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UNM Professor Develops Cheap DNA Mapping
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Jeremy Edwards' job is to bring down the cost of sequencing the human genome to less than $1,000, but he thinks he can beat that figure.

"I think we can do it for less than $300 a genome," said Edwards, a University of New Mexico professor of molecular genetics and microbiology. The process now costs at least $20,000.

New tools for sequencing DNA developed by UNM and Harvard Medical School, where Edwards did post-doctoral work a decade ago, promise to make genome sequencing a routine tool in fighting cancer and other diseases, he said.

"Maybe we'll get to a $100 genome by the end of our project" in 2013, he said.

A genome is all of an organism's genetic material. Genetic sequencing, or the detailed mapping of that material, is likely to offer therapies for many diseases once researchers understand their genetic causes, he said.

"Probably most diseases will have some kind of genetic component, but we just don't know what it is," he said.

Edwards, a researcher at the UNM Cancer Center, received a three-year $2.8 million grant in September 2010 from the National Institutes of Health to bring the cost of sequencing the human genome under $1,000.

As a cancer researcher, Edwards wants to find a fast, inexpensive way to analyze the genomes of cancerous cells "and figure out the exact cause of the cancer," he said.

"Eventually, we'll start sequencing the genomes of people who come into the (UNM) Cancer Center," he said.

Researchers one day hope to develop customized drugs that target specific illnesses such as cancer.

The first step is to develop a routine technique for studying the genomes of diseased cells in thousands of patients, then search for specific mutations that make those cells dangerous, Edwards said.

Genetic sequencing involves cutting the genome into millions of segments, then reproducing each segment in quantities large enough to allow researchers to identify the sequence of cytosine, guanine,

adenine and thymine — the four molecules that comprise DNA.

The technique that offers the most promise for cheap genome sequencing involves rolling genetic fragments into circles that can turn like a printing press, creating copies of itself in long threads with a DNA sequence identical to the original fragment.

This technique, called "rolling circle amplification," creates a threadlike bundle of genetic material about 200 nanometers wide, or one-billionth of a meter, Edwards said. Next, these thread bundles are applied to a glass surface and photographed, producing a field of colored dots that allow researchers, with the help of computers, to sequence the entire genome. The whole process now requires about 2,000 photographs and takes about three days, he said.

Much of the process takes place in a refrigerator-sized machine called a "Polonator," made by Danaher Motion, a Washington, D.C.-based equipment manufacturer.

"We're working with several companies to make this all commercialized," he said.

Edwards expects to begin sequencing the genomes of UNM Cancer Center patients within about two years. Then they will start the more difficult job of searching for specific mutations that make cancer cells deadly, he said. The genomes of cancer cells probably contain millions of mutations, of which only a few make it dangerous to the patient, Edwards said.

"We won't even know what to look for initially," he said.

Once researchers identify those harmful mutations, they can begin searching for drugs and therapies that combat the harmful effects of cancerous cells, he said.