Downloaded from symposium.cshlp.org on December 26, 2012 - Published by Cold Spring Harbor Laboratory Press

Cold Spring Harbor Symposia on Quantitative Biology

Human Versus Chimpanzee Chromosome-wide Sequence Comparison and Its Evolutionary Implication

Y. SAKAKI, H. WATANABE, T. TAYLOR, et al.

Cold Spring Harb Symp Quant Biol 2003 68: 455-460
Access the most recent version at doi:10.1101/sqb.2003.68.455

References This article cites 13 articles, 5 of which can be accessed free at:
http://symposium.cshlp.org/content/68/455.refs.html

Email alerting service Receive free email alerts when new articles cite this article - sign up in the box at the top right corner of the article or **click here**

To subscribe to *Cold Spring Harbor Symposia on Quantitative Biology* go to:
http://symposium.cshlp.org/subscriptions

Copyright © 2003 Cold Spring Harbor Laboratory Press

Downloaded from symposium.cshlp.org on December 26, 2012 - Published by Cold Spring Harbor Laboratory Press

Human Versus Chimpanzee Chromosome-wide Sequence Comparison and Its Evolutionary Implication

Y. SAKAKI,* H. WATANABE,* T. TAYLOR,* M. HATTORI,* A. FUJIYAMA,* A. TOYODA,* Y. KUROKI,* T. ITOH,* N. SAITOU,† S. OOTA,† C.-G. KIM,† T. KITANO,† H. LEHRACH,‡ M.-L. YASPO,‡ R. SUDBRAK,‡ A. KAHLA,‡ R. REINHARDT,‡ M. KUBE,‡‡ M. PLATZER,¶¶ S. TAENZER,¶¶ P. GALGOCZY,¶¶ A. KEL,§ H. BLÖECKER,** M. SCHARFE,** G. NORDSIEK,** I. HELLMANN,†† P. KHAITOVICH,†† S. PÄÄBO,†† Z. CHEN,‡‡ S.-Y. WANG,‡‡ S.-X. REN,‡‡ X.-L. ZHANG,‡‡ H.-J. ZHENG,‡‡ G.-F. ZHU,‡‡ B.-F. WANG,‡‡ G.-P. ZHAO,‡‡ S.-F. TSAI,¶¶ K. WU,¶¶ T.-T. LIU,§§ K.-J. HSIAO,*** H.-S. PARK,††† Y.-S. LEE,††† J.-E. CHEONG,††† AND S.-H. CHOI††† (THE CHIMPANZEE CHROMOSOME 22 SEQUENCING CONSORTIUM)

**RIKEN, Genomic Sciences Center, Yokohama 230-0045, Japan; †National Institute of Genetics, Japan; ‡Max-Planck-Institut for Molekulare Genetik, Germany; ¶Institute of Molecular Biotechnology, Germany; §BIOBASE GmbH, Germany; German Research Centre for Biotechnology, Germany; ††Max-Planck-Institut of Evolutionary Anthropology, Germany; ‡‡Chinese National Human Genome Center at Shanghai, China; ¶¶National Health Research Institutes, Taiwan; §§Veterans General Hospital-Taipei, Taiwan; ***National Yang-Ming University, Taiwan; and †††Genome Research Center, KRIBB, Korea*

Homo sapiens is a unique organism characterized by its highly developed brain, use of complex languages, bipedal locomotion, and so on. These unique features have been acquired by a series of mutation and selection events during evolution in the human lineage and are mainly determined by genetic factors encoded in the human genome. It is of great interest and also of great importance from biological and medical viewpoints to understand what kind of genetic factors are involved in these complex human features and how they have been established during human evolution (Carrol 2003). Recent completion of the human genome sequence provided a solid platform for addressing these issues. However, the information obtained from the human genome alone is insufficient to discover genetic changes specific to human. The genomes of several experimental organisms such as mouse, fly, and nematode have successfully been used to characterize the human genome, but they are evolutionarily too distant to zoom in on the human-specific changes. Therefore, we definitely need the genome sequence of the closest organism to human. Detailed molecular anthropological studies have now established that the chimpanzee (and bonobo) is the closest organism to human, followed by the gorilla (see, e.g., Sibley and Ahlquist 1984; Saitou 1991; Chen and Li 2001; Wildman et al. 2003). The chimpanzee genome is thus the best for comparison with the human genome to elucidate the genetic changes that have occurred on the human lineage in the past 5–6 million years, providing us with important clues to address the above issues.

A number of pilot studies have already been done comparing human and chimpanzee genomes (see Olson and Varki 2003). For example, we previously showed through chimpanzee BAC end sequencing that the genomic difference between human and chimpanzee in terms of nucleotide substitution is 1.23% (Fujiyama et al. 2002). Frequent insertions and deletions were detected (Frazer et al. 2003). When insertions and deletions (indels) were compared, about 5% of the genome was shown to differ between human and chimpanzee (Britten 2002). Duplication, translocation, and transposition events have been also reported (Bailey et al. 2002). However, these data were obtained from various parts of the genomes by using several different technologies including sequence-based comparison, chip technology, and cytogenetic analysis, so that it is difficult to draw an integrated picture of dynamic changes of the genome to evaluate the overall consequence of these genetic changes to human evolution. For these reasons, we conducted a human–chimpanzee whole-chromosome comparison at the nucleotide sequence level. We chose human chromosome 21 and its genomic ortholog in chimpanzee, namely chromosome 22, because human chromosome 21 is one of the most well-characterized human chromosomes (Hattori et al 2000) and contains regions and units representing characteristic features of the human genome such as GC-rich/gene-rich regions and AT-rich/gene-poor regions, many repeated structures, duplications, housekeeping genes and tissue-specific genes, genes with a variety of functions such as transcriptional factors and receptors, members of large gene families and singleton genes.

RESULTS AND DISCUSSION

Mapping and Sequencing

At first, a BAC clone map of chimpanzee chromosome 22 was constructed based on the sequence similarity of BAC end sequences to human chromosome 21. Some gaps were then filled by screening chromosome-22-specific libraries or by PCR amplification. Finally, only two clone gaps remained at positions corresponding to gaps in human chromosome 21 (Hattori et al. 2000). A nucleotide sequence totaling 32.7 Mb of the mapped clones was then