(IIB-1) Towards a Chemogenomic Future

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Toxicogenomics data -- with its potential to highlight common patterns of response and illuminate underlying mechanistic pathways across toxicology domains – holds great promise for improving predictive toxicology capabilities. Chemogenomics, the integrated use of genomic and chemical information, has been applied in pharmacology and toxicology for enhancing target identification/validation, efficacy evaluation, and toxicity assessment. These methods have been applied to predicting a chemical's potential toxicity based on a limited profile of data for the chemical of concern, or available data for related chemicals. The most success has been achieved in the pharmaceutical/commercial domain with the use of a diverse array of information, including toxicogenomics data in combination with chemical, bioactivity, and histopathology data, to determine predictive toxicological signatures. This success, while serving as proof-of-principle, also demonstrates the abundant information resources necessary to complete such a study. The environmental regulatory domain typically lacks access to the data resources of the commercial and pharmaceutical efforts, where large focused data gathering efforts are undertaken to support such capabilities and most of these data are proprietary. Hence, major hurdles to transferring these successes to environmental and industrial chemicals and wider public access, include: lack of publicly available, standardized, reference genomic/bioactivity databases; lack of chemical structure indexing for public genomic and toxicity databases; and scattered, fragmented sources of toxicity and genomic data. In addition new methodologies and considerations must be employed to potentially compare data across laboratories and platforms, and to address issues of extrapolation (species, doses, chemicals, and endpoints) that are of direct relevance to health risk assessment. Progress will be reported on the development of tools and methodologies that will further the integration and leveraging of public data for use in predictive toxicology. These involve integration of DSSTox chemical standards and data resources with public genomic repositories, and include collaborations with the EBI's (European Bioinformatics Institute) ArrayExpress and NCBI's (National Center for Biotechnology Information) GEO (Gene Expression Omnibus) repositories.