

# Conquering conker canker

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Scientists have decoded the genome of a bacterium that is threatening the UK's historic landscape.

The horse chestnut has become an iconic sight in Britain since its introduction in the 1500s but in 2002 a new lethal disease appeared that now infects over 70 per cent of trees in some areas. Bleeding canker, caused by the bacterium *Pseudomonas syringae pathovar aesculi* (*Pae*), causes lesions which bleed like open sores and in severe cases can kill large mature trees within one to two seasons.

"Comparing the genomes of British strains of the [bacterium](#) has shown us they are very similar and probably originated from a single introduction into the UK within the last few years," said Dr David Studholme who led the analysis of the [DNA sequences](#) at The Sainsbury Laboratory in Norwich.

"Detecting the origin of *Pae* is important from a biosecurity perspective," said Dr Sarah Green, a tree pathologist with Forest Research. "There has been an unprecedented rise in invasive plant diseases, possibly linked to the rise in international travel and in the global plant trade."

"We now have the first clues to the [evolutionary origin](#) of the disease and to its ability to spread so fast. *Pae* might have been accidentally introduced to Europe through importation in the plant trade. We need to prevent it being introduced to new geographical areas such as North America," said Dr Green.

Before the European epidemic, the only reported case of *Pae* was in India. A similar strain infects the Indian horse chestnut but causes only minor lesions in the leaves. The strains that emerged in Europe appear to be more aggressive and attack the woody trunk and branches.

"This pathogen spread quickly through Western Europe and Britain and the information from the sequencing will help us discover how it is dispersed," said Dr Rob Jackson from the University of Reading. "It may be that it can cause precipitation so it is swept into the atmosphere before being rained back down in new locations, or it may be carried by some kind of vector such as insects."

The success of the pathogen may be helped by a cluster of genes that help it to acquire iron, an essential nutrient for virulent bacteria. *Pae* also has an unusual cluster of genes which may be involved in the degradation of compounds derived from woody tissues. A plant will normally produce nitric oxide as part of its defence mechanism, but *Pae* may have the ability to inhibit this response via two genes identified by the scientists.

The differences between the Indian and British strains give the first clues to its virulence on European horse chestnut. The British strains contain additional genes that enable it to live off the sucrose found in the tree sap.

The genome sequence will allow scientists to determine which genes might be necessary for infection of a tree host so they can be targeted to control the disease.

"Emerging human and animal diseases are routinely sequenced and this research shows the usefulness of doing the same for plant pathogens," says Professor Kamoun from the Sainsbury Laboratory.

"We can quickly generate large amounts of genetic information on emerging plant diseases that is valuable for combating current and future biosecurity threats."

Provided by Norwich BioScience Institutes

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