Whole-genome study of metastatic tumors provides a catalog of genetic features of metastatic cancer

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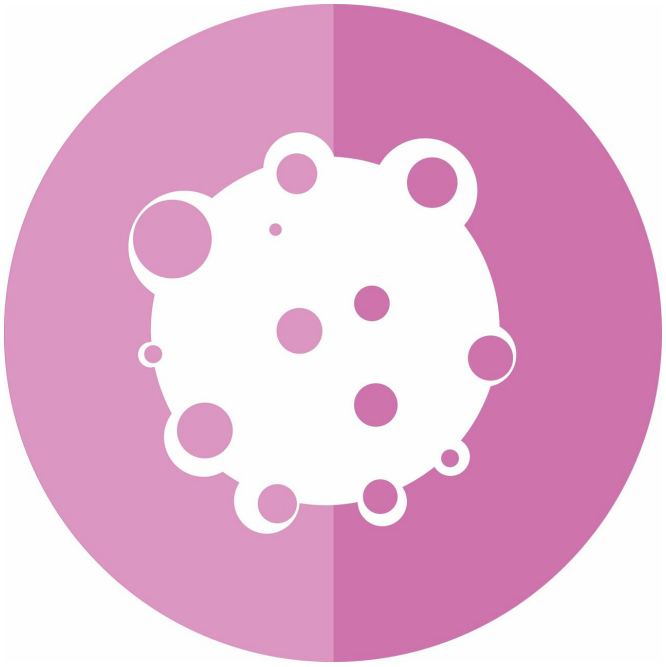

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A team of researchers with members affiliated with multiple institutions in The Netherlands and Australia has conducted the largest-ever whole-genome study of metastatic solid tumors. In their paper published in the journal *Nature*, the group describes their study and the benefits it has already provided. Jillian Wise and Michael Lawrence with the Massachusetts General Hospital Cancer Center and Department of Pathology have published a News & Views piece describing the work by the team in the same journal issue.

When people develop breast cancer or skin cancer, death isn't caused by what it does to the originating organs—patients die because cancer cells from the original tumor break away and travel to other more vital parts of the body, such as the lungs or the brain, where they grow into new tumors. The process is referred to as metastasis, and it is the area of cancer research that gets the most study, precisely because it is so deadly. To advance that work, the team with this new effort has conducted the largest of its kind whole-genome study of metastatic solid tumors and cataloged what they found. They also sequenced blood cells from the same patients that donated the tumors as a means of comparison. The researchers explain that the exercise was needed because it has become clear that metastatic tumor cells undergo genetic changes as they travel through the body. By looking at the genomes of the same types of cancers traveling in different patients, medical researchers can spot trends, which in turn could lead to new treatment therapies.

The work involved carrying out whole-genome sequencing on 2,520 tumor samples from 2,399 cancer patients, and doing the same with blood samples. As each was sequenced, the information describing it was entered into a catalog that grew larger as the study progressed. The researchers note that the most important part of the data is the information that describes genetic mutations. They note also that the catalog will be added to others that have been developed providing researchers with a much larger dataset to use in their work. Notably, the researchers found that variants associated with treatment outcomes were identified in 62 percent of the patients whose tumors they studied.

More information: Peter Priestley et al. Pan-cancer whole-genome analyses of metastatic solid tumours, *Nature* (2019). DOI: 10.1038/s41586-019-1689-y