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Editorial

Advances in translational research in breast cancer; a bridge to future therapies

The past 10–15 years have witnessed remarkable new developments in tissue analytical methods and in the conceptual understanding of cancer. Only a few years ago, investigators could only study one gene at a time and techniques to measure more than one molecular variable in human cancers were slow and cumbersome. Today it is possible to perform high resolution comparative genomic hybridisation on a small cancer biopsy and perform a genome-wide survey of DNA copy number abnormalities.[1] The same biopsy can be simultaneously processed for comprehensive gene expression analysis with DNA microarrays to provide semi-quantitative measurements of essentially all mRNA transcripts in the tissue. Mass spectrometry based DNA sequencing allows rapid screening for mutations and polymorphisms in hundreds of genes.[2] High throughput protein and small metabolite detection methods are also being developed and will probably catch up shortly with the more mature analytical tools that exist to study nucleic acids. Not surprisingly, these new technologies have revealed previously unrecognised complexities in biology. Entirely new RNA classes have been discovered, the functional importance of non-coding DNA sequences has been established and it has also become apparent that most human cancers harbour a large number of potentially functionally important abnormalities at the DNA, RNA and protein levels.[3,4] In the wake of these discoveries a new field of biology, systems biology, has emerged.[5]

Simultaneously, important advances have been made in the conceptual framework of cancer biology. Interactions between tumour cells and stroma have been established as important contributors to cancer behaviour, and angiogenesis and hypoxia play important roles in tumour progression and can be exploited for therapeutic purpose. The long held paradigm of tumour heterogeneity has acquired added complexity due to the identification of tumour stem cells. The development of technologies to isolate and study circulating tumour cells has made it possible to study these rare cells in previously unprecedented detail. Molecular analysis has revealed that breast cancer is not a single disease with heterogeneous morphology and biomarker profiles but a collection of molecularly distinct neoplastic diseases that quite plausibly originate from different cells within the breast.

These technological and conceptual advances drive some of the most promising contemporary translational research directions that may lead to new drugs, novel treatment strategies and more accurate biomarkers for breast cancer. It is almost impossible for any individual today to follow the entire breadth of the scientific literature that is relevant for a particular disease which has therefore motivated the creation of this special issue of the *European Journal of Cancer*. The purpose of this issue was to collate a series of reviews that cover some of the most important new developments in translational research in breast cancer. We realise that a comprehensive coverage of all interesting research directions is not possible even in a dedicated volume like this. We have attempted to focus on areas that have already shown promise in clinical application. Drs. Sherene Loi and Lisa Carey and colleagues will review the molecular analysis of two important subsets of breast cancer hormone receptor-positive and triple-negative cancers, respectively.[6,7]

Drs. Fabrice Andrée and colleagues, Andrew Tutt and colleagues, Brian Leyland Jones and colleagues and Carlo Croce and colleagues will cover important new diagnostic technologies including gene expression profiling, proteomics and microRNA profiling.[8–11] These powerful high throughput molecular analytical tools produce results that can be easily misleading and their analysis requires specialised bioinformatics expertise. Dr. Richard Simon will discuss problems and pitfalls in translating these molecular observations to clinical practice.[12] Dr. Angelo Di Leo and colleagues will discuss recent developments in using topoisomerase alpha II as a potential marker of anthracycline sensitivity.[13] Drs. Adrian Harris and colleagues, Kornelia Polyak and Christoph Klein will review three important new concepts in breast cancer biology including the role of hypoxia in cancer progression, tissue microenvironment and stem cells and metastatic precursor cells, respectively.[14–16] Dr. Dimitris Mavroudis will discuss the implications of detecting micrometastatic disease in the blood.[17] Drs. Jose Baselga and colleagues, and Francisco Esteva and colleagues will summarise the current status of targeted therapies in breast cancer and new developments in the therapy of HER2-positive breast cancer, respectively.[18,19] Magnetic resonance imaging (MRI) has emerged as a powerful and very sensitive tool to detect cancer in the breast. It is readily available in the clinic but frequent false positive findings and costs limit its use. Dr. Jennifer Zakhireh and colleagues will discuss the current

controversies and practice recommendations for using MRI in the screening and management of breast cancer.[20]

We hope that this special issue of the Journal will serve as a useful reference for the readers to navigate the complex literature of contemporary breast cancer research and will help to disseminate important new ideas that will likely impact the future therapy of breast cancer.

Conflict of interest statement

None declared.

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