

Human, malaria-causing parasite genomes sequenced

THE human genetic instruction book just got more readable. Nearly a decade after the Human Genome Project assembled the genome's three billion chemical units, an international consortium has revealed how the components fit together into sentences and chapters.

Already, the genome's tales are revealing how genetic variants contribute to disease, giving researchers insights into human evolution and even changing how scientists define a gene.

Director of the United States National Human Genome Research Institute, which coordinated and funded the mammoth Encyclopedia of DNA Elements, or ENCODE, project, Eric Green, said: "The questions we can now ask are more sophisticated and will yield better answers than the ones we were asking nine years ago."

Results from ENCODE, which involves more than 400 researchers around the globe, appear in the September 6 *Nature*, with more than 30 companion papers published in *Science*, *Genome Research*, *Genome Biology*, *Cell* and *BMC Genetics*.

Also, scientists at Case Western Reserve University and the Cleveland Clinic Lerner Research Institute, United States, have discovered that the parasite that causes the most common form of malaria share the same genetic variations — even when the organisms are separated across continents.

The discovery raises concerns that mutations to resist existing medications could spread worldwide, making global eradication efforts even more difficult.

The researchers, including Cleveland-based David Serre and Peter Zimmerman, Didier Menard (Institut Pasteur-Cambodia) and Arsene Ratsimbaoa (Madagascar National Malaria Control Program) are the first to sequence the genome of the parasite *Plasmodium vivax*, taken from patients at coverage needed to verify genome-wide DNA sequence variation. The genome contains all of the organism's inheritable information.

View the original article here: [Human, malaria-causing parasite genomes sequenced](#)