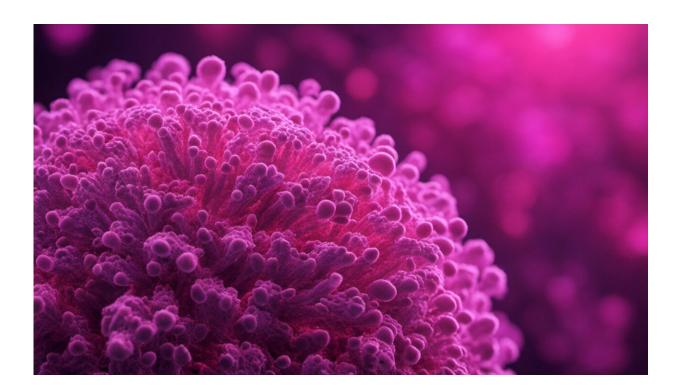# Single cell focus reveals hidden cancer cells

May 16 2017

Credit: AI-generated image (disclaimer)

Researchers have found a way to identify rogue cancer cells which survive treatment after the rest of the tumour is destroyed, by using a new technique that enables them to identify and characterise individual cancer cells.

Recent breakthroughs are revolutionising cancer treatment, enabling doctors to personalise chemotherapy for each patient. However, although

these new treatments are often highly effective, all too often the cancer grows back, eventually causing relapse.

An international research team, led by Professors Adam Mead and Sten Eirik Jacobsen at the University of Oxford and Karolinska Institutet in Sweden, have found a way to identify rogue cancer cells which survive treatment after the rest of the tumour is destroyed, by using a new technique that enables them to identify and characterise individual cancer cells.

Professor Adam Mead of Oxford University's Radcliffe Department of Medicine, said: 'It is increasingly recognised that tumours contain a variety of different cell types, including so-called cancer stem cells, that drive the growth and relapse of a patient's cancer. These cells can be very rare and extremely difficult to find after treatment as they become hidden within the normal tissue.

'We used a new genetic technique to identify and analyse single cancer stem cells in leukaemia patients before and after treatment. We found that even in individual cases of leukaemia, there are various types of cancer stem cell that respond differently to the treatment. A small number of these cells are highly resistant to the treatment and are likely to be responsible for disease recurrence when the treatment is stopped. Our research allowed us uniquely to analyse these crucial cells that evade treatment so that we might learn how to more effectively eradicate them.

'This technique could be adapted to analyse a range of different cancers to help predict both the likely response to treatment, and the risk of the disease returning in the future. This should eventually enable treatment to be tailored to target each and every type of cancer stem cell that may be present.'

Molecularly targeted therapies for cancer frequently induce impressive

remissions, however, complete disease elimination remains rare, and patients remain at risk of disease relapse. At a cellular level this is likely to reflect differences between individual cancer cells, so-called intratumoural heterogeneity, which underlies this differential response to treatment.

The researchers from the Weatherall Institute of Molecular Medicine at Oxford's Radcliffe Department of Medicine used a technique called single-cell analysis to study thousands of individual cancer cells in a type of blood cancer called chronic myeloid leukemia (CML) before and after treatment. Being able to identify each subpopulation using this single cell analysis technique will be an important step towards tailoring treatment to each patient.

  More information: Alice Giustacchini et al. Single-cell transcriptomics uncovers distinct molecular signatures of stem cells in chronic myeloid leukemia, *Nature Medicine* (2017). DOI: 10.1038/nm.4336

Provided by University of Oxford