Most popular ovarian cancer cell lines do not resemble ovarian cancer

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(Medical Xpress)—Researchers from Memorial Sloan-Kettering Cancer Center recently discovered that the most frequently used cancer cell lines in ovarian cancer research are not suitable models of ovarian cancer. Their findings are the result of a detailed review of genomic data that recently became publicly available. Their methods, published in this week's *Nature Communications*, could provide a usable framework for other researchers to better assess cell lines' validity for future use in this and in other types of cancer research.

Computational biologists Nikolaus Schultz and Rileen Sinha, and biochemist Silvia Domcke, focused their review on high-grade serous ovarian cancer (HGSOC), the most commonly diagnosed and frequently studied subtype of ovarian cancer. Using datasets from The Cancer Genome Atlas and the Cancer Cell Line Encyclopedia, which detail and define the genomic features of numerous clinical samples and cell lines, the team analyzed and then ranked several cell lines by their genomic similarities to tissue samples and, in doing so, uncovered multiple discrepencies between the cell lines and actual human tumors.

"Our review showed that the two most utilized cell lines, accounting for almost 60 percent of all published research studies, do not resemble HGSOC well at all," explained Dr. Schultz, the paper's lead author. "The problem with this is, investigators assumed they were studying high-grade serous ovarian cancer, when in reality they were looking at something else. So conclusions drawn from this work might be misleading."

Cancer cell lines are generated and grown indefinitely in laboratories around the world, but are ultimately derived from human tumors. For the past several decades, they have been the most popular model for the study of cancer because they are inexpensive and easy to replicate. However, the origin of some cell lines is not well established, and through years in culture, they can acquire additional changes, making them less desirable.

"With the explosion of genomic data now at our fingertips and the potential for more to become available, it's our hope that this approach can be used by our colleagues to choose optimal cell lines, as we do expect similar discrepencies in other tumor types," said Dr. Schultz. "Overall, we believe these findings should greatly benefit the study of cancer."

Provided by Memorial Sloan-Kettering Cancer Center