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Comparing relatives

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Stephen Pincock

Email: Stephen@thescientisteurope.com

BERLIN - A better understanding of the genetic makeup of our closest and most distant mammalian relations is shedding new light on the human genome, researchers told the [Human Genome Meeting](#) here on Monday (April 5).

At the distant end of the spectrum, Australian researchers want to begin large-scale sequencing of the kangaroo genome. With about 180 million years of independent evolution separating humans from the jumping marsupials, there are few mammals that are more distant from us, and that offers unique opportunities.

"The platypus is even more distantly related, and they're going to be important too, but the platypus isn't your normal experimental animal," [Jenny Graves](#) from the Australian National University told us. For one thing, she said, they are nearly impossible to breed in captivity.

Focusing on the kangaroo as a good example of a remote relative is "turning out to be a very effective way to spot genes and control sequences," Graves told the conference.

"Because they're so different, everything in the genome other than those elements that really matter will 'rot away' over time, and that will leave the blocks of sequence that are really important," she explained. "There will be blocks of sequence similarity that really jump out at you. And that's already happened. We've already found genes and control elements."

Some extensive sequence comparisons have already been completed. One interesting finding has been about prion proteins, which are similar in kangaroos and humans. "Of course, there are a lot of questions about the prion protein... Obviously, it's not there to cause mad cow disease, it must do something for the genome," she said.

Although Graves' focus is mostly evolutionary, her group's funders - who include the Australian dairy industry - are interested in what the research can do for "the people of Australia." For example, there's a great deal of interest around lactation in kangaroos, which produce three different types of milk for different stages of the development of their offspring. Understanding this could help the dairy industry, she said.

Meanwhile, the kangaroo project is moving from its current gene-by-gene approach to full genome sequencing. "That's obviously a vast leap in funding and a vast leap in resourcing," Graves said. "We're talking with the US National Institutes of Health on how they might collaborate on a two-fold sequencing."

Turning to humanity's closest evolutionary relative, sequencing of the [chimpanzee genome is largely complete](#), [Svante Paabo](#) from the Max Planck Institute for Evolutionary Anthropology in Leipzig, Germany, said. A rough draft of the genome has been available since Christmas, and researchers involved in the project team are currently writing up a final paper that is expected this summer, he told us.

That sequence is already throwing up interesting findings. For example, there is growing evidence of differences in gene expression in the brain between chimps and humans. The latest experimental results have solidified evidence of a roughly 10% difference in gene expression from several regions of the brain.

"This is pretty new," Paabo told us. "Earlier there was data from a single region of the brain, but now we've looked at six different regions, and we really know that it holds up."

The researchers have confirmed their findings in four regions of the cerebral cortex, and in the cerebellum and the caudate nucleus. On the other hand, evidence relating to the linear accumulation of differences over time means "we are coming to believe that these are not all functionally relevant," Paabo added.

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