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Speaking of Science

A second look at the gorilla genome shows just how similar we are

By Rachel Feltman April 1 at 11:39 AM

A gorilla named Sue, formerly of the Lincoln Park Zoo, is showing scientists just how similar her species is to our own. In a study published Thursday in Science, researchers presented a new, more complete genome sequence for the animal based on her blood sample.

Gorillas are some of our closest relatives, edged out only by chimpanzees and bonobos. This latest genome sequence confirms that just 1.6 percent of their genes diverge from our own. For reference, chimps and bonobos tie for 1.2 percent divergence, and after gorillas there's a sharp drop-off to 3.1 percent in orangutans — great apes with Asian instead of African origins. The genomes of individual humans differ from one another by around 0.1 percent.

Because gorillas are so close to us on the family tree, their genomes are especially valuable to study. "The differences between species may aid researchers in identifying regions of the human genome that are associated with higher cognition, complex language, behavior and neurological diseases," study author Christopher Hill of the University of Washington told Reuters.

Last year, for example, scientists at Duke University pinpointed a gene regulator — a gene that tells other genes how strongly to present themselves and when — that makes human brains grow big. They found it by tracking the differences between human and chimpanzee genomes in areas related to brain development.

The more we know about the genes of our close relatives, the better we can understand what tiny changes have made us so different from them. And understanding those differences can enrich research on everything from language to disease.

"My motivation in studying human and great ape genomes is to try to learn what makes us tick as a species," lead author Evan Eichler of the University of Washington said in a statement. Eichler and his colleagues used more recent sequencing techniques for their genome than the one published in 2012. In addition to finding new, previously unknown coding segments, the team noted that the older method of sequencing had thrown away

some of the duplicates of segments that were repeated. Strings of genetic code repeat frequently in organisms over time, and seeing how many redundancies there are can help scientists figure out the history of the species.

For example, the new sequence shows that a population bottleneck that occurred some 50,000 years ago — a time when the population was small and the species became inbred — was probably worse than the first sequence had suggested.

"I'd like to see a re-doing of all the great ape genomes, including chimpanzee and orangutan, to get a comprehensive view of the genetic variants that distinguish humans from the great apes. I believe there is far more genetic variation than we had previously thought. The first step is finding it," Eichler said. He also hopes that humans having their genome sequenced for clinical reasons will one day be able to expect such accuracy and detail.

Unfortunately, he estimates that the sequencing method costs "$80,000 a pop." Since other methods for human sequencing have hit the $1,000 milestone, that might be a hard sell. Then again, the cheaper process cost $100 million just 15 years ago — so it's all relative.

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Rachel Feltman runs The Post's Speaking of Science blog.
