Scientists: cancer genome decoded

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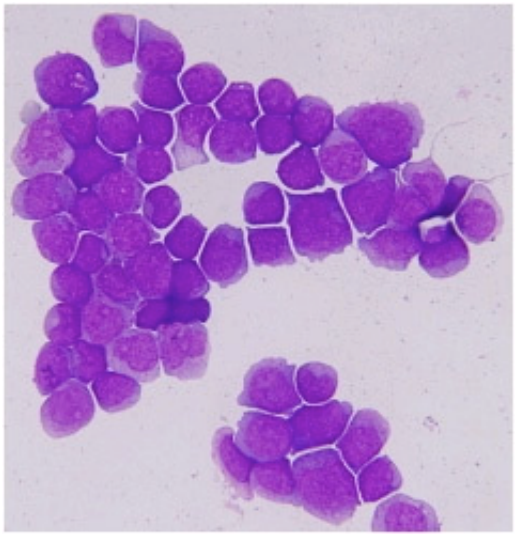
Courtesy Nature and World Science staff



The genome of the cancerous tissue of an individual patient has been sequenced for the first time, identifying mutated genes with a likely a role in development of the cancer, researchers say.

The data came from a patient with acute myeloid leukaemia, a cancer of white blood cells that affects around 13,000 adults yearly in the United States alone and kills about a third.

The gene sequencing technique used in the study could be applied to other cancers and aid the design of targeted treatments, according to the researchers, who reported their findings in this week's issue of the research journal Nature.

Cancer, really a group of diseases rather than one, occurs when genetic mutations cause cells to become abnormal and start reproducing out of control. This leads to a sometimes deadly growth of diseased tissue.

The researchers, Elaine Mardis of the Washington University School of Medicine in St. Louis, Mo. and colleagues, sequenced cancerous and normal tissue from the patient and compared the two sequences, or full sets of genetic code.

Ten mutated genes were identified, according to Mardis and colleagues. Of these, two were previously reported to be associated with acute myeloid leukaemia whereas the others probably represent new genes that are involved in the development of the disease.

"Our study establishes whole-genome sequencing as an unbiased method for discovering cancer initiating mutations in previously unidentified genes," the researchers wrote. The technique may be "the only effective means for discovering all of the mutations" relevant to the disease process, they added, noting that some of the mutations "may respond to targeted therapies."

Image; Marrow cells used in the study. (Courtesy Dr. Tim Ley)