

Translational quantitative systems pharmacology

crossing borders between experimental and computational drug development using zebrafish as model organism

Rob van Wijk, Elke Krekels, Wanbin Hu, Astrid van der Sar, Sharka Dijkema, Dirk-Jan van den Berg, Rida Bahi, Jeremy Liu, Theo Verboom, Fons Verbeek, Ulrika Simonsson, Herman Spaink, Piet van der Graaf

PAGE Lewis Sheiner Student Session 2020

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Learning versus confirming in (pre)clinical



CLINICAL PHARMACOLOGY & THERAPEUTICS

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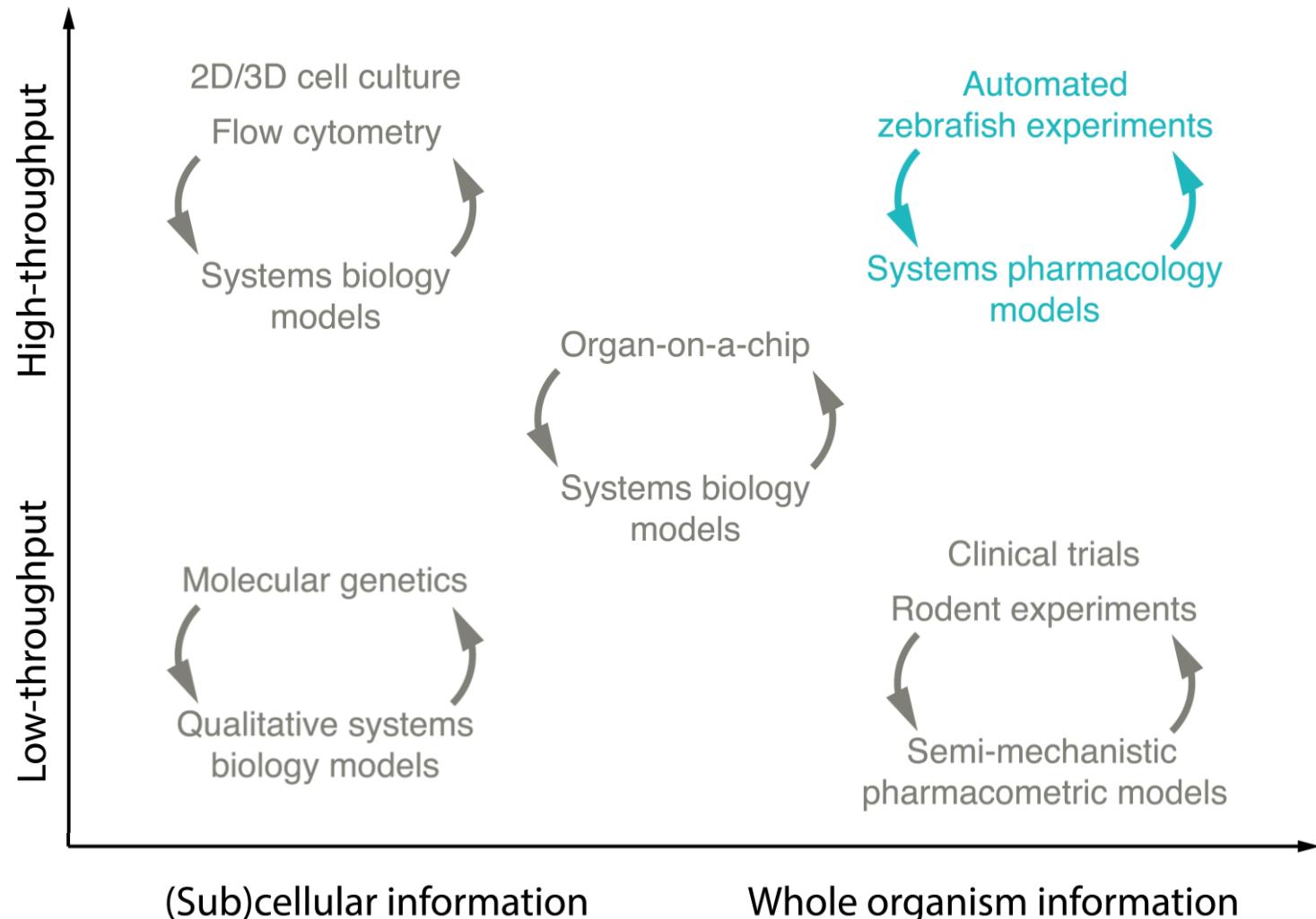
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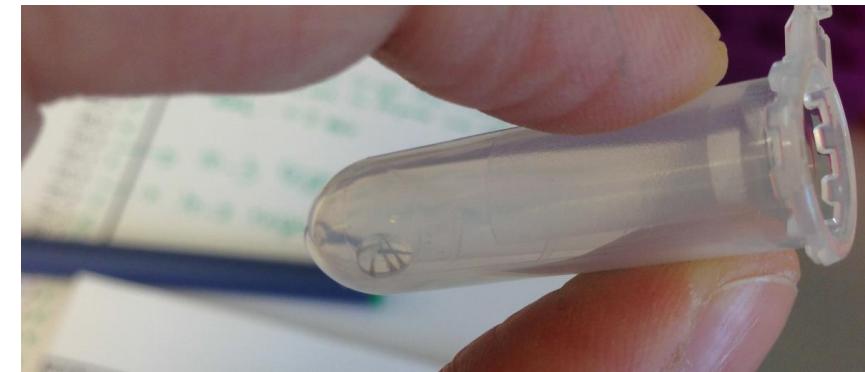
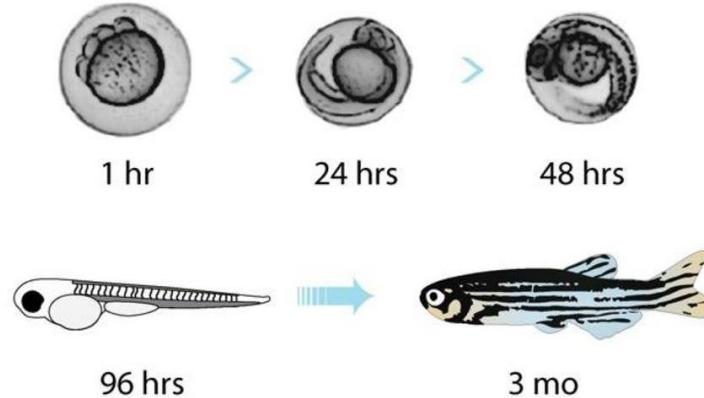
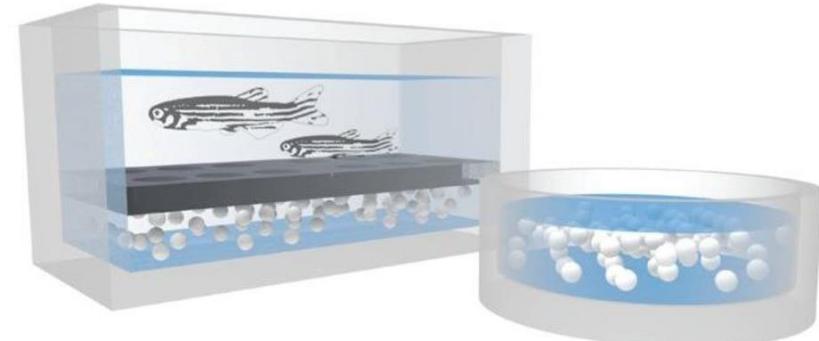
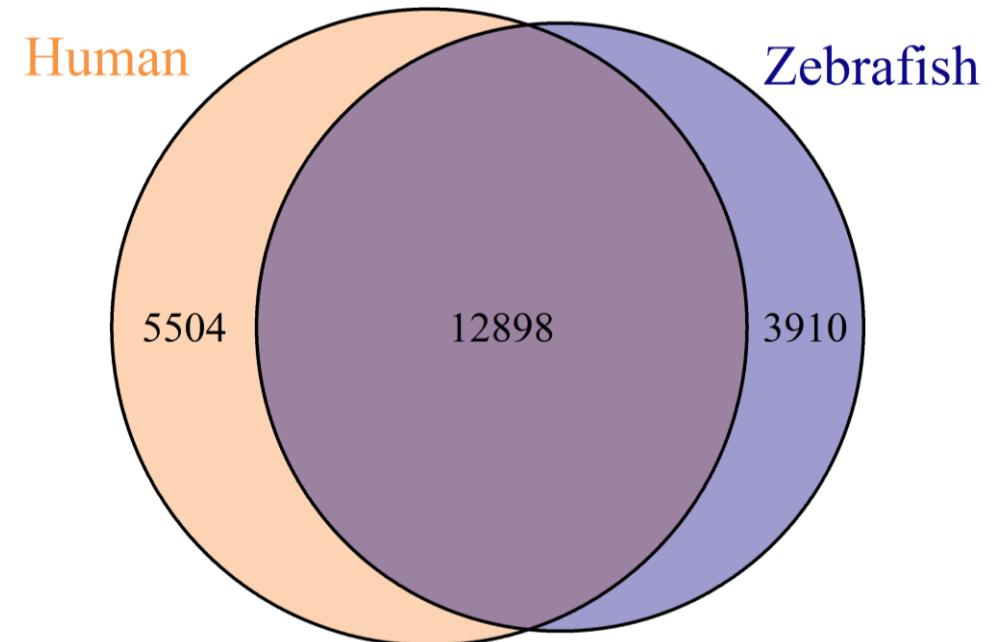
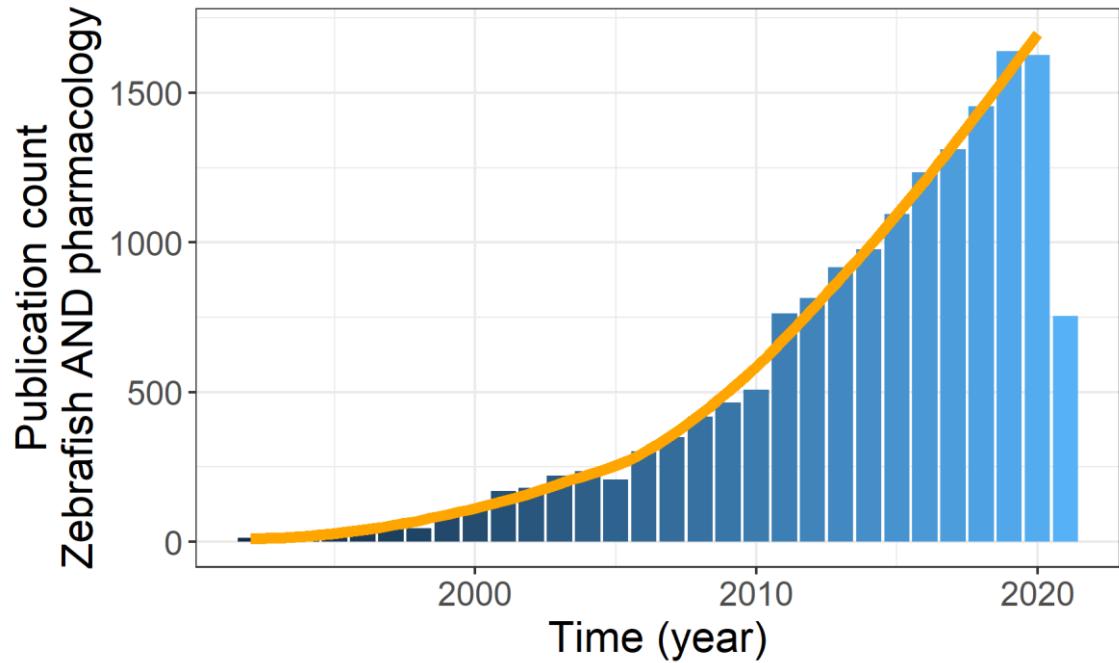
Learning versus confirming in clinical
drug development

Lewis B. Sheiner, MD *San Francisco, Calif.*

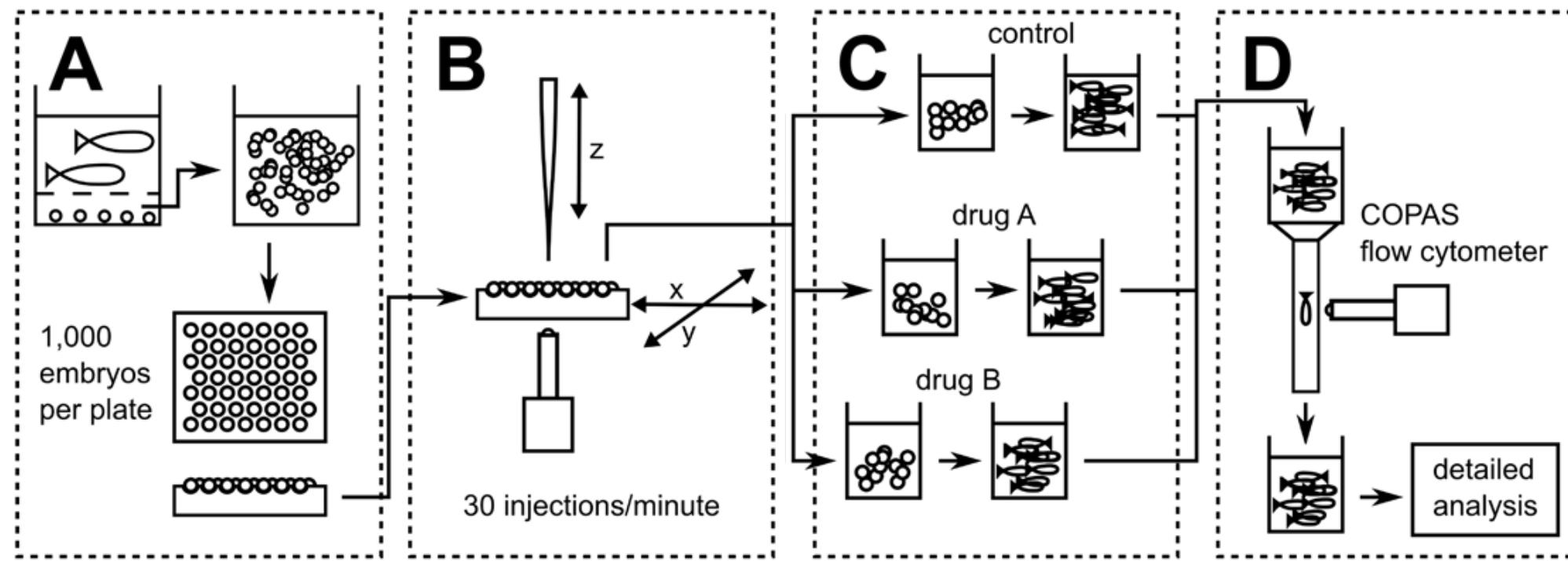
Quantitative systems pharmacology requires high-throughput data



Zebrafish as experimental vertebrate

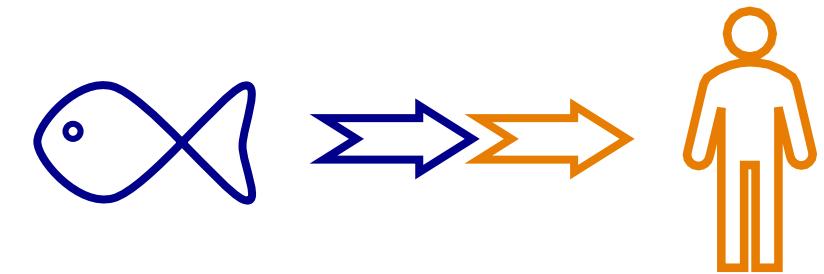
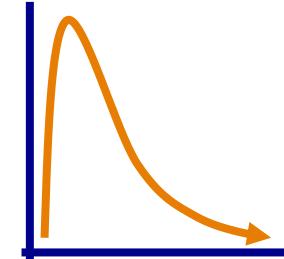


Imaging based high throughput infection study

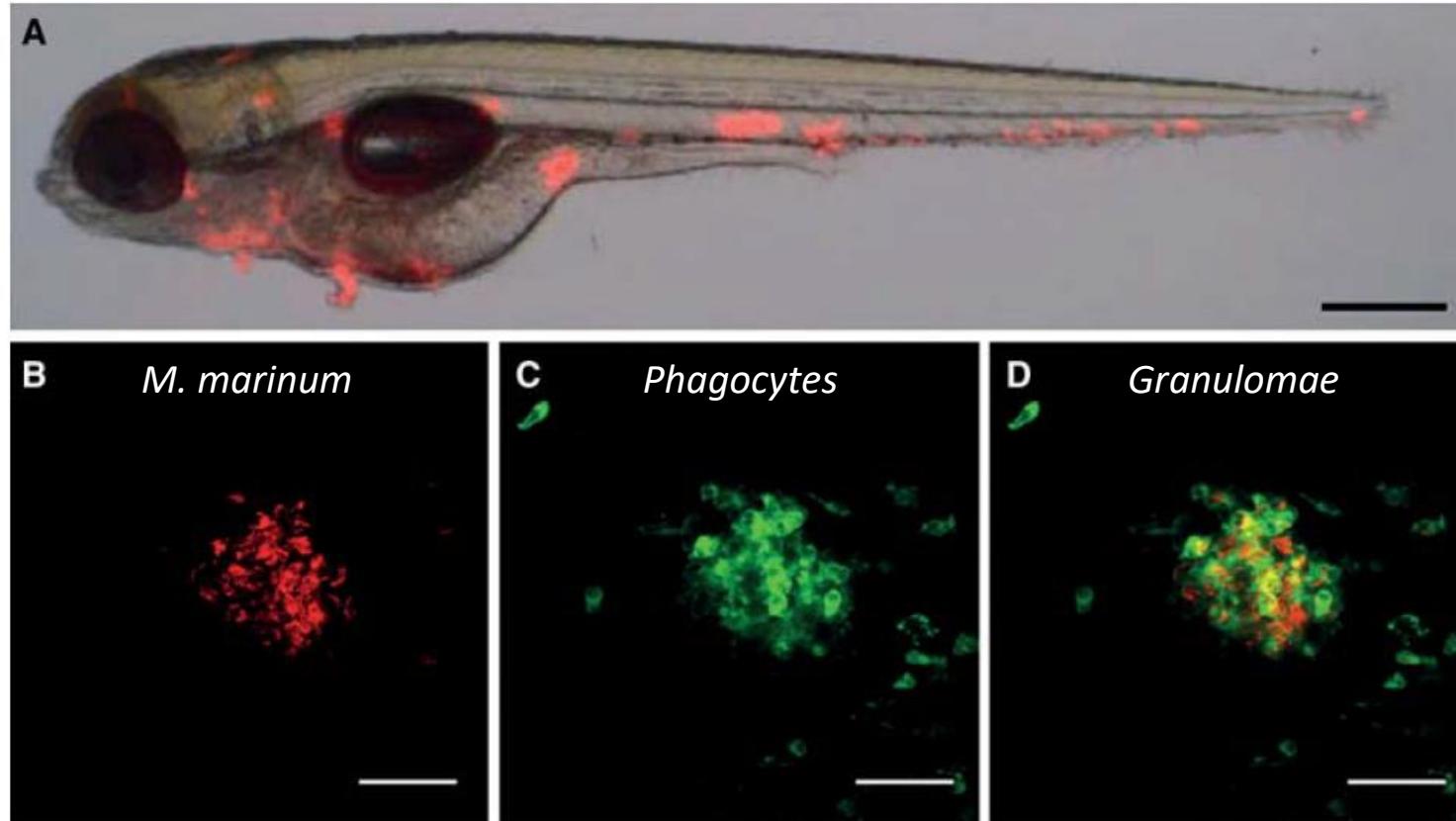


Challenges for zebrafish in QSP

- Quantification of internal drug exposure
- Quantification of between-species differences in disease and disease progression



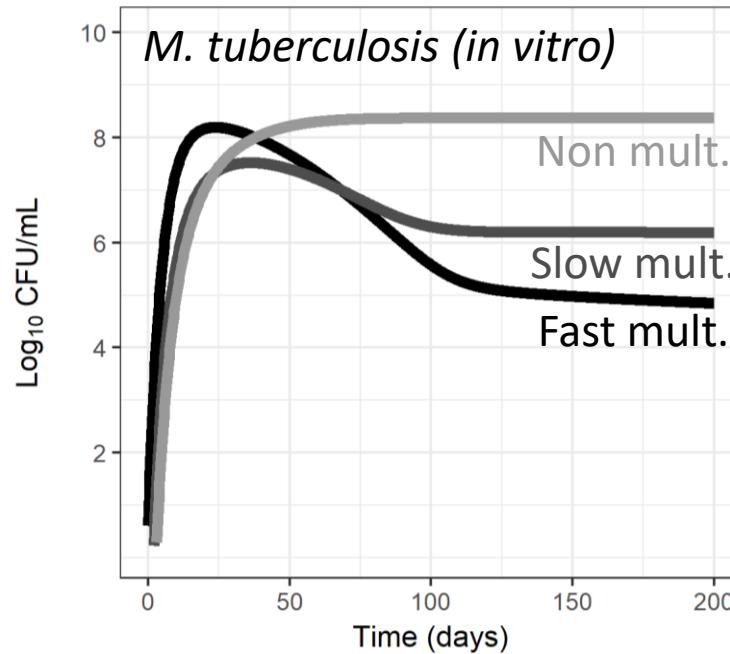
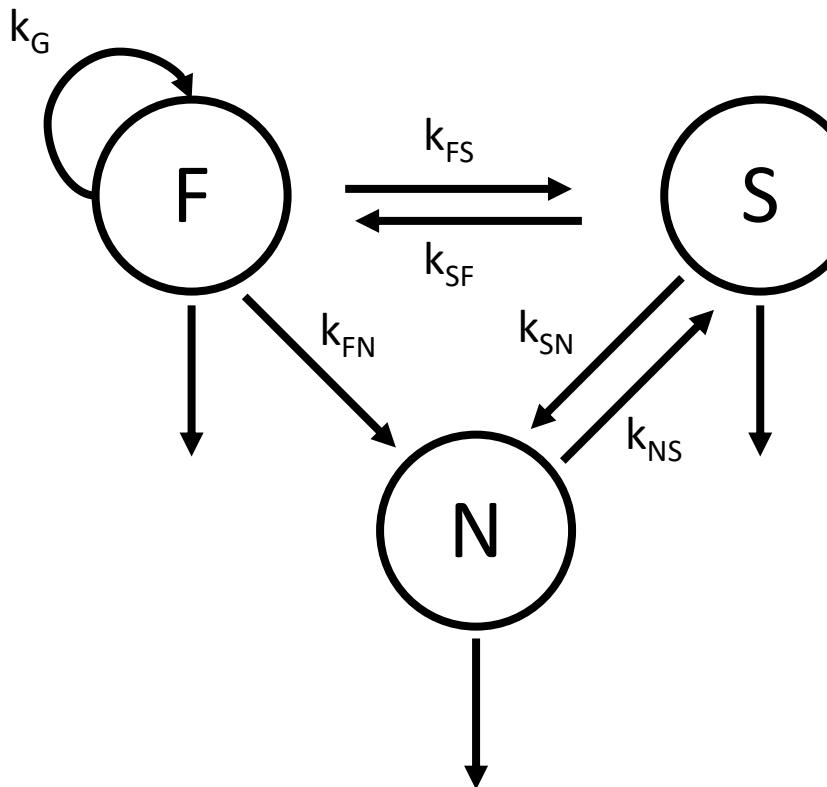
Zebrafish as disease model for tuberculosis



Zebrafish shows TB hallmark of granuloma formation after *Mycobacterium marinum* infection

Quantify between-species differences in TB

Mycobacterium tuberculosis: fast, slow, or non multiplying state

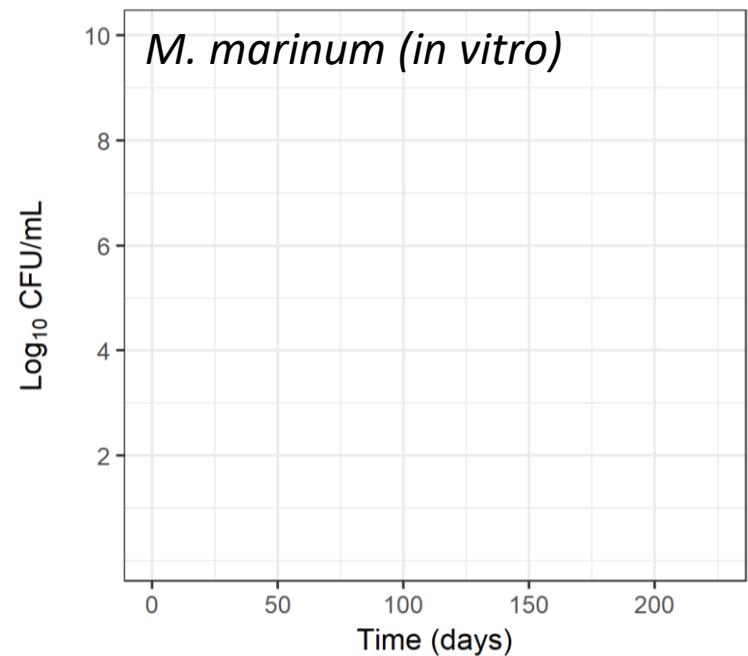
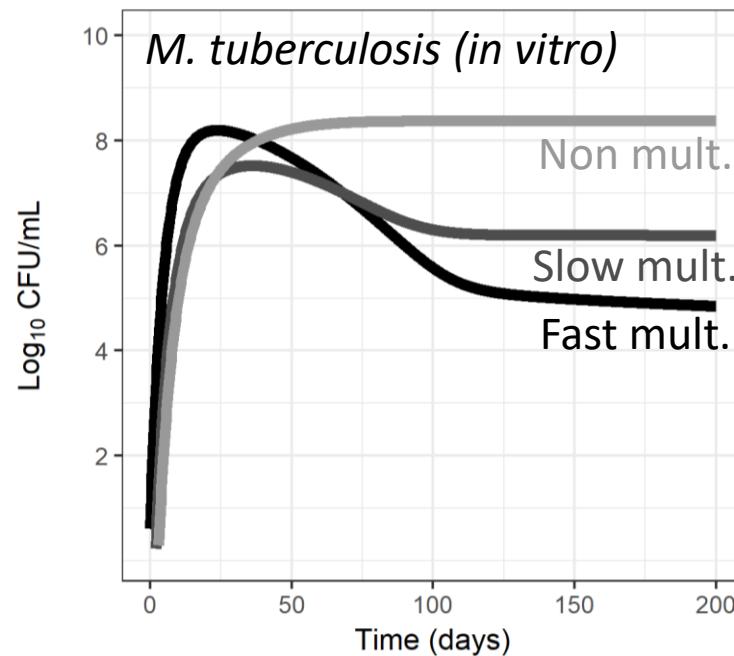
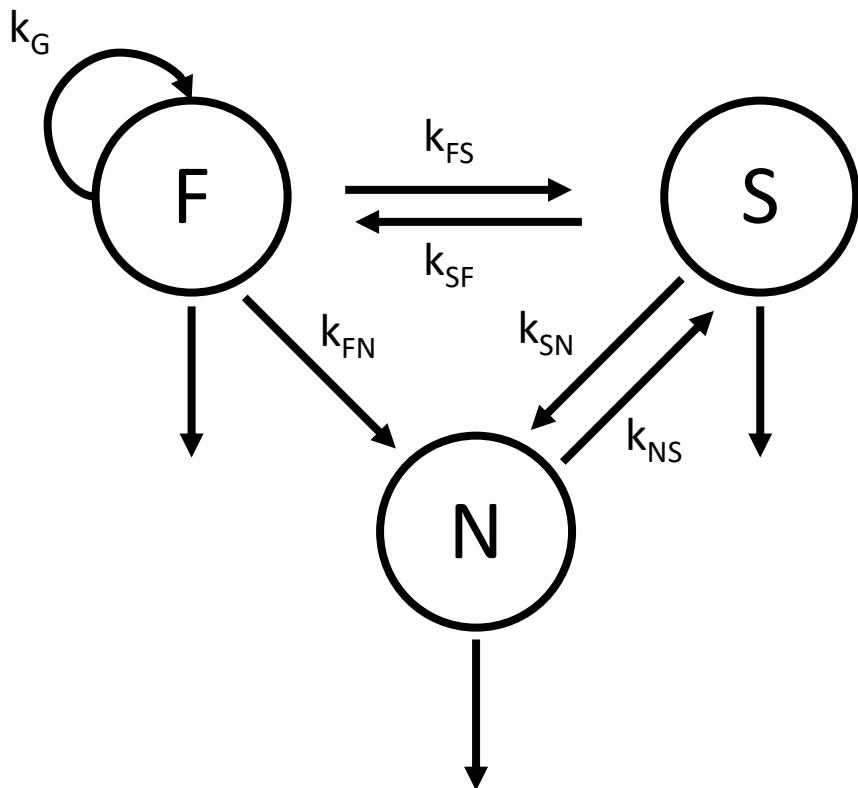


Successful prediction:
- *in vitro*
- Mice
- Patients

Multistate Tuberculosis Pharmacometric (MTP) model

Quantify between-species differences in TB

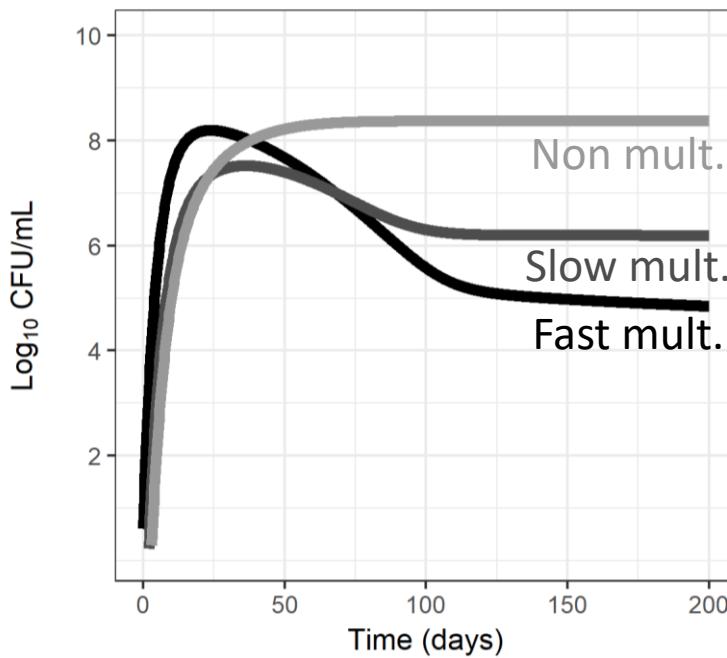
Mycobacterium tuberculosis compared to *Mycobacterium marinum*



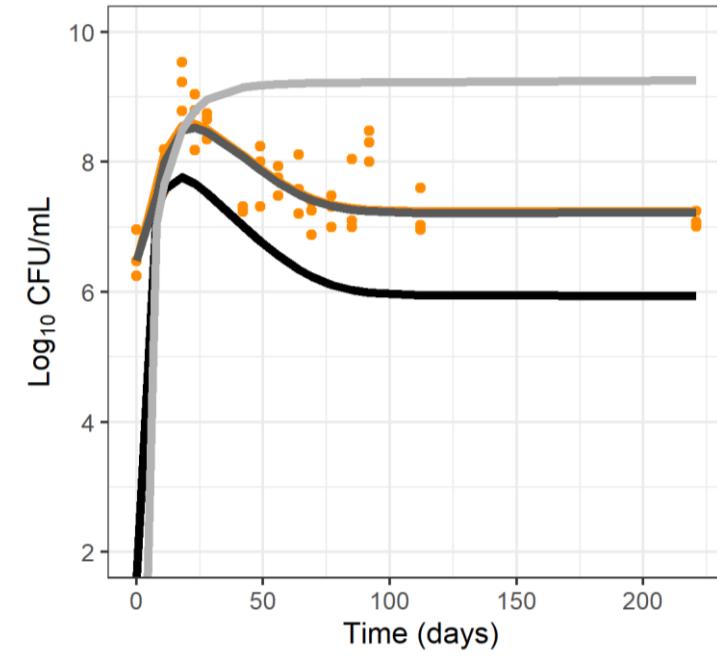
Multistate Tuberculosis Pharmacometric (MTP) model

Quantify between-species differences in TB

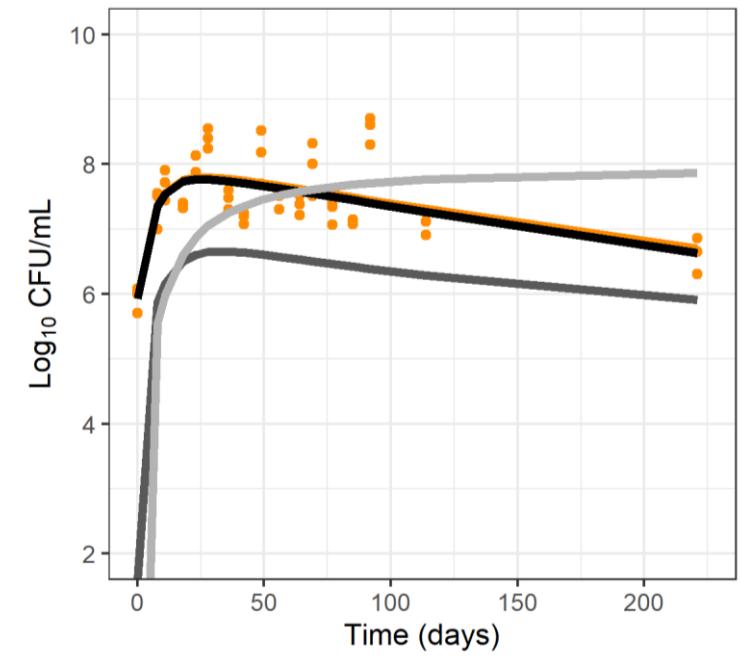
Mycobacterium tuberculosis compared to *Mycobacterium marinum*



M. tuberculosis (in vitro)

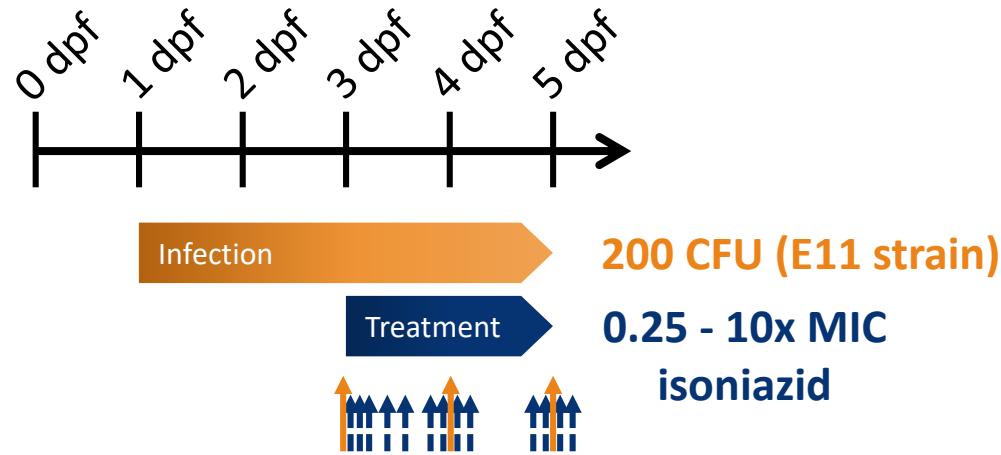


M. marinum (E11, in vitro)



M. marinum (M-USA, in vitro)

Experimental design to quantify PKPD in zebrafish



Sampling

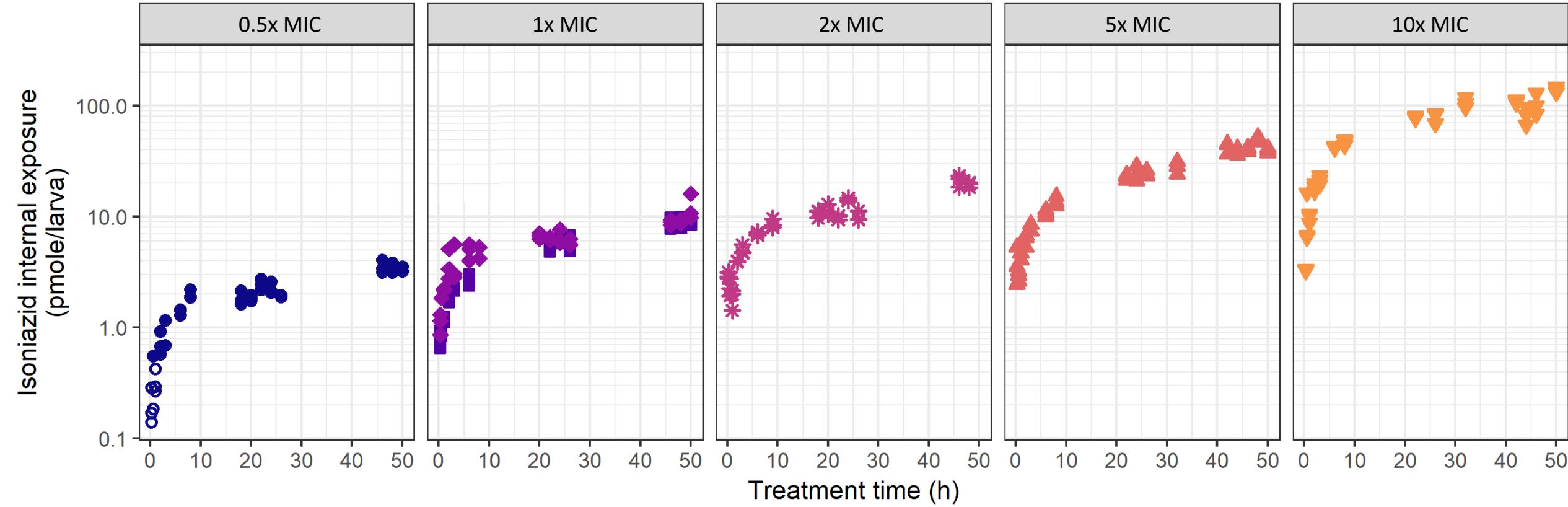
PK: Larval homogenate
Blood



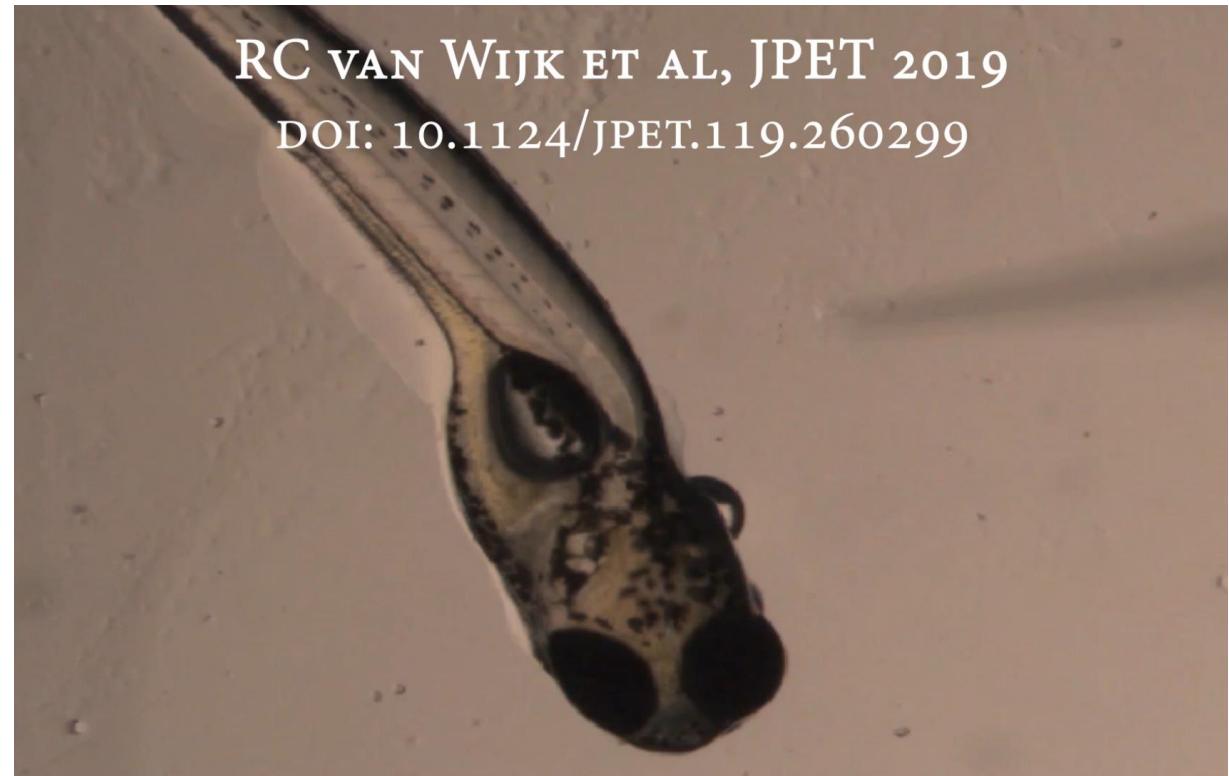
PD: Mycobacterial fluorescence



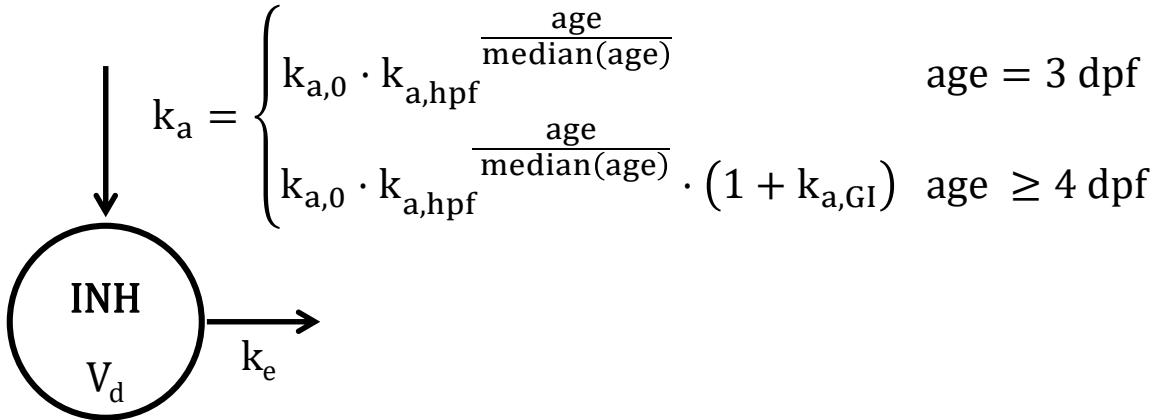
Isoniazid exposure in larval homogenates



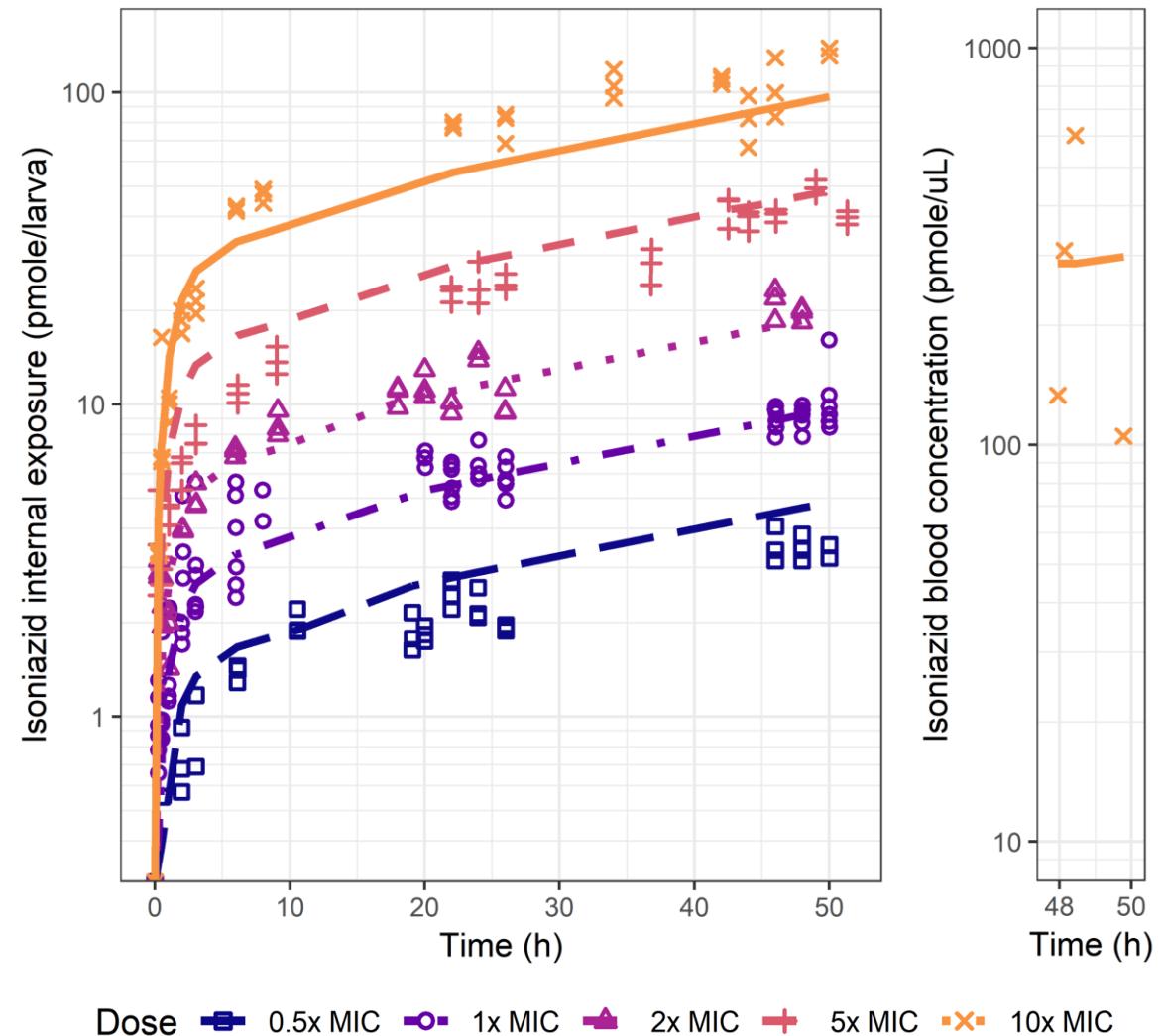
Nanoscale blood sampling



Integrated pharmacokinetics modelled

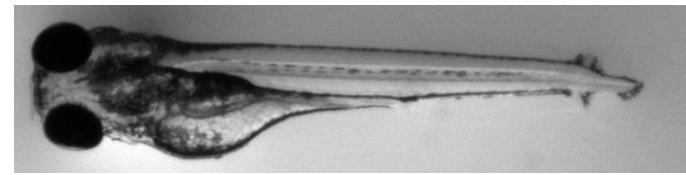
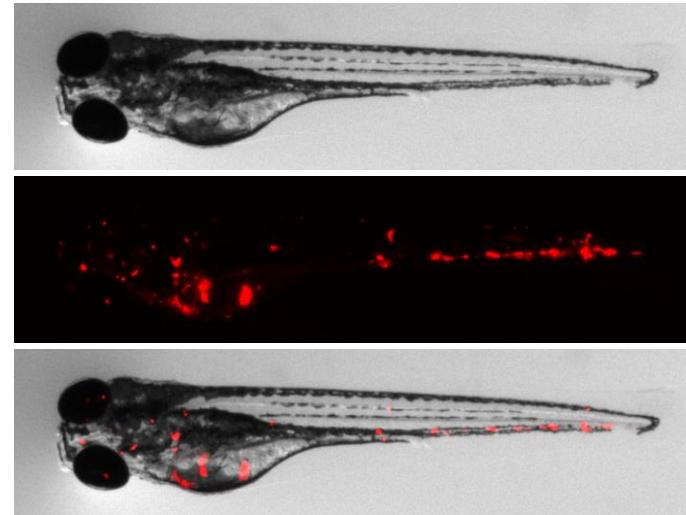
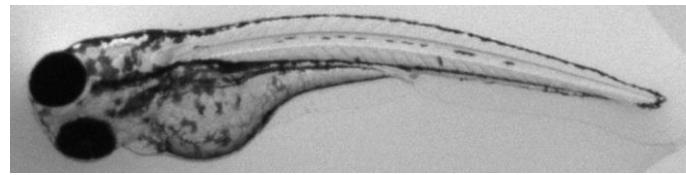
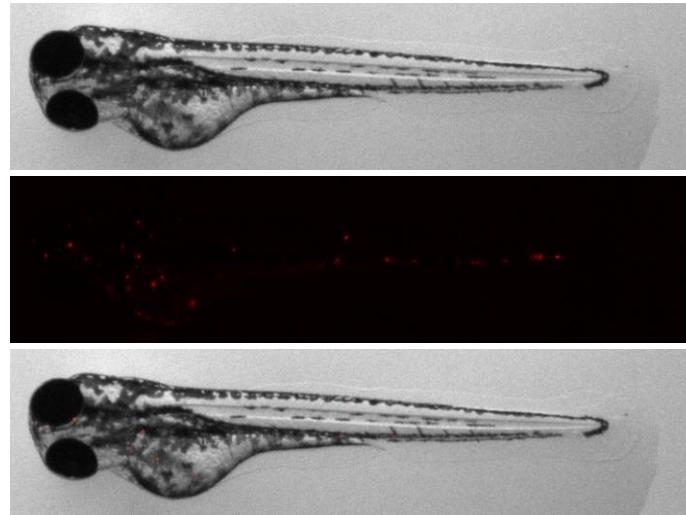


Parameter	Estimate	Relative standard error (%)
$k_{a,0}$ ($\mu\text{L}/\text{h}$)	0.00349	25
$k_{a,hpf}$	7.61	17
$k_{a,GI}$	0.171	51
k_e (/h)	0.580	32
V_d (μL)	0.325	36

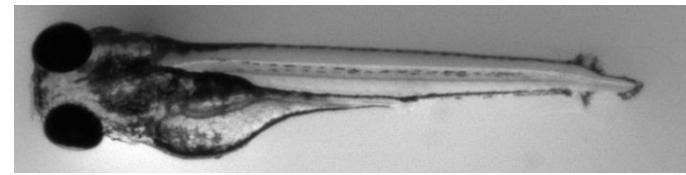
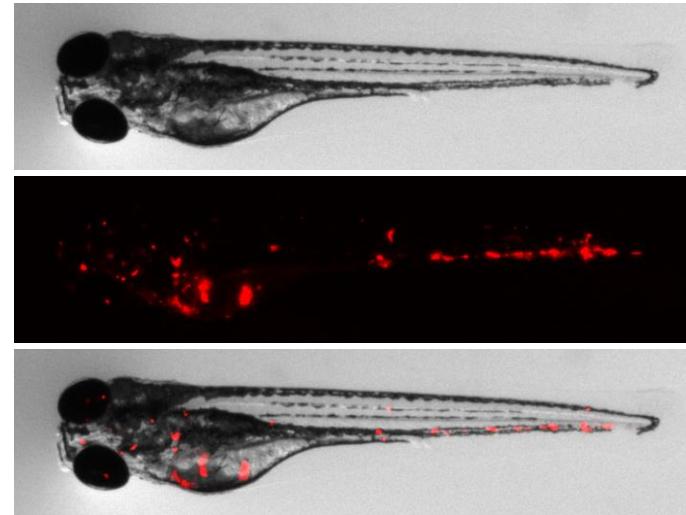
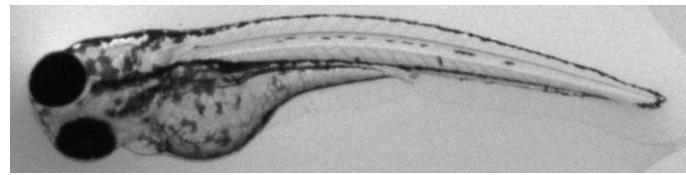
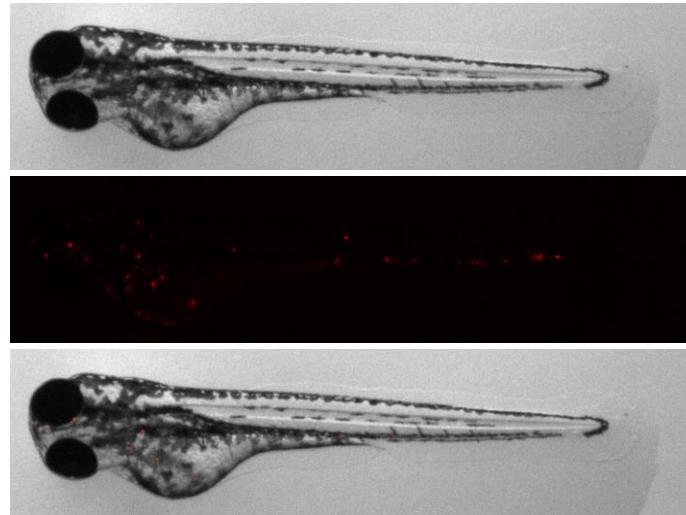


Fluorescence microscopy shows infection

Control



5x MIC

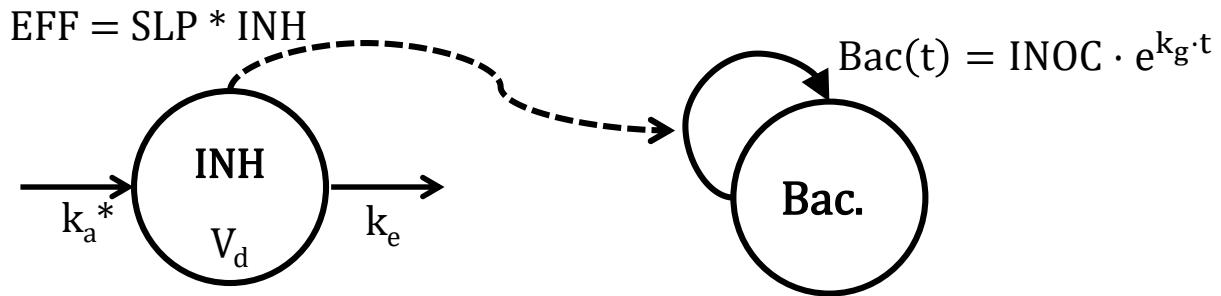
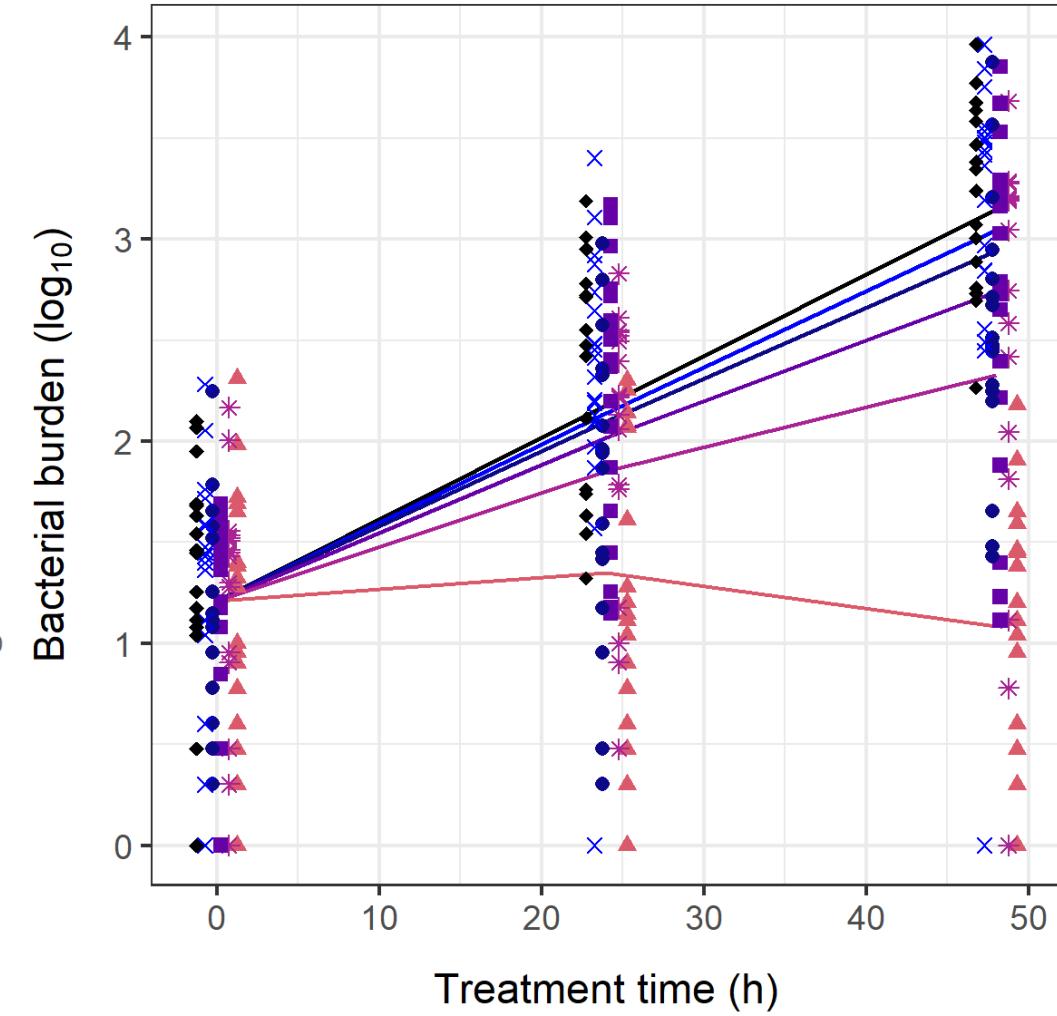
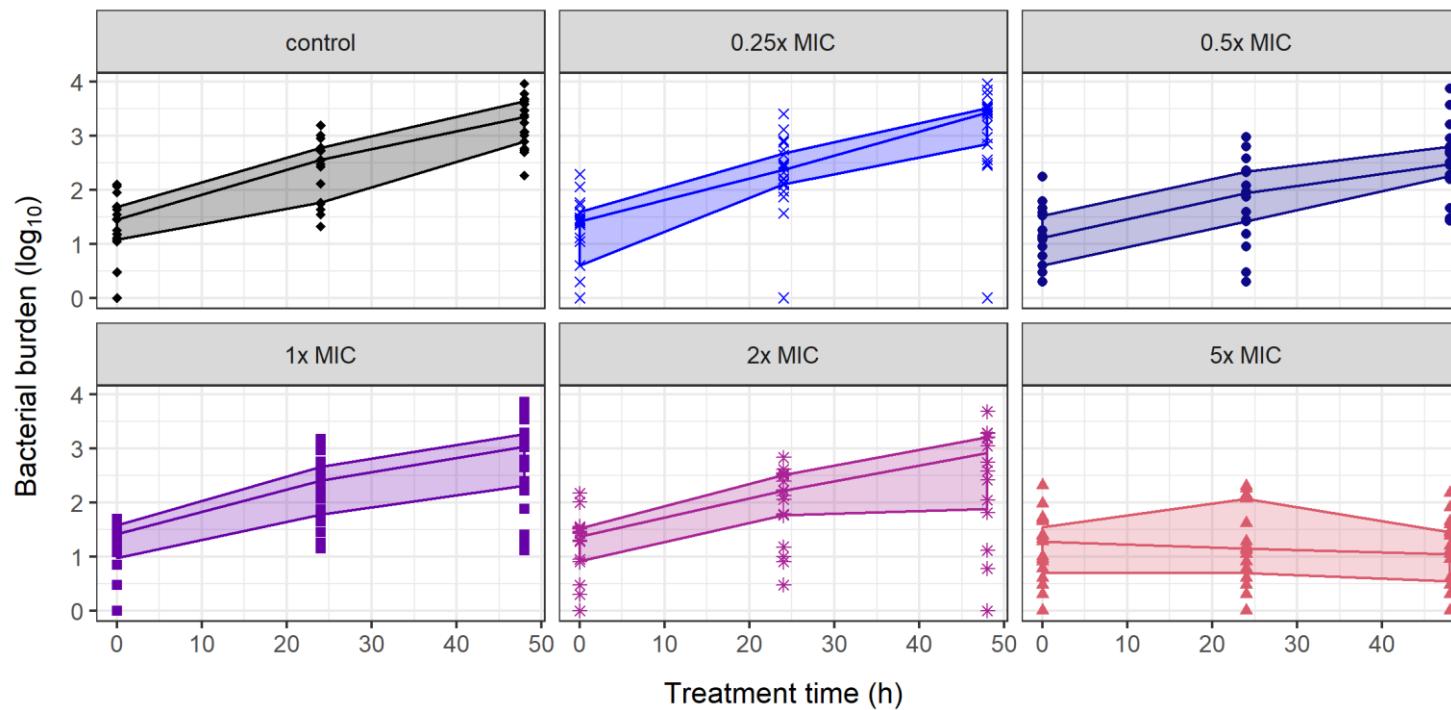


2 dpi

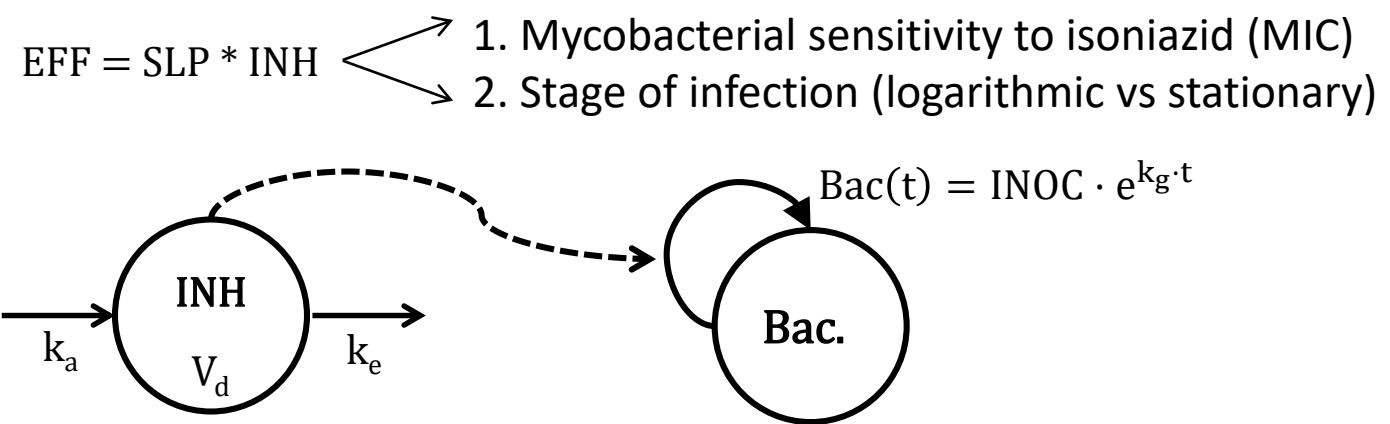
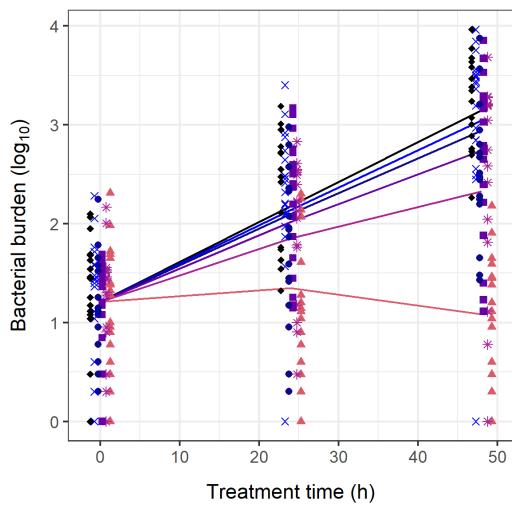
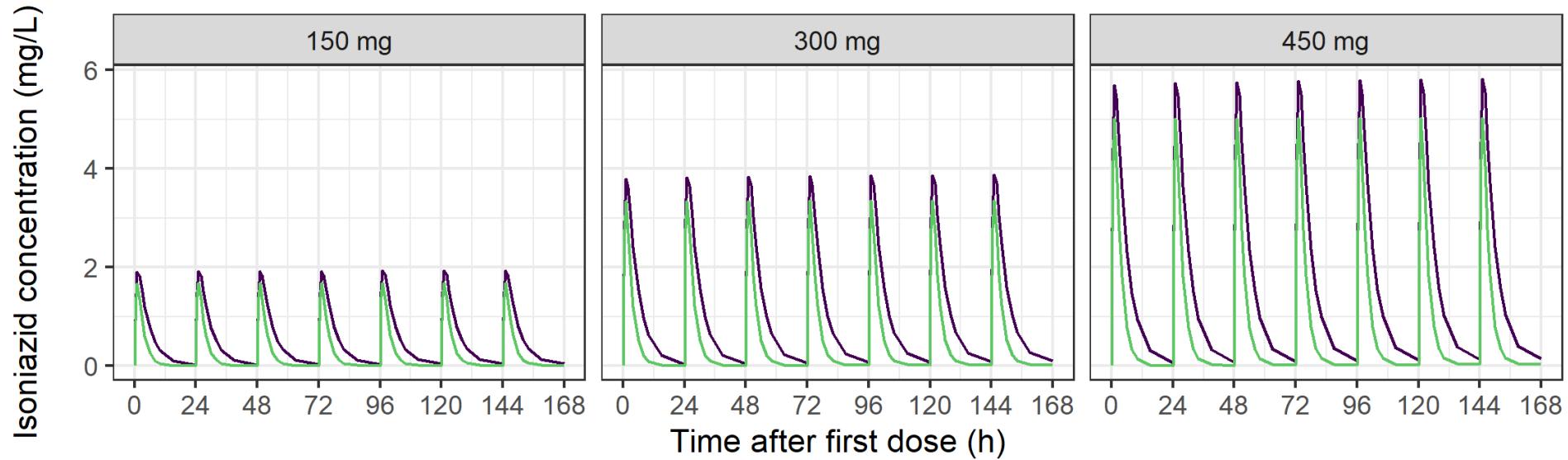
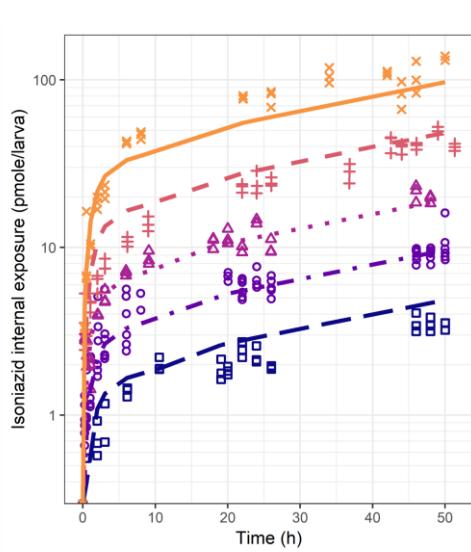
3 dpi

4 dpi

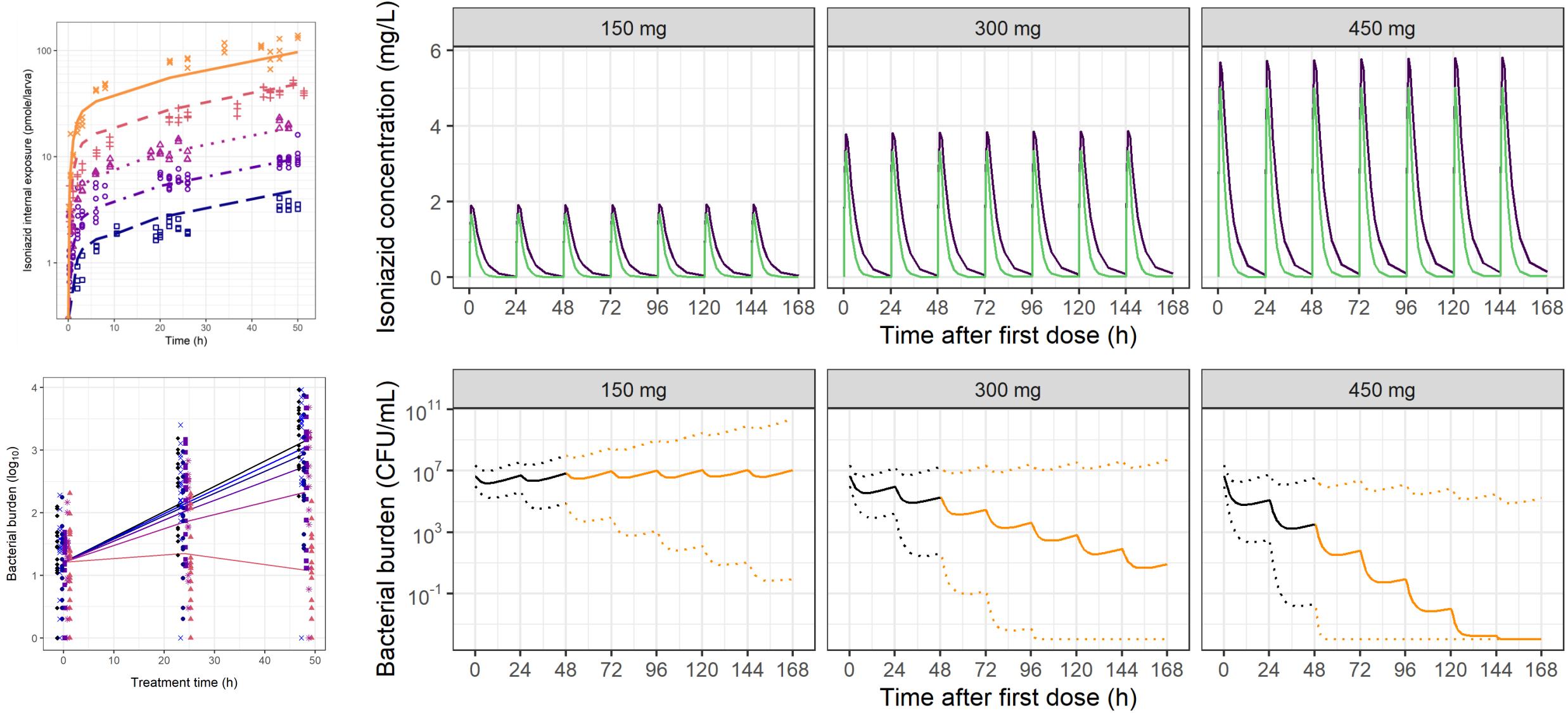
Concentration-effect relationship quantified



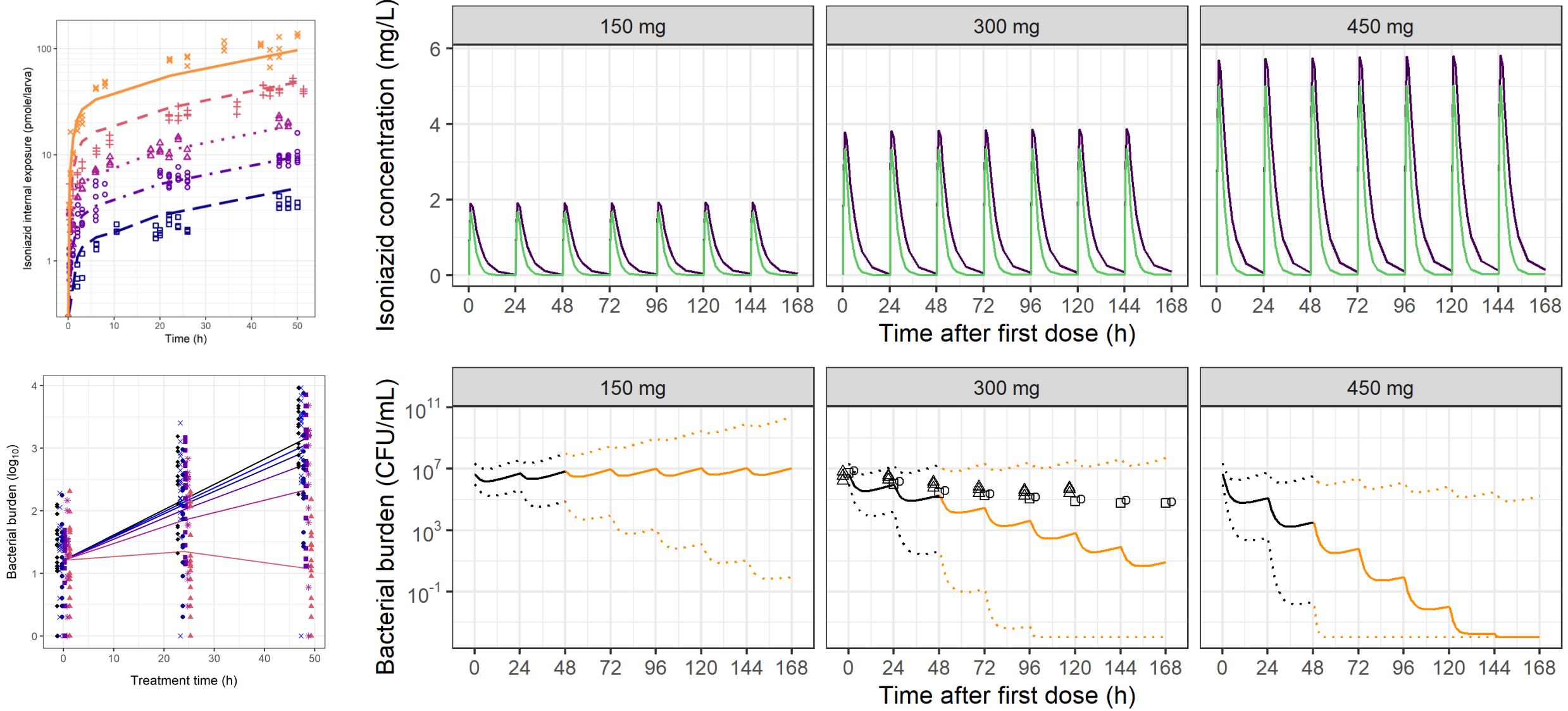
Translate from zebrafish to human?



Translate from zebrafish to human?

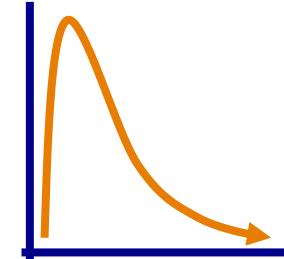


Translate from zebrafish to human!

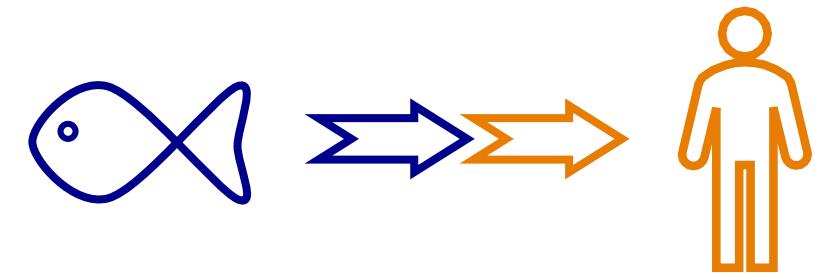


Conclusion

Internal drug exposure
quantified to determine the
exposure-response relationship



Promising translation from
zebrafish to humans based on
between-species differences



Translational quantitative systems pharmacology

crossing borders between experimental and computational drug development using zebrafish as model organism

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