

Quantitative Systems Toxicology Modeling of Cisplatin Nephrotoxicity Using *in vitro* Assays of Proximal Tubule Epithelial Cells for Mechanistic Toxicity Pathways

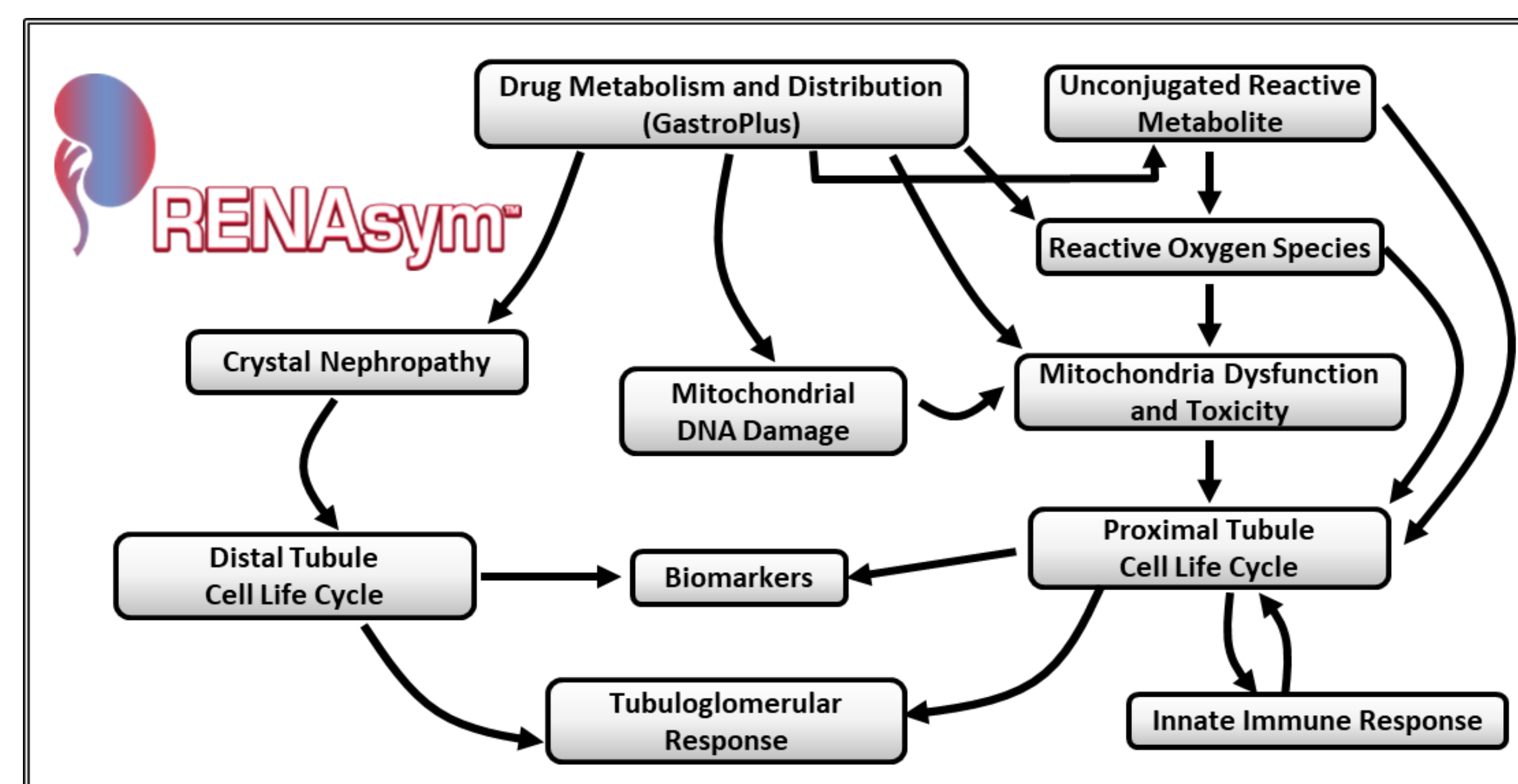
Yeshitila Gebremichael, Nader Hamzavi, Jeffrey L. Woodhead, Shailendra Tallapaka, Scott Q. Siler, and Brett A. Howell

DILsym Services, Inc., a Simulations Plus company, Research Triangle Park, NC, USA

BACKGROUND

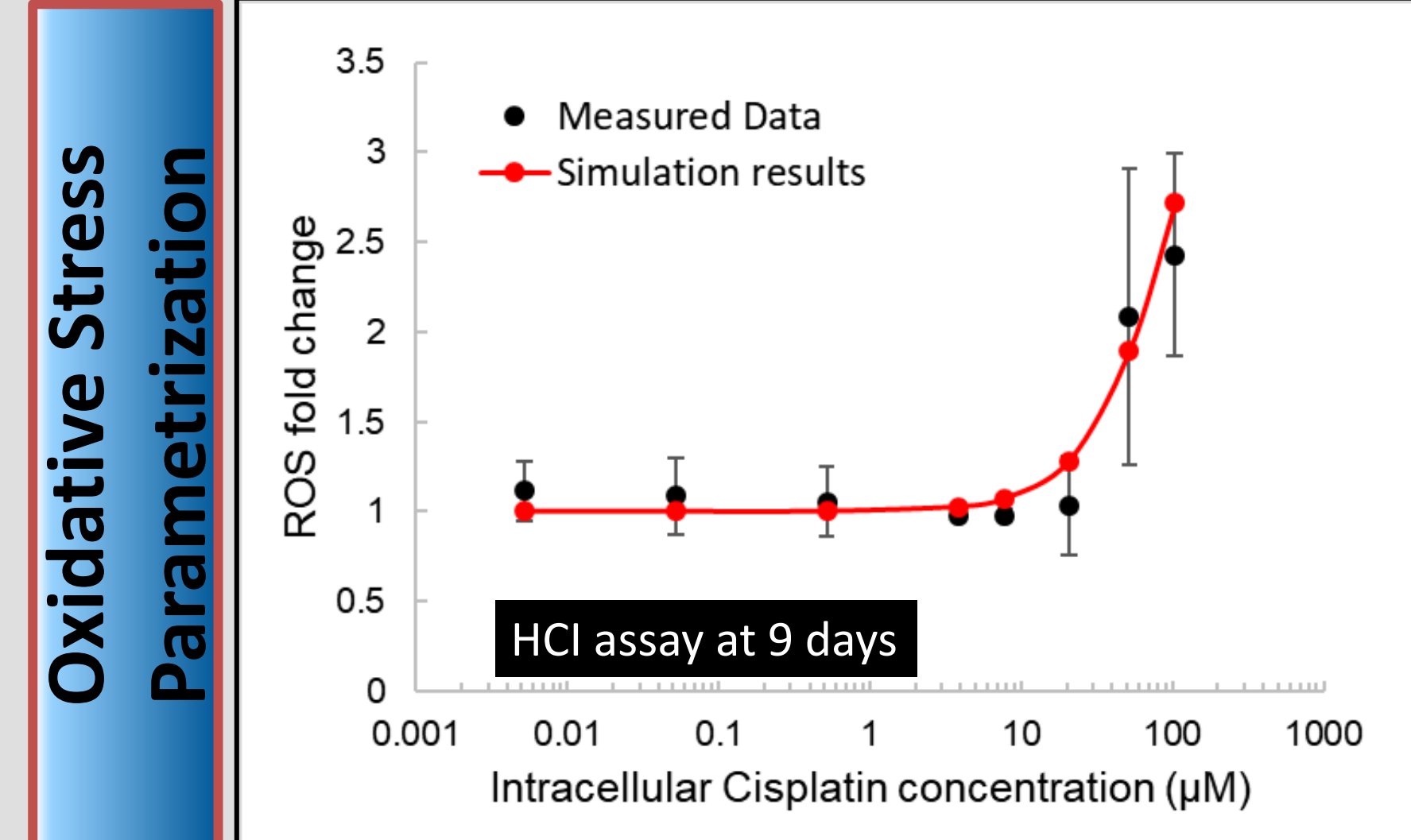
- Cisplatin-induced nephrotoxicity results in acute kidney injury (AKI) and is caused by various cellular mechanisms, including mitochondrial dysfunction, oxidative stress, and others.
- AKI mechanisms of cisplatin and several other nephrotoxic drugs remain incompletely understood.
- Quantitative system toxicology (QST) offers promise for better understanding of drug induced AKI through mechanistic representation of the underlying toxicity pathways.
- We developed a QST model of cisplatin induced AKI using *in vitro* assay data to characterize injury pathways.

METHODS



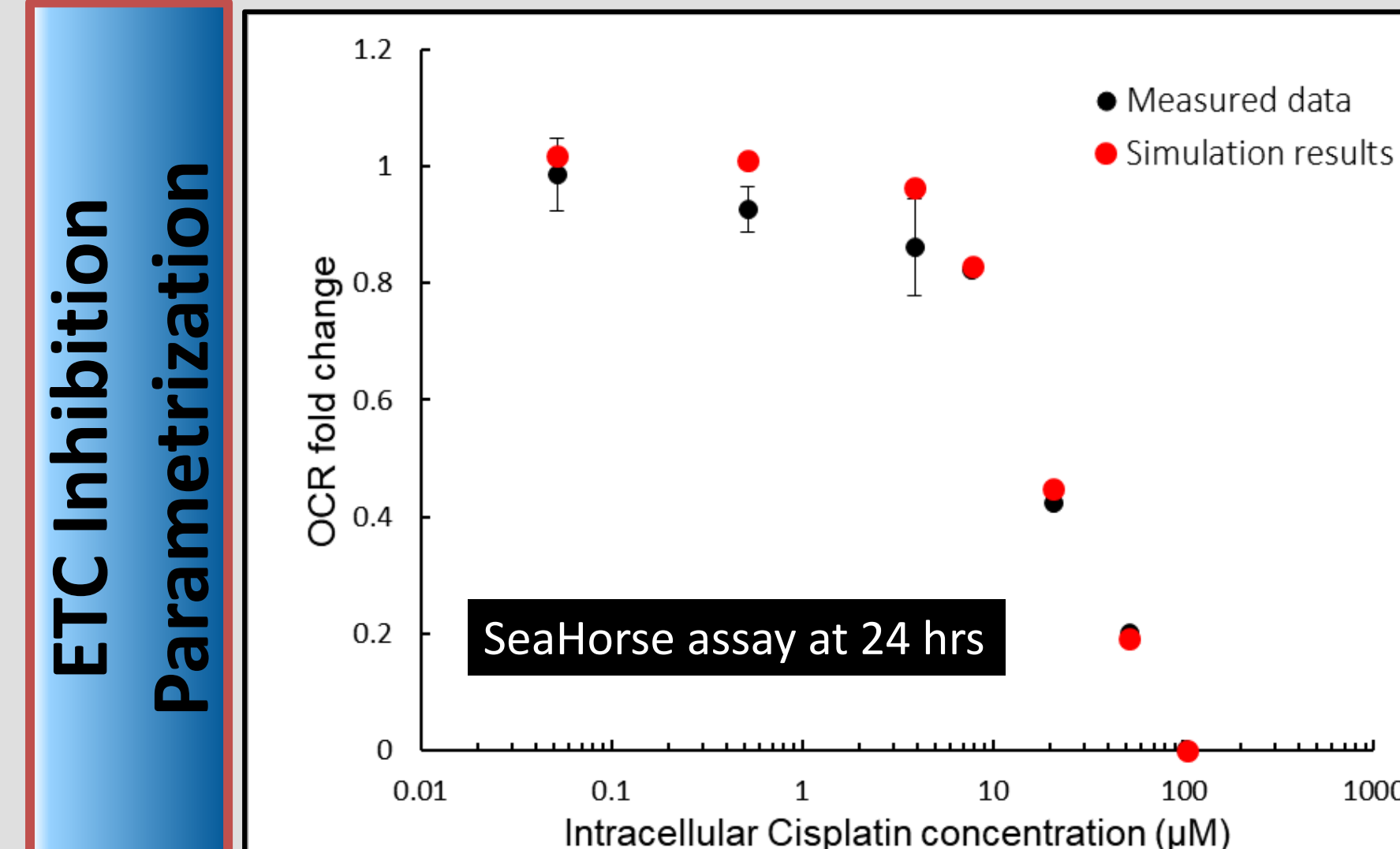
- We employed RENAsym®, a QST model of drug-induced acute kidney injury that is currently under development.
- RENAsym® represents aspects of renal proximal tubule epithelial cells (RPTCs), including cell life cycle, bioenergetics, drug-induced cell death pathways, and biomarker (α GST) responses.
- For mechanistic representation of cisplatin induced AKI, we analyzed data from a 2D *in vitro* assay (measured by Cyprotex, Inc.) of RPTEC.
- Seahorse XF analyzer and high content imaging (HCI) were used to quantify cisplatin-induced mitochondrial dysfunction and oxidative stress.

Model Parametrization using *in vitro* Data



In vitro data measured by Cyprotex in RPTEC was utilized to parameterize the oxidative stress (RNS/ROS) production and clearance of cisplatin.

- HCl assay of RPTEC was used to measure an increase in cisplatin-induced reactive oxygen species.



Oxygen consumption rate (OCR) decline measured using SeaHorse was fit using MITOsym, a model of *in vitro* mitochondrial bioenergetics (1).

- Rate constants for ETC inhibition from MITOsym were converted to RENAsym® parameters using a conversion factor.

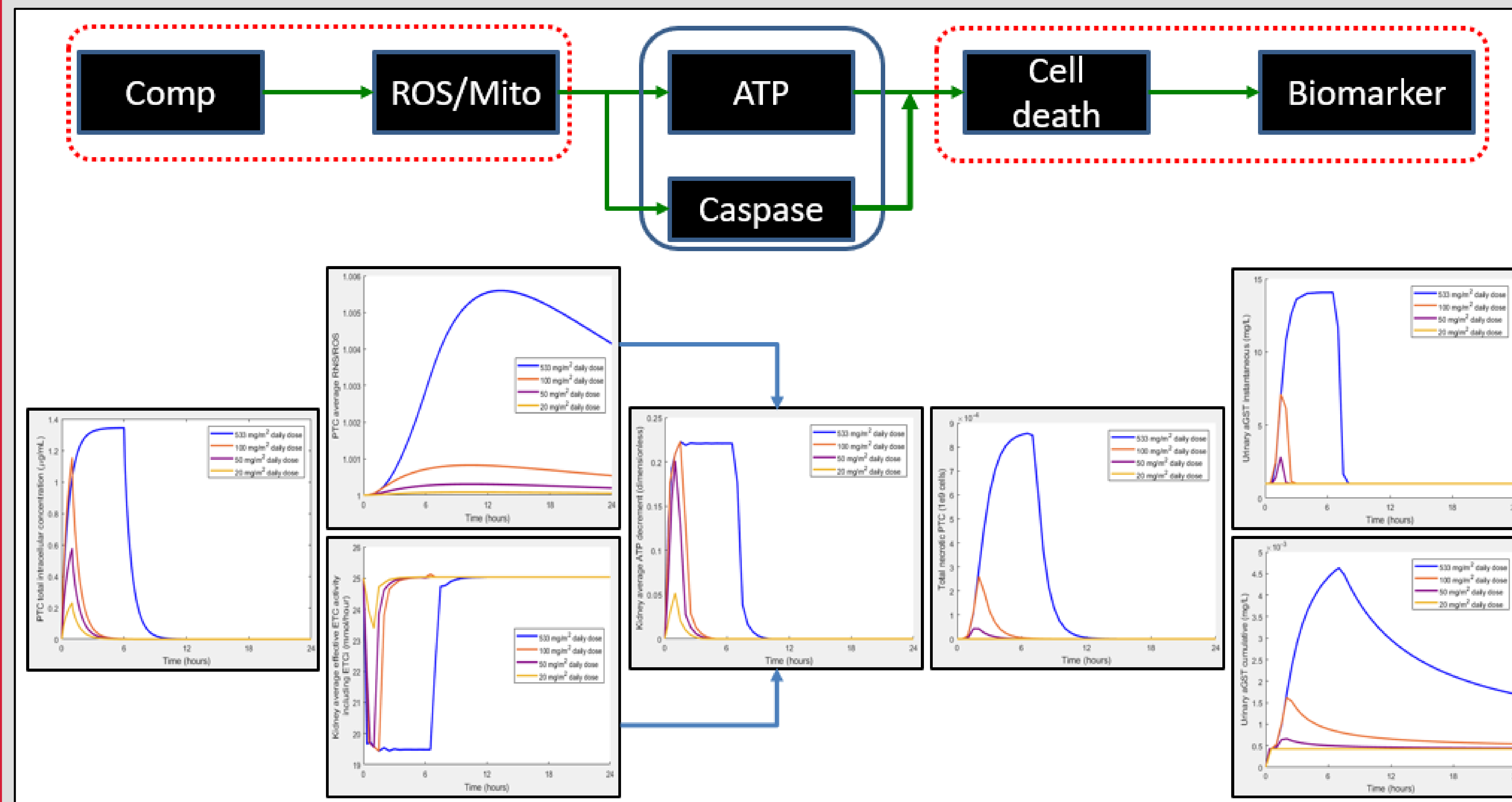
Mechanism	Parameter	Unit	Cisplatin Value*
Oxidative Stress	Liver RNS/ROS production rate Vmax 4	1/hour	0.067
	Liver RNS/ROS production rate Km 4	µM	57.68
	Liver RNS/ROS production rate Hill 4	Dimensionless	1.45
Mitochondrial Dysfunction	Coefficient for ETC Inhibition 3	µM	2.34
	Max inhibitory effect for ETC inhibition 3	Dimensionless	1.025

Table: Summary of toxicity parameters for drug-induced mitochondrial dysfunction and oxidative stress production. The parameters were determined by fitting the *in vitro* data using MITOsym for mitochondrial dysfunction parametrization and RENAsym® for oxidative stress parametrization. These parameters were then incorporated in RENAsym® for predicting drug-induced AKI.

CONCLUSION

- Simulations predict dose-dependent cisplatin toxicity as quantified by elevations in α GST, a biomarker that marks RPTEC death.
- A simulated single high dose of 533 mg/m² i.v. cisplatin results in 14-fold change in α GST, while a simulated clinical dose of 100 mg/m² shows 7 fold increase.
- The 100 mg/m² result is in qualitative agreement with 3.4-fold change observed in a clinical study where patients administered 100 mg/m² i.v. cisplatin exhibited 20% incidence of AKI [3].
- RENAsym® shows promise in combining QST modeling and *in vitro* assay data to provide a unique tool for drug-induced AKI prediction.

Simulation Predictions for dose dependent responses of cisplatin exposure



- RENAsym® is designed to integrate drug exposure, *in vitro* toxicity, and kidney physiology to predict drug-induced AKI.
- Urinary biomarkers offer early detection of AKI. Model predicts α GST as a key biomarker that signals cellular death.
- The figure shows the intermediate mechanistic pathways that link between drug exposure and biomarker responses.
- The relation between cell death and α GST is parameterized using literature data (2).

- Simulations based on RPTEC *in vitro* toxicity assay show cisplatin-induced toxicity that is dominated by ETC inhibition.

REFERENCES

- [1] Yang Y, et al. Pharm Res. 2015 Jun;32(6):1975–92.
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- [3] Ummer V, et al. International journal of Bioscience, Biochemistry and Bioinformatics. 2012 July; 2(4): 224-226

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