MedicalXpress

Low-cost method for examining single leukemia cells could transform treatment

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Leukemia is a disease in which each cell can exhibit different genetic traits, and now Swedish researchers have found a cheap way to examine the individual cells. Reported in *Nature Communications*, the breakthrough could transform leukemia treatment.

Cells are packed with genetic information that can be used to improve treatment of diseases such as cancer, but the RNA sequencing methods typically used today have one limitation: they don't identify in which cells the genetic activity is taking place.

In the recent issue of *Nature Communications*, Swedish researchers presented a new method they used to examine individual tumor cells in patients with chronic lymphocytic leukemia (CLL) – an important advance considering the team found the leukemia tumors to be comprised of cells with entirely different gene expressions.

"We found that CLL cells do not consist of a single cell type, but of a number of sub-clones that exhibit entirely different gene expression," says Joakim Lundeberg, a professor of Gene Technology at KTH Royal Institute of Technology in Stockholm and director of the Science for Life Laboratory's genomics platform.

Typically, RNA sequencing will provide information about what RNA molecules are present in a biological sample, but not where or in which cells they are active.

"With this new, highly cost-effective technology, we can now get a whole new view of this complexity within the blood cancer sample. Molecular resolution of single cells is likely to become a more widely-used therapy option," he says.

Lundeberg says the method provides analysis of all mRNA molecules in individual cells by binding a location tag to the molecules.

Individual cells are sorted on a specially-made glass surface and using analysis of RNA molecules with next-generation sequencing, one can tell which genes are active. The spatial information on the glass surface tells which cell a specific RNA molecule is to be found in.

"We have also developed an open, available software which combines images of individual cells with information from the sequencing, that is, which genes are expressed and at what level.

"With the new method, and the software, we can study thousands of cells in a day," he says.

More information: Sanja Vickovic et al. Massive and parallel expression profiling using microarrayed single-cell sequencing, *Nature Communications* (2016). DOI: 10.1038/NCOMMS13182

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