

# Mouse genome will help identify causes of environmental disease

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Research on the DNA of 15 mouse strains commonly used in biomedical studies is expected to help scientists determine the genes related to susceptibility to environmental disease. The body of data is now publicly available in a catalog of genetic variants, which displays the data as a mouse haplotype map, a tool that separates chromosomes in to many small segments, helping researchers find genes and genetic variations in mice that may affect health and disease.

The haplotype map appearing online in the July 29th issue of *Nature* is the first published full descriptive analysis of the “Mouse Genome Resequencing and SNP Discovery Project” conducted by the National Institute of Environmental Health Sciences (NIEHS), part of the National Institutes of Health.

“These data allow researchers to compare the genetic makeup of one mouse strain to another, and perform the necessary genetic analyses to determine why some individuals might be more susceptible to disease than another. This puts us one step closer to understanding individual susceptibility to environmental toxins in humans. We also hope that pharmaceutical companies developing new treatments for environmental diseases will find these data and this paper as a valuable resource,” said David A. Schwartz. M.D., NIEHS Director.

The paper describes in detail the laborious and technology-driven approaches that were used to identify 8.27 million high quality SNPs distributed among the genomes of 15 mouse strains. Single Nucleotide

Polymorphisms, or SNPs (known as snips), are single genetic changes, or variations, that can occur in a DNA sequence.

Much of the project was conducted through a contract between the National Toxicology Program at NIEHS and Perlegen Sciences, Inc. of Mountain View Calif.

“The database of mouse genetic variation should facilitate a wide range of important biological studies, and helps demonstrate the utility of this array technology approach,” said David R. Cox, M.D., Ph.D., chief scientific officer at Perlegen Sciences, Inc.

The Perlegen scientists used C57BL/6J the first mouse strain to undergo DNA sequencing as their standard reference to conduct the re-sequencing on the four wild-derived and eleven classical mouse strains. The technology used, the oligonucleotide array, was also used to discover common DNA variation in the human genome.

The arrays looked at about 1.49 billion bases (58 percent) of the 2.57 billion base pair of their standard reference strain. The data were then used to develop the haplotype map which contains 40,898 segments.

“The data will be a valuable resource to many, including the National Toxicology Program,” Schwartz says. The National Toxicology Program (NTP) is an interagency program, headquartered at NIEHS, with the mission to coordinate, conduct and communicate toxicological research across the U.S. government.

“The NTP is looking forward to exploring the responses of these strains of mice to various environmental agents,” said John Bucher, Ph.D., the new associate director of the NTP.

Frank M. Johnson, Ph. D., an NTP research geneticist and one of the

authors of the Nature paper, adds that systematically characterizing even more mouse strains for susceptibility to toxins will not only help with genetic analysis, but better position researchers to do intervention studies.

Source: National Institute of Environmental Health Sciences

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