IN SILICO DISCOVERY OF POTENTIAL DEHYDROGENASES FOR DEOXYNIVALENOL BIODEGRADATION

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INTRODUCTION

The conventional method for **preventing animal mycotoxicosis** consists in the application of feed additives to adsorb mycotoxins. However, this is often inefficient due to the toxins' structural diversity, particularly in the case of **deoxynivalenol** (DON), whose characteristic physicochemical properties make it **resistant to standard adsorption methods**.

DON primarily **compromises intestinal integrity** and exerts **strong immunotoxic effects**, leading to **severe animal health issues** and **major economic losses** (Sabater-Vilar et al., 2007). Because conventional adsorbents have proven limited mitigation of DON's toxicity, there is an **urgent need for developing alternatives**, such as **enzymatic biotransformation**, to **convert DON into less toxic compounds** like **3-keto-DON** (Abraham et al., 2022).

OBJECTIVE

The aim of this study was to **identify and select dehydrogenase candidates for DON degradation** using computational discovery tools. The strategy was divided into **data compilation**, **massive virtual screening**, and **candidate validation**.

MATERIALS AND METHODS

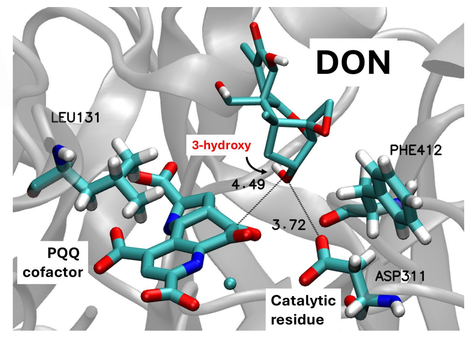
GENOMIC SEARCHES (bioinformatics)	**VIRTUAL SCREENING** (artificial intelligence + modelling)	**CANDIDATE VALIDATION**

Bibliography research: DON degrading enzymes → **Retrieval of Protein Sequences** BLAST, HMMer → **Predicting 3D structures** AlphaFold → **Molecular modelling of protein flexibility** Modeller → **Docking of DON to the active sites:** AutoDock VINA → **Candidate selection from docking** → **Result: Protein Hits**

REFERENCE SEQUENCE:
Sorbose dehydrogenase from
Ketogulonicigenium vulgare *(Li et al., 2023)*

- **1st iteration:** BLAST search against GenBank
- **2nd iteration:** Hidden Markov Models (HMMer) search against Uniprot

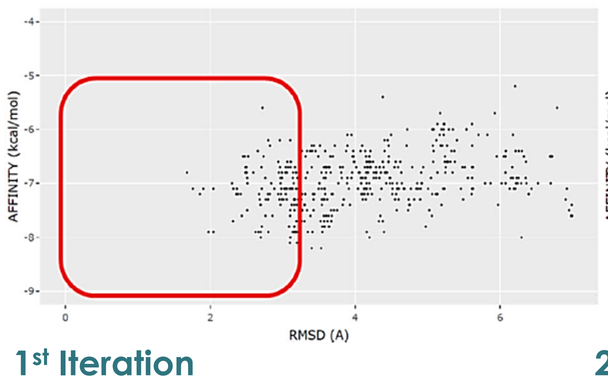
DOUBLE SELECTION CRITERIA:
1- High binding affinity
2- Structural similarity (RMSD) to reference binding mode



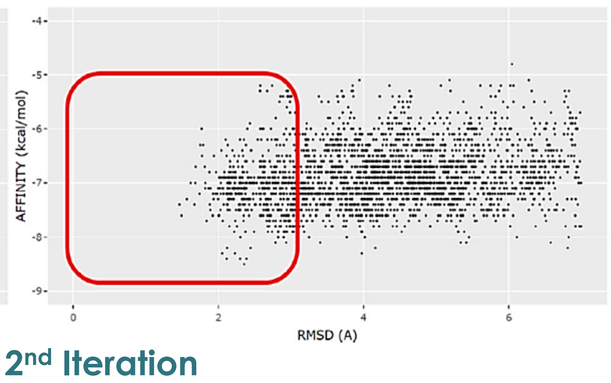
Model of the reference binding mode of DON to the active site of DepA from *Devosia sp.*

RESULTS

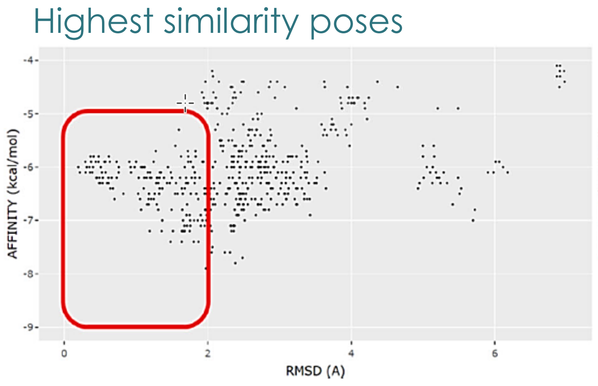
1st Iteration
Highest binding affinity poses



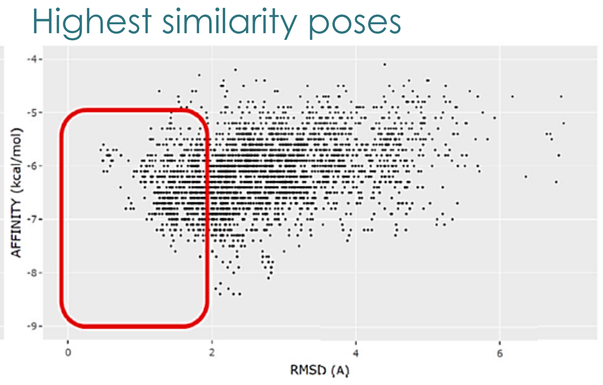
2nd Iteration
Highest binding affinity poses



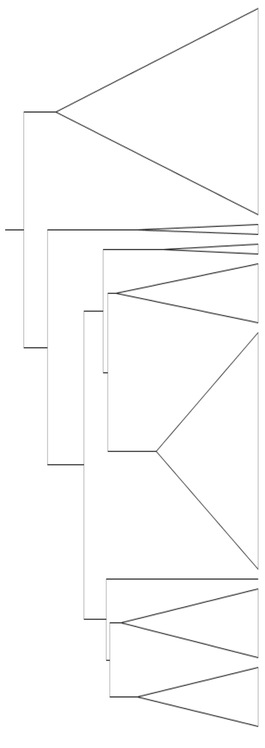
1st Iteration
Highest similarity poses



2nd Iteration
Highest similarity poses



Clustering of candidate enzyme sequences



HIGHLIGHTS:

74 **DEHYDROGENASE ENZYME CANDIDATES IDENTIFIED** FROM GENOMIC SEARCH PHASE

10 **HIT DEHYDROGENASE ENZYME CANDIDATES SELECTED** FROM CANDIDATE VALIDATION

4 **MAIN PHYLOGENETIC GENERA**

- *Pseudogluconobacter*
- *Devosia*
- *Acidobacteria*
- *Ketogulonicigenium*

CONCLUSIONS

This study explores **enzymatic biotransformation** as an **alternative** to conventional mycotoxin mitigation strategies, focusing specifically on **dehydrogenases for DON conversion**. The ***in silico* evaluation** employed a high-throughput pipeline that integrated **bioinformatics-driven genomic searches with AI-guided structural modelling** for the discovery of new dehydrogenase candidates. This roadmap offers **valuable insights** for guiding **future experimental research into biotechnological detoxification solutions** for the animal nutrition industry.

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