Molecular-ecological Studies on Bile Acid Degrading Bacteria in Soil for Assessment of Plant Protection Products

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Introduction

- The metabolic performance of soil bacteria is primarily assessed by nitrification1, but changes in microbial communities following the introduction of substances are not considered.
- Specific carbon and energy sources, which are only used as substrates by certain taxa, could be used to correlate metabolic activity with the structure of the soil microbial community.
- Bile acids, released by all vertebrates, are degraded by a limited number of bacterial genera such as Comamonas, Pseudomonas, Rhodococcus, or bacteria from the family Sphingomonadaceae2.
- Possibility to assess the functional capacity of the microbial metabolism of bile acids by specific bacterial taxa in the soil to provide information on the effects of plant protection products (PPP).

Aim of the study

Development of methods to measure soil bile acid degradation and identify related bacteria, then studying how pesticide pollution affects this microbial community’s ability to degrade bile acids.

Material & Methods

- Thiram fungicide
- Propamocarb fungicide
- Cholate (CA)
- Ursodeoxycholate (UDCA)

Results

- ISO15685: Inhibition of nitrification compared to control: Propamocarb: 19%, Thiram: 100%
- Minimal inhibition of propamocarb on nitrification and bile acid degradation
- High inhibition of thiram on nitrification and bile acid degradation
- Functionality of bile acid degradation in soil could serve as a parameter for analysing the effects of PPP on soil microorganisms
  - considers not only impairment of function but also the associated taxa → Structure-function correlation
- Repetitions with different soils and other PPP, veterinary drugs or other relevant substances
- Consider qPCR analysis with less robust genera
- To quantify only bacteria relevant in bile acid degradation, use already known and important genes for bile acid degradation
- Accumulation of steroid compounds that may be present extracellularly during bacterial degradation → Impairment of other important soil organisms3

Conclusion

- qPCR analysis of the specific genera Pseudomonas and Comamonas
  - Inhibition of Pseudomonas (Thiram + CA) and Comamonas (Propamocarb + UDCA), was observed with both, qPCR and Metabarcoding, consistently.

Cultivation of bile acid-degrading soil bacteria

- Significantly increased growth of bile acid-degrading bacteria in soils spiked with the CA and UDCA.
- Thiram: Significantly inhibited growth of CA degrading bacteria with, clear tendency with UDCA-degrading bacteria.

Outlook

- Repetions with different soils and other PPP, veterinary drugs or other relevant substances
- Consider qPCR analysis with less robust genera
- To quantify only bacteria relevant in bile acid degradation, use already known and important genes for bile acid degradation
- Accumulation of steroid compounds that may be present extracellularly during bacterial degradation → Impairment of other important soil organisms

4 All figures in Material & Methods are created with Biorender.com