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Forest Research has monitored a new episode of acute oak decline spreading since 2006 through the Midlands and South East England, mainly on mature trees of both of Britain's native oaks (*Quercus robur* and *Quercus petraea*).

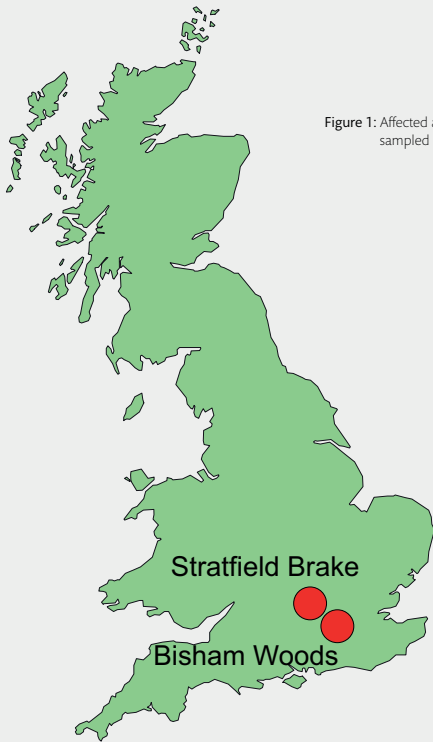
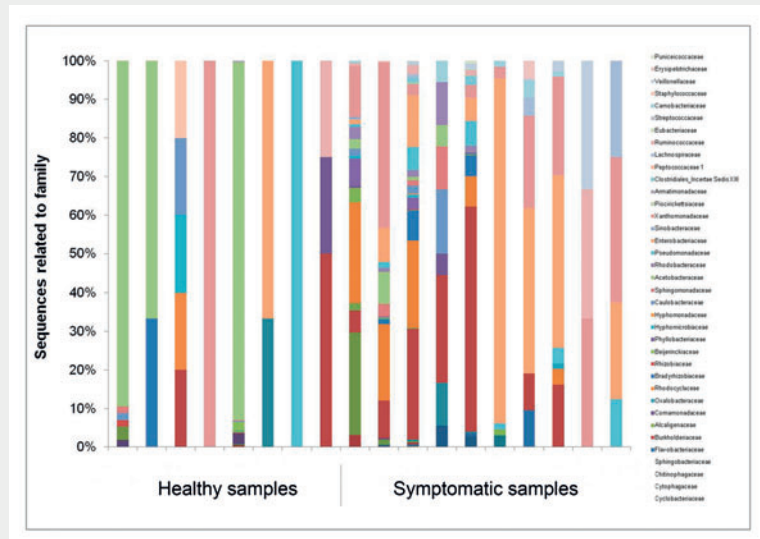


Figure 1: Affected and healthy trees sampled at 2 locations



Figure 2: Lesions and necrotic patches form in the stem tissues underlying the weeping points; the galleries of *Agrilus biguttatus* are in close proximity to necrotic patches

Figure 3: Next generation (Roche 454) amplicon sequencing of a 16S rRNA gene fragment from oak tissues indicate higher bacterial diversity in symptomatic, relating to wider bacterial taxonomic variation at family level than found in healthy tissue samples.



Alignment of 16S rRNA gene (Fig. 4) and *gyrB* sequences (Fig. 5) with those in curated databases identified *Brenneria goodwinii* and *Gibbsiella quercinecans* in symptomatic but not healthy tissues. These bacteria have also been isolated as suspect plant pathogens at Forest Research.

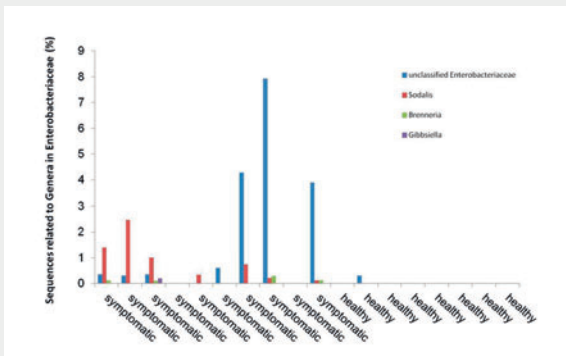


Figure 4: Relative abundances of *Enterobacteriaceae* using 16S rRNA genes classified using RDP.

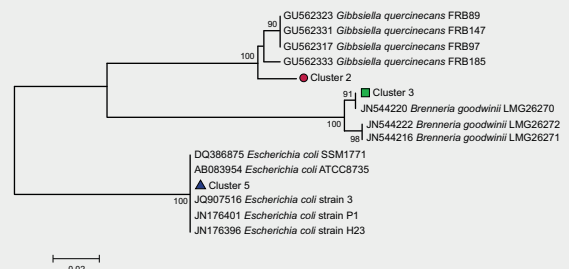


Figure 5: Neighbor-Joining tree based on *gyrB* sequences

Acknowledgements

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