

# Crowdsourcing to kickstart comeback from ash dieback

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On Friday scientists from The Sainsbury Laboratory and the John Innes Centre will publish the first RNA sequence data on the ash dieback fungus causing an epidemic of disease.

They will release the data via a website to a system designed for "social coding" of software. The system, called GitHub, was also used to crowdsource expertise during the 2011 *E. coli* epidemic in Germany.

Experts from around the world will be able to access the RNA sequence and start to analyse it immediately, speeding up the process of discovery. It will also allow live peer review of analysis, helping produce more accurate findings more quickly.

"Bringing together knowledge and data through technologically-oriented social media is one of the most vital steps in beginning to understand this outbreak," said Dr Dan MacLean of The Sainsbury Laboratory, a research centre focused on the science of plant-microbe interactions.

"The tiny amount of data we have so far is already suggesting interesting insights and we want others to start poring over it straight away," said Professor Sophien Kamoun, head of The Sainsbury Laboratory.

Drs Diane Saunders and Kentaro Yoshida from The Sainsbury Laboratory took cuttings of infected ash in Ashwellthorpe wood in Norfolk, where the [fungus](#) was first identified in the natural environment in the UK. They sampled pith from the twig, extracted RNA and

sequenced it.

The sequence data is a mixture of both ash and fungus so one of the first jobs through the crowdsourcing exercise will be to search it against existing sequence databases and sort it out. They have already identified a sizeable proportion of fungal RNA, some of which appears to code for toxin proteins.

"By looking at what genes are expressed at this time of year when the fungus is active in the woody tissue of ash, we might be able to home in on genes that enable it to spread so rapidly," said Professor Allan Downie from the John Innes Centre, an institute strategically funded by the BBSRC.

"You need to know your enemy before you can start to come up with solutions and this work will enable us to do that," said Dr Joan Webber from the Forestry Commission's Forest Research agency, which is a research partner in the project.

In the longer term, the scientists hope to be able to discover how the fungus causes disease, where it originated from, how it spread to the UK and how different strains are related.

The GitHub system allows contributions from other scientists to be attributed and tracked. Scientists would normally withhold sequence data until they have carried out an analysis and had a paper accepted for publication in a scientific journal.

"Crowdsourcing will give us access to the expertise of many more people," said Professor Kamoun.

"It will speed up analysis and, through live peer review, it will speed up how that analysis is checked and then corroborated or rejected."

**More information:** The OpenAshDieback: [oadb.tsl.ac.uk/](https://oadb.tsl.ac.uk/)

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