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Presenter Biography: Carlie LaLone is a bioinformaticist with the U.S. Environmental Protection Agency in Duluth MN. She is the principle investigator for the development of a web-based tool, Sequence Alignment to Predict Across Species Susceptibility (SeqAPASS), for evaluating protein sequence/structural similarity across taxa to predict susceptibility to chemicals with known molecular targets. Her research interests and published work include topics related to species extrapolation, adverse outcome pathway development, effects of pharmaceuticals in the environment, and ecotoxicology. Additionally, she is an editorial board member for the Society of Environmental Toxicology and Chemistry. She received bachelor's degrees in Biochemistry/Molecular Biology and Chemistry from the University of Minnesota Duluth in 2003 and a Ph.D. in Genetics from Iowa State University in 2009. From 2010-2015 Carlie was both a federal and University of Minnesota postdoctoral researcher for the Office of Research and Development in the U.S. Environmental Protection Agency.

Presentation Title: Cross-species Evaluation of Molecular Target Sequence and Structural Conservation as a Line of Evidence for Identification of Susceptible Taxa to Inform Toxicity Testing

Abstract: The 1985 U.S. Environmental Protection Agency Guidelines for Deriving Aquatic Life Criteria require acute and chronic toxicity testing with a fixed list of taxa that cover a broad spectrum of aquatic organisms from vertebrate, invertebrate, and plant families. In considering revisions to the Guidelines, there is interest in employing new technologies that could inform chemical-specific selection of test species based on scientific evidence for susceptibility as a means to eliminate unnecessary animal testing, reduce cost, and gain the most applicable data for decision making. Further, when toxicity testing is completed on selected organisms, advances in methods for species extrapolation could be implemented to gain a greater understanding of how representative the data are of other species from the same taxonomic group. A currently available computational method for informing such considerations is the U.S Environmental Protection Agency's Sequence Alignment to Predict Across Species Susceptibility (SeqAPASS) tool. Developed as a product under the Chemical Safety for Sustainability Research Program, SeqAPASS facilitates cross species comparisons of chemical molecular targets based on evaluation of protein sequence and structure. The assumption underlying this approach is that if a chemical is known to act on a specific protein to initiate toxicity in one species, conservation of that protein in another species provides a line of evidence that the second species could also be susceptible to a given chemical. Depending on the degree of characterization of the selected protein and the existing knowledge about the chemical-protein interaction, the SeqAPASS tool derives susceptibility predictions by calculating percent similarities from alignments of primary amino acid sequences, functional domains (e.g., ligand-binding domain), and individual amino acid residue(s) important for maintaining protein structure or for direct interaction with the chemical. Such data can be used to identify both species that are likely susceptible and those unlikely susceptible to a given chemical, therefore aiding in selection of appropriate test species. Another application for the data would be in understanding how broadly toxicity test data derived from one species may be extrapolated to others. In short, evaluation of cross species protein and structural conservation using SeqAPASS provides a rapid and cost effective method for deriving a line of evidence for chemical-specific testing strategies that may be of utility in the revised Aquatic Life Criteria Guidelines. *The contents of this abstract neither constitute nor reflect official US EPA policy.*