



Application of Early Molecular Measurements to Develop Points of Departure for Risk Assessment

Society of Toxicology Workshop Leah Wehmas, U.S. EPA, Chair Connie Mitchell, HESI, Chair March 13, 2024 (1:30 PM to 4:45 PM)

This presentation does not represent U.S. EPA policy or endorsement and I have no conflicts to disclose.

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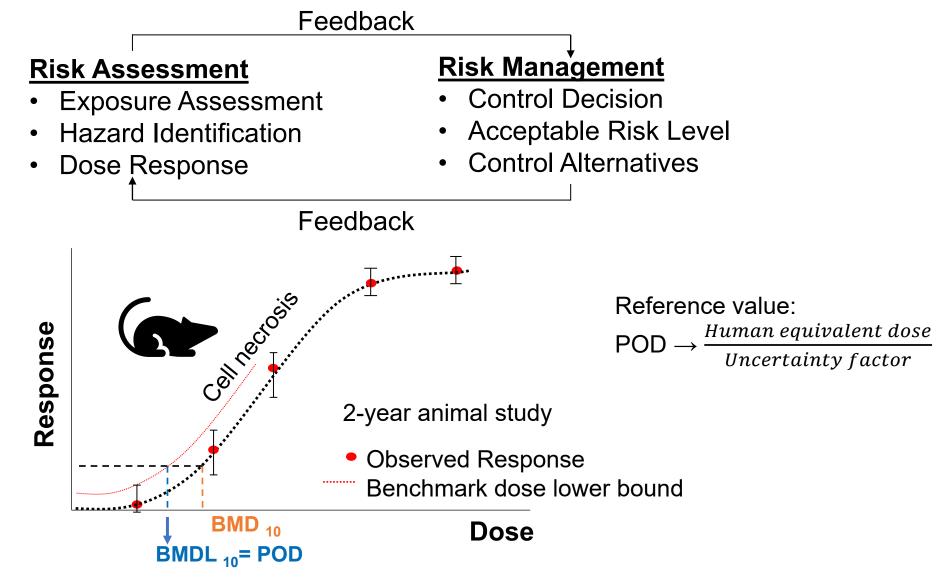
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Application of Early Molecular Measurements to Develop Points of Departure for Risk Assessment

Leah Wehmas (US EPA)	Introduction	1:30 PM to 1:35 PM
David Rouquie (Bayer)	Integration of NAMs and omics for determining points of departure	1:35 PM to 1:55 PM
Joshua Harrill (US EPA)	Evaluating the Impact of Cell Line Choice on Determination of Human Health Protective Molecular Points-of-Departure.	1:55 PM to 2:15 PM
Celeste Carberry (UNC)	Incorporating extracellular vesicle mediators of PFAS toxicity into NAMs-based points of department: a comparison against transcriptomic-based risk values	2:15 PM to 2:35 PM
Julia Malinowska (JCR- ISPRA)	Derivation of metabolic point of departure using high-throughput in vitro metabolomics: investigating the importance of sampling time points on benchmark concentration values in the HepaRG cell line	2:35 PM to 2:55 PM
Richard Currie (Syngenta)	Using omics for decision making and regulatory applications by Industry.	2:55 PM to 3:15 PM
Tara Barton-Maclaren (Health Canada)	Evaluating in vitro transcriptomics data for regulatory testing and assessment - Are we there yet?	3:15 PM to 3:35 PM
Panel Discussion	Q&A	3:35 PM to 4:15 PM



Traditional chemical assessments rely on chronic animal studies

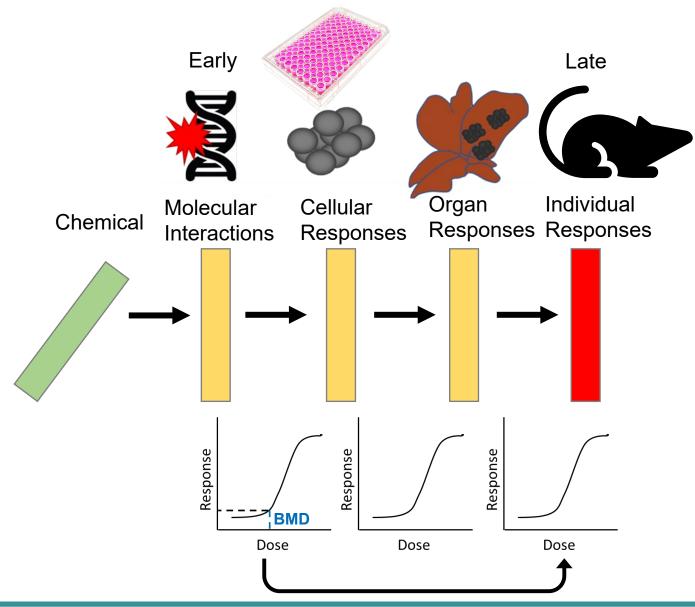


Benchmark dose (BMD) response modeling identifies point of departure (POD)



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Dose response assessment can be applied to molecular data



- Molecular changes occur with chemical exposure
- Changes often coincide or precede health effects
- Changes are measurable and dose dependent
- Coordinated changes across multiple genes, metabolites, miRNAs can identify a POD indicative of chronic toxicity

EPA transcriptomic assessment product