Characterising the profile of breast cancer metastases for improved treatment

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Researchers at the Jules Bordet Institute - Université libre de Bruxelles, VIB and KU Leuven published this 21 of April an important study offering a better understanding of the progression of breast cancer. The conclusions could have an impact on care for patients suffering from a metastatic breast cancer. This is one of the first studies based on the analysis of multiple metastases obtained at the time of patient autopsies.

A global understanding of the dissemination of the disease

To date, the choice of treatment for metastases was based on the analysis of the primary tumour. A better understanding of the metastatic disease was crucial to arrive at an improved treatment. Unfortunately, the study of the dissemination of breast cancer, from the primitive tumour to the metastatic disease, is virtually impossible as it would require an analysis of all the patient's metastases over time. Studying the different metastases obtained at the time of the autopsy of patients who have unfortunately died of breast cancer therefore represents one of the only options for characterising the disease in its globality.

Discovery of a unique metastatic precursor

The team from the Breast Cancer Translational Research Center (BCTL) J.-C. Heuson laboratory at the Jules Bordet Institute – ULB-Cancer Research Center, Université libre de Bruxelles, investigated the biology

of different metastases and of the primary tumour of 10 patients, thereby making it possible to reconstitute the history of the cancer's progression. This study, carried out in cooperation with VIB, KU Leuven and the University of Budapest, revealed that in the majority of cases all the metastases originate in a single metastatic precursor and do not result from independent multiple dissemination events from the primary tumour.

In the case of certain recurrences that occur shortly after the initial diagnosis, the characteristics of the metastases were close, from a genomic point of view, to those of the primary tumour. On the other hand, in the case of later recurrences, the molecular differences proved to be greater. Moreover, the genomic profile of the various metastases in the same patient could be very different, providing a potential explanation for the heterogeneous nature of the response to anti-cancer treatment sometimes observed in a hospital environment in the same patient.

Study conclusions

This study suggests that at least one metastatic lesion (if possible several) should be biopsied and analysed at the time of the breast cancer recurrence, especially if the recurrence comes several years after the initial cancer given the possible modifications in the particular genomic profile of the metastatic disease. The determination of the genomic profile using high throughput sequencing techniques targeting a set of predefined and clinically relevant aberrations could be useful for making the therapeutic decision, in particular for the choice of targeted treatments.

More information: David Brown et al. Phylogenetic analysis of metastatic progression in breast cancer using somatic mutations and copy number aberrations, *Nature Communications* (2017). DOI:

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