



A study of drug metabolism in zebrafish larvae using MALDI-MS Imaging

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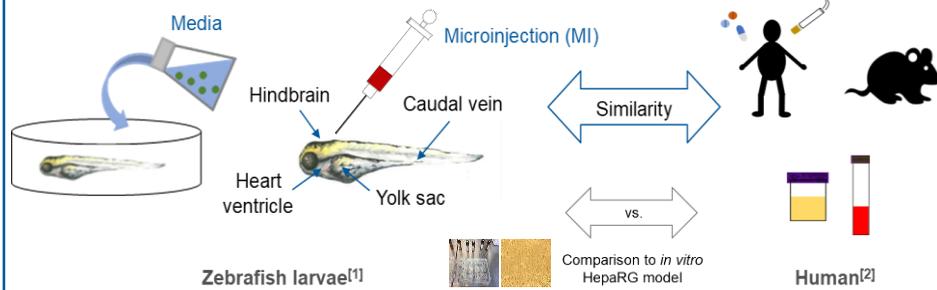
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Introduction

In this study we identified metabolites of a drug and the distribution of its metabolites in zebrafish larvae using LC-MS/MS and MALDI-MSI. Zebrafish (*Danio rerio*, abbr. ZF) larvae have been investigated as a promising vertebrate model to study drug metabolism (DM) due to their easy handling in high-throughput *in vivo* metabolite identification workflows. Mass spectrometry imaging (MSI) is a powerful technology allowing for visualization and analysis of the spatial distribution of molecules without labelling or staining. Matrix-assisted laser desorption/ionization (MALDI)-MSI has previously been proven to be suitable for the analysis of small molecules such as drugs and their metabolites in tissue samples.

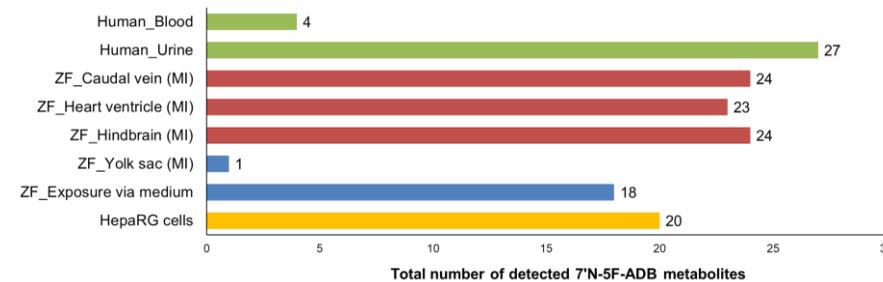
New approach of ZF larvae to study *in vivo* DM

Can ZF larvae help to predict human drug metabolism?

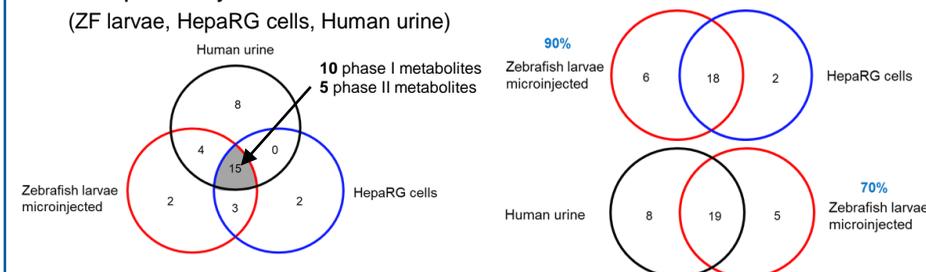


Results

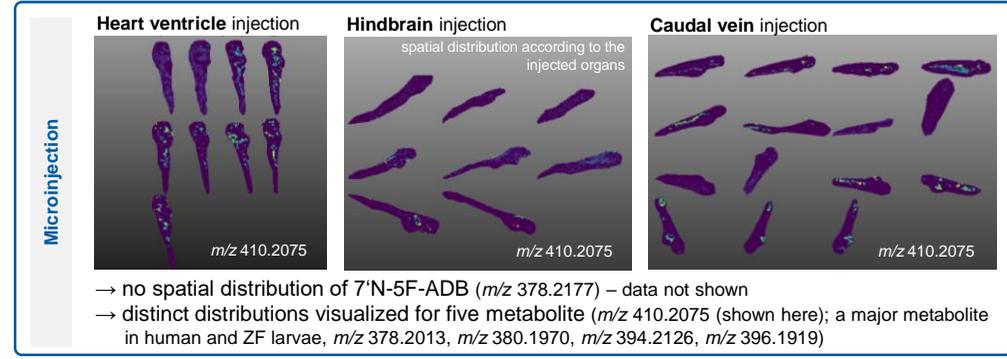
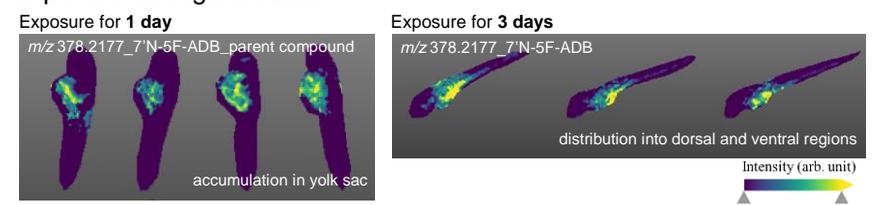
Comparison of the detected metabolites following different administrations



Comparability of the metabolites detected in three models (ZF larvae, HepaRG cells, Human urine)



Visualization of the spatial distribution of the parent drug in ZF larvae after exposure through medium



Summary

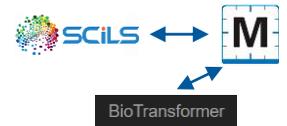
- Metabolites were compared among three different models (i.e., ZF larvae, HepaRG cells, human urine)
- Microinjection in different organs was applied in ZF drug metabolism model
- The distribution of 7*N-5F-ADB and its metabolites was studied using MSI

Conclusions

- ZF larvae model is a promising tool to study human drug metabolism
- MSI can help to optimize compound administration in DM model of ZF larvae

On-going works

- Application of new drugs to MSI method in ZF larvae
- Optimization of MSI method in zebrafish larvae
- Data interpretation integrated by DM and MSI results



Ref. ^[1] Richter LHJ et al., Drug Test Anal 2019, 11, 305-317, ^[2] Richter LHJ et al., Toxicol Lett 2019, 305(1), 73-80, ^[3] Kirla KT et al., Toxicol Sci 2016, 154(1), 183-193, ^[4] Djoumbou Feunang Y et al., J Cheminform 2019, 11 (1), 2.

Method

