, as was seen during the wheat stem rust outbreak that occurred in 2013 in Germany (Olivera Firpo *et al.*, 2017). This supports the need for enhanced vigilance and monitoring across cereals and grasses in the UK.

## Acknowledgements

We thank Matt Heaton, Andrew Davis (JIC) and Joe Win (TSL) for photography. This project is funded by the UK Biological Sciences Research Council (BBSRC; BB/S003975/1) and European Union's Horizon 2020 research and innovation programme under grant No 773311 (RustWatch). G.V.R. is additionally supported by a BBSRC Discovery Fellowship (BB/S011005/1) and D.G.O.S by the European Research Council (no. 715638), BBSRC Institute Strategic Programmes BB/J004553/1 and BB/P012574/1 and the John Innes Foundation.

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Figure 1



Figure 2



Figure 3



Figure 4



Figure 5

**To cite this report:** Orton ES, Lewis CM, Davey PE, Radhakrishnan GV, Saunders DGO, 2019. Stem rust (*Puccinia graminis*) identified on spring barley in the UK adjacent to infected *Berberis vulgaris*. *New Disease Reports* **40**, 11.

<http://dx.doi.org/10.5197/j.2044-0588.2019.040.011>

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