New cheaper method for mapping disease genes

May 27 2008

Scientists at the Swedish medical university Karolinska Institutet have developed a new DNA-sequencing method that is much cheaper than those currently in use in laboratories. They hope that this new method will make it possible to map disease genes in large patient groups, which in turn can mean quicker breakthroughs for new treatments for a wide variety of diseases.

By mapping DNA, scientists can trace disease genes, understand how bacteria and viruses cause infection and chart the evolution of mankind and other species. When the HUGO project mapped the first human genome not so long ago, it cost over a billion kronor and took over ten years. Today, there are instruments on the market that can do the same thing in a matter of months for less then ten million kronor. However, if scientists are to have opportunities to study disease genes in detail, and from hundreds of patients, the process must be much, much cheaper.

A Swedish team, led by Sten Linnarsson at the Department of Medical Biochemistry and Biophysics at Karolinska Institutet, has now developed a new DNA-sequencing method that can one day make it possible to map out the human genome for one-tenth of today's cost. The method is presented in the online edition of the scientific journal Nature Biotechnology.

The scientists took DNA from the enteric bacteria E. coli and split it into tiny fragments, each with a length of approximately 200 nucleotides (the building blocks of DNA: A, C, G and T). These fragments were then

spread out and fixed onto a microscope slide so that several million fragments could be analysed simultaneously. These fragments were then rinsed in a fluid containing short DNA sequences of five nucleotides, marked with a fluorescent dye, which allowed them to examine which of the short DNA sequences adhered to each fragment.

After having rinsed all possible short DNA sequences over several million fragments, the scientists were able to then digitally piece together the sequences into one complete chain of the entire bacteria genome, a total of 4.5 million nucleotides long.

“Everything takes place in our own specially built instrument, which comprises a microscope powerful enough to take pictures of DNA fragments, an automated pipette and a small flow chamber with a glass surface on which the reaction itself occurs,” says Sten Linnarsson.

This is not the first time that Swedish scientists have successfully developed new methods of DNA sequencing. Ten years ago Pål Nyrén and his colleagues from the Royal Institute of Technology published Pyrosequencing, one of the most common methods of mapping DNA in use today.

Source: Karolinska Institutet