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Chimp genome released

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A first draft of the chimpanzee genome sequence has been completed, US researchers [announced](#) Wednesday (December 10). Investigators, funded by the National Human Genome Research Institute (NHGRI), also aligned the chimp sequence with the human sequence to facilitate comparisons.

All data from the draft sequence, which covered most of the chimp's 3.1 billion bases, has been made [publicly available](#). Scientists in the United States, Europe, and Japan will now begin analyzing that data and comparing it to the human sequence in hopes of finding clues to genome evolution, disease genes, and regulation. Comparing humans' sequence to that of our closest relative also may help researchers start to address an age-old question: "Everybody sort of wonders what makes us human," Kerstin Lindblad-Toh, codirector of the Genome Sequence and Analysis Program at the Massachusetts Institute of Technology's (MIT's) Center for Genome Research, told us.

"This is a notification more to the scientific community than to the public that the sequence is done, the assembly is done, it's out there," Richard Wilson, director of the Genome Sequencing Center at Washington University in St. Louis, told us. "And that there are a couple of really good computational tools that you can use to start getting into that sequence and start finding your favorite human gene in the chimp." The sequencing effort, which cost approximately \$20 million, was undertaken by sequencing centers at Washington University and the Eli and Edythe L. Broad Institute of MIT.

According to [white papers](#) written by University of Washington scientists Maynard Olson, Robert Waterston and others, the sequencing project's rationales included identifying sites of sequence differences between the chimp and human; investigating the genomic basis of differences in chimp and human gene expression that have been measured with microarrays; comparing physiology, anatomy, and pathology, such as different rates of epithelial cancers and the progression of HIV to AIDS; and conducting evolutionary and population genetic studies to compare, for instance, regions of rapid evolution and differences in polymorphism rate.

Some scientists have already begun to analyze and compare chimp and human genomes and make assertions about human evolution. In a separate work published in [Science](#) on Friday (December 12), scientists at Celera Diagnostics report their own comparison of regions of the human and chimp genomes, concluding the processes like hearing and olfaction evolved at a relatively fast rate in humans.

"In general you'd expect evolution to work at the level of the gene," senior author Michele Cargill of Celera told us. "But for a few of these categories, it seems to be acting on the class of gene."

Researchers used polymerase chain reaction primers to show positive selection in humans for 1600 coding sequences of the approximately 20,000 genes analyzed. They found that human genes involved in olfaction, hearing, amino acid catabolism, and other processes had more genes than expected undergoing positive selection. In the case of hearing, for example, this positive selection may suggest that humans evolved to have different sensitivities to different frequencies of sound that are important for developing speech and understanding language. Having the chimp genome sequence in hand will now enable researchers to extend their chimp-human comparisons to potentially important noncoding sequences, which comprise about 98% of the chimp genome.

Started in January of this year, the NHGRI-funded genome sequencing of the chimp has fourfold coverage, meaning each base has been sequenced an average of four times. The human genome has 10-fold coverage, and the mouse genome about sevenfold.

The completed human sequence provided a sort of reference to expedite the assembly. According to Wilson, the chimp sequencing, despite employing fewer sequencing centers, was completed at least twice as fast as the generation of the human draft done in 1998, 1999, and 2000. "With chimp and human, we're looking for the differences. And with mouse and human, we were looking for the similarities," said Lindblad-Toh.

The chimp genome's similarity to the human's, however, may make it a less useful tool for disease gene finding than the genome of a more distant relative. "Every gene has its best model organism," Wilson said. "For some disease genes, the chimp's going to tell you a lot. For others it won't tell you much because it's too close to the human."

There are currently no plans for an additional draft of the chimp genome, though Wilson and Waterston advocate doing additional sequencing to fill in the gaps and get better coverage, improve accuracy, and better understand the level of variation.

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