# Forest Research

# Revealing the complex pathology of Acute Oak Decline, a major threat to Britain's native oak

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# Background:

- Decline-diseases are complex syndromes involving multiple biotic and abiotic agents, and are becoming problematic globally.
- Currently the UK is facing an episode of Acute Oak Decline (AOD), which represents a serious threat to native oak species (*Quercus robur* and *Q. petraea*).
- AOD is characterised by stem bleeds, morbid inner bark, and larval galleries of the native buprestid Agrilus biguttatus, all of which disrupt the normal health and function of the tree.
- Several novel species of bacteria are consistently associated with AOD lesions, but the origin and pathogenicity of these bacteria is unknown.



# Fig. 1 a-c. Symptoms of Acute Oak Decline



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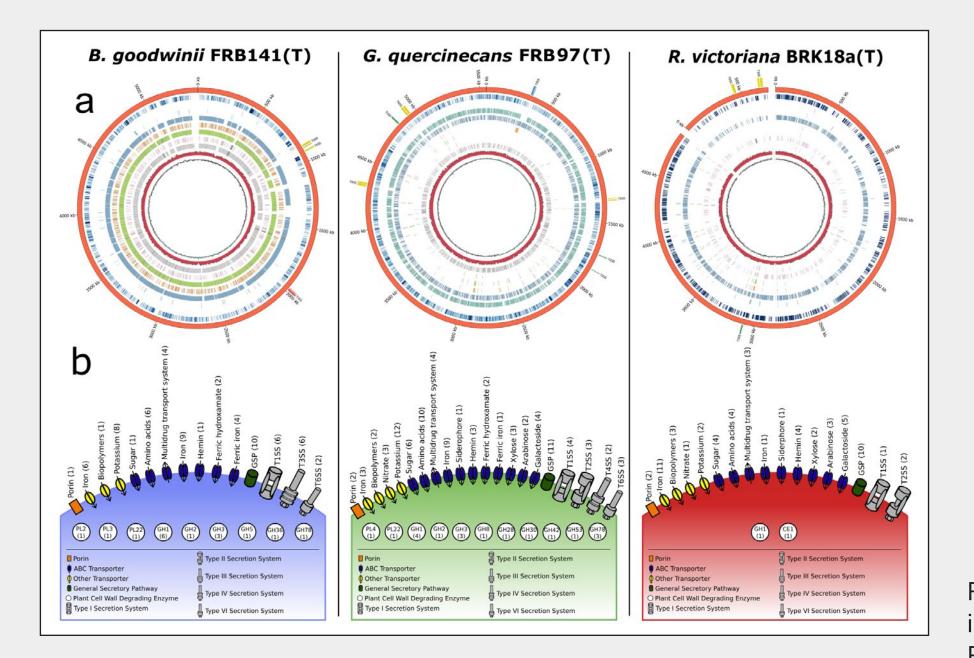
Aims and objectives:

- The aim of this work was to identify the causal agents of tissue necrosis in AOD lesions.
- In the absence of a single potential causal agent of AOD lesions, a multifaceted approach was required using DNA sequencing technologies and infectivity studies to identify the key causal agents of necrosis within AOD lesions.

Fig. 1a. (Left) External symptoms showing stem bleeding Fig. 1b. (Right top) Decomposing innerbark tissue under the weeping patches Fig. 1c. (Right bottom) Larval galleries of *A. biguttatus* associated with AOD stem lesions in the innerbark tissues

# Results:

- Three bacterial species, Brenneria goodwinii, Gibbsiella quercinecans and Rahnella victoriana are consistently abundant in AOD lesions and possess virulence genes that are expressed in the decomposing tissues.
- Inoculation tests demonstrated that B. goodwinii and G. quercinecans cause tissue necrosis, but when combined cause more damage, and when inoculated together with A. biguttatus, produce the diagnostic symptoms of AOD.



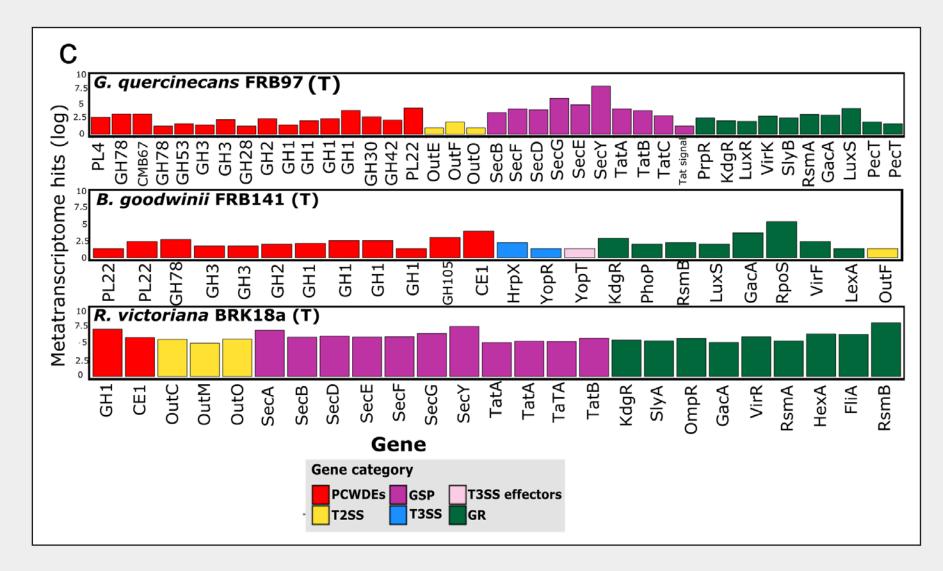


Fig. 2. (Left) Genome sequences of bacteria consistently associated with AOD lesions indicating presence of pathogenicity and virulence genes

Fig.3. (Right) Expression of bacterial pathogenicity and virulence genes in AOD lesions

# Fig. 4 a-h. Infectivity tests demonstrating bacterial lesion formation and interaction with A. biguttatus larvae

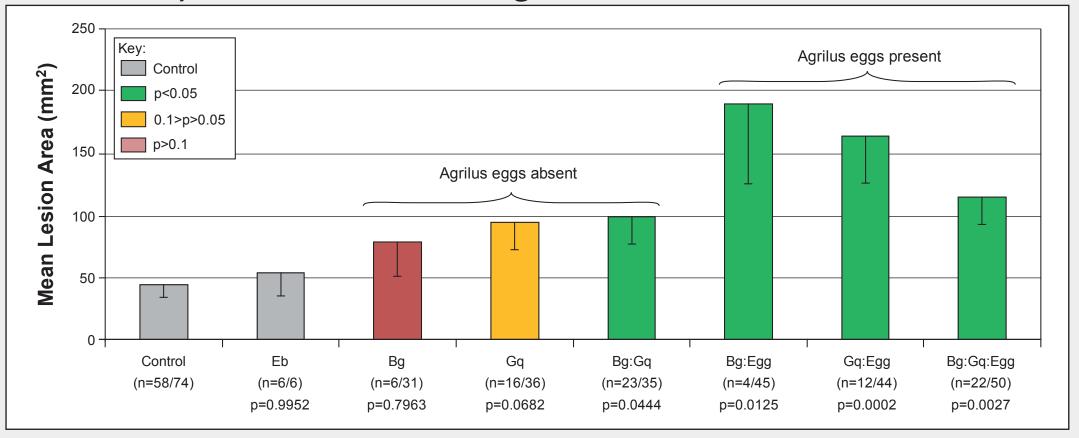


Fig. 4a. Mean lesion area caused by bacterial strains with or without larvae of A. *biguttatus* (Eb = *Erwinia billingiae*, Lqb = *Lonsdalea quercina* ssp *britanica*, Bg = *Brenneria goodwinii*, Gq = *Gibbsiella quercinecans*). Larvae were derived from A. *biguttatus* eggs produced *in vitro* and applied to log tests as egg clusters or as individual day old larvae.



Fig. 4b. Wound response in wounded control treatment

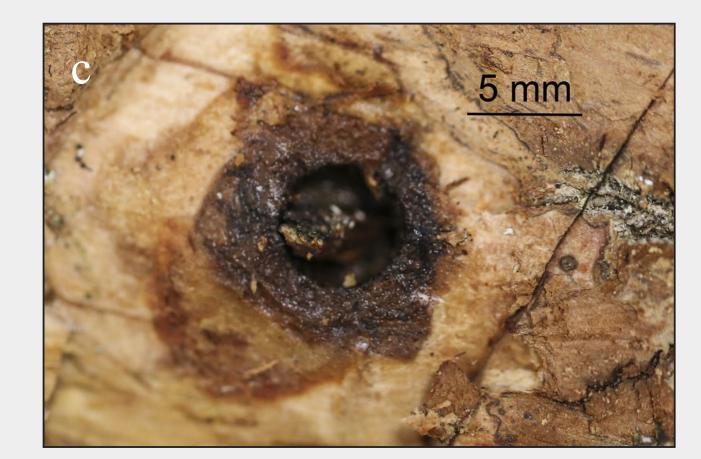
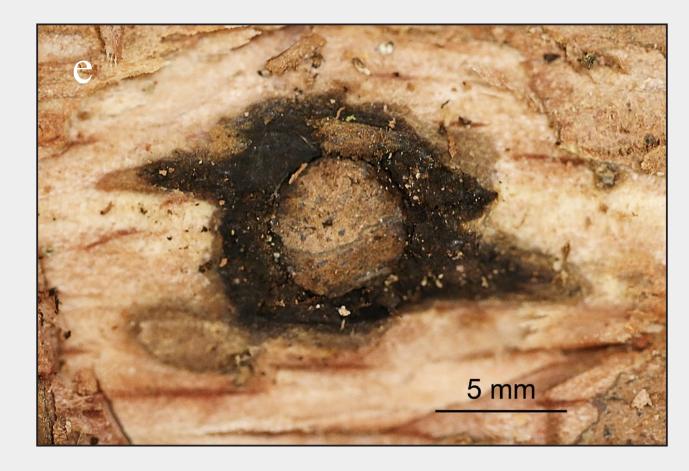


Fig. 4c. Tissue necrosis caused by Brenneria goodwinii





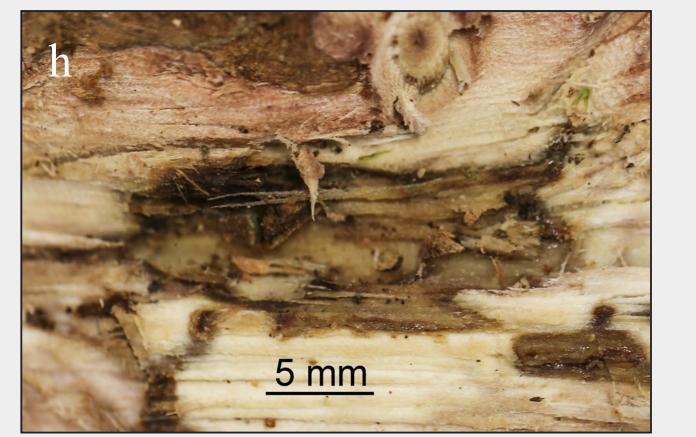
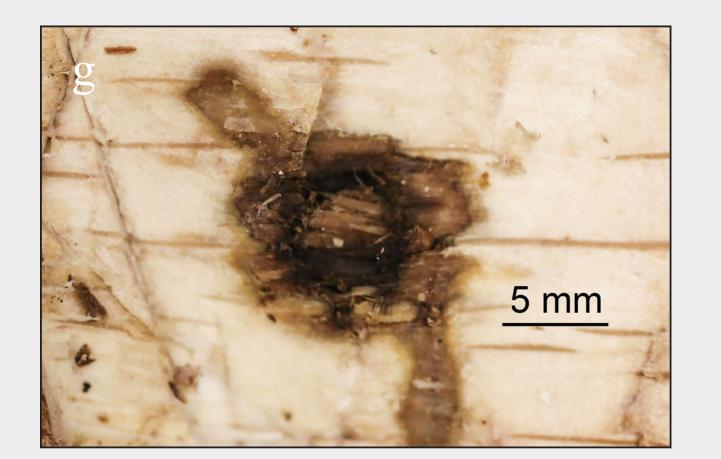


Fig. 4d. Tissue necrosis caused by Gibbsiella quercinecans
Fig. 4e. Tissue necrosis caused by a mixture of Brenneria goodwinii and Gibbsiella quercinecans
Fig. 4f. Tissue necrosis caused by Brenneria goodwinii and





# Conclusions:

- Agrilus biguttatus larvae
- Fig. 4g. Tissue necrosis caused by *Gibbsiella quercinecans* and larvae of *Agrilus biguttatus*.
- Fig. 4h. Tissue necrosis caused by Brenneria goodwinii, Gibbsiella quercinecans and Agrilus biguttatus.

## Acknowledgements:

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- AOD lesions are caused by a polybacterial complex, providing novel insights into polymicrobial interactions in tree disease.
- The prevailing paradigm that plant diseases are caused by a single pathogen (Koch's postulates) requires contemporary adaptation for complex polymicrobial diseases.
- We present a novel conceptual and methodological template to address the role of microbial communities in disease in future studies of plant health.



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