

## **Overview of Genomic Studies on Rodent Tumors and its Translational Relevance**

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The National Toxicology Program's signature rodent cancer bioassays have provided invaluable cancer hazard identification information on more than 600 chemicals/agents. The NTP calls of carcinogenicity are primarily based on the pathology data. However, the advent of next generation sequencing technologies has provided an unprecedented opportunity to investigate the molecular alterations underlying chemical carcinogenicity by examining genomic and epigenomic alterations in tumors from the rodent cancer bioassays. The genomic data such as mutation signatures, driver genes, copy number alterations, and transcriptomic alterations as well as epigenomic data such as global methylation changes, and miRNA alterations provide an avenue to understand the mechanisms of chemical carcinogenicity, to identify biomarkers of exposure and disease, and to provide a translational context to the rodent cancer data. This presentation will focus on some of these approaches and discuss how these approaches can add value to the cancer hazard identification program at the NTP.