Effect of age, health and location on the chemical composition of ash (*Fraxinus excelsior*) wood

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Introduction

Bacterial canker of ash is a disease caused by the pathogen *Pseudomonas savastanoi* pv. *fraxini* (***Psf***)[1]. The disease can be recognized by the presence of canker lesions on the bark. Although the pathogen was described in the 1980s there is still a significant gap in the knowledge of this disease. Aiming to understand how ash trees respond to bacterial infection and if the tree produces any antibacterial metabolites, an untargeted metabolomics analysis was performed on **healthy and symptomatic ash trees from Wytham woods (UK).** Knowing that variables such as age and location cause differences in the tree metabolome[3], **the metabolic profile of healthy saplings, young and mature trees were also evaluated**.

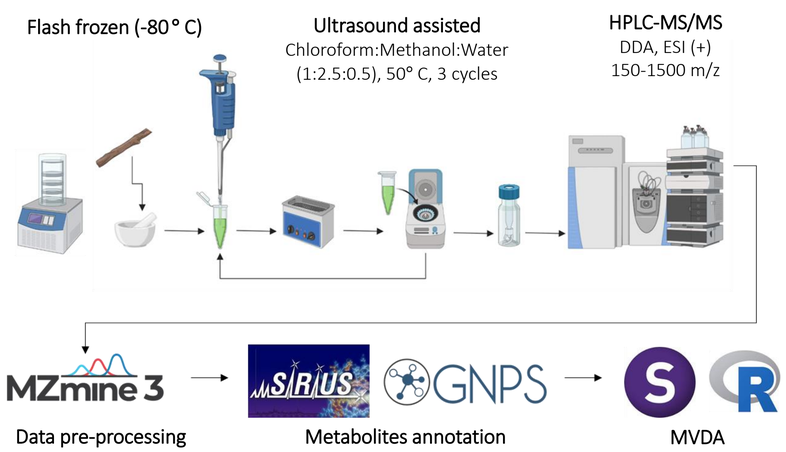
Fig 1. Ash bacterial canker[2]

Methods

Table 1. Ash tree groups considered for sampling in the present research

Group ID	Age group	Health	Tissue	Location/origin
Sapling	< 1 year-old	Healthy	Healthy	BIFoR (collected during winter 2022)
Young	1-3 year-old	Healthy	Healthy	Woodland near East Dereham (collected during winter 2021)
Diseased – Healthy	>10 years-old	Diseased	Healthy	Wytham woods
Canker	>10 years-old	Diseased	Canker	Wytham woods
Healthy	>10 years-old	Healthy	Healthy	Wytham woods
Healthy - BIFoR	>10 years-old	Healthy	Healthy	BIFoR (possibly parental trees of the sapling group)

Fig 2. Untargeted metabolomics pipeline



Results

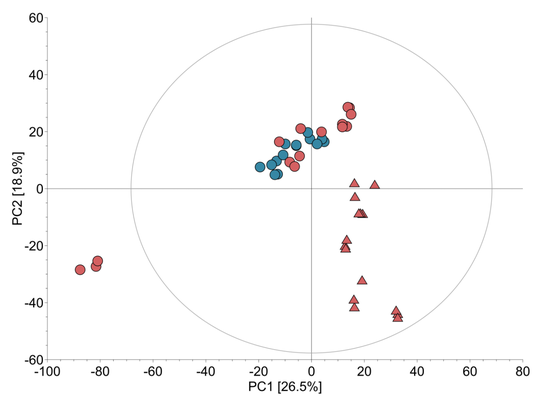


Fig 3. PCA of the mass spectral data collected from ash wood obtained at Wytham and BIFoR from healthy trees of different age.

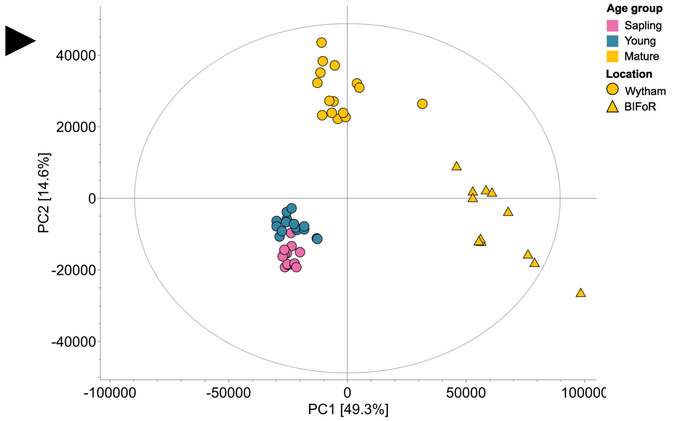


Fig 4. PCA of the mass spectral data collected from ash wood obtained at Wytham woods from healthy and diseased trees.

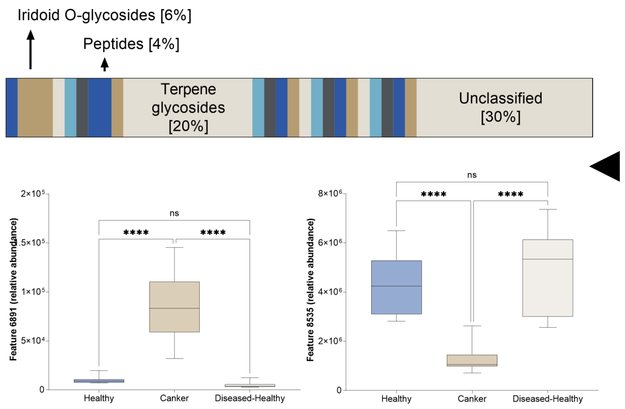


Fig 5. Antibacterial activity of the extracts obtained from ash wood against *Psf 1006.*

Fig 6. VIP features (n=50, top) and their abundance variation (bottom) on healthy or diseased tissue obtained from healthy and disease ash trees at Wytham woods. Significant differences are shown as (ns) no significant, (*) p≤0.05, (**) p ≤ 0.01, (***)p ≤0.001, (****) p<0.0001.

Conclusions and future work

- ✓ **Ash metabolomes from healthy wood and cankers are significantly different**. The difference is related to the abundance of metabolites from the prenol lipid class.
- ✓ The data suggests that **the response of the tree against *Psf* is localized.**
- ✓ **Location and age affect the tree metabolism** and the production of antibacterial metabolites.
- ✓ Current work is being done to **identify these compounds.**
- ✓ These observations seem to indicate that young ash trees are particularly susceptible to bacterial infection, thus an analysis of **antimicrobial activity against other ash pathogens would be worth assessing.**

References

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2. Grace, E.R., Rabiey, M., Friman, V.-P. & Jackson, R.W. (2021). Plant Pathology, 70 :1987– 2004. https://doi.org/10.1111/ppa.13465
3. Rodrigues, A.M., Miguel, C., Chaves, I. and António, C. (2021). Mass Spec Rev, 40: 126-157. https://doi.org/10.1002/mas.21603

* Fig 2 was made in **Biorender**

Acknowledgments

COOPER GROUP MASS SPECTROMETRY

Wytham WOODS the natural place for science