NEWS

All about Craig: the first 'full' genome sequence

Controversial genomics pioneer Craig Venter has sequenced his own genome. In a preliminary analysis published this week (S. Levy *et al. PLoS Biol.* 5, e254; 2007), Venter's team has picked apart the sequences belonging to both chromosomes in each of the 23 chromosome pairs found in his cells, providing the first glimpse of the variation found within a single genome.

The paper also highlights some features of Venter's genome. The sequence of his *ABCC11* gene, for example, indicates that Venter is likely to have wet earwax, as opposed to dry. In a finding likely to disappoint some critics of the maverick scientist, Venter has four repeat sequences located just before his *MAOA* gene. Having only three of the repeats is associated with an increased risk of antisocial behaviour. On a more sobering note, Venter's *APOE* sequence is associated with a higher risk of Alzheimer's and cardiovascular diseases, and his *SORL1* gene also contains several variants that are associated with Alzheimer's disease.

For more about his personal genomic and

family history, Venter aficionados can refer to his upcoming book, *A Life Decoded*. Venter has placed references to how his genome sequence may have affected his life throughout the book, says Jan Witkowski, executive director of the Banbury Center at Cold Spring Harbor Laboratory in New York, who is reviewing the book for the 4 October issue of *Nature*.

Venter's sequence also provides important new information about the human genome. Previous sequencing efforts have not distinguished between the two copies of each chromosome, or even between DNA from different donors. "What we were doing was mixing up alleles," says Samuel Levy — who led the study at the J. Craig Venter Institute in Rockville, Maryland — referring to DNA sequences from specific spots on the chromosome. "We were creating Frankenstein versions of chromosomes."

This time, armed with an additional 13 million sequences — added to the 19 million generated from Venter's own DNA during the first genome project — and fresh algorithms

designed to pick apart sequences from different versions of the same chromosomes, Levy and his team could look at the variation within the genome. They found more than 4 million vari-

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Genomes within genomes

Another team of genome researchers at the J. Craig Venter Institute in Rockville, Maryland, which has been investigating the DNA of a rather less salubrious organism, this week reports a surprise discovery: the DNA of fruitfly *Drosophila ananassae* contains the entire genome of a parasitic bacterium of the *Wolbachia* genus. Smaller parts of the parasite's genetic material also turned up in worms and wasps.

Bacteria commonly swap DNA with each other. But transfer of bacterial genes into animals was thought to be rare. The new work, published in *Science* (J. C. Dunning Hotopp *et al. Science* doi:10.1126/science.1142490; 2007), suggests that gene flow from bacteria to animal hosts happens on a larger scale and more commonly than suspected. And it hints that the

Invader: *Wolbachia* bacteria (yellow) inside a developing fruitfly egg (red).

bacterial genome may have provided some sort of evolutionary advantage to its host. "You're talking about a significant portion of [the fruitfly] DNA that is now from *Wolbachia*," says Julie Dunning Hotopp, who led the study. "There has to be some sort of selection to carry around that much extra DNA."

But Dunning Hotopp's former

colleague Jonathan Eisen of the University of California, Davis, contests this. "One cannot conclude that some DNA is advantageous simply because it is there," he says.

Up to 75% of insect species are plagued by *Wolbachia*, which lives inside testes and ovaries and passes from one female generation to another through infected ova. To ensure its spread, *Wolbachia* can skew insect birth ratios towards females and even prevent infected males from successfully mating with disease-free females. The bacterium's close association with egg cells means there's ample opportunity for bacterial DNA to get permanently sewn into a host's nuclear genome, says Dunning Hotopp.

When Dunning Hotopp and her colleagues analysed the DNA of *D. ananassae* uninfected by

Wolbachia, they found 44 of the 45 *Wolbachia* genes they searched for. Because these selected genes are so widely spread throughout *Wolbachia* DNA, this suggests that the rest of its more than 1-million-base-pair genome is also likely to be found in fruitflies.

Many of the *Wolbachia* genes were infiltrated by strands of insect DNA that jump around the genome, and so are unlikely to be functional. But the researchers showed that at least 28 of the bacteria's 1,206 genes are active in the flies. More genes that have seeped from bacteria into animals are certain to be found, the researchers say, particularly in reptiles and amphibians. But finding bacterial genes in mammals is unlikely because no bacteria are known to infect their sperm and egg cells. ■

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