New analytical method enhances the possibility of selecting optimal cancer treatment

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For a cancer treatment to be adapted to each individual patient, a large number of tumor samples need to be examined carefully. Collaboration between a company and Uppsala University has now led to a method that makes this process ten times more efficient than in the past.

New cancer treatments that target specific molecules in the tumor are under development. But for this to be effective, it's necessary to know first what mutations caused the tumor. By analyzing the sequence of genes that are often mutated in certain tumor forms, it is possible to increase the possibility of selecting optimal treatment for each patient.

Researchers at the Department of Immunology, Genetics, and Pathology at Uppsala University are collaborating with the company Halo Genomics in a project designed to identify mutations that cause cancer of the large intestine. The scientists selected 560 genes in 192 tumor samples, and Halo Genomics produced a so-called HaloPlex PCR-analysis that covered all the genes.

"With this analytical method it took a week for one person to prepare the 192 samples for sequencing, without any need for special equipment. This increases productivity by a factor of up to ten compared with conventional methods," says Professor Mats Nilsson, who has directed the project.

The samples are now being sequenced at SciLifeLab in Uppsala. The researchers expect to be able to identify exactly what molecules are affected in tumor cells from individual patients.

"This will be of significance when it comes to selecting the right kind of targeted treatment for patients in the future," says Mats Nilsson. "The method is promising for use in diagnostics because of its low cost and high efficiency."

Provided by Uppsala University