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# Differential carbohydrate-active enzymes and secondary metabolite productions by the grapevine trunk pathogen Neofusicoccum parvum Bt-67 grown on a host and non-host biomass

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## Introduction

## Experiments

Neofusicoccum parvum is one of the most aggressive Botryosphaeriaceae species in grapevine, commonly reported as one of the causal agent of Botryosphaeria dieback. This species may secrete cell wall-degrading enzymes capable of overcoming the plant cell wall barriers [1]. Furthermore, *N. parvum* produces toxic secondary metabolites that may contribute to its virulence. To increase knowledge on the mechanisms underlying pathogenicity and virulence, we evaluated the capacity of N. parvum to produce Carbohydrate-Active enZymes (CAZymes) and secondary metabolites when grown in vitro on two lignocellulosic biomasses: grapevine canes (GP) and wheat straw (WS), and with glucose (GLU) as control. For this purpose, we combined enzymology, transcriptomic, and metabolomic analyses [2].





#### **Metabolites production**



Lignocellulose degradation analysis using infrared spectroscopy



#### Most discriminant compounds:

- In GP condition:
  - ✓ Phospholipids (*e.g.*, phosphatidylcholine)
- In WS condition ✓ Mycotoxins (*e.g.*, ovalicin)
- In GLU condition ✓ Dipeptides (*e.g.*, phenylalanylthreonine)

Wheat straw **Grapevine** canes

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Relative degradation (<1) or enrichment (>1) of carbon bonds representative of the lignocellulose polymers (\* indicate statistical significance, *P*<0.05)

## **Conclusion and future work**

- $\checkmark$  Np Bt-67 showed a differential production of pathogenicity- and virulence-related factors depending on the lignocellulosic biomass.
- Transcriptomic revealed that the cellulolytic enzymes, such as LPMOs, glucosidases,  $\checkmark$ and endoglucanases were the most represented CAZymes.
- Enzymatic activities and lignocellulose biomass degradation were higher when the  $\checkmark$ fungus grew with the non-host biomass (WS).
- $\checkmark$  Some differentially produced metabolites, such as phospholipids and ovalicin, appear to be relevant to the plant-microbe interaction.
- ✓ Our future works will focus on the purification and characterization of both CAZymes and toxic secondary metabolites.



PCA analysis of metabolomic data showing segregation according to carbon source

#### Acknowledgements

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#### References

[1] Belair M, Restrepo-Leal JD, Praz C, Fontaine F, Rémond C, Fernandez O, Besaury L. 2023. Botryosphaeriaceae gene machinery: Correlation between diversity and virulence. Fungal Biology 127:1010–1031. DOI: 10.1016/j.funbio.2023.03.004 [2] Restrepo-Leal JD, Belair M, Fischer J, Richet N, Fontaine F, Rémond C, Fernandez O. (in press). Differential carbohydrateactive enzymes and secondary metabolite productions by the grapevine trunk pathogen *Neofusicoccum parvum* Bt-67 grown on a host and non-host biomass. Mycologia.