



# **DILIsym Training Session 10:**

# **Reactive Metabolites in DILIsym®**

**January 7, 2016**

Jeff Woodhead

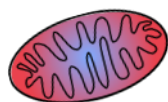
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# Reactive Metabolites in DILIsym®

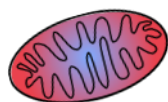
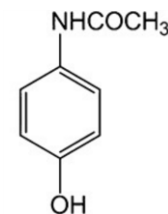
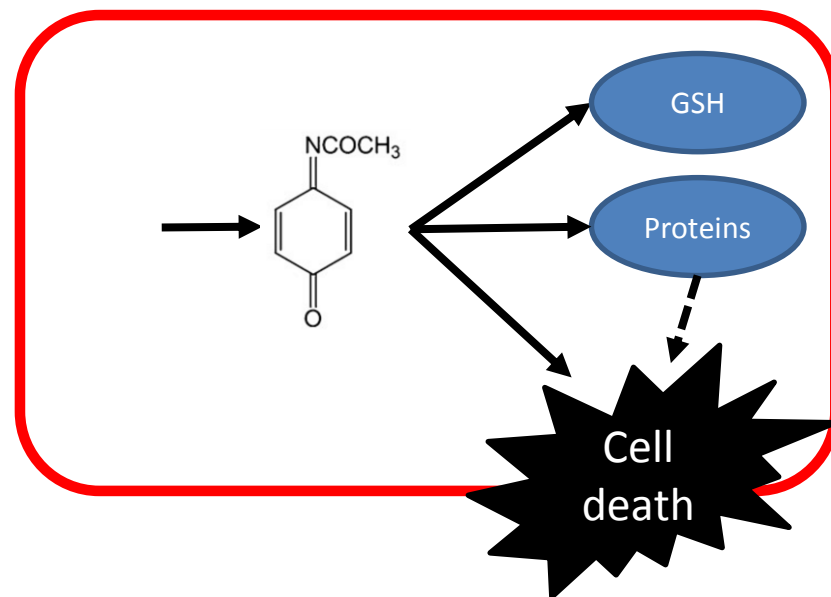
## Review Session Agenda

- Reactive Metabolite Generation in DILIsym®
- Fate of Reactive Metabolites in DILIsym®
- Reactive Metabolite Examples

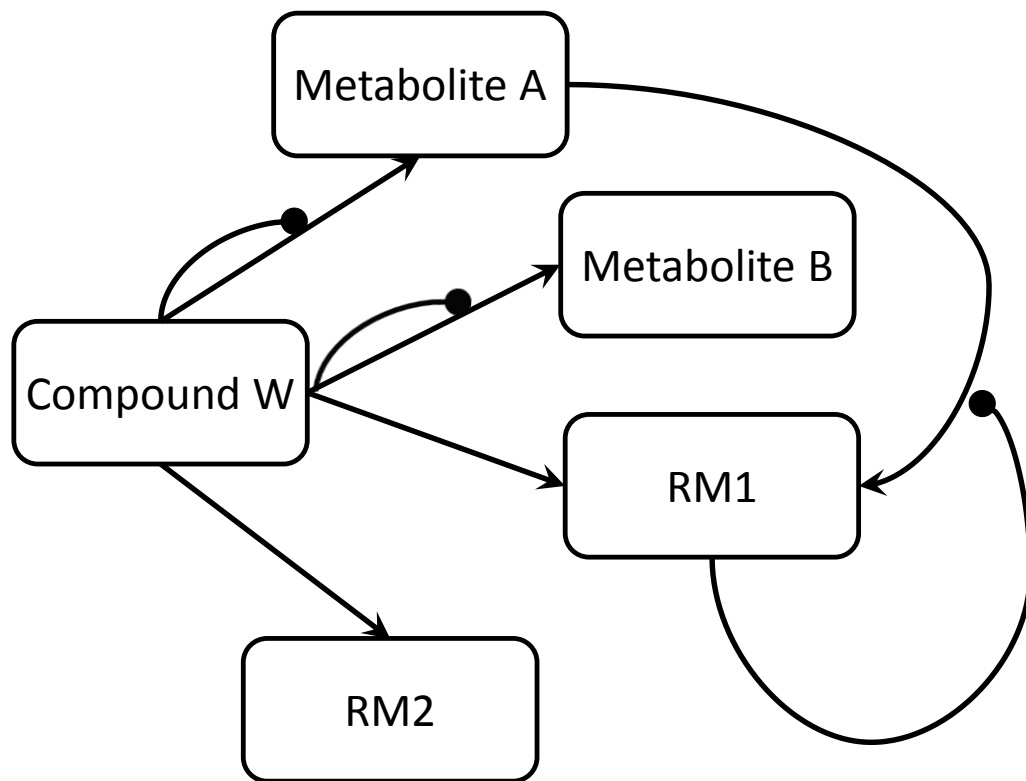


# Reactive Metabolite-Mediated DILI

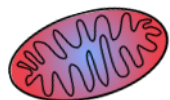
- Reactive metabolites (RM) are extremely labile metabolites generated in the liver that can covalently bind to cellular proteins or cellular antioxidants
- Ability to cause toxicity determined by amount of reactive metabolite generated and ability of the reactive metabolite to cause cellular stress
  - Reactive metabolites often, but not always, cause oxidative stress
  - Reactive metabolites themselves or adducts to cellular proteins can cause toxicity
- Examples of drugs that have reactive metabolites
  - Acetaminophen
  - Furosemide
  - Cocaine
  - Methapyrilene







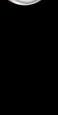
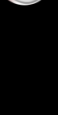
# Compound Metabolism Representation in DILIsym® Includes Two Reactive Metabolites

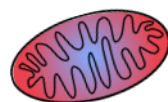


- DILIsym® metabolic scaffold involves four potential metabolic pathways
  - Two stable metabolites and two reactive metabolites
- Reactive metabolites can be generated from parent compound or from Metabolite A
- Metabolism to RM values are difficult to calculate directly
  - Usually need information on RM fate (GSH depletion, protein adducts) from microsomal data in order to properly determine RM metabolism



# Input Panel Document Provides Insight into Data Needed for RM Determination

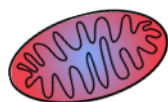
	Inputs or Data Needed	Commonly Used Systems/Assays	DILIsym® Preferred Systems	
	Concurrent GSH depletion, parent compound disappearance (and metabolite appearance if possible), protein adduct formation,	Primary hepatocytes; immortalized cell lines transfected with cytochrome P450s or other metabolising enzymes; <sup>14</sup> C or <sup>3</sup> H label for protein adducts	Primary hepatocytes; parent compound should be measured in the cells if possible, but can be estimated if not; comparisons to immortalized cells lines (HepG2) are useful from a metabolite perspective; data from cell lines transfected with drug metabolising enzymes are useful when available	
	ATP depletion	Primary hepatocytes; immortalized cell lines transfected with cytochrome P450s or other metabolising enzymes; whole-cell ATP	Primary hepatocytes; comparisons to immortalized cells lines (HepG2) are useful from a metabolite perspective; data from cell lines transfected with drug metabolising enzymes are useful when available	
	ROS/RNS indicators	Primary hepatocytes; immortalized cell lines transfected with cytochrome P450s or other metabolising enzymes; TBARS; peroxynitrite; lipid hydroperoxide, fluorescent probes (DCFDA, DHR123);	Primary hepatocytes; comparisons to immortalized cells lines (HepG2) are useful from a metabolite perspective; data from cell lines transfected with drug metabolising enzymes are useful when available	



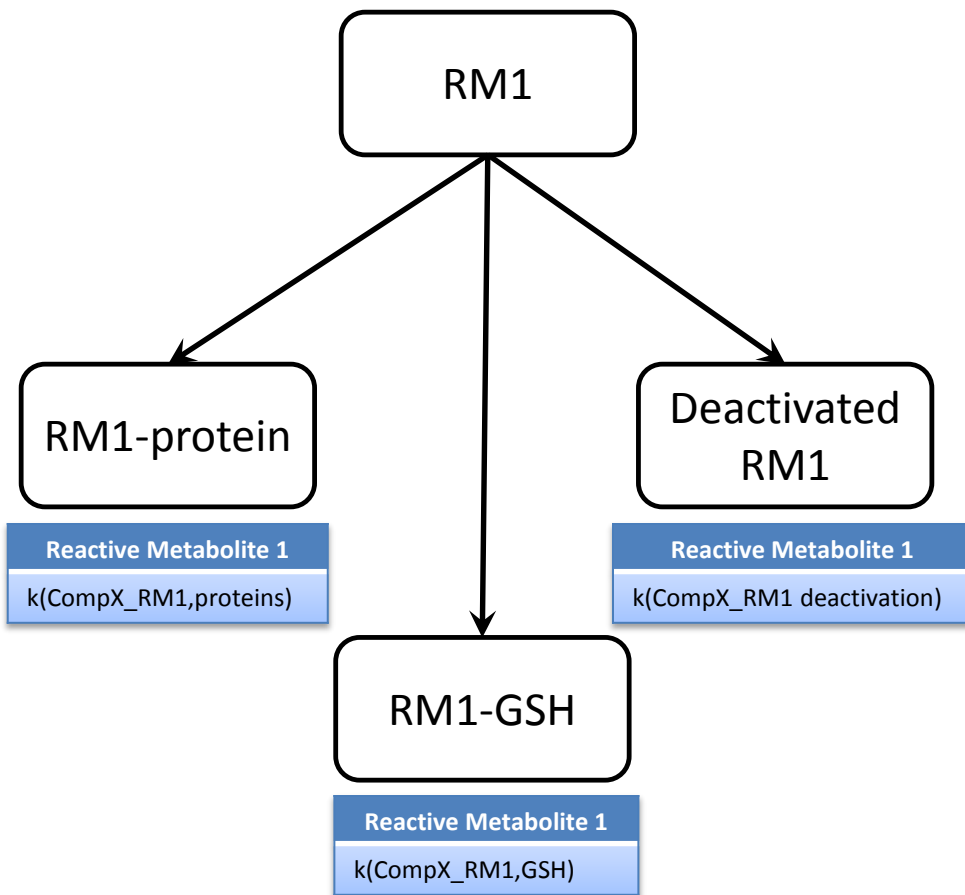
# Reactive Metabolites in DILI<sup>®</sup>

## Review Session Agenda

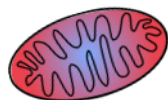
- Reactive Metabolite Generation in DILI<sup>®</sup>
- Fate of Reactive Metabolites in DILI<sup>®</sup>
- Reactive Metabolite Examples



# Reactive Metabolites Can Be Cleared in Several Ways

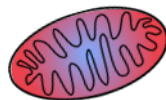
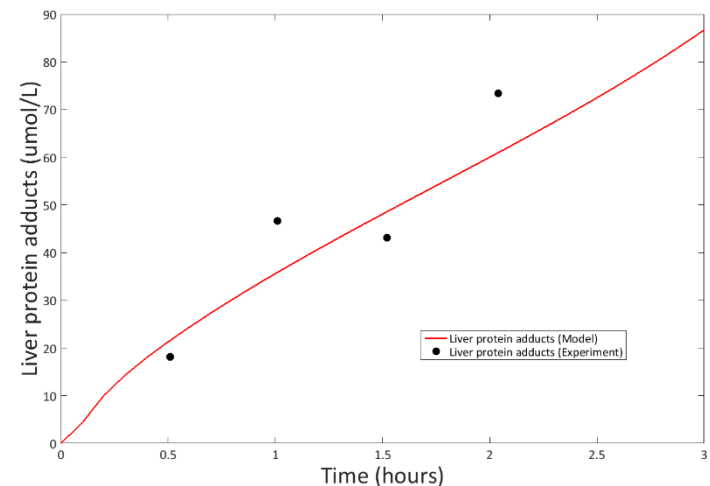
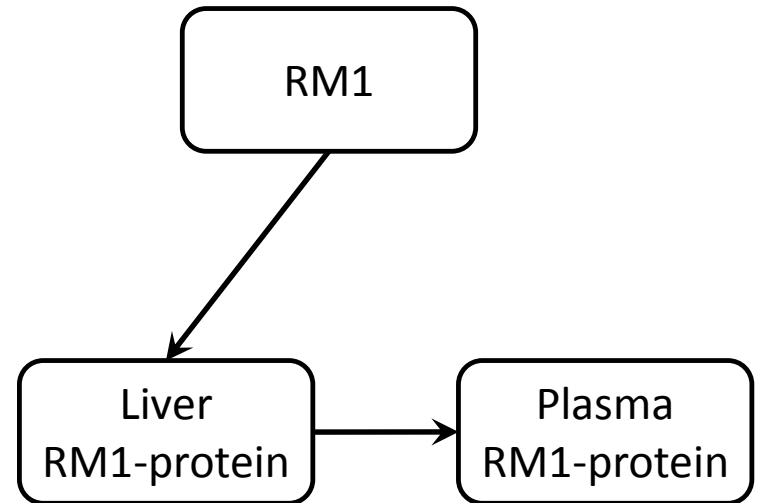


- Reactive metabolites have three potential modes of clearance
  - Adduction to cellular proteins
  - Conjugation with glutathione
  - Deactivation
  - Each is represented by a first-order process relative to the RM
- *In vitro* data determine which method(s) of clearance to model
  - GSH trapping assay can determine whether GSH conjugation is occurring
  - Protein binding is generally present with reactive metabolites
  - Deactivation occurs when the reactive metabolite is an intermediate; downstream metabolites will appear in a microsomal study



# Protein Adducts in DILIsym<sup>®</sup>

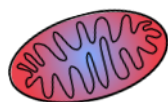
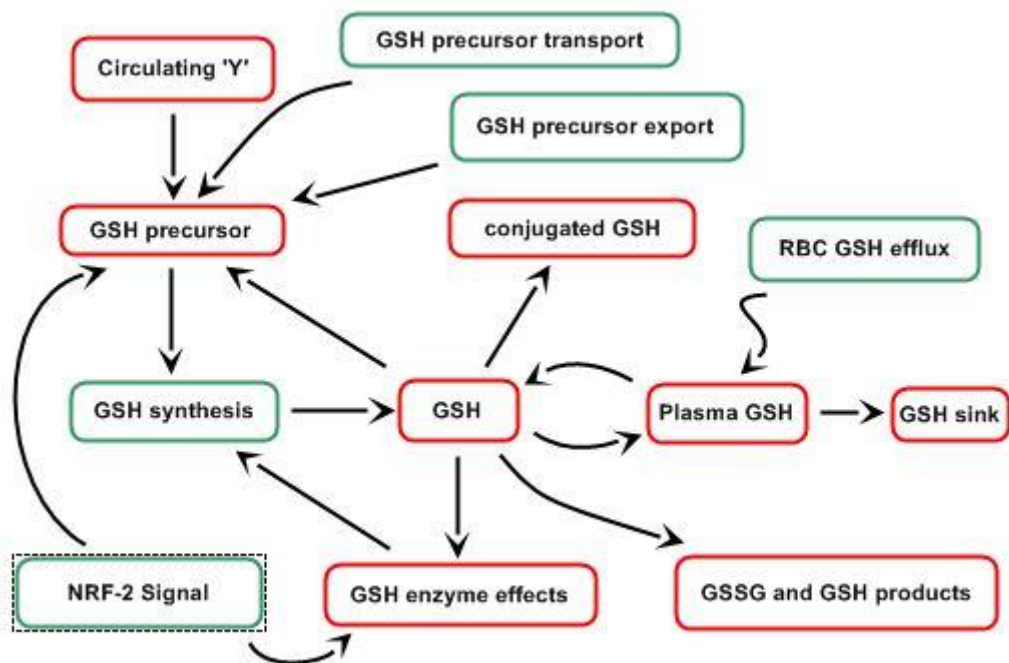
- Protein binding is a first-order process
- Protein adducts can cause toxicity
  - All DILIsym<sup>®</sup> toxicity mechanisms available to protein adducts
  - Adducts do not cause ROS in current APAP model
- Protein adducts are actively transported out of the hepatocyte
  - Adducts cleared from plasma by half-life
- Adducts can serve as a biomarker for validation
  - Example: APAP adducts in rat liver validated with data from Speeg 1985





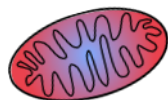
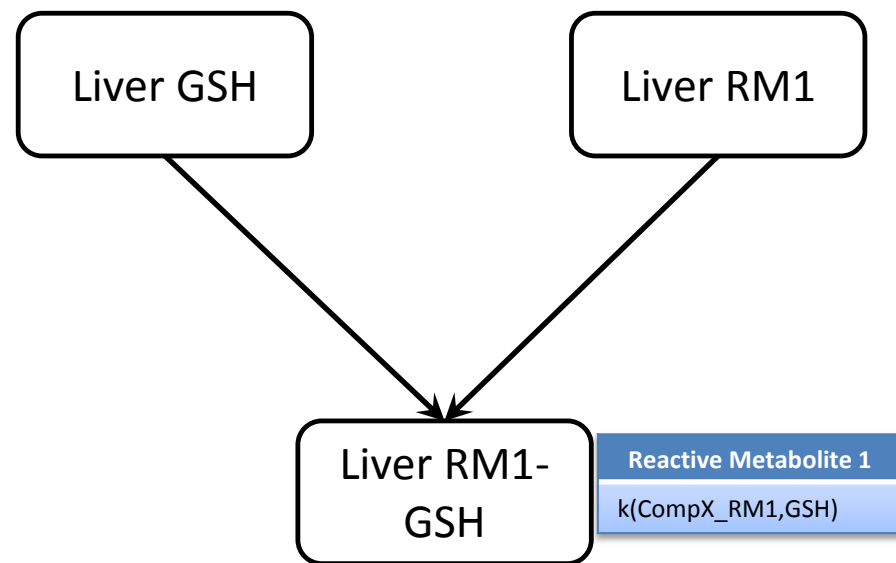
# Glutathione (GSH) Model in DILIsym®

- DILIsym contains a model of GSH homeostasis and conjugation to reactive metabolites
  - Will be explored more in depth in future review sessions
- In DILIsym®, GSH exists only for conjugation by reactive metabolites
  - GSH is not affected by cellular oxidative stress from other sources
- Baseline GSH can vary across a population
  - Important for susceptibility to RM-mediated toxicity
- N-acetylcysteine can serve as a GSH precursor, boosting GSH levels
  - Uses existing Compound Y scaffold



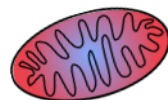
# GSH Binds and Neutralizes Reactive Metabolites

- RM-GSH reaction is second-order (first order with respect to both molecules)
  - Allows GSH depletion to occur
- RM-GSH is **not** available to cause toxicity
- Rate constant is extremely high in APAP case in order to reflect immediate reaction
  - Other RMs might not conjugate with GSH as readily
  - Rate constant can be determined by using *in vitro* GSH binding assays if expected to be in competition with other RM reactions *in vivo*



# Reactive Metabolite Clearance Assumptions

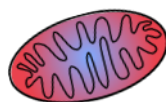
- Reactive metabolites exist in the liver only
  - RM scaffold cannot be used to represent stable metabolites that require plasma tracking
  - Upon cell death, intracellular RM turns into plasma RM protein adducts
- Deactivated RM and RM-GSH are not cleared from the liver
  - Cumulative amount of each produced on a per-cell basis is calculated over the course of the simulation
  - Not released into the blood stream after cell death



# Reactive Metabolites in DILIsym<sup>®</sup>

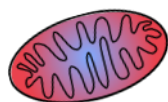
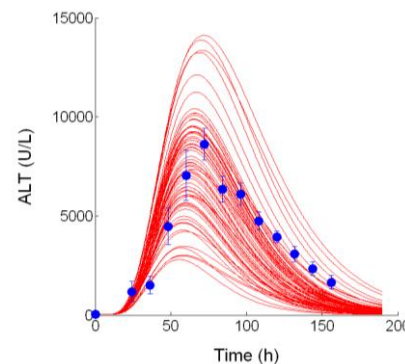
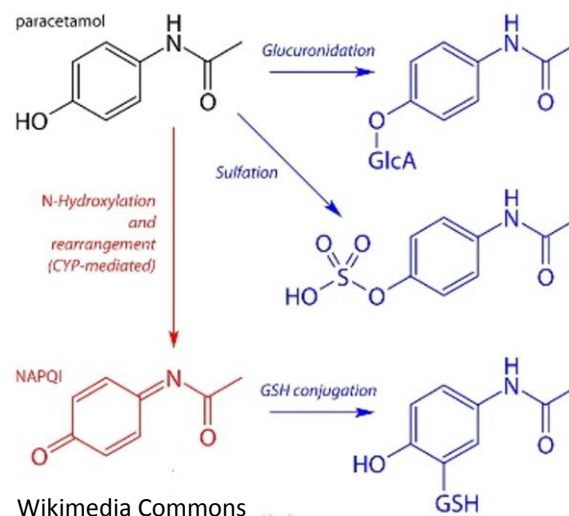
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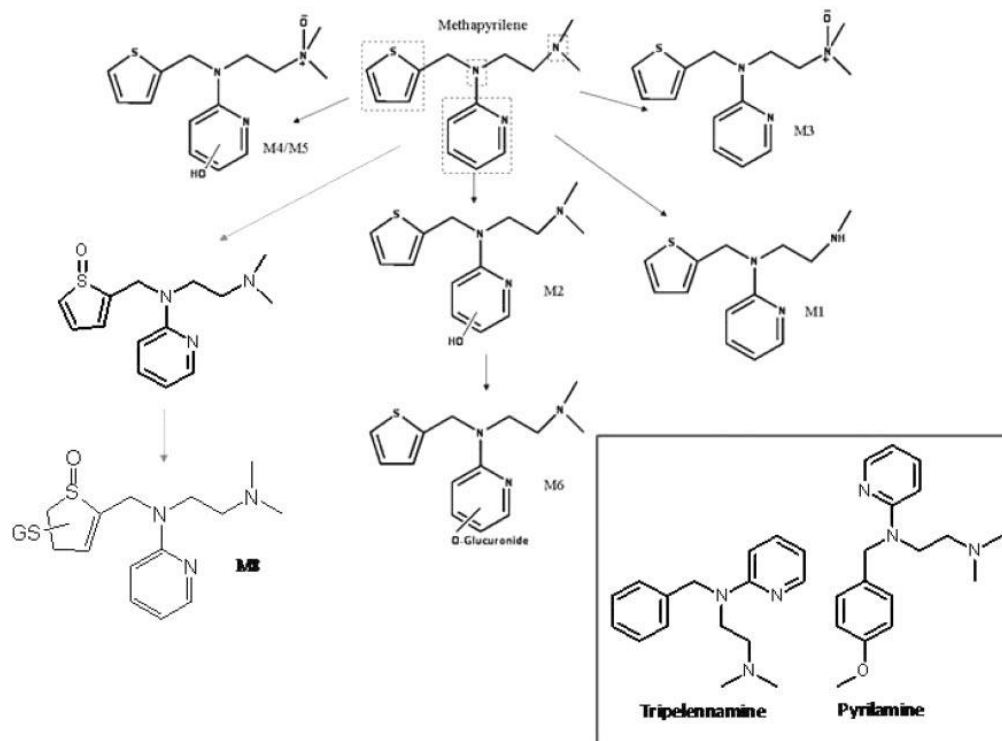
# Acetaminophen Toxicity is Represented Extensively in DILIsym<sup>®</sup>

- Acetaminophen (APAP) is the drug most commonly implemented in DILI in the US and Europe
- APAP is metabolized into three metabolites, including NAPQI, which is reactive
  - Significant species differences in metabolism
- GSH quenches NAPQI easily; toxicity occurs when GSH is depleted and NAPQI can accumulate, causing oxidative stress
- Oxidative stress model in DILIsym<sup>®</sup> was calibrated using APAP data in rats, mice, and humans
  - Immune response model also frequently leverages data from the APAP literature

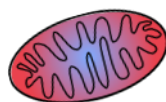


# Representing Methapyrilene Requires Combining Several Metabolites from Microsome Studies

- Graham 2008 contains microsome metabolism data used to parameterize methapyrilene metabolism parameters
  - Percentage of initial incubation of MP transformed into various metabolites was reported
- $V_{\max}$  values are determined by calculating the values of  $V_{\max}$  that produce the appropriate percentages after the correct amount of time
  - $K_m$  values are assumed from reported values for similar metabolism pathways
  - $K_m$  could be calculated using microsome incubations at different concentrations; in practice, these data rarely exist
- GSH depletion dynamics similar to acetaminophen
  - Can assume same GSH binding rate constant

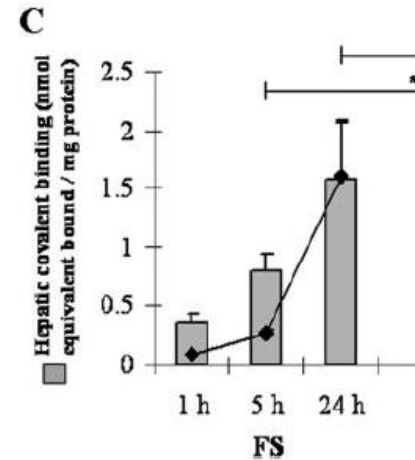


Graham JPET 2008

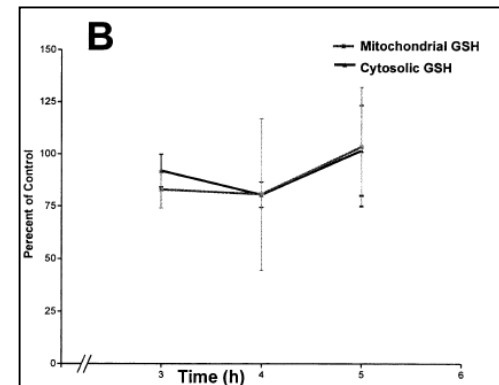


# Furosemide Has a Reactive Metabolite But Does Not Deplete Glutathione

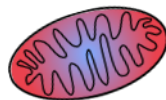
- Furosemide causes hepatotoxicity in mice at high doses
- Covalent binding in mouse studies implicates a reactive metabolite
  - Microsomal metabolism data backs this up
- GSH is not depleted in furosemide-treated mice
  - Reactive metabolite binds to proteins but not GSH
  - Also suggestive of a toxicity mechanism other than oxidative stress (in this case, increased ATP utilization)



Williams, JPET 2007; CD-1 mice, 400 mg/kg

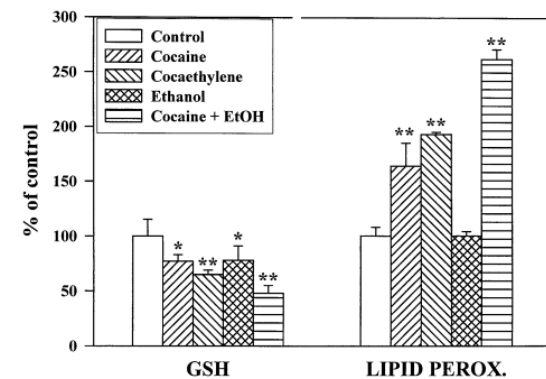
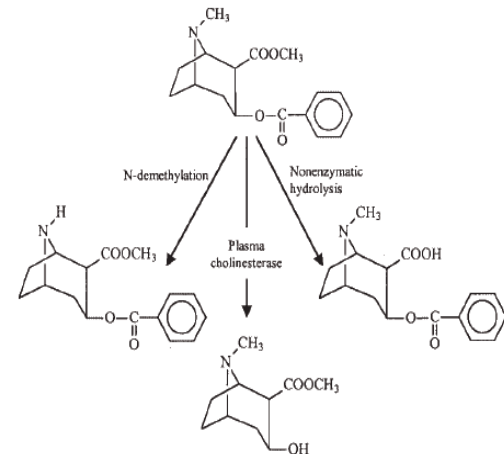


Wong Tox Letters 2000; Swiss CD-1 mice, 400 mg/kg

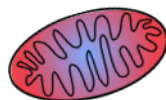


# IVIVE with Cocaine Requires Use of *In Vitro* Lipid Peroxidation and GSH Data

- Cocaine is metabolized to three main metabolites, one of which is reactive
  - Increase in lipid peroxidation suggests N-demethylated metabolite causes oxidative stress
- GSH assay shows some mild depletion *in vitro*, suggesting weaker GSH binding than APAP
  - Microsomal data is less abundant, so a lower GSH binding constant than the one used for APAP/MP can be assumed



Ponsoda Biochem Pharm 1999





# General Summary of Metabolism Data Used for RM Determination

- Microsomal metabolism data is key to the determination of reactive metabolite generation rates
  - RM and its products are often not easily measured *in vivo*
  - Also key to determining GSH binding rate, protein adduction rate, etc.
  - Training sessions contain detailed steps for converting microsomal metabolism data to  $V_{\max}$  and  $K_m$  for input into DILIsym®
- In vivo* data can be used to eliminate certain pathways
  - Furosemide example: no GSH depletion *in vivo* means that pathway can be ignored
- Mechanistic data are still required for determining active toxicity pathways
  - ROS is usually the appropriate pathway but not always

Other (mol/mL soln)	C(calculated)	C	Covalent bind	Vmax Km	3.25E-08 mol/mL soln/hour 500 uM
0.00E+00	2.00E-07	200	0.00E+00	Vmax	4.92E-05 mol/hour/kg^0.75
6.32E-09	1.90E-07	189.744	0.00E+00	Km	5.00E-07 mol/mL
1.26E-08	1.79E-07	179.4968	1.48E-11		
1.86E-08	1.70E-07	169.695	4.45E-11		
2.44E-08	1.60E-07	160.3283	8.85E-11	Vmax	2.49E-08 mol/mL soln/hour
2.98E-08	1.51E-07	151.3862	1.46E-10	Km	500 uM
3.50E-08	1.43E-07	142.8576	2.17E-10	Vmax	3.77E-05 mol/hour/kg^0.75
4.00E-08	1.35E-07	134.7312	3.00E-10	Km	5.00E-07 mol/mL
4.46E-08	1.27E-07	126.9952	3.96E-10		
4.91E-08	1.20E-07	119.6376	5.02E-10		
5.33E-08	1.13E-07	112.6463	6.20E-10		
5.73E-08	1.06E-07	106.0087	7.48E-10	Vmax	1.58E-07 mol/mL soln/hour
6.11E-08	9.97E-08	99.71247	8.87E-10	Km	1000 uM
6.47E-08	9.37E-08	93.74502	1.03E-09	Vmax	2.39E-04 mol/hour/kg^0.75
6.81E-08	8.81E-08	88.09378	1.19E-09	Km	1.00E-06 mol/mL
7.13E-08	8.27E-08	82.74623	1.36E-09		
7.43E-08	7.77E-08	77.68993	1.53E-09		
7.71E-08	7.29E-08	72.91256	1.71E-09	Covalent binding rate	
7.98E-08	6.84E-08	68.40196	1.90E-09	k(proteins, RM)	2.66E-02 1/hour
8.23E-08	6.41E-08	64.14618	2.09E-09	GSH adduct	
8.47E-08	6.01E-08	60.13347	2.29E-09	to protein adduct	
8.70E-08	5.64E-08	56.35238	2.50E-09	ratio at 6 hours	11.04762
8.91E-08	5.28E-08	52.79171	2.72E-09	% going to protein	9.051724
9.11E-08	4.94E-08	49.44057	2.93E-09	versus GSH	
9.29E-08	4.63E-08	46.28841	3.16E-09		
9.34E-08	4.80E-08		3.16E-09		
9.29E-08	4.63E-08		3.16E-09		
2.38E-19	2.94E-18		2.07E-47		
0.000511421			Sum of Sq	2.07E-29	

