Title: Using a Sequence Homology-Based Predictive Strategy to Address Current Demands for Focused Toxicity Testing in Ecological Risk Assessment

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The lack of resources available for comprehensive toxicity testing, international interest in limiting the quantity of animals used in testing, and a mounting list of anthropogenic chemicals produced world-wide have led to the exploration of innovative means for identifying chemicals that are potentially hazardous to the environment and its inhabitants. Predictive toxicological approaches, which utilize publically available, *a priori*, knowledge of a chemical and its known molecular, cellular, or whole organism interactions, show promise for focusing current toxicity testing strategies. Using modern bioinformatic techniques, we have created a computational tool, which mines the extensive genomic and proteomic sequence repositories available through the National Center for Biotechnology Information and strategically compares homology metrics associated with primary and secondary protein sequences/structural domains across taxa. These comparisons are used to identify and rank species most likely to be susceptible to a chemical acting through a known molecular initiating event and can therefore aid in designing toxicity studies for species of concern. This presentation will identify the domains of applicability for this tool and describe examples related to predicting species sensitivities to pharmaceuticals and pesticides. An assessment of honey bee sensitivity to various pesticides will demonstrate the applicability of this tool for existing questions in risk assessment. *The contents of this abstract neither constitute nor reflect official US EPA policy.*