Media Release

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Roche Scientists Exceed Expectations of Genetic Discoveries
More than 18,000 mouse SNPs identified in 27 months

Roche scientists have progressed faster than expected in uncovering important knowledge that will lead to improvements in diagnosing and treating disease. During the past 27 months, scientists at three Roche research centers along with colleagues at Washington University in St, Louis, Mo., and the Center for National Genotyping in Paris, France, discovered 18,035 single nucleotide polymorphisms (SNPs) – variations that help determine genetic makeup – of the mouse genome. The new SNPs, derived from analysis of 15 commonly used mouse strains, are now publicly available via a website (http://mouseSNP.roche.com).

The work is part of a National Institutes of Health (NIH)-funded project that will provide the basis for discovering how genetic factors determine disease susceptibility. Using proprietary methodology to help identify SNPs, Roche scientists were able to far exceed the expectations of the original NIH grant, initiated in 2000, which called for 300 SNPs to be discovered over a three-year period.

In order to understand how variations in the human genome determine disease susceptibility, it is necessary to first understand the genetic effects in a model organism. The mouse is the preferred experimental model organism for scientists.

"The precise analysis of genetic variation among these mouse strains will help scientists understand how diseases develop in humans," said Gary Peltz, Ph.D., head of Genetics, Inflammatory Diseases Unit at Roche Bioscience, Palo Alto. "This knowledge, in turn, provides critical information for human disease analysis and will impact the way in which disease is diagnosed and treated.

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Using its proprietary computational methodology, Roche expects to reach 25,000 SNPs by the end of the grant, and to provide the largest collection of polymorphisms across mouse strains. The 60-fold increase in the number of SNPs discovered in this project results from improvements made by Roche in its computational methods for analyzing DNA sequence. An earlier version of the methodology for identifying SNPs was described in a paper published in the journal Science on June 8, 2001.

This information will allow scientists to scan the entire mouse genome for disease-associated risk factors. The resulting data can then be used to identify genetic risk factors in the human genome. Results of these new discoveries have already been applied at several institutions, including Duke University and the Jackson Laboratories, where the information enabled scientists to positionally clone genes in the mouse genetic models they were studying.

"This project has generated an extensive amount of raw data that can be utilized for mouse genetic studies," said Russell Higuchi, Ph.D., associate director, Human Genetics at Roche Molecular Systems. "It is our intention that the wealth of information coming out of this project will benefit the scientific community at large. At the same time, it will also help Roche scientists to more easily identify genetic factors associated with diseases and provide more effective diagnostic tools and medicines."

The research is supported in part by a $1.2 million, 3-year grant from the National Human Genome Research Institute (NHGRI) of the NIH, the first such grant awarded by NHGRI to a pharmaceutical company.

About Roche

Headquartered in Basel, Switzerland, Roche is one of the world's leading research-orientated healthcare groups. The company's two core businesses in pharmaceuticals and diagnostics provide innovative products and services, that address prevention, diagnosis and treatment of diseases, thus enhancing people's health and quality of life. The two core businesses achieved a turnover of 19.3 billion Swiss Francs in the first three quarters of 2002 and employed about 57'000 employees world-wide.