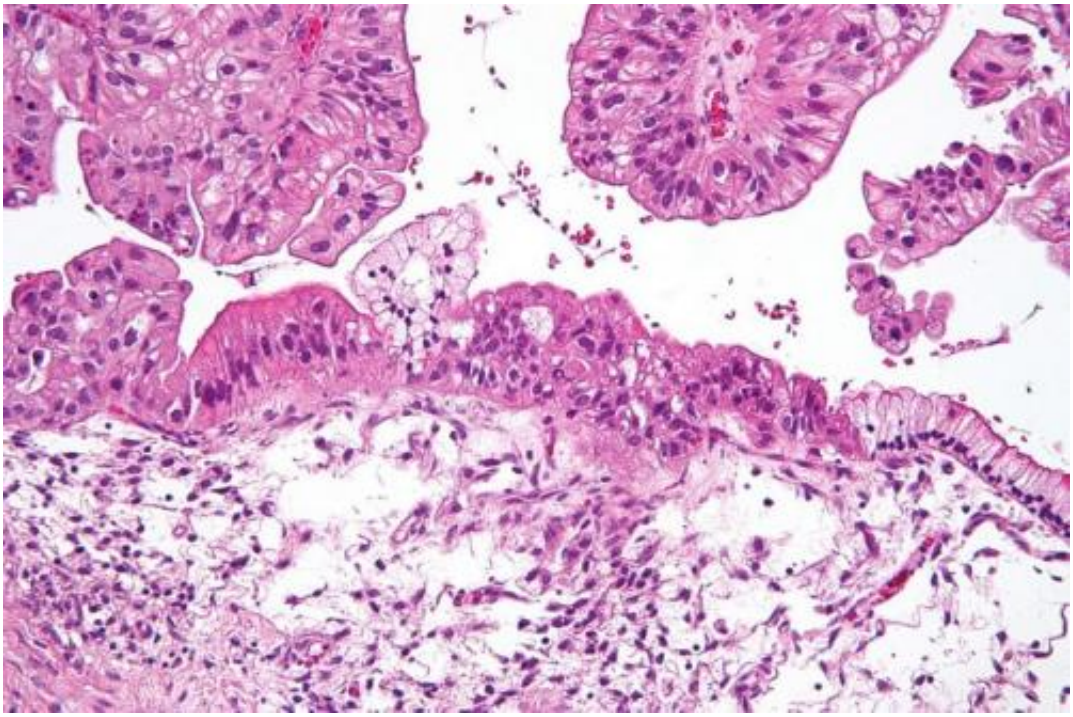
Scientists closer to finding the cell of origin for ovarian cancer

February 10 2020



Intermediate magnification micrograph of a low malignant potential (LMP) mucinous ovarian tumour. H&E stain. The micrograph shows: Simple mucinous epithelium (right) and mucinous epithelium that pseudo-stratifies (left - diagnostic of a LMP tumour). Epithelium in a frond-like architecture is seen at the top of image. Credit: Nephron /Wikipedia. CC BY-SA 3.0

Researchers at the University of Oxford are now closer to finding the cell of origin of ovarian cancer, and their ultimate aim of developing a much needed screening tool for ovarian cancer.

Ovarian cancer is the sixth most common cancer in women, with around 7,500 new cases diagnosed in the UK each year. Currently only 35% of patients in England will live 5 years beyond their diagnosis. Less than 1 in 3 patients in England are diagnosed at Stage 1 where survival rates are as good as 95%. The development of screening tools have transformed survival rates for other cancers such as cervical and breast cancer.

The new technique is called single cell RNA sequencing. It examines all the RNA molecules in a cell, whereas the traditional technique can only look at a group of cells at a time. In this study, the researchers used single-cell sequencing to look at the RNA in individual normal cells from the inner layer (epithelium) of Fallopian tubes, which carry eggs from the ovaries to the uterus, and which is the origin of the vast majority of ovarian cancers. By doing so, they were able to identify new subtypes of normal Fallopian tube cells.

Surprisingly, the molecular fingerprints of these subtypes were mirrored in individual ovarian cancers. Scientists discovered that single cell sequencing of the normal Fallopian tube can identify a particular group of ovarian cancer patients who have the poorest chance of surviving the disease and do not benefit from current treatments. Focussing on new treatments for this particular group of patients will be an important way to improve overall survival rates.

Professor Ahmed Ashour Ahmed, Director of the Ovarian Cancer Cell Laboratory at the MRC Weatherall Institute of Molecular Medicine at Oxford University, said: "Identifying the type of cancer cells is an important early step in choosing which drugs and treatments to use because different types of cells respond differently to treatment. The "Oxford Classic", our new tumour classifier should give us much more accurate predictions for disease outcome in patients as well as helping us to develop targeted therapies for each type of cancer."

Zhiyuan Hu, first author on the paper, said: "The discovery of new types of cells sheds new light onto the complexity of ovarian cancers. This research should take us a step closer to identifying the cell of origin of ovarian cancer and to developing a new tool for screening. It also opens the door for similar research for other types of cancers."

Cary Wakefield, Chief Executive of charity Ovarian Cancer Action who funded the research, said: "We fund world-class research to address the low survival rate women diagnosed with ovarian cancer currently face. These exciting findings take us closer to both a screening tool and personalised treatments, the two key elements we know will transform the lives of women diagnosed with ovarian cancer today and for generations to come."

The full paper, 'The repertoire of serous ovarian cancer non-genetic heterogeneity revealed by single-cell sequencing of normal fallopian tube epithelial cells,' can be read in *Cancer Cell*.

Provided by University of Oxford

Citation: Scientists closer to finding the cell of origin for ovarian cancer (2020, February 10) retrieved 20 April 2024 from https://medicalxpress.com/news/2020-02-scientists-closer-cell-ovarian-cancer.html