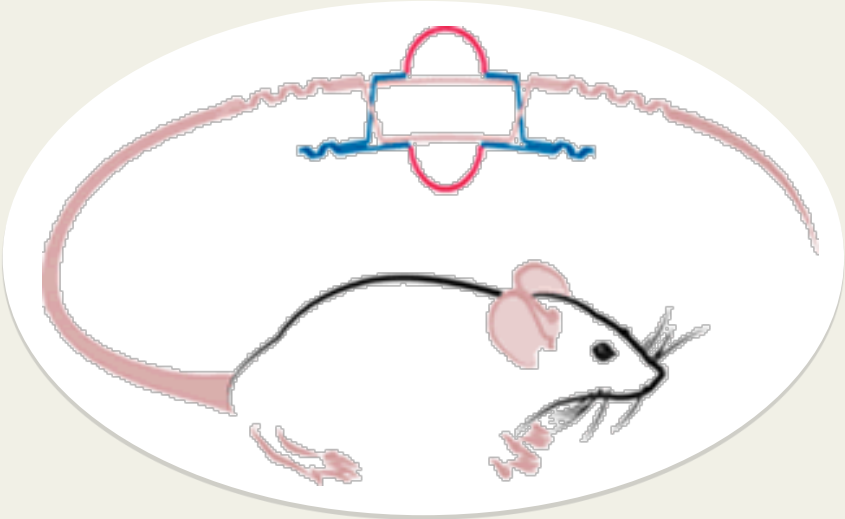
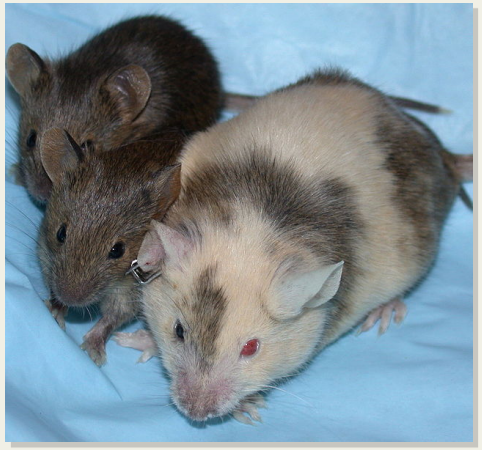
The Knockout Mouse Project (KOMP)
&
KOMP Phenotyping (KOMP^2)

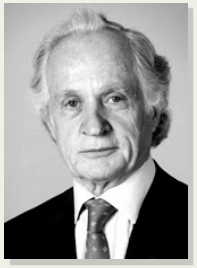


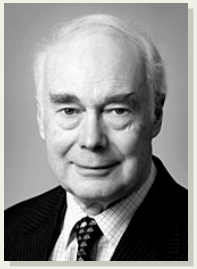
Jane Peterson, Ph.D.
June 6, 2010

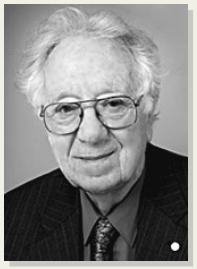
Mice in Biomedical Research

- The laboratory mouse has been considered the premiere experimental model of human biology and disease since 1902 when it was first used to demonstrate how genetic traits could be transferred from parents to offspring via classical or “Mendelian” inheritance in mammals.
- In just over a century, an impressive array of genetic tools, reagents and processes has been developed in the mouse, including:
  - Homozygous inbred strains
  - Recombinant inbred and consomic strains
  - Transgenic and knockout methods
  - Monoclonal antibodies
  - iPS cells
- Evidence that mice have played a key role in biomedical research is provided by the fact that at least 18 Nobel prizes have been awarded for work done using the mouse. Most recently, the 2007 Nobel Prize was awarded to Mario Capecchi, Martin Evans, and Oliver Smithies for their discovery of the "principles for introducing specific gene modifications in mice by the use of embryonic stem (ES) cells.”

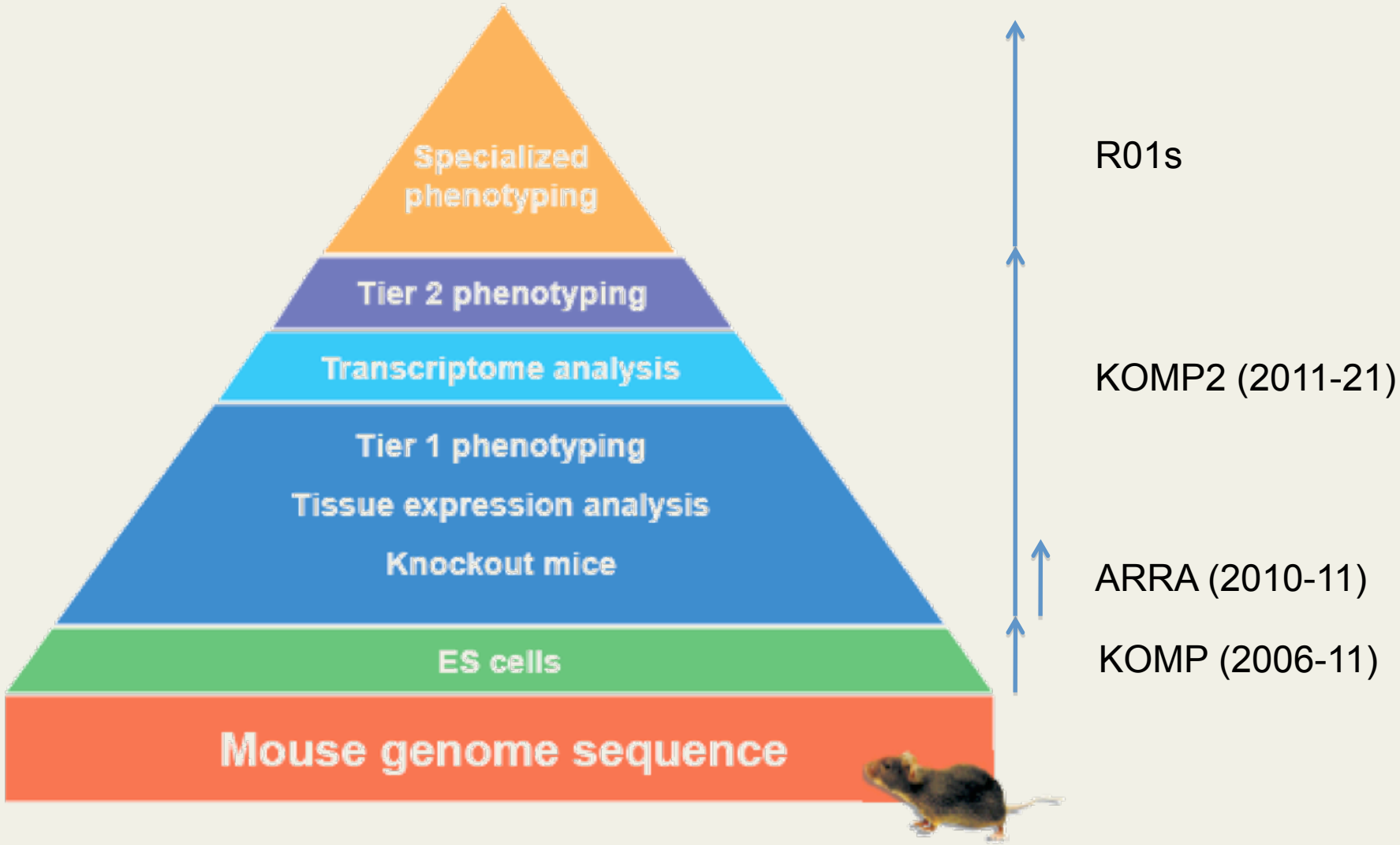






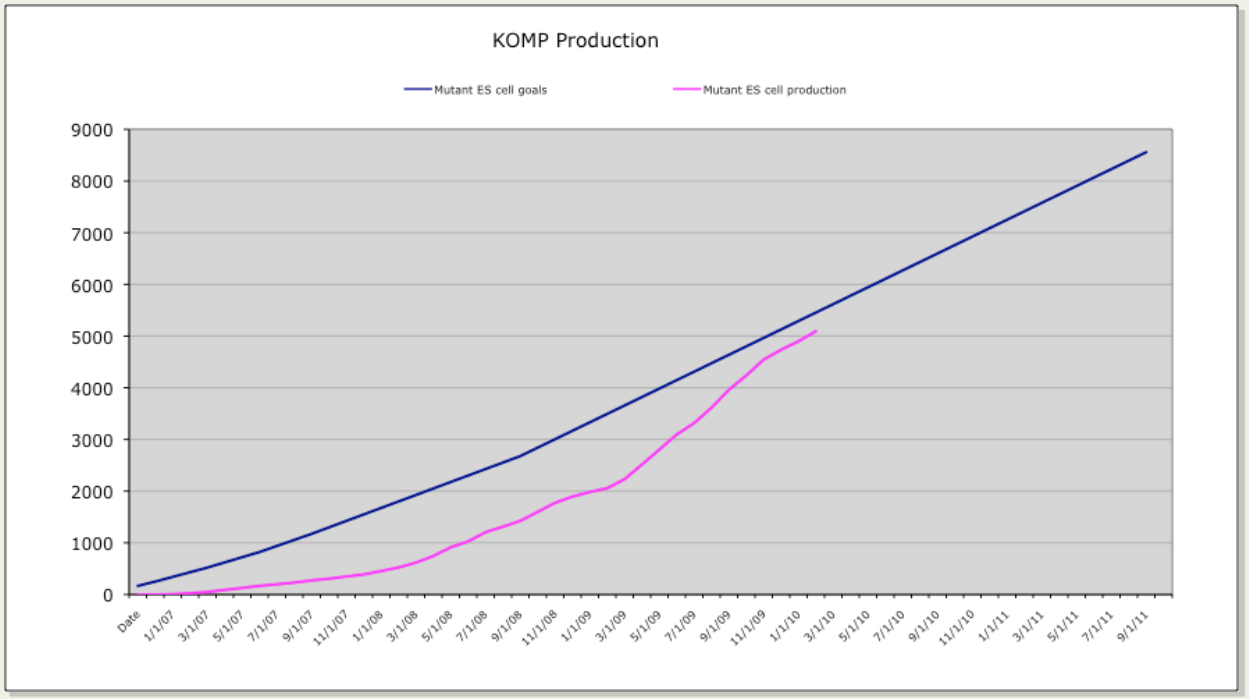


KOMP Vision



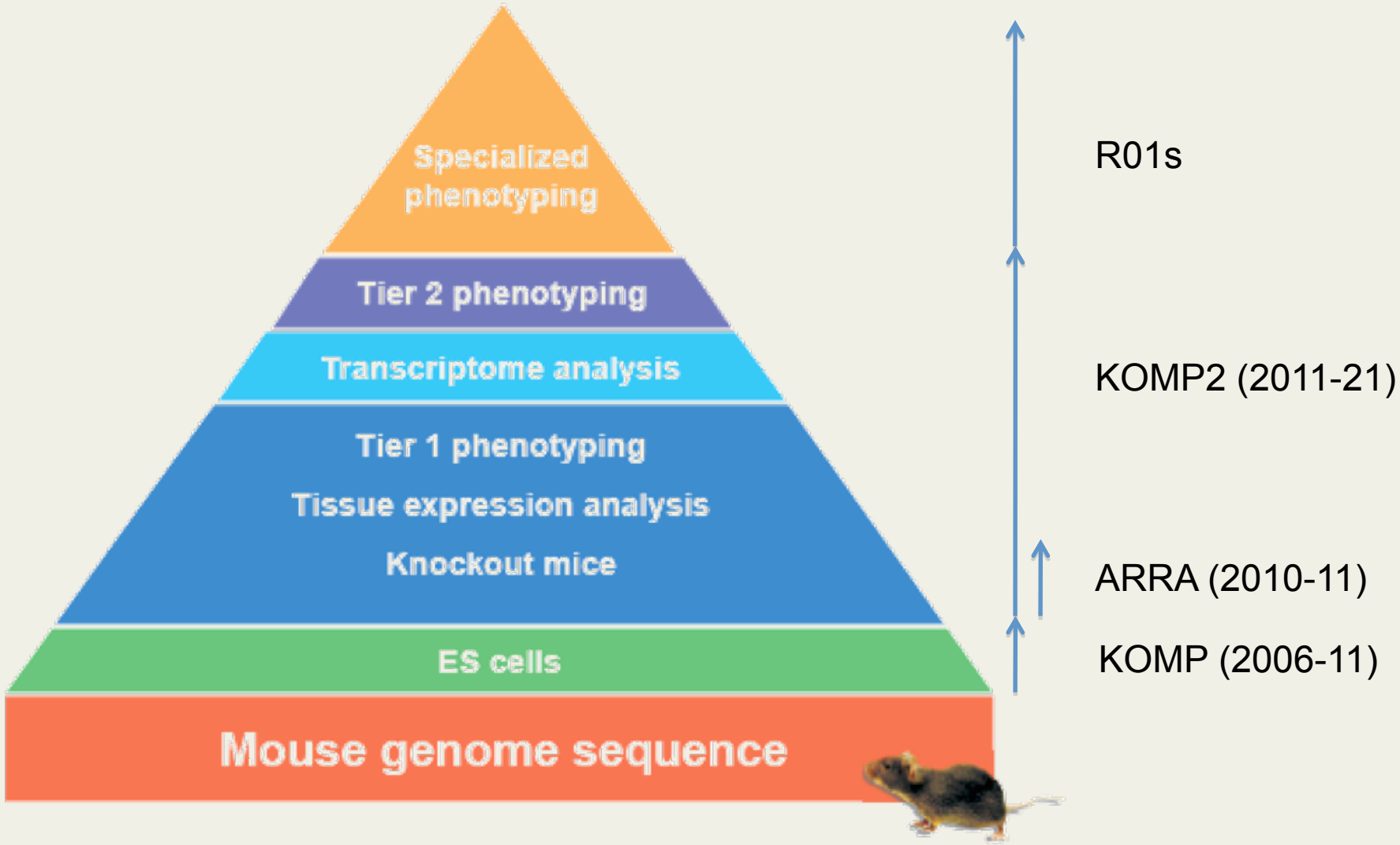
Austin et al., Nature Genetics, 2004

Goals and Progress



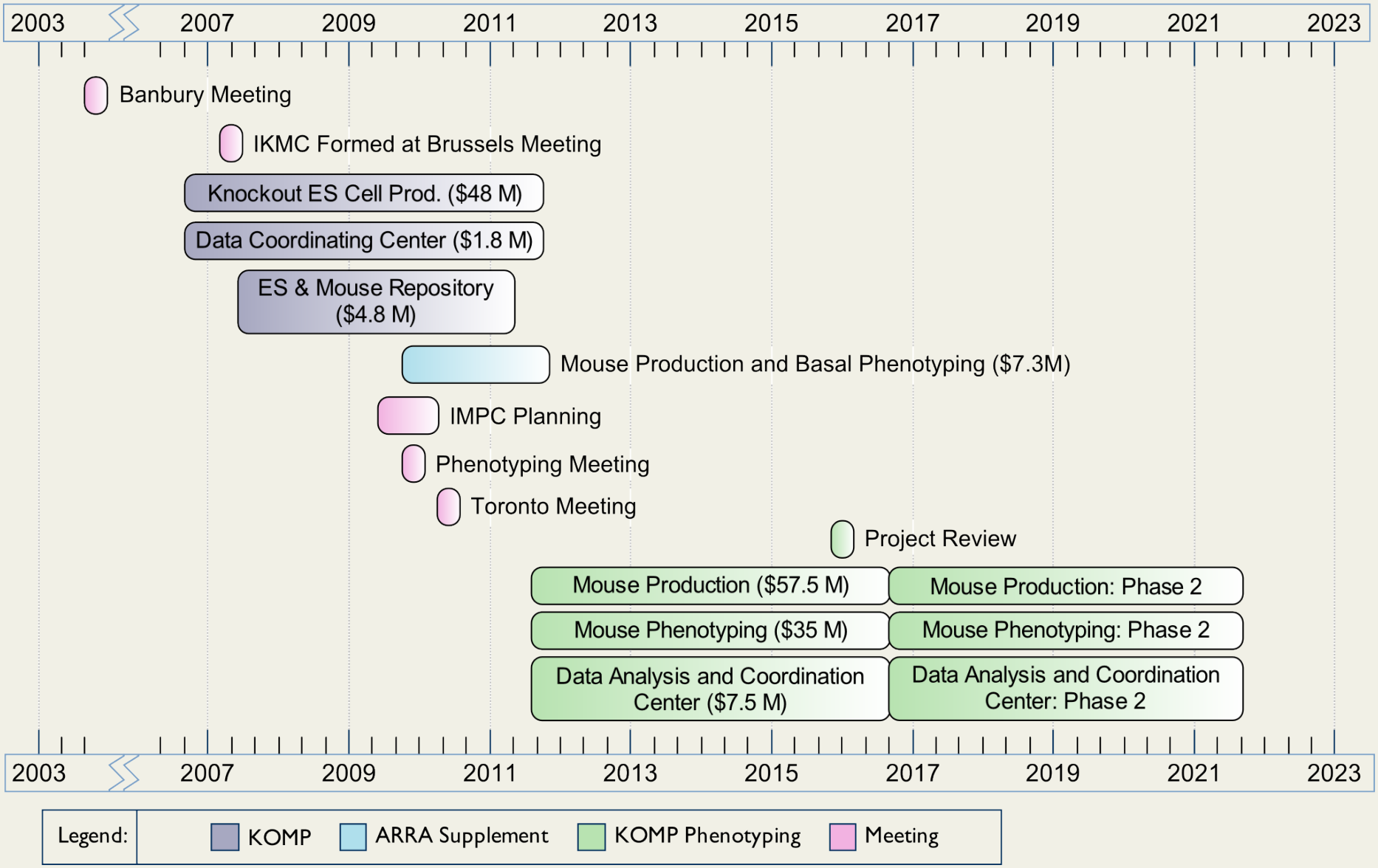
	CSD	Regeneron	EuCOMM	NorCOMM	TIGM	Total
Goal (ES)	5,000	3,500	8,000	500		17,000
Vectors	4991	3116	4271	596		
Targeted ES	3064	2038	2883	236		8,221
Mice	189	160	351	12		700

KOMP Vision



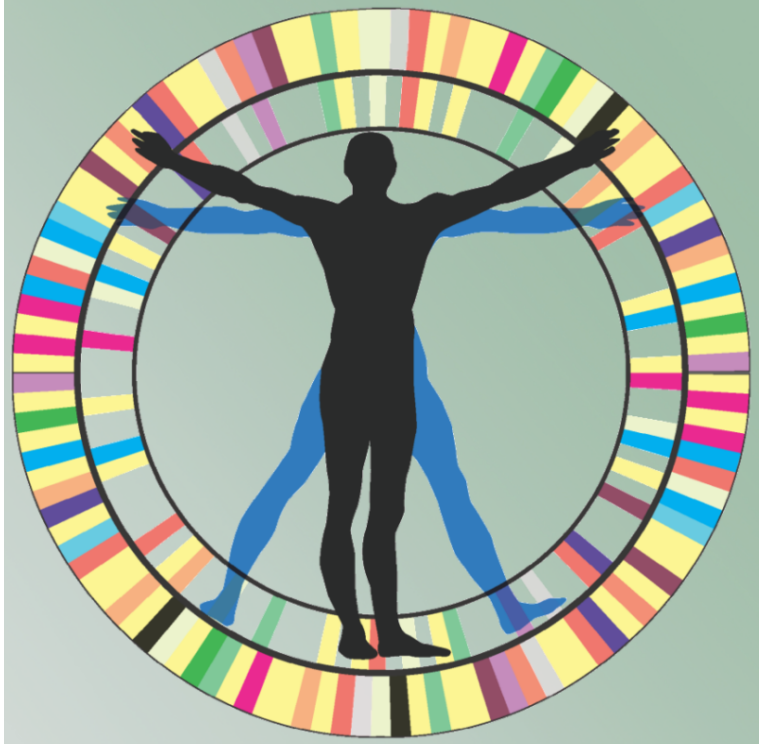
Austin et al., Nature Genetics, 2004

KOMP – KOMP^2 Timeline



Goal: Phenotype 2,500 mice in Phase 1 and 6,000 in Phase 2

NIH Roadmap Human Microbiome Project



NIH Human Microbiome Project

Goal:

1. **Catalog the microbes that inhabit the human body**
2. **Examine whether changes in the microbiome can be related to health and disease**
3. **Generate a community resource to support and enable metagenomics-based projects that investigate the role of microbial communities in human health.**

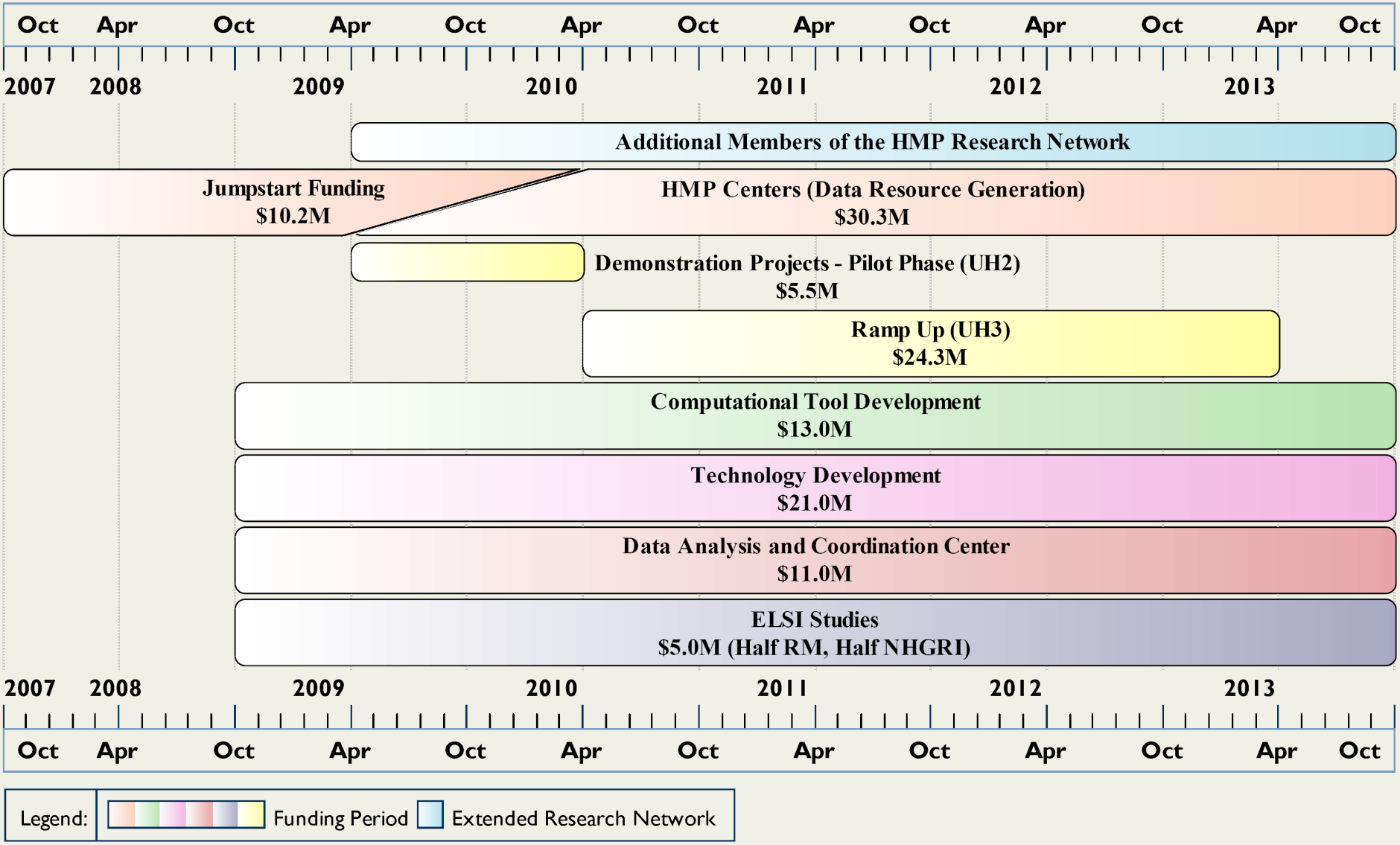
- **Timeline: five-year project**
- **Budget: $157 million**
- **Data Release: All data and resources will be released immediately (community resource project).**

URLs: http://nihroadmap.nih.gov/hmp/

http://hmp.nih.gov

http://www.hmpdacc.org

HMP Initiatives



Contact PI	Application Title
Blaser, Martin	Evaluation of the cutaneous microbiome in psoriasis
Storch, Gregory	The human virome in children and its relationship to febrile illness
Fraser-Liggett, Claire	The thrifty microbiome: The role of the gut microbiota in obesity in the Amish
Li, Huiying	Metagenomic study of the human skin microbiome associated with acne
Wu, Gary	Diet, genetic factors, and the gut microbiome in Crohn's disease
Fortenberry, Dennis	Urethral microbiome of adolescent males
Tarr, Phillip	The neonatal microbiome and necrotizing enterocolitis
Pei, Zhiheng	Foregut microbiome in development of esophageal adenocarcinoma

Contact PI	Application Title
Ravel, Jacques	The microbial ecology of bacterial vaginosis: A fine scale resolution metagenomic analysis
Li, Ellen	Effect of Crohn's disease risk alleles on enteric microbiota
Young, Vincent	The role of the gut microbiota in ulcerative colitis
Versalovic, James	The Human Microbiome in Pediatric Abdominal Pain & Intestinal Inflammation
Segre, Julia	Skin Microbiome in Disease States: Atopic Dermatitis and Immunodeficiency
Buck, Gregory	The Vaginal Microbiome: Disease, Genetics and the Environment
Fraser-Liggett, Claire	Metagenomic Analysis of the Structure and Function of the Human Gut Microbiota in Crohn’s Disease

Human Microbiome Project DACC - Home - Mozilla Firefox

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http://hmpdacc.org/

HUMAN MICROBIOME PROJECT

DACC

BACTERIAL STRAINS | MICROBIOME SAMPLING | ANALYSIS | PROTOCOLS & STANDARDS | PARTICIPANT INFO | RESOURCE REPOSITORY | OUTREACH

Welcome

Welcome to the Data Analysis and Coordination Center (DACC) for the Human Microbiome Project (HMP). The HMP was launched by the National Institutes of Health Roadmap for Medical Research and is designed to fuel research into the multitude of microbes that live in the various environments of the human body. A major goal of the HMP is to look for correlations between changes in the microbiome and human health. More information about the project can be found on the NIH Roadmap website at http://nihroadmap.nih.gov/hmp.

The HMP DACC is the central repository for all HMP data, providing specialized data management and analysis infrastructure to facilitate discoveries about the microbiome. The HMP-DACC web site will provide web-based query and visualization tools, comprehensive computational analysis of HMP data, quality control measures, and links to well-documented Standard Operating Procedures. The DACC is also strongly committed to outreach and training. Please visit the above tabs for more information on each of these topics.

Projects

Reference Genomes

Approximately 600 microbes from cultured and uncultured bacteria, plus several non-bacterial microbes will be sequenced during the HMP. Combined with existing and other currently planned efforts, the total reference collection should reach 1000 genomes.These sequences will provide a benchmark against which further sequence data can be compared.

16S RNA Sequencing

16S RNA sequencing will be used to characterize the complexity of microbial communities at individual body sites, and to determine whether there is a core microbiome at each site. Several body sites will be studied, including the gastrointestinal and female urogenital tracts, oral cavity, nasal and pharyngeal tract, and skin.

Metagenomic WGS

Expanding on the 16S data, Whole Genome Shotgun (WGS) sequencing will be performed on samples taken from human subjects. Coupled with the other data generated during the project, this will provide insights into the genes and pathways present in the human microbiome.

We Welcome Community Feedback

We encourage and welcome feedback from the scientific community on the selection of strains to include in the reference collection as well as which of these strains should be prioritized for finishing (only about 15% of strains can be finished). The current list of strains included in the project can be found under the "Bacterial Strains" tab at the top of this page. The list of strains that are currently slated for a higher level of finishing beyond the standard draft stage can be found here. In addition, projects listed on the main strains list (under the strains tab) which are marked "targeted" may still require sources of cells or DNA. If you have such materials you are willing to share please contact us. Click here to provide feedback or information that you wish to share with the HMP.

For internal use

- FTP
- Collaboration Site
- Clinical Data Collection Center (EMMES)

Other Resources

DACC Member Organizations

- The Institute for Genome Sciences
- The Joint Genome Institute
- Lawrence Berkeley National Laboratory
- University of Colorado at Boulder

NIH Sites

- NIAID Microbial Sequencing centers
- NIDCR Human Oral Microbiome Database
- BRC Central
- NMPDR RAST Annotation Server
- NMPDR RAST Metagenome Annotation Server

Jumpstart Center Sites

- J. Craig Venter Institute
- Broad Institute
- Baylor College of Medicine
- Washington University

International Sites

- INRA
- MetaHIT

Contact | Policy