Breast cancer cells change and adapt during disease progression

A diagnosis of breast cancer usually includes characterisation of the breast cancer cells: determining if the tumour cells have hormone receptors and other proteins which will help to decide the best treatment options for the patient. This information is usually gathered from a biopsy and forms part of the initial patient diagnosis. The knowledge will be used to choose the most suitable drugs and will help to shape the patient's treatment plan.

For some patients, tumour cells become resistant to the drugs and can grow back to form a new tumour, either in the breast or at another site in the body such as the liver or bone. Until recently, it was frequently assumed that these tumour cells still had the same characteristics as the original cells.

In this study by McBryan et al, 3 patients each had tumour samples collected from their breast, lymph node and liver. All tumour samples were profiled in detail using a technique known as RNA-sequencing. This technique looks not only at standard tumour characteristics that are tested for in the hospital, but at all expressed genes in the cell to provide a complete picture or profile of the cells. This is the first study of its kind to profile matched tumours (breast, lymph node and liver) from the same patients.

The results suggest that tumour cells undergo a process of change and adaptation during disease progression. The changes are quite unique to each patient but share a common theme of adapting to a new environment. Genes involved in cell to cell communication are found in tumour cells in the liver that originated from a breast cancer. The patients in this study all received tamoxifen, chemotherapy and radiotherapy. Further research will be needed to determine the impact of treatment in driving these adaptations.

The results emphasise the need to re-evaluate cancer cell biology and provide personalised medicine throughout disease management. In line with these results, new clinical guidelines published in July 2015, based on worldwide research, now recommend that new tumours be characterised where possible before deciding further treatment plans.

Publication

Transcriptomic Profiling of Sequential Tumors from Breast Cancer Patients Provides a Global View of Metastatic Expression Changes Following Endocrine Therapy.
McBryan J, Fagan A, McCartan D, Bane FT, Varešlija D, Cocchiglia S, Byrne C1, Bolger J, McIlroy M, Hudson L, Tibbitts P, Ó Gaora P, Hill AD, Young LS

Clin Cancer Res. 2015 Aug 3