

Massive genomic study identifies six types of liver cancer

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In the largest genomic study ever targeting single-organ cancers, Japanese researchers have completed a whole-genome analysis of 300 liver cancer patients, discovering that liver cancer among Japanese can be broken down into six types.

The study, jointly carried out by a number of institutions including the National Cancer Center, the Riken research institute and the University of Tokyo, hopes to contribute to the development of new diagnostic methods and personalized drug therapies.

In a paper in the journal Nature Genetics, the researchers extracted DNA and RNA from blood samples of 300 liver cancer patients and put them through next-generation genome sequencers, identifying a wide variety of mutations that have taken place.

To analyze the vast genomic data — totaling more than 300 terabytes — the scientists used Shirokane, a supercomputer used specifically for life science research at the University of Tokyo.

The study found that liver cancer is caused by mutations or abnormalities in nearly 40 genes, including more than 10 that had never before been linked to liver cancer. Depending on the mix of these factors, types of liver cancer among Japanese can be divided into roughly six types.

These findings could contribute to the development of new drugs that target key molecules involved in cancer cell growth, called molecular target therapy. Furthermore, patients might one day be able to choose therapies based on their genomic characteristics, according to Hidewaki Nakagawa, a Riken researcher involved in the project.

Read full, original post: [Massive whole-genome study finds six types of liver cancer](#)