

The same test, regardless of cancer type

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Researchers at the Institute for Cancer Genetics and Informatics at Oslo University Hospital (OUS), have developed a method that can assess the seriousness of a patient's cancer and what treatment is required.

A test can help understand the development of almost all types of [cancer](#), and the results are now published in *The Lancet Oncology*: "Chromatin organization and cancer prognosis: a pan-cancer study."

Today, there is no common test to diagnose and predict cancer. Instead, a variety of tests and methods are used for different types of cancer. Very few of them can provide a certain answer as to how cancer will develop.

The consequence is that it is difficult to distinguish [patients](#) who need more treatment after surgery from those who do not need any. A significant number of patients today receive too much treatment, which may cause unnecessary side effects, damage and at worst, death.

The fresh research results are based on more than 20 years of collaboration between the Department of Cancer Genetics and Informatics at OUS and the Department of Informatics at The University of Oslo (UiO).

Initially, the method will be particularly useful for finding patients with Stage II intestinal cancer who will need more treatment after surgery, usually chemotherapy. Experiments show that the method can also be used for [ovarian cancer](#), uterine cancer and prostate cancer.

Large amounts of data

The study is based on chromatin analysis of 461,000 digital images of DNA-stained cancer cells from 390 patients from the OUS, all treated for stage 1 or II intestinal cancer. In addition, the same analytical method is applied to samples from six independent patient groups from different countries, mainly Norway and the United Kingdom. One of the groups consists of colon cancer patients from the UK corresponding to the Norwegian group. In all patient groups, those patients who had many cancer cells with high chromosome heterogeneity died of cancer.

Looking for chaos

Although different cancers have different characteristics, there are some common features that can be used in understanding the severity and treatment needs. One of them is that cancer often starts with an injury to the DNA that the body is unable to repair.

Human DNA contains about 23,000 genes, in addition to the areas that control the gene activity. DNA is formed as a double helical thread where the genes are in line with each other. When cell division occurs, the DNA molecules nest up around proteins and are called chromosomes. It has long been known that a heterogeneous or "messy" organization is a sign of poorer prognosis for the patient. Nevertheless, until now no one has yet managed to transform this knowledge into a method of prognosis of cancer.

The method now developed is based on a technology called automated image analysis. Images of cell and tissue samples are transferred to the computer from the microscope and studied bit by bit. At ICGI, one has chosen to call the [method](#) "nucleotyping."

The new research results show that nucleotyping provides a very good basis for assessing whether cancer will continue to develop.

The results are now included in the DoMore research project, which will use new technology to solve the challenges of over and undertreatment of cancer. The technological development of the last few years has opened up opportunities for gaining much more insight into what is happening in a tumour that we have so far reviewed. Using methods and tools like big data, deep learning and machine learning, researchers allow machines to compare huge amounts of data, including microscopic images.

More information: Andreas Kleppe et al. Chromatin organisation and cancer prognosis: a pan-cancer study, *The Lancet Oncology* (2018). [DOI: 10.1016/S1470-2045\(17\)30899-9](https://doi.org/10.1016/S1470-2045(17)30899-9)

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