

New diagnostic method finds aggressive tumors

October 18 2019



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Researchers at Karolinska Institutet in Sweden have developed a new, cheap method that can identify highly heterogeneous tumors that tend to be very aggressive, and therefore need to be treated more aggressively.

The technique is presented in the scientific journal *Nature Communications*.

A common feature of cancer cells is alterations in the number of copies in which each chromosome or gene is present in the genome—a phenomenon known as copy number alterations or CNAs. Within the same tumor, cells belonging to different anatomical parts of the tumor may carry different CNAs. Tumors with many CNAs are typically very aggressive and tend to reform more often, even after harsh treatments.

Now, the Bienko-Crosetto Laboratory at Karolinska Institutet and Science for Life Laboratory (SciLifeLab) in Sweden have developed a new genomic method, named CUTseq, which can assess the amount and type of CNAs in many different parts of the same tumor, at a much lower cost than existing technologies.

"I expect that CUTseq will find many useful applications in [cancer diagnostics](#)," says Nicola Crosetto, senior researcher at the Department of Medical Biochemistry and Biophysics, Karolinska Institutet, and one of the senior authors of the paper. "Multi-region tumor sequencing is going to be increasingly used in the diagnostic setting, in order to identify patients with highly heterogeneous tumors that need to be treated more aggressively. I believe that our method can play a leading role here."

The method works with DNA extracted from multiple biopsies and even from very small portions of thin tissue sections—the type of sample that pathologists commonly rely on to make a diagnosis of cancer under the microscope.

By tagging the DNA extracted from multiple regions of the same tumor sample with unique molecular barcodes, a comprehensive picture of the heterogeneity of CNAs in a tumor can be obtained with a single

sequencing experiment.

Applications of CUTseq are not only limited to cancer diagnostics, according to the researchers behind the new method.

"For example, CUTseq could be used as a platform for cell line authentication and to monitor genome stability in large cell line repositories and biobanks," says Magda Bienko, senior researcher at the same department and the other senior author of the paper. "It could also be applied in ecology, as an alternative to other reduced representation genome sequencing methods, such as RAD-seq, to assess biodiversity in a cost-effective way."

More information: *Nature Communications* (2019). [DOI: 10.1038/s41467-019-12570-2](https://doi.org/10.1038/s41467-019-12570-2)

Provided by Karolinska Institutet

Citation: New diagnostic method finds aggressive tumors (2019, October 18) retrieved 3 May 2024 from <https://medicalxpress.com/news/2019-10-diagnostic-method-aggressive-tumors.html>

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