Developing in vitro assay annotations to provide context and facilitate interpretation toward toxicological endpoints

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In vitro assays, especially high-throughput screening (HTS) assays, can generate an abundance of mechanistic data to inform on chemical effects on biochemical endpoints and molecular and cellular signaling pathways. However, interpreting HTS data in the context of organism-level outcomes can be challenging. Assay descriptions are often focused on technological features such as cell line, receptor type, and reporter used. Contextualization can be further complicated when cell lines have a transfected target molecule from a different species, or when the assay's measured endpoint (e.g., a change in the expression of a gene transcript) is different from the process the assay is intended to inform on (e.g., activity of a receptor that mediates the expression of that gene transcript). For stakeholders unfamiliar with HTS assays, the lack of context may lead to either misinterpretation of the data or a hesitancy to use the data at all. This presentation describes how annotating HTS assays with complementary technological and biological target pathway information can provide context needed to improve accessibility of these data to a broader range of stakeholders. Focusing on the curation of HTS data within the National Toxicology Program's Integrated Chemical Environment (https://ice.ntp.niehs.nih.gov/), we will demonstrate the use of knowledge organization systems and controlled terminology to facilitate human and machine-accessible data interpretation in support of chemical evaluation for toxicological hazard characterization. This project was funded by the National Institute of Environmental Health Sciences, National Institutes of Health, under Contract No. HHSN273201500010C.