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Press Release

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Neandertal Genome to be Deciphered

The Max Planck Institute for Evolutionary Anthropology and 454 Life Sciences Corporation unveil plan to sequence the Neandertal Genome

The Max Planck Institute for Evolutionary Anthropology in Leipzig, Germany, and 454 Life Sciences Corporation, in Branford, Connecticut, have announced an ambitious plan to complete a first draft of the Neandertal genome within the next two years. Prof Svante Pääbo, Director of the Institute's Department of Evolutionary Anthropology, and Dr. Michael Egholm, Vice-President of Molecular Biology for 454 Life Sciences will jointly direct the project, made possible by financing from the Max Planck Society. 454 Life Sciences' newly developed sequencing technology has made it possible to extract and sequence nuclear DNA from Neandertal fossils, a hopeless task using traditional techniques. As a trial, the collaborators have already sequenced approximately one million base pairs of nuclear Neandertal DNA from a 38,000-year-old Croatian fossil.

This August marks the 150th anniversary of the discovery of the first Neandertal fossil in the Neander Valley near Dusseldorf, Germany. Ever since that time, paleontologists and anthropologists have been striving to uncover the role of these stockily-built early humans in modern human evolution who lived in Europe and parts of Asia until they disappeared about 30,000 years ago. Pääbo, a pioneer in the field of ancient DNA research, brought the world closer to understanding our relationship to Neandertals when he sequenced Neandertal mitochondrial DNA in 1997. This breakthrough suggested that Neandertals did not make a substantial contribution to the modern human gene pool, even though the Neandertals and modern humans coexisted for thousands of years. Together with 454 Life Sciences, Pääbo is now gearing up to take the next leap in Neandertal research and sequence the entire 3 billion base pairs that made up their genome. They will then compare the Neandertal genome to the already sequenced human and chimpanzee genomes. This will clarify the evolutionary relationship between humans and Neandertals as well as help identify those genetic changes that enabled modern humans to leave Africa and rapidly spread around the world starting around 100,000 years ago.

Extracting, identifying and sequencing ancient DNA from fossils is a technically challenging task. When an organism dies, its tissues are overrun by bacteria and fungi. Much of the DNA is simply destroyed, and the small amount remaining is broken into short pieces and chemically modified during the long period of fossil formation. This means that when scientists mine tiny samples of ancient bones for DNA, much of the DNA obtained is actually from contaminants such as bacteria, fungi, and even scientists who have previously handled the bones. Over

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the last twenty years, Pääbo's research group has developed methods for demonstrating the authenticity of ancient DNA results, as well as technical solutions to the problems of working with short, chemically-modified DNA fragments. Together with 454 Life Sciences they will now combine these methods with a novel high-throughput DNA sequencing that is ideally suited to analyze ancient DNA.

Until now, ancient DNA researchers have targeted mitochondrial DNA (mtDNA), a small circle of DNA found in the cell's energy-producing mitochondria. Each mitochondrion contains multiple copies of mtDNA, so it tends to persist in fossils and bits can be retrieved by a technique called the polymerase chain reaction (PCR). Pääbo and other experts in ancient DNA research have therefore focused on sequencing the mtDNA of ancient organisms such as the woolly mammoth and cave bears. However, mtDNA comprises only about 0.001% of a mammal's entire genome and is inherited exclusively through the female line. It therefore provides only limited insights into how ancient organism differed from those living today.

In order to sequence an entire mammalian nuclear genome, millions of PCR reactions would have to be performed requiring kilograms of Neandertal bones. Until 454 Life Sciences' development of the Genome Sequencer 20 System, sequencing the entire nuclear genome of ancient organisms therefore seemed impossible. This technology makes such an endeavor feasible by allowing about a quarter of a million single DNA strands to be amplified individually by PCR from small amounts of bone and sequenced in only about four hours by a single machine. The DNA sequences determined by the Genome Sequencer 20 System are 100-200 base pairs in length, which coincides neatly with the length of ancient DNA fragments. Over the next two years, the Neandertal sequencing team will determine about 60 billion bases from Neandertal fossils in order to reconstruct a draft of the 3 billion bases that made up the genome of Neandertals. The team will use samples from several well-preserved Neandertals. The Rheinisches Landesmuseum in Bonn and Dr. Ralf W. Schmitz have generously agreed to provide a sample from the original Neandertal type specimen, discovered 150 years ago.

On July 20th scientists from the Institute together with representatives from 454 will be available at a press conference to present further details of the project and answer questions. You can follow the press conference live over the Internet beginning at 15:00 CET [1]. Questions can be submitted via email to Neandertal@eva.mpg.de both before and during the conference.

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Related Links:

[1] press conference online

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