

Researchers tackle top UK barley disease

Rhynchosporium is a difficult disease to control, but we are closer to understanding how to improve barley's natural resistance to it. *Sarah Henly* reports on fundamental research

■ The number-one pathogen of UK barley is estimated to be causing average yield losses of 10%, even where fungicides are used, which equates to an annual loss of £7.2m.

"It is not surprising that growers have difficulty in controlling the disease when you consider the complexity of the rhynchosporium pathogen and its often asymptomatic development, says Anna Avrova of the James Hutton Institute.

"The natural resistance genes present in some UK barley varieties are largely being overcome by new strains of the pathogen."

Rhynchosporium produces many proteins to help evade barley's immune system. Some of these proteins can be detected by barley, leading to resistance. If scientists can find barley material that recognises the proteins essential to infection, they can incorporate these "protective" genes into new varieties.

Dr Avrova first sequenced the genome of the pathogen to identify the proteins that can be involved in the infection of barley.

Then she looked at whether these proteins are present and conserved

in all sequenced strains of pathogen. With this knowledge, she can predict how durable any resistance found is likely to be.

"The reason resistance mechanisms have broken down is that they involve recognition of non-essential proteins. The pathogen simply stops using the proteins and thus avoids recognition," she explains.

The two main resistance genes incorporated into Recommended List varieties are Rrs1 and Rrs2. Dr Avrova points out that Rrs1 recognises protein missing in more than 45% and modified to avoid recognition in many more pathogen isolates. Similarly, while most new resistant spring barley cultivars carry Rrs2, their continued use has led to rapid breakdown of this resistance.

The James Hutton Institute has an extensive collection of barley landraces from the centre of barley diversity.

A project funded by the BBSRC Crop Improvement Research Club is exploiting this collection and the rhynchosporium genome sequence to identify and characterise novel sources of resistance.



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Louise Gamble is using the latest genomics to identify key rhynchosporia resistance genes that could be exploited by breeders.

Research reasons



HGCA

This project should greatly improve our understanding of rhynchosporium biology and the infection process, helping us develop durable disease resistance in barley to reduce reliance on fungicides.

Project: Identification and characterisation of rhynchosporium genes activating barley resistance (PhD)

Timescale: October 2012-October 2015

Researchers involved: James Hutton Institute (JHI)

Funders: HGCA and JHI PhD sponsorship programme

Cost: HGCA funding of £37,500; JHI funding of £30,000

Key points

■ The super-virulent strain AU2 is capable of causing disease symptoms in most barley varieties, even those with major resistance genes

■ Rhynchosporium genes activated at the early stages of infection are being used to identify new sources of barley resistance

HGCA perspective by *Ellie Marshall*

Research and knowledge transfer manager, HGCA

■ "Rhynchosporium remains the most damaging disease of barley in the north and west of the UK.

"Selecting barley varieties with good disease resistance ratings is recommended where disease pressure is high. However, sustainable strategies for rhynchosporium management depend on further understanding the biology of the pathogen and its interactions with barley.

"In particular, we need to get a better handle on crop/pathogen genetics to assist with the development of varieties with durable disease resistance."

