

Addressing Population Variability in Risk Assessment: Challenges and Opportunities

SRP Risk e-Learning Webinar
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Conflict of Interest Statement

Neither myself nor any of my coauthors, including members of our immediate families, have any financial interest or affiliation with a commercial organization that has a direct or indirect interest in the subject matter of my presentation.

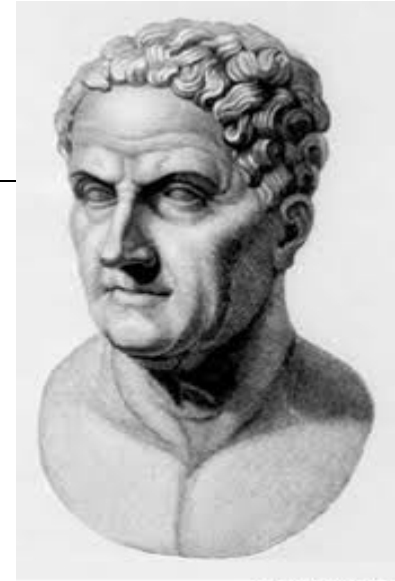
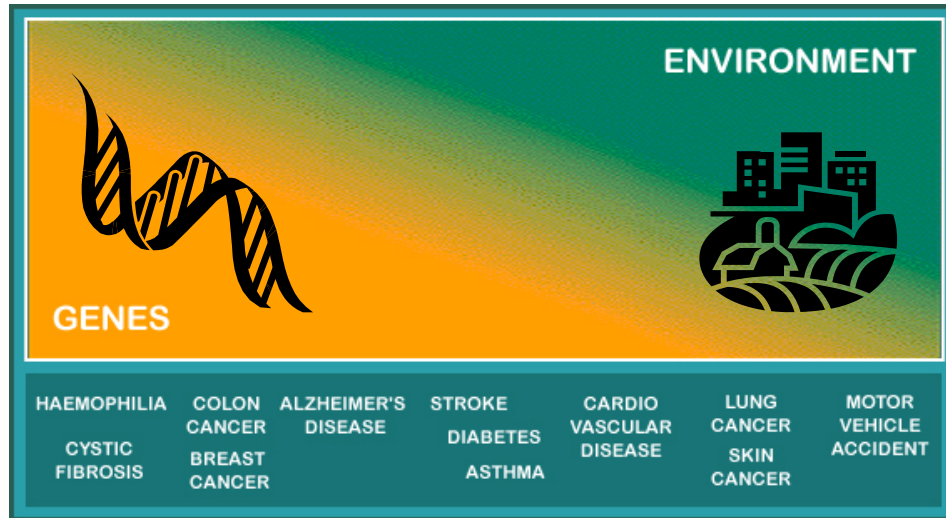
Outline

- Motivation for addressing population variability and susceptibility
- Opportunities using emerging population-based in vivo, in vitro, and in silico approaches
 - Hazard identification and mechanisms of toxicity
 - Dose-Response Assessment
- Challenges in risk characterization

Claudius Galenus (Galen of Pergamum)

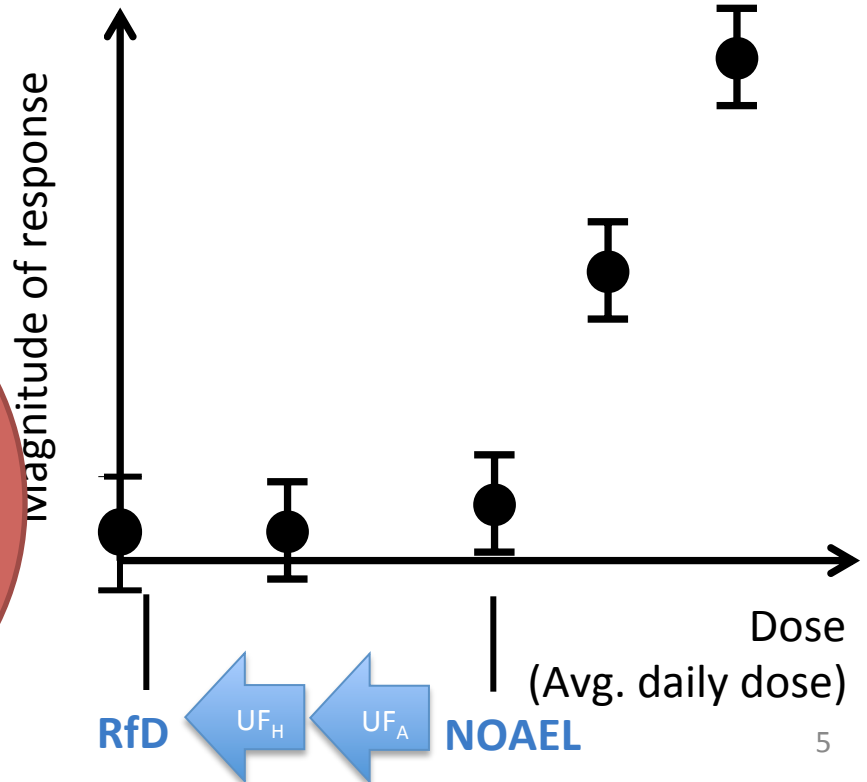
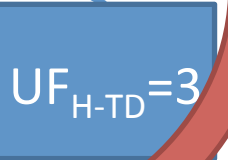
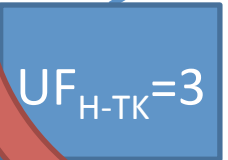
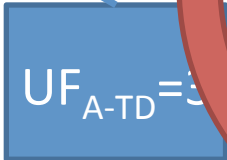
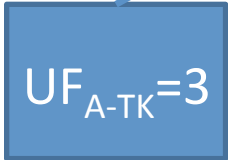
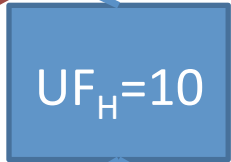
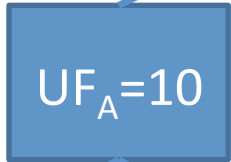
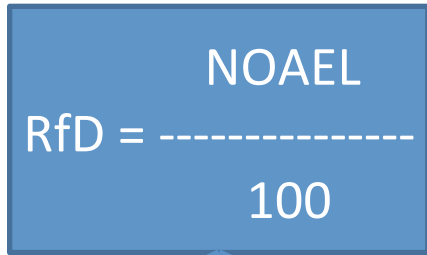
129-217 AD

“But remember throughout that no external cause is efficient without a predisposition of the body itself. Otherwise, external causes which affect one would affect all.”

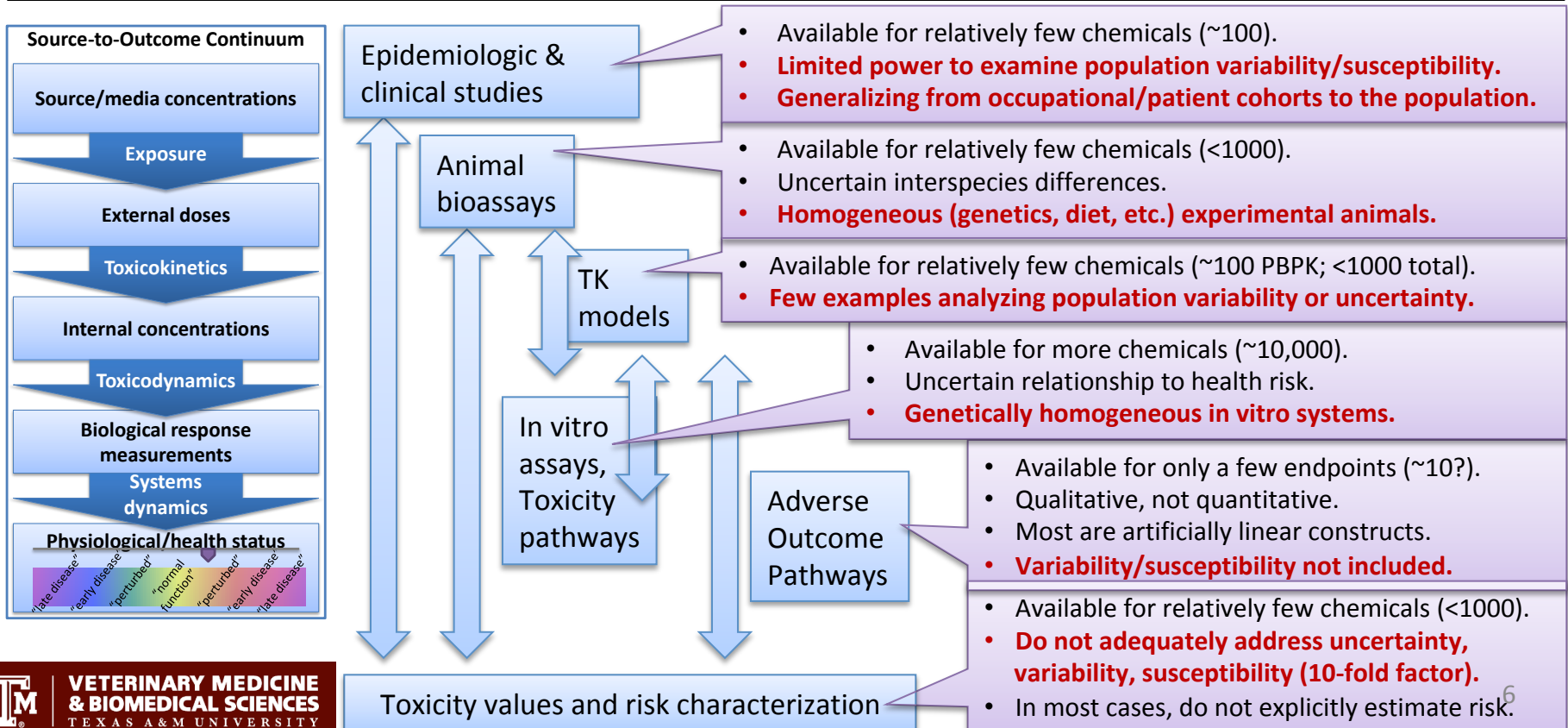


Library of Congress

“Uncertainty” or “Safety” Factors



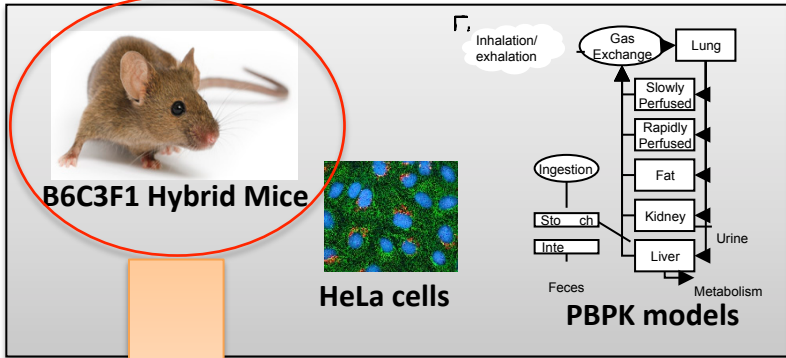
How well can we characterize variability?



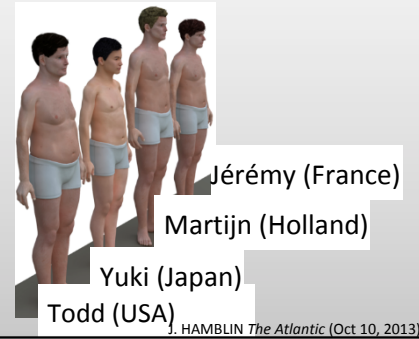
Population Variability in Susceptibility Remains a Risk Assessment Challenge

Animals, *in vitro*,
or *in silico* data

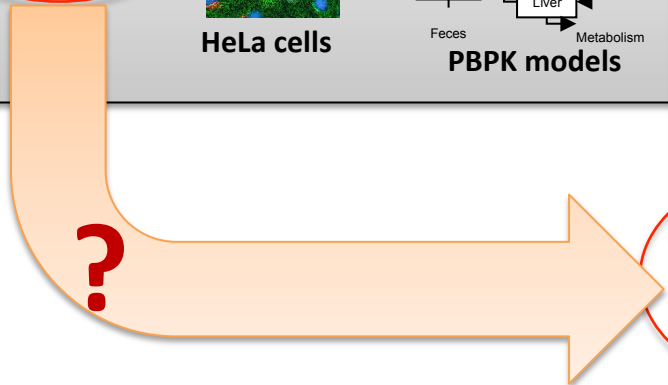
Humans



Predictions
for an Average
Male (or Female)



Individual



Predictions
for a Variable
Population



Population

New Population-Based Approaches and Tools

- Genetically diverse mouse populations
 - Diversity Panel
 - Collaborative Cross, Diversity Outbred
- Populations of human cells
 - Cell lines
 - Inducted pluripotent stem cells
- Computational modeling of populations

All involve studying populations instead of individuals in an experimental and/or computational setting.

Challenges for Hazard Identification

Animals, *in vitro*,
or *in silico* data

Humans



B6C3F1 Hybrid Mice



Predictions
for an Average
Male (or Female)



Jérémy (France)

Martijn (Holland)

Yuki (Japan)

Todd (USA)

J. HAMBLIN *The Atlantic* (Oct 10, 2013)



Predictions
for a Variable
Population



Individual

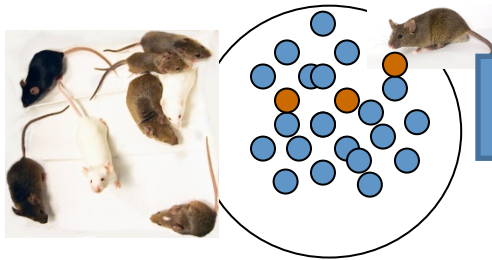
Population

- Human relevance of single strain rodent (positive and negative findings)
- No information about human population variability

Hazard Identification: Why Use Population-Based Models?

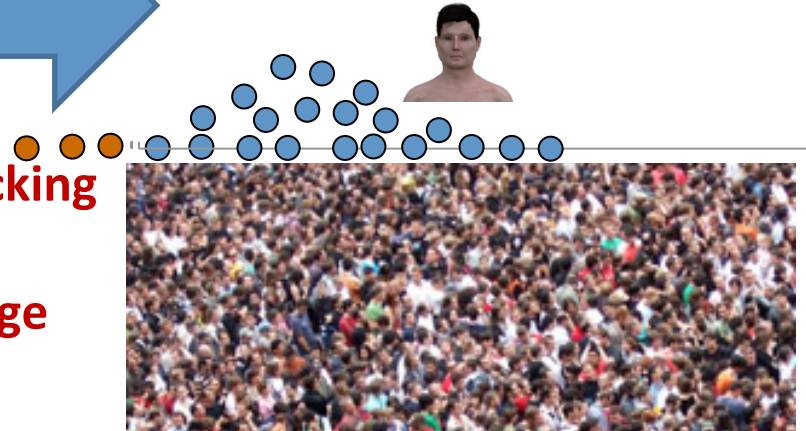
Mouse

- Poor models of humans
- Good models of humans



Extrapolation

Range of Human Responses



- Reduce chances of being “unlucky” and picking a strain that is a “poor” model of humans
- Obtaining information about potential range of population variability

Mouse Diversity Panel (MDP)

- Comprised of dozens of conventional inbred strains
- Each line is genetically distinct
- Many strains have a high degree of genetic relatedness between them, potentially limiting degree of genetic diversity across strains

Strain
Selection



Founder Strains: A/J,
C57BL/6J, 129S1/SvImJ,
NOD/ShiLtJ, NZO/H1LtJ,
CAST/EiJ, PWK/PhJ,
WSB/EiJ

F1 Diallel Cross → F1 Crosses

Establish Inbreeding Funnels

Collaborative Cross (CC)

- >100 RI lines available
- Each RI line is genetically distinct
- Within each RI line, all mice are genetically identical

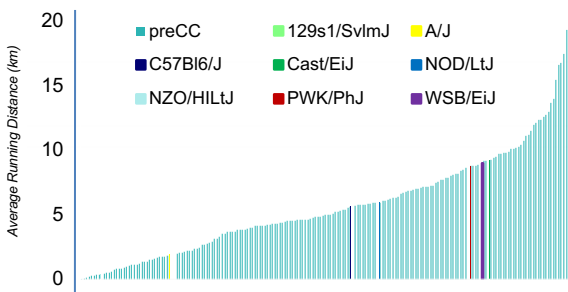
Diversity Outbred (DO)

- Large population of genetically unique individuals
- High level of genomic heterozygosity
- Each individual animal is genetically unique

Initiation: Interbred 144
segregating CC lines between
G2:F4 and G2:F12 generations

Harrill & McAllister (2018) <https://doi.org/10.1289/EHP1274>

Extreme Transgressive Variation Average Daily Running Distance

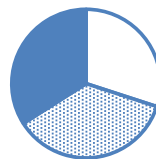


AJP - Endocrinology and Metabolism, 2011

Mouse and Human Response Phenotypes to Ebola Virus Infection

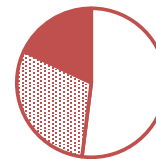
Mouse (47 strains)

Human (n=86)



- Resistant or Partially Resistant
- Lethal w/o HF
- Lethal w/ HF

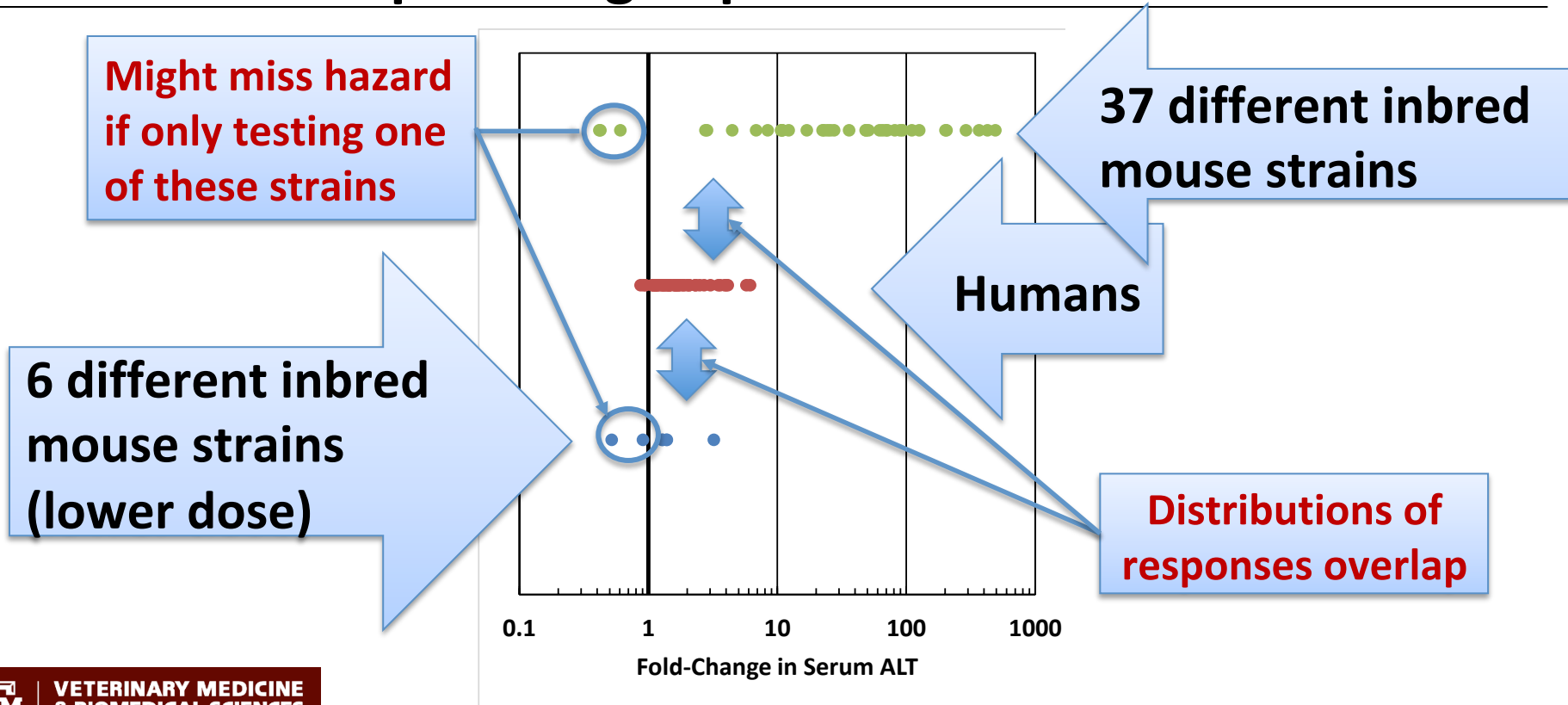
- Resistant or Partially Resistant
- Lethal w/o HF
- Lethal w/ HF



Sources: Rasmussen et al. 2014 (mouse), McElroy et al. 2014 (human)

Hazard Identification:

Proof of Principle Using Population-Based Mouse Models



Challenges for Characterizing Mechanisms of Toxicity and Susceptibility

Animals, *in vitro*,
or *in silico* data

Humans



B6C3F1 Hybrid Mice



Predictions
for an Average
Male (or Female)



Jérémy (France)

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J. HAMBLIN *The Atlantic* (Oct 10, 2013)



Predictions
for a Variable
Population



Individual

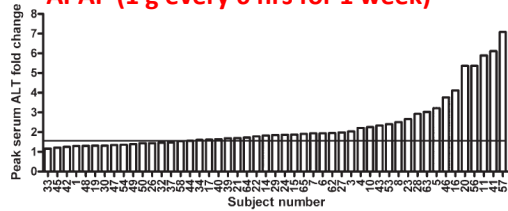


Population

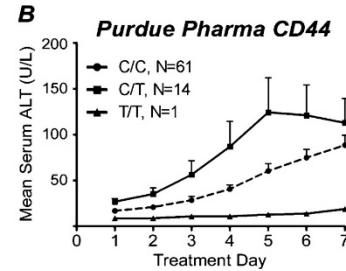
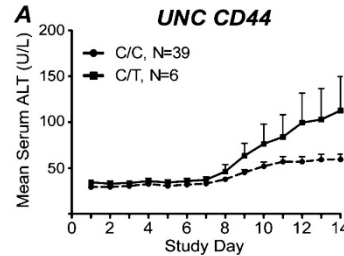
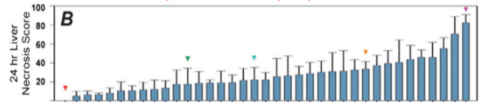
- Knockout studies probe one gene at a time
- Difficult to distinguish inter- and intra-species susceptibility differences

Mechanisms of Toxicity and Susceptibility: Proof of Principle Using Population-Based Mouse Models

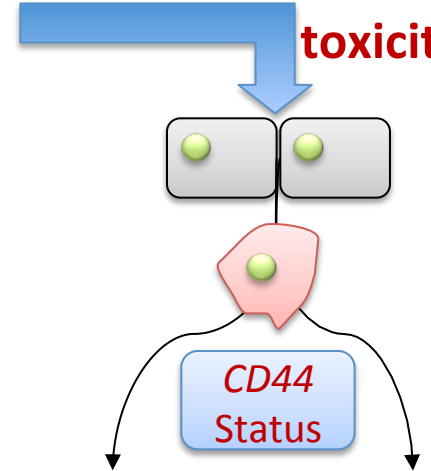
Liver toxicity: Humans
APAP (1 g every 6 hrs for 1 week)



Liver toxicity: Mouse population



**Insights into
mechanism of
toxicity**

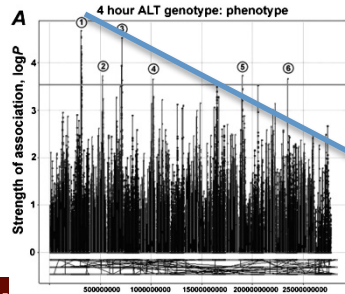


**Confirmed
in human
cohorts**

**CD44 Candidate
Susceptibility Gene**

Recovery

**Apoptosis &
Inflammation**



**GWAS in
mice**

Challenges for Dose-Response Assessment

Animals, *in vitro*,
or *in silico* data

Humans



B6C3F1 Hybrid Mice

$\div 10$

Predictions
for an Average
Male (or Female)



Jérémy (France)
Martijn (Holland)
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J. HAMBLIN *The Atlantic* (Oct 10, 2013)

$\div 10$

Predictions
for a Variable
Population



Individual

Population

- Single strain dose-response assumed to be representative of population
- 10-fold inter- and intra-species factors assumed to be adequate (conservative?)

Population Variability in Toxicokinetics

$$\text{NOAEL} \\ \text{RfD} = \frac{\text{NOAEL}}{\text{UF}_A \times \text{UF}_H}$$

$$\text{UF}_A = 10$$

$$\text{UF}_H = 10$$

$$\text{UF}_{A\text{-TK}} = 3$$

$$\text{UF}_{A\text{-TD}} = 3$$

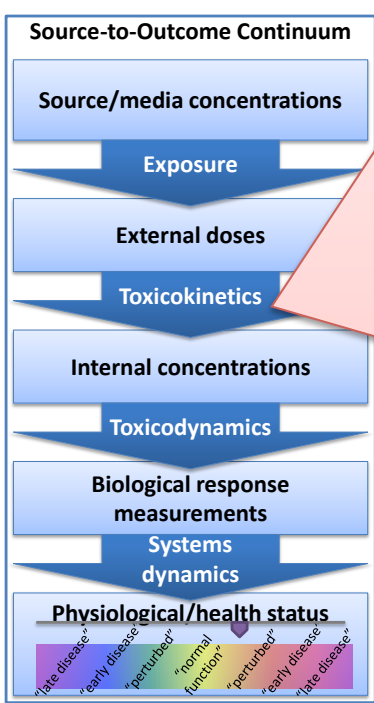
$$\text{UF}_{H\text{-TK}} = 3$$

$$\text{UF}_{H\text{-TD}} = 3$$

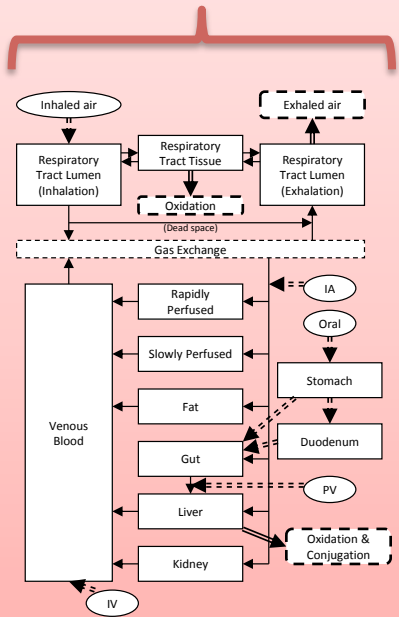
Population-based Physiologically-Based Pharmacokinetic (PBPK) Models

- Monte Carlo simulation
- Bayesian approaches
- Emerging experimental models

Human population variability of trichloroethylene pharmacokinetics



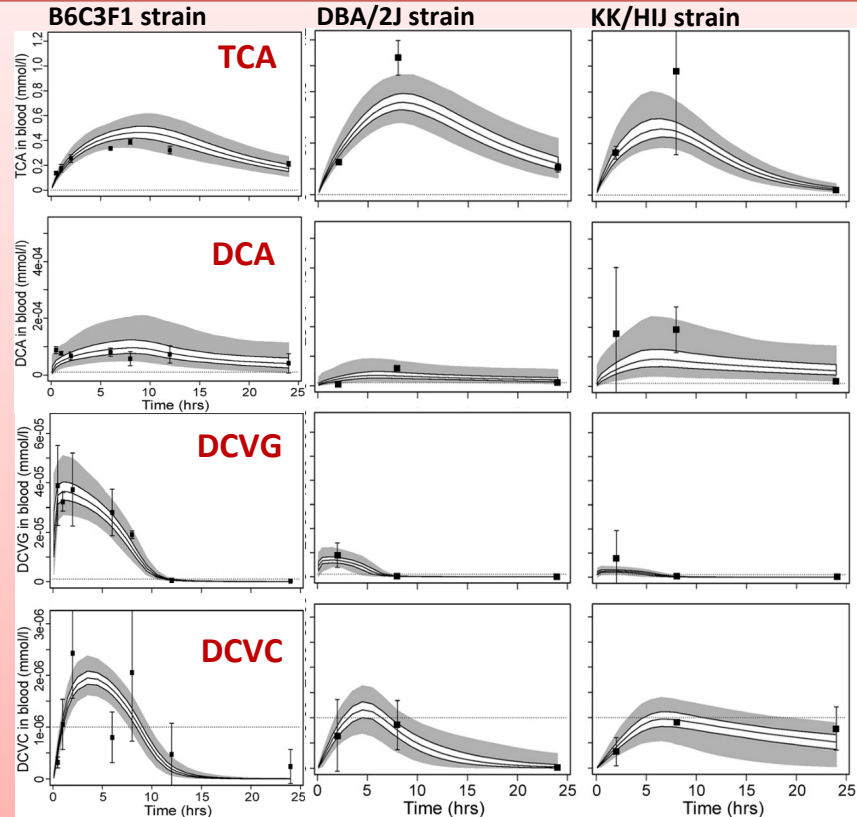
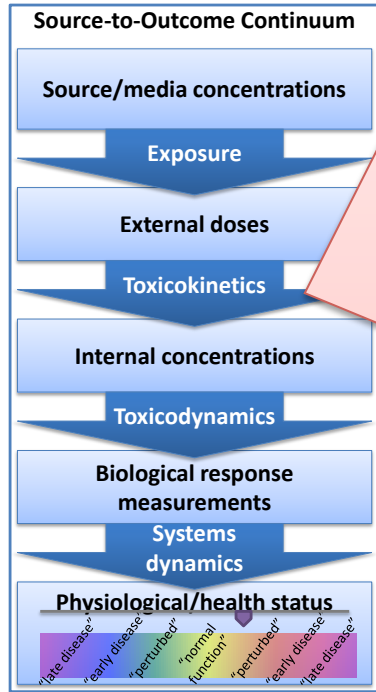
Bayesian Population PBPK Model
 parameters vary by individual
 [~50 individuals total]



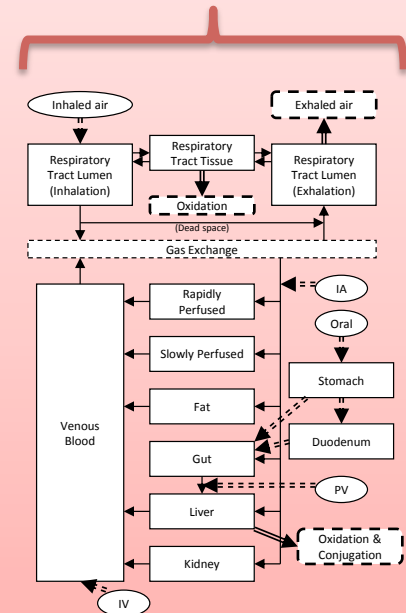
	Ratio of 95th percentile/ 50th percentile individual
	Human inter-individual variability
TCE oxidized by P450	1.11 (1.05, 1.22)
Total TCA produced	2.09 (1.81, 2.51)
TCE conj. with GSH	6.61 (3.95, 11.17)

Depending on the toxic moiety (which may be different for different effects), humans could have very low or very high variability.

Using a population of mouse strains to address TCE toxicokinetic variability

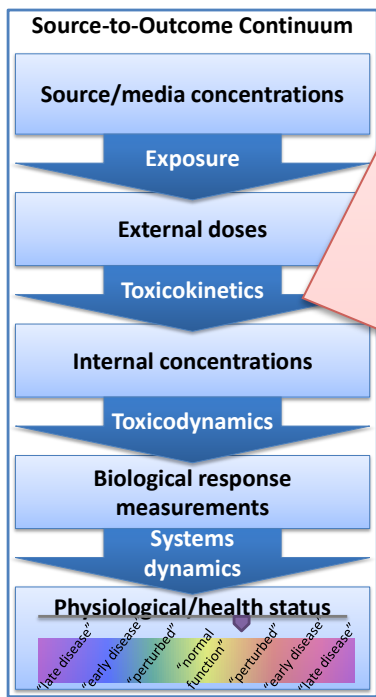


Bayesian Population PBPK Model
parameters vary by strain
[17 strains total]



Source: Chiu et al., 2014

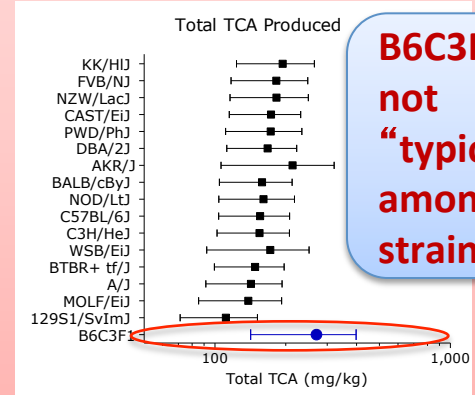
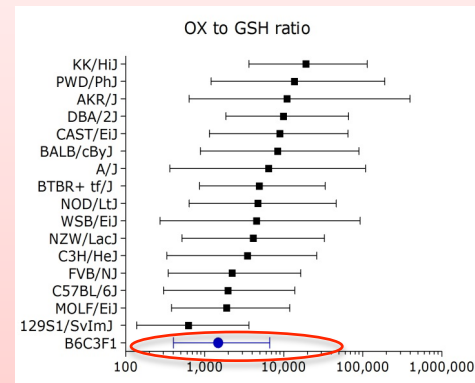
Using a population of mouse strains to address TCE toxicokinetic variability



	Ratio of 95th percentile/50th percentile individual or strain*	
	Human inter-individual variability	Mouse inter-strain variability
TCE oxidized by P450	1.11 (1.05, 1.22)	1.05 (1.01, 1.27)
Total TCA produced	2.09 (1.81, 2.51)	1.77 (1.36, 2.99)
TCE conj. with GSH	6.61 (3.95, 11.17)	7.12 (3.43, 20.7)

*Median and 95% CI

Estimates of mouse population variability from multi-strain experiments are consistent with estimates of human population variability from controlled human exposure studies.



B6C3F1 is not "typical" among strains

Population Variability in Toxicodynamics

$$\text{RfD} = \frac{\text{NOAEL}}{\text{UF}_A \times \text{UF}_H}$$

$$\text{UF}_A = 10$$

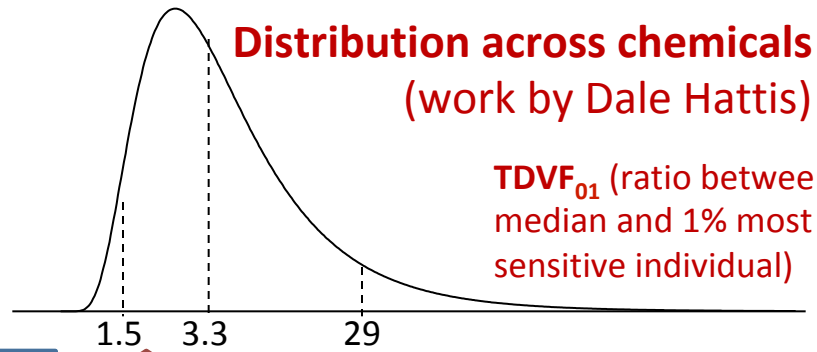
$$\text{UF}_H = 10$$

$$\text{UF}_{A\text{-TK}} = 3$$

$$\text{UF}_{A\text{-TD}} = 3$$

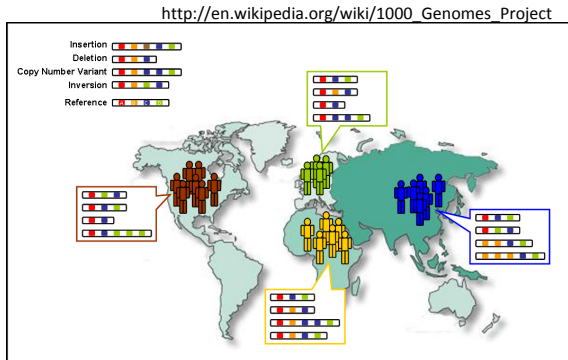
$$\text{UF}_{H\text{-TK}} = 3$$

$$\text{UF}_{H\text{-TD}} = 3$$

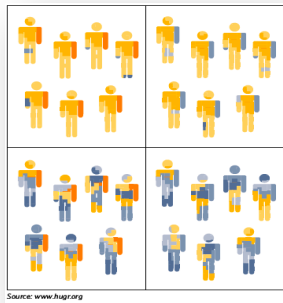


- Some idea as to the range of possible toxicodynamic variability, based on existing data mostly from drugs.
- Virtually no other examples for chemical-specific estimates of toxicodynamic variability.

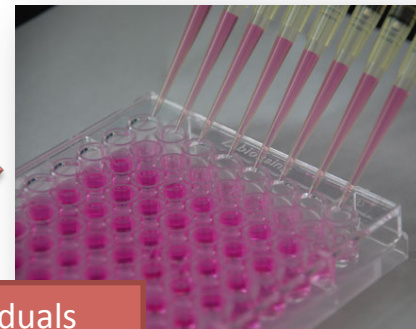
Genetically diverse human population



Genetically defined sample of population

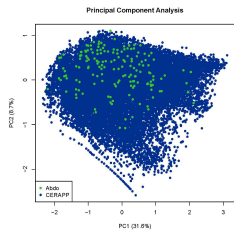


High throughput *in vitro* model system



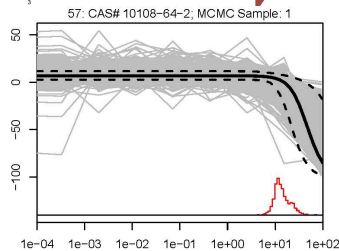
~1000 individuals
cytotoxicity screening

Structurally diverse chemical population

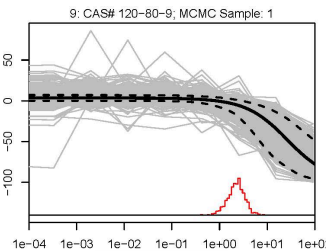


~170
compounds

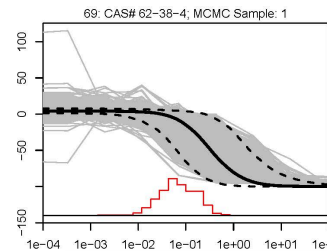
Chemical-Specific TD Variability Factor (TDVF₀₁):
The factor estimated to protect up to the most sensitive 1% for human toxicodynamic variability for a chemical



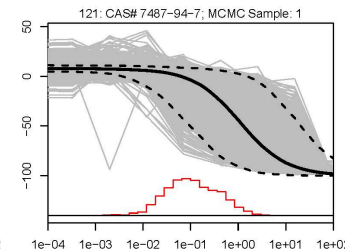
Cadmium Chloride
~2-fold



Catechol
~3-fold



Organic and inorganic mercury compounds
>8-fold

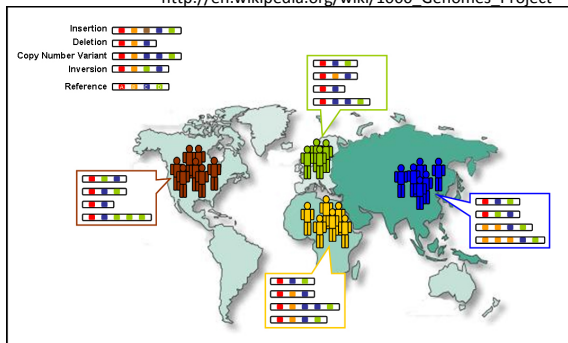


Abdo et al., 2015
Chiu et al., 2017

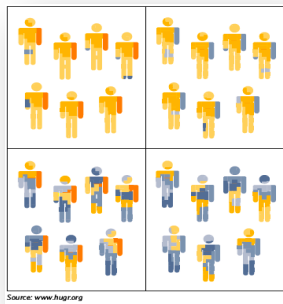
<https://doi.org/10.14573/altex.1608251>

Genetically diverse human population

http://en.wikipedia.org/wiki/1000_Genomes_Project

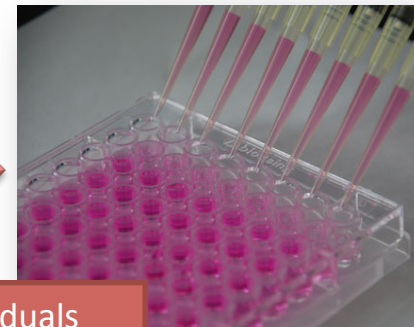


Genetically defined sample of population



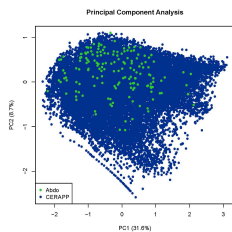
Source: www.hug.org

High throughput *in vitro* model system



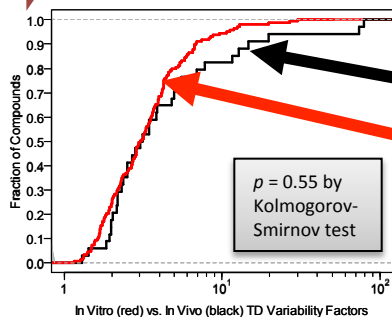
~1000 individuals
cytotoxicity screening

Structurally diverse chemical population



~170
compounds

Chemical-Specific TD Variability Factor (TDVF₀₁):
The factor estimated to protect up to the most sensitive 1% for human toxicodynamic variability for a chemical



Consistent estimates of
toxicodynamic variability *in vitro* and
in vivo.

	Human <i>In vitro</i>	Human <i>in vivo</i>
TD variability factor*	3.04 (1.33, 12.6)	3.10 (1.40, 74.3)

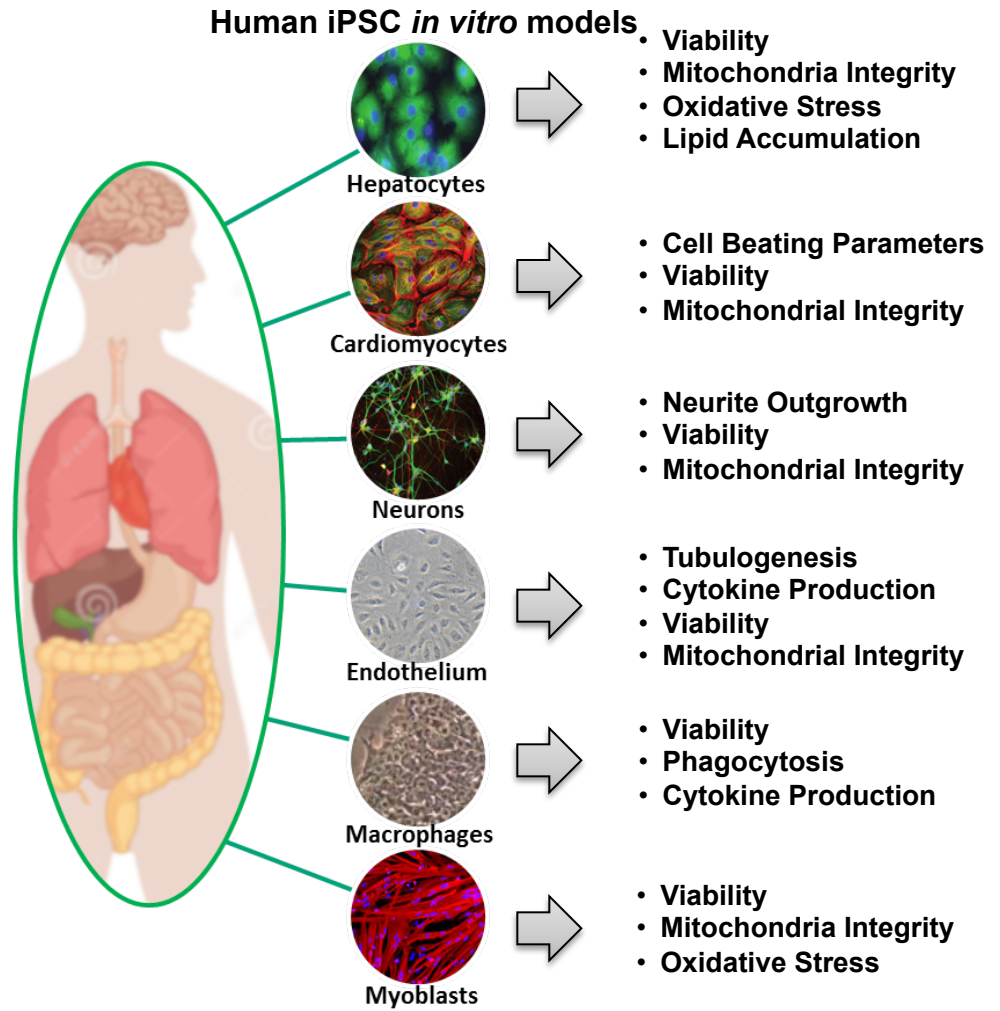
Abdo et al., 2015

Chiu et al., 2017

<https://doi.org/10.14573/altex.1608251>

Next Step: Other Cell Types and Phenotypes

- Induced pluripotent stem cells (iPSC)
 - Multiple cell types, eventually from multiple individuals
 - Cell-type-specific measures of function/toxicity



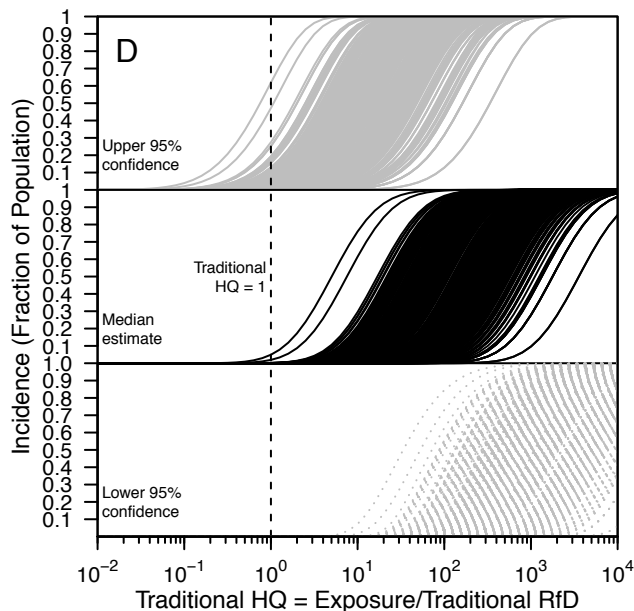
Challenges to Risk Characterization

Acknowledging that “safe” exposures are **not risk-free**.

- Uncertainty – can never achieve 100% certainty
- Variability – can never ensure 100% of population is protected



What is the risk at the RfD?



- Applied WHO/IPCS probabilistic framework to >1500 endpoints for >600 chemicals
- Exposure at the RfD implies upper 95% confidence bound population incidence of several percent.
- Noted that there is wide range of severity of the associated effects, from clinical chemistry to mortality (!).

Confirmation that the RfD is not 100% risk-free!

Challenges to Risk Characterization

Emerging data and methods have the potential to identify **who** may remain at risk.

- Risk-based policies presume individuals are unidentifiable.
- Precedent in cardiovascular health for calculating individual risk profiles.
- What if toxicity testing were done on each individuals' cells?

Heart Risk Calculator

Home About Contact

Age (years)

Gender Male
 Female

Race African American
 Other

Total cholesterol (mg/dL)

HDL cholesterol (mg/dL)

Systolic blood pressure (mmHg)

Diastolic blood pressure (mmHg)

Treated for high blood pressure No
 Yes

Diabetes No
 Yes

Smoker No
 Yes

Calculate

Calculate your 10-year risk of heart disease or stroke using the ASCVD algorithm published in 2013 ACC/AHA Guideline on the Assessment of Cardiovascular Risk.

This calculator assumes that you have not had a prior heart attack or stroke. If you have, generally it is recommended that you discuss with your doctor about starting aspirin and a statin. Furthermore, if you have an LDL-cholesterol (bad cholesterol) greater than 190, it is also generally recommended that you discuss with your doctor about starting aspirin and a statin.

Unfortunately, there is insufficient data to reliably predict risk for those less than 20 years of age or greater than 79 years of age and for those with total cholesterol greater than 320.

UPDATE (6/30/16) – The calculator has been vetted against the final guidelines from the USPSTF for initiating aspirin therapy.

UPDATE (9/18/15) – The calculator now also incorporates draft guidelines from the USPSTF for initiating aspirin therapy.

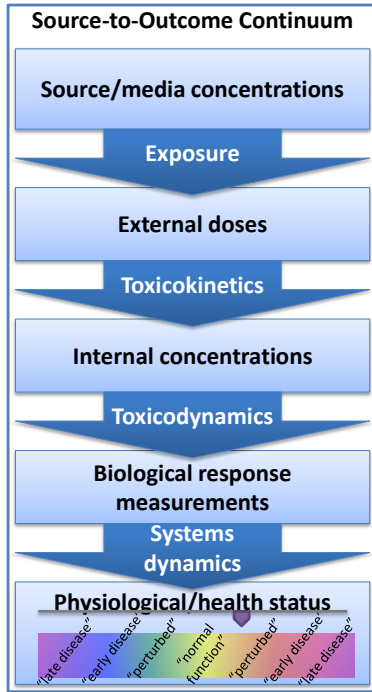
UPDATE (5/26/14) – The calculator now also incorporates guidelines from JNC-8 for blood pressure management. An excel spreadsheet is also available for download.



23andMe

And Beyond...

Summary and Conclusions: Addressing Population Variability and Susceptibility



- **Hazard identification: Multiple opportunities for improvement**
 - Population-based experimental models are more likely to overlap with human population responses
 - Genetic-based analyses of experimental populations have potential to identify mechanisms of toxicity and susceptibility
- **Dose-Response Assessment: Multiple opportunities for improvement**
 - Population PBPK modeling of toxicokinetic variability facilitated by new population-based in vivo and in vitro data
 - Emerging genetically diverse cell-based systems, including iPSC-based technologies, for assessing toxicodynamic variability
 - Potential for directly estimating population dose-response experimentally in toxicity testing using genetically diverse populations
 - Probabilistic dose-response modeling necessary to integrate population-based data for characterizing risk
- **Risk Characterization: Challenges to communication and policy**