

# Mouse DNA to aid biomedical research

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Researchers announced today that they have successfully resequenced the DNA of 15 mouse strains most commonly used in biomedical research. More than 8.3 million single nucleotide polymorphisms (SNPs) were discovered among the genomes of the 15 mouse strains and the data are now publicly available. These new data will help researchers better understand complex genetic traits, such as why some individuals are more susceptible to certain diseases, and will serve as a valuable resource in determining how environmental agents influence the development of disease.

Single Nucleotide Polymorphisms, or SNPs (known as "snips"), are single genetic changes, or variations, that can occur within a DNA sequence. Because mice and humans share many of the same fundamental biological and behavioral processes, including gene functions, these data will help researchers understand human genetic susceptibility to almost 200 diseases such as Parkinson's, cancer, diabetes, heart and lung diseases, reproductive diseases, and asthma and other childhood diseases, which are affected by exposure to environmental substances.

"Making this wealth of data freely available to the research community is a significant milestone," said David A. Schwartz, M.D., director of the National Institute of Environmental Health Sciences (NIEHS), part of the National Institutes of Health, which funded the research. "Each mouse strain is genetically unique. Now that we know the DNA variations for these mouse strains, we can compare the genetic makeup of one strain that acquires a certain disease to another strain that does

not get the same disease. In this way researchers gain insight into the same processes that may cause one human to get a disease while another human in the same environment remains disease-free."

The "Resequencing and SNP Discovery Project" began less than two years ago through a contract between the National Toxicology Program at NIEHS and Perlegen Sciences, Inc. of Mountain View CA. Perlegen scientists conducted the project using as a standard reference the 2003 DNA sequencing of the C57BL/6J mouse strain -- the very first mouse strain to undergo DNA sequencing. The mouse models included in the resequencing project are: 129S1/SvImJ, A/J, AKR/J, BALB/cByJ, BTBR T+ tf/J, C3H/HeJ, CAST/EiJ, DBA/2J, FVB/NJ, MOLF/EiJ, KK/HIJ, NOD/LtJ, NZW/LacJ, PWD/PhJ, and WSB/EiJ. The 15 mouse strains were carefully chosen because of their routine use as research models and their genetic diversity. The project used the same high-density oligonucleotide array technology that was used to discover common DNA variation in the human genome.

"Perlegen Sciences was excited to perform this scientific work, because it promised to provide an extremely valuable resource. We believe the data will generate a lot of knowledge about complex genetic traits," said Kelly Frazer, Vice President of Genomics at Perlegen Sciences, Inc.

"This project was highly anticipated by scientists. Now, we can go to our computer, click on the mouse strain we want to use, see the sequence variations for that strain and compare it to the others," said David Threadgill, Ph.D., an expert in mouse models of disease at the University of North Carolina, Chapel Hill. "If we use multiple strains, we can then look at the data after the animals are exposed to an environmental substance and compare the genetic differences between the strains that acquired a disease and those that did not. This will help us begin to identify causes of differential susceptibility to disease."

"These mouse data will aid in our understanding of 'counterpart' genes in humans, the corresponding molecular and biological pathways the lead to disease susceptibility, and the environmental agents that trigger the development of disease in susceptible people," said David Christiani, M.D., Professor of Medicine at Harvard Medical School and Professor of Occupational Medicine and Epidemiology at Harvard School of Public Health. "The data will also be a great resource for pharmaceutical companies that are developing new treatments for disease."

Source: National Institute of Environmental Health Sciences

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