Press Release

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New Tool Scans the Genome for Disease-relevant Variations

Investigating the genetic background of major diseases has now become easier. As part of a European-Japanese Consortium (STAR), Dr. Kathrin Saar and Prof. Norbert Hübner from the Max Delbrück Center for Molecular Medicine (MDC) Berlin-Buch, Germany, have constructed a genome map with more than 300 different rat strains. The researchers are convinced that this new tool can help understand the development of cardiovascular diseases or diabetes in laboratory rats as well as in humans. The paper of the STAR consortium has been published online in the current issue of the journal *Nature Genetics (Vol. 40, No. 5, pp. 560 – 566, 2008).**

Laboratory rats are particularly suited for analyzing the genetic causes of epidemiological-relevant diseases. For over 150 years, scientists have been using laboratory rats as model animals in clinical research laboratories. It is known that the DNA sequence of every organism shows natural variations called “single nucleotide polymorphisms” or SNPs. Typically, the genome of an individual has several million SNPs and, thus, he or she differs at this level from others within the same species. Scientists investigate these SNPs to clarify whether they are linked to or influence the development of certain diseases. The MDC researchers and their colleagues in Europe and Japan have now identified three million SNPs in the genome of the rat. Thus, they were able to expand and improve upon the existing genomic map which until now was based on the analyses of only three rat strains.

SNP and haplotype mapping for genetic analysis in the rat

The STAR Consortium[1]

The complete list of authors is as follows:

The STAR Consortium: Kathrin Saar[1], Alfred Beck[2], Marie-Thérèse Bihoreau[3], Ewan Birney[4], Denise Brocklebank[3], Yuan Chen[4], Edwin Cuppen[5], Stephanie Demonchy[6], Paul Flicek[4], Mario Foglio[6], Asao Fujiyama[7,8], Ivo G. Gut[6], Dominique Gauguier[3], Roderic Guigo[9], Victor Guryev[5], Matthias Heinig[1], Oliver Hummel[1], Niels Jahn[10], Sven Klages[2], Vladimir Kren[11], Heiner Kuhl[2], Takashi Kuramoto[12], Yoko Kuroki[7], Doris Lechner[6], Young-Ae Lee[1], Nuria Lopez-Bigas[9], G. Mark Lathrop[6], Tomoji Mashimo[12], Michael Kube[2], Richard Mott[3], Giannino Patone[1], Jeanne-Antide Perrier-Cornet[6], Matthias Platzer[10], Michal Pravenec[11], Richard Reinhardt[2], Yoshiyuki Sakaki[7], Markus Schilhabel[10], Herbert Schulz[1], Tadao Serikawa[12], Medya Shikhagaie[9], Shouji Tatsumoto[7], Stefan Taudien[10], Atsushi Toyoda[7], Birger Voigt[12], Diana Zelenika[6], Heike Zimdahl[1] & Norbert Hübner[1]

[1]Max-Delbrück-Center for Molecular Medicine (MDC), Robert-Roessle-Strasse 10, 13125, Berlin, Germany. [2]Max Planck Institute for Molecular Genetics, Berlin, Germany. [3]Wellcome Trust Centre for Human Genetics, University of Oxford, Oxford, UK. [4]European Bioinformatics Institute, Hinxton, UK. [5]Hubrecht Institute, Utrecht, The Netherlands. [6]CEA/Institut de Génomique, Centre National de Génotypage, Evry, France. [7]RIKEN Genomic Sciences Center, Kanagawa 230-0045, Japan. [8]National Institute of Informatics, Tokyo 101-8430, Japan. [9]Centre de Regulacio Genomica, Barcelona, Spain. [10]Leibniz-Institut für Altersforschung - Fritz-Lipmann-Institut, Jena, Germany. [11]Institute of Physiology, Czech Academy of Sciences and 1st Medical Faculty, Charles University, Prague, Czech Republic. [12]Institute of Laboratory Animals, Graduate School of Medicine, Kyoto University, Yoshidakonoe-cho, Sakyo-ku, Kyoto 606-8501, Japan.

A graph can downloaded from the internet at:
http://www.mdc-berlin.de/en/news/2008/index.html

Barbara Bachtler
Press and Public Affairs
Max Delbrück Center for Molecular Medicine (MDC) Berlin-Buch
Robert-Rössle-Straße 10; 13125 Berlin; Germany
Phone: +49 (0) 30 94 06 - 38 96
Fax: +49 (0) 30 94 06 - 38 33

e-mail: presse@mdc-berlin.de
http://www.mdc-berlin.de/en/news

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