Representation of Crizotinib and Pazopanib-mediated Drug-Induced Liver Injury (DILI) Using Quantitative Systems Toxicology (QST) Guncha Taneja¹, Tamas Szalai², Brett Howell¹, Scott Siler¹, Jeffrey L. Woodhead¹

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INTRODUCTION

- Crizotinib and pazopanib are oral receptor tyrosine kinase inhibitors (TKIs).
- Crizotinib is used for treatment of locally advanced or metastatic nonsmall-cell lung cancer (NSCLC); pazopanib is prescribed for metastatic renal cell carcinoma and soft tissue sarcoma.
- In the clinic, serum ALT elevations were observed in 57% of patients (6% had >5X ULN) treated with standard doses of crizotinib {Source: Livertox}.
- In clinical trails of pazopanib, >5X ULN elevations in ALT and bilirubin were observed in only 1-2% of patients {Source: *Livertox*}.
- In vitro experiments to determine whether these TKIs inhibit bile acid





plasma concentrations at single dose for crizotinib (left) and multiple dose for humans administered pazopanib (right). Simulated plasma profiles (red) are within two standard deviations of the average measured

Liver/ Plasma Kp (Crizotinib) = 39

transporters, induce production of reactive oxygen species, and/or inhibit mitochondrial electron transport chain activity were performed.

DILIsym, a QST model of DILI that incorporates drug/metabolite disposition, multiple mechanistic pathways of DILI (e.g. oxidative stress, bile acid transporter inhibition, mitochondrial dysfunction), the hepatocyte life cycle, and liver injury biomarkers, was used to assess the potential contribution of each mechanism to the observed toxicity.

METHODS

Determining TKI toxicity mechanism parameters from *in vitro* experiments MITOsym[®], a mitochondrial modeling platform used to mimic *in vitro* experimental conditions¹, was used to determine parameter values for TKI-mediated mitochondrial uncoupling by fitting simulated results to Seahorse XF96 basal respiration data for HepG2 cells exposed to crizotinib and pazopanib³. Conversion factors translated the predicted results from HepG2 cells to human hepatocytes. The ROS production constant parameter was found by sweeping through potential values until the DILIsym "in vitro-like" simulation yielded ROS effects in line with the data. The BSEP/MRP3 IC₅₀ for crizotinib and the BSEP IC₅₀ for pazopanib were used to represent the appropriate inhibition constants (K_i) in DILIsym². Further studies performed in transporter-overexpressing vesicles determined IC₅₀ values for MRP3, MRP4, and NTCP which were used for both compounds. The mode of inhibition was assumed to be mixed with $\alpha = 5$.

Physiologically-based pharmacokinetic (PBPK) model development Human PBPK models were developed in DILIsym using available in vitro and in vivo pharmacokinetic data. Distribution parameters were then optimized to get the best fit.

Simulation of crizotinib and pazopanib responses Previously SimPops that include variability in species-specific constructed parameters within the BA, ROS, and mitochondrial submodels in DILIsym were used to predict the hepatotoxic effects of crizotinib (250 mg BID, 60 days) and pazopanib (800 mg daily, 60 days) at the population level.

Mechanistic Analysis To identify the most important toxicity mechanism associated with TKI-mediated DILI in humans, each mechanism was individually inactivated and predicted ALT elevation frequencies for each simulation were compared. DILIsym[®] Overview



CONCLUSION

- Mitochondrial Uncoupling and ROS production were the primary drivers of predicted increases in ALT with crizotinib and pazopanib administration respectively.
- In general, tox parameters derived from intracellular concentrations better predict clinically observed liver signals compared to nominal, but further investigations to understand discrepancies in crizotinib hepatotoxicity are ongoing.
- Quantitative systems toxicology (QST) models can be used to evaluate DILI mechanisms and investigate observed differences among drugs in the same class.

Temple's Corollary Range Normal Rang Peak ALT x ULN

500 mg BID, 60 **Crizotinib-Simulated** days (2X clinical (Kp assumption)

(Nominal assumption)	days	(285/285)
Pazopanib – Simulated	800 mg, 60	0.7%
(Kp assumption)	days	(2/285)

Each mechanism was simulated as the sole contributor to study its individual effect on toxicity in humans. ALT elevation frequency declined for pazopanib when ROS was inactivated; Mitochondrial Uncoupling was the main driver of ALT with crizotinib at 2X dose. The elimination of other mechanisms did not have an effect on the simulated ALT elevation frequency. Previously constructed SimCohorts that include variability in BA, ROS, and mitochondrial submodels within DILIsym (n=16) were used for this analysis.

Mechanistic Analysis

87.5%

(14/16)

	Oxidative Stress	BA Inhibition	Mitochondrial Uncoupling	ALT >3X ULN
Pazopanib	Yes	Yes	-	1/16
Pazopanib	No	Yes	-	0/16
Pazopanib	Yes	No	-	1/16
Crizotinib (2X)	Yes	Yes	Yes	14/16
Crizotinib (2X)	No	Yes	Yes	14/16
Crizotinib (2X)	Yes	No	Yes	14/16
Crizotinib (2X)	Yes	Yes	No	0/16

References: 1. Yang, Y. et al. "MITOsym[®]: A Mechanistic, Mathematical Model of Hepatocellular Respiration and Bioenergetics." Pharmaceutical Research (2015). 2. Howell, BA et al. "In vitro to in vivo extrapolation and species response comparisons for drug-induced liver injury (DILI) using DILIsym[™]: a mechanistic, mathematical model of DILI." Journal of Pharmacokinetics & Pharmacodyn. (2012). 3. Paech, Franziska, Jamal Bouitbir, and Stephan Krähenbühl. "Hepatocellular Toxicity Associated with Tyrosine Kinase Inhibitors: Mitochondrial Damage and Inhibition of Glycolysis." Frontiers in Pharmacology 8 (2017).







S⁺ A SIMULATIONS PLUS COMPANY

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