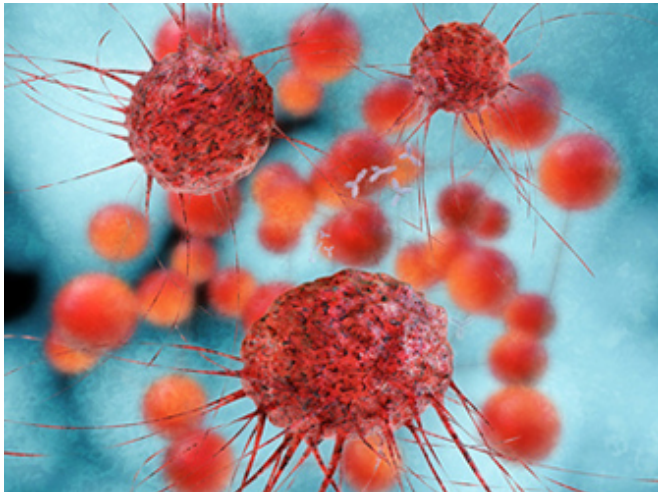


New technology developed to diagnose cancer cells

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Credit: Medical University of Vienna

In pathology, cells and cell nuclei are usually examined using a microscope for bio-marker expressions in tumours. This analysis is used to weigh up the treatment options for patients who have cancer, for example. The certainty of the diagnosis depends greatly on the individual pathologist. A study led by Lukas Kenner at the MedUni Vienna at the Clinical Institute of Pathology, as well as at the Ludwig Boltzmann Institute for Cancer Research (LBI-CR) and the VetMedUni Vienna, has demonstrated that two independent pathologists only agreed on one in three diagnoses. New computer software that has been developed jointly will help in future to double diagnostic certainty.

This is the outcome of the recent study, which has now been published in the highly respected journal PlosOne. The scientists investigated and analysed 30 liver cell carcinomas and were able to classify them into categories ranging from "negative" to "strongly positive" using the software developed jointly by the MedUni Vienna and the Vienna-

based firm "Tissuegnostics".

This study measured the expression of the proteins STAT5AB and JUNB in an aggressive T-cell lymphoma. The software uses certain algorithms and highly sensitive digital photography, enabling it to represent the matrix of cells and the cell nucleus better than under the microscope. STAT5 plays an important role in the development of leukaemia and [liver cancer](#). The JUNB gene is involved in the development of tumours in lymph gland tissue.

Paving the way towards more accurate specification of changes in [cancer cells](#)

Says Kenner: "The new program of course does not make pathologists redundant, however it is a supplementary method that considerably increases diagnostic certainty." The MedUni Vienna expert also anticipates that the new technology will contribute to the changes in [cancer](#) cells, which are currently classified into four categories, being specified in much more detail in the future. It may in future be possible to create much more detailed categories, giving clinicians a further tool with which to choose the correct and tailored therapy option.

"Cancer therapies are expensive. This new software will also help us to assess more effectively where expensive therapy is justified, but also which cases do not need it, thereby also sparing the patient," says Kenner.

More information: Schleder M, Mueller KM, Haybaeck J, Heider S, Huttary N, et al. (2014) "Reliable Quantification of Protein Expression and Cellular Localization in Histological Sections." *PLoS ONE* 9(7): e100822. [DOI: 10.1371/journal.pone.0100822](#)

Provided by Medical University of Vienna

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