



Population-Based Rodent Resources for Environmental Health Sciences

AGENDA

Day One – March 18, 2015

8:30 a.m.	Welcoming Remarks Linda Birnbaum, <i>National Institute of Environmental Health Sciences</i>
8:40 a.m.	Introduction/Purpose/Background Kim McAllister, <i>National Institute of Environmental Health Sciences</i>
Session One	Overview of Mouse/Rat Resources Chair: Allan Balmain, <i>University of California, San Francisco</i>
9:00 a.m.	The Collaborative Cross: What We've Learned From Randomized, Structured Populations David Threadgill, <i>Texas A&M University</i>
9:45 a.m.	Diversity Outbred Gary Churchill, <i>Jackson Laboratory</i>
10:30 a.m.	Hybrid Diversity Panel Brian Parks (<i>Jake Lusis' laboratory</i>), <i>University of California, Los Angeles</i>
11:15 a.m.	Recombinant Inbred Rats: Genetics, Transcriptomes, and Use for Identifying Phenotypic Determinants Boris Tabakoff, <i>University of Colorado School of Medicine</i>
12:00 p.m.	Q&A
12:30 p.m.	Lunch
Session Two	Diverse Applications Chair: Mathew Pletcher, <i>Pfizer</i>
1:30 p.m.	"Fit-For-Purpose," Population Study Designs To Address Specific Hypotheses Ivan Rusyn, <i>Texas A&M University</i>
2:00 p.m.	Mouse Populations Enable Translational Pharmacogenomic Approaches for Understanding and Predicting Adverse Drug Events Alison Harrill, <i>University of Arkansas for Medical Sciences</i>
2:30 p.m.	Identifying G X E Interactions and Thresholds for Toxicity in Diversity Outbred Mice Jef French, <i>National Institute of Environmental Health Sciences</i>
3:00 p.m.	A Diversity Outbred ES Cell Platform for In Vitro Genetics Ted Choi, <i>Predictive Biology, Inc.</i>
3:30 p.m.	Q&A
Session Three	Poster Session
4:00 p.m.	Poster Session
6:00 p.m.	Adjourn for the Day



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Day Two – March 19, 2015

Session Four Computational Tools and Analysis Approaches

Chair: Daniel Pomp, *University of North Carolina, Chapel Hill*

8:30 a.m. Advancing Risk Assessment with Population-based Experimental Resources

Weihshueh Chiu, *Texas A&M University*

9:00 a.m. Mixed Model and Meta-analysis Methods for G X E Analysis in Mouse Studies

Eleazar Eskin, *University of California, Los Angeles*

9:30 a.m. Computational Mapping Tools

Dan Gatti, *Jackson Laboratory*

10:00 a.m. Q&A

Session Five Disease Applications

Chair: Cheryl Marks, *National Cancer Institute*

10:30 a.m. Genetic Regulatory Variation and Environmental Response

David Aylor, *North Carolina State University*

11:00 a.m. Harnessing Diversity in the CC and DO Populations for the Study of Behavior

Elissa Chesler, *Jackson Laboratory*

11:30 a.m. Genetic Diversity in Ebola Response

Martin Ferris, *University of North Carolina, Chapel Hill*

12:00 p.m. Q&A

12:30 p.m. Lunch

Session Six Breakout Groups Highlighting Experimental Designs/Test Cases: Challenges and Opportunities for Utilizing These Population-based Rodent Resources

1:30 p.m. Initial Charge

Nigel Walker

1:45 p.m. Breakouts

(Note: Selected assignments below are attempting to distribute expertise among some of the invited speakers, chairs, and other confirmed researchers, but all other participants are invited to join in and contribute as well!)

Breakout Group One:

Co-chairs: Warren Casey, Terry Kavanagh

Heather Patisaul

Igor Pogribny

William Valdar

Mathew Pletcher

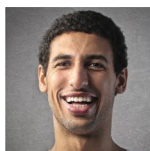
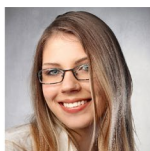
David Threadgill

Ivan Rusyn

Eleazar Eskin

David Aylor

Notetaker/Scribe: Rick Paules/Leroy Worth



1:45 p.m.

Breakouts *(continued)*

Breakout Group Two:

Co-chairs: Fernando Pardo Manuel de Villena, Paul Foster

Samir Kelada

Laura Saba

John Bucher

Gary Churchill

Allan Balmain

Cheryl Marks

Dan Gatti

Notetaker/Scribe: June Dunnick/Sri Nadadur

Breakout Group Three:

Co-chairs: Tim Wiltshire, Mike Devito

Jessica Mayeux

Brian Bennett

Arun Pandiri

Daniel Pomp

Brian Parks

Elissa Chesler

Jef French

Notetaker/Scribe: Dan Shaughnessy/Fred Tyson

Breakout Group Four:

Co-chairs: Jonathan Pollock, David Dix

Greg Crawford

Amelie Baud

Alison Harrill

Weihshueh Chiu

Byron Jones

Martin Ferris

Ted Choi

Boris Tabakoff

Notetaker/Scribe: Keith Shockley/Jonathan Hollander

2:45 p.m.

Prepare Report-back

3:00 p.m.

Report-backs by Co-chairs of Each Breakout Group (Approx. 10-15 minutes each)

4:00 p.m.

Final Wrap-up/General Recommendations of Next Steps

4:30 p.m.

Adjourn the Meeting

Poster List

1. ***Accounting for population structure in gene-by-environment interactions in genome-wide association studies using mixed models.*** Michael Bilow, UCLA Department of Computer Science
2. ***Baseline brain co-expression networks in the HXB/BXH recombinant inbred rat panel.*** Laura Saba, Skaggs School of Pharmacy and Pharmaceutical Sciences, University of Colorado Anschutz Medical Campus
3. ***Determining the interactive effects of maternal diet and genetic factors on germline epigenetic reprogramming.*** Jing Xue, Nutrition Research Institute, University of North Carolina at Chapel Hill, Kannapolis, North Carolina
4. ***Distinct genetic factors influence different stages of cancer development and progression.*** Kyle Halliwill, University of California, San Francisco
5. ***Diversity outbred mice indicate idiosyncratic drug-induced liver injury potential.*** Lascelles Lyn-Cook Jr., University of Arkansas for Medical Sciences
6. ***Efficient detection of trans-eQTL in a collaborative cross study.*** Wesley Crouse, University of North Carolina at Chapel Hill
7. ***Estimation of heritability from inbred mouse strains.*** Dat Duong, University of California, Los Angeles
8. ***Genetic determinants of cell state in mouse induced pluripotent stem cells.*** Tiffany Garbutt, North Carolina State University
9. ***Genetics basis of social effects – A pilot study on indirect genetic effects in laboratory mice.*** Amelie Baud, EMBL – European Bioinformatics Institute
10. ***Heterogeneity in quantum dot induced lung inflammation and toxicity in recombinant inbred mouse strains of the collaborative cross.*** David Scoville, University of Washington
11. ***Host genetic determinants of diversity in viral-induced disease pathology.*** Candice Brinkmeyer-Langford, Texas A&M University
12. ***Identification of causal genes for complex traits.*** Farhad Hormozdiari, University of California, Los Angeles
13. ***Identification of genetic regulators of the atherosclerosis-associated metabolite trimethylamine-n-oxide in the diversity outbred mice population.*** Brian Bennett, University of North Carolina at Chapel Hill
14. ***Susceptibility to multi-walled carbon nanotube-induced acute lung pathology varies with mouse strain.*** Megan Cartwright, University of Washington
15. ***Systems genetics approach uncovers Dusp7 as a novel phosphatase regulating skeletal muscle insulin signaling.*** Marcus Seldin, University of California, Los Angeles
16. ***Systems genetics of microbial abundance, host transcriptome, and disease in the collaborative cross.*** Jason Bubier, The Jackson Laboratory
17. ***The collaborative cross as a source of new models for human disease.*** Andrew Morgan, University of North Carolina at Chapel Hill
18. ***The effects of a high fat diet on male diversity outbred mice.*** Michael DeVito, National Institute of Environmental Health Sciences (Division of National Toxicology Program, National Toxicology Program Laboratory)
19. ***The Oncology Models Forum: A translational research collaborator.*** Cheryl Marks, National Cancer Institute
20. ***Using variation in micronucleus response to benzene exposure in diversity outbred (J:DO) mice to identify population-based exposure thresholds and genetic factors influencing genotoxicity.*** Kristine Witt, National Institute of Environmental Health Sciences/National Toxicology Program