Submitter Name: Molly A. Bogue
Submitter email: Molly.Bogue@jax.org

# Mouse Phenome Database 2.0: New tools and data resources for curated and integrated primary mouse phenotype data

Molly A. Bogue[1], Gaurab Mukherjee[1], Stephen C. Grubb[1], David O. Walton[1], Vivek M. Philip[1], Matthew Dunn[1], Georgi I. Kolishovski[1], Timothy Stearns[1], Vinita Sinha[1], Beena Kadakkuzha[1], Gregg TeHennepe[1], Govind Kunde-Ramamoorthy[1], Elissa J. Chesler[1]

[1]The Jackson Laboratory

The Mouse Phenome Database (MPD; phenome.jax.org) is a widely used resource that provides access to primary experimental data, protocols and analysis tools for mouse phenotyping studies. Data are contributed by investigators around the world and represent a broad scope of phenotyping endpoints and disease-related characteristics in naïve mice and those exposed to drugs, environmental agents or other treatments. MPD was recently re-engineered using Web 2.0 technologies to facilitate interactive data exploration and quantitative analysis. We are curating data from inbred strains and other reproducible strains, including KOMP mice, Collaborative Cross (CC), CC-RIX, and founder strains. We are also collecting primary data from mapping populations, including historic mapping crosses and advanced high-diversity mouse populations such as Diversity Outbred mice. We are developing a new data submission interface for data contributors so that they, as domain experts, may annotate their own data with relevant ontology terms and provide detailed information for protocols and animal environmental conditions as required by the ARRIVE guidelines. These data will be exposed to analysis tools within MPD and through an API to other systems. Rigorous statistical analyses are implemented in R, and dynamic D3 visualizations are available through MPD. New tools and analyses are under continual development and include multivariate outlier detection, replicability analysis, and multi-trait, multi-population mapping. Tools will be integrated with other systems genetics resources, including GeneNetwork. Tools and features from the re-engineered MPD system will be presented, including tools for QTL analysis across studies.