Clinical utility of circulating tumour DNA analysis in hormone receptor positive breast cancer patients

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Breast cancer is the most frequently diagnosed cancer worldwide and in women, the second most common cause of cancer death. Approximately 70% of breast cancers are Hormone Receptor positive (HR+) cancers with about half of the patients with HR+ breast cancer responding well to anti-estrogenic therapies. Nonetheless, around 25% of patients with the disease will relapse during treatment and follow-up. Advances in diagnosis and treatment have resulted in substantial improvement in disease free survival in the last few decades but still there is considerable need to develop better tools to establish who is at risk of relapse following treatment due to the development of resistance mechanisms to these therapies.

Circulating tumor DNA (ctDNA), thought to be released from cells mostly through apoptosis and necrosis, and possibly also by active secretion, can be detected in the circulation of breast cancer patients by identifying genomic aberrations. Levels of ctDNA fluctuate with treatment during cancer therapy and broadly correlate with disease response and relapse thus offering the potential for non-invasive monitoring of disease status in both the early and the metastatic settings.

Although levels of ctDNA detected in HR+ breast cancer tend to be the at the lower end in any of the different breast cancer subtypes, recent advances in pre-analytical approaches, as well as analytical techniques, have allowed the interrogation of these circulating nucleic acids from patient's samples undergoing therapy. The ability to interrogate ctDNA in HR+ breast cancer patients presents us with a new paradigm for the developing of novel therapies to treat the disease, allowing the tailoring of novel adjuvant, as well as metastatic therapies to the genetic makeup of these patients.