UNRAVELING THE ZEARALENONE DEGRADATION PATHWAY USING A POLY-OMICS APPROACH

Laura De Mets1, Kris Audenaert1, Arnau Vidal Corominas2, Filip Van Nieuwerburgh3, Leen De Gelder1

1Department of Applied Biosciences, Faculty of Bioscience Engineering, laura.demets@ugent.be; 2Department of Bioanalysis, Faculty of Pharmaceutical Sciences, 3Department of Pharmaceutics, Faculty of Pharmaceutical Sciences

Introduction

The microbial detoxification of mycotoxins is a promising tool to mitigate mycotoxins. However, the degradation pathway and metabolites need to be well defined to meet legislative requirements. Using a poly-omics approach, including a genomic and transcriptomic analysis, we aim to unravel the degradation pathway of the ergotistic mycotoxin zearalenone (ZEN) by Actinobacteria.

The toxicity of ZEN lies in its lactone ring and the C-4 hydroxy group. Cleavage of the lactone ring followed by spontaneous dehydroxylation as well as cleavage of the aromatic ring are shown to induce lowered toxicity. However, in multiple studies toxicity is not tested; no degradation products can be identified or degradation products show higher toxicity which is detrimental for the application! Can a poly-omics approach be the solution?

Objective

- Obtain zearalenone-degrading Actinobacteria and understand the circumstances wherein the degradation takes place.
- Obtain a high-quality full genome sequence and conduct a transcriptomic RNAseq analysis to find differentially expressed genes and pinpoint important degradation steps and enzymes.
- Find a gateway towards practical application in pre- and post harvest remediation.

Workflow

 Screening of the Actinobacteria strain collection

Poly-omics approach

Application in pre- and post-harvest remediation

First results – Screening of Actinobacteria

18 Actinobacteria have been screened for the detoxification an degradation of 5 ppm ZEN, both in a rich medium and a minimal medium.

Degradation

Table 1: Degradation of ZEN by relevant strains in rich growth medium after 3 days. Percentages are calculated based on the initial concentration of 5 ppm ZEN. Results obtained via LC-MS/MS after QuECHERS extraction.

<table>
<thead>
<tr>
<th>Strain</th>
<th>Degradation in 3 days</th>
<th>Adsorption by pellet in 3 days</th>
</tr>
</thead>
<tbody>
<tr>
<td>S. cerevisiae R189</td>
<td>85.50%</td>
<td>0.97%</td>
</tr>
<tr>
<td>B. subtilis IAM1</td>
<td>58.38%</td>
<td>7.24%</td>
</tr>
<tr>
<td>S. carbonicus 16.25</td>
<td>76.60%</td>
<td>4.42%</td>
</tr>
<tr>
<td>B. coagulans 4.92</td>
<td>86.82%</td>
<td>3.10%</td>
</tr>
</tbody>
</table>

- Degradation resulting in both higher and lower toxicity
- Degradation products can be more toxic
- Low adsorption by bacterial cell pellets

Conclusion

- Degradation of mycotoxins by microorganisms is a promising tool to be implemented in integrated crop management systems.
- Degradation of zearalenone does not always entail detoxification.
- Rhodococcus and Streptomyces strains show divergent ZEN metabolism.
- The poly-omics approach will allow to identify biodegradation genes and enzymes, important for application in pre- and post-harvest remediation of grains.

References

1. Vanhaecke et al. (2018) Bio 15.1394/1916.05.01