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Editorial

Translating cancer-omics into function

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Cancer is a complex disease and its progression and aggressiveness depends on a number of factors such as patient's genetic background, tumor mutational landscape and the cancer microenvironment. Cancer also exhibits vast patient- and tumor-specific heterogeneity, which is often reflected in low rates of response to therapy or after initial response, in local and metastatic relapse. To meet the challenges that arise from such complexity and heterogeneity, personalized medicine approaches based on fine-grained analyses of the patient's tumors and thus more sophisticated diagnoses have become an integral part in current therapeutic strategies and drug development.

The "omics" approach, that is the ability to measure thousands parameters simultaneously such as by RNA-sequencing and metabolomics screens, is key to define 'personal' at the molecular and metabolic level (Lorendeau et al., 2015). Actually, gene expression signatures obtained from tumors using whole exome arrays, have demonstrated strong predictive power and are currently used in the clinic for diagnostic purposes (Alshalalfa et al., 2015). In addition, next-generation sequencing is now used to identify new fusion protein kinases in cancer that have proved as important drug targets (Davare and Tognon, 2015). Indeed, identification of oncogenic drivers and pathways in a particular case can now be used to assign a drug combination that will inhibit a particular oncogene and in parallel a hyper active pathway (Wolfson et al., 2015).

Two areas that have perhaps received less attention from the "omics" research community but do offer exciting therapeutic opportunities are the tumor-blood brain barrier interaction in the context of brain metastasis and brain cancers, as well as regulation of selective protein synthesis. First, brain cancers and metastasis are particularly deadly and their treatment challenging as often drugs do not pass the blood brain barrier. Advances in our understanding of the tumor-blood brain barrier interaction is now leading to new paradigms in drug design and combinatorial therapy of these diseases (Blecharz et al., 2015). Second, while genetic and transcriptional profiling are by far the most prevalent "omics" analyses in cancer, recent advances in our understanding of how selective RNA translation is regulated in the context of cancer has highlighted new pathways that promote the adaptation of cancer cells to the tumor microenvironment.

Despite these revolutionary advancements owing to these "omics" technologies, the scientific community needs now to make the next step in actually connecting these diverse genetic and molecular findings and to translate novel discoveries into improved outcomes for cancer patients. In fact, the success of personalized medicine depends on the detailed knowledge of cellular pathway/drug interactions and molecular markers that can predict therapeutic response. Accordingly, this themed issue on *"Translating cancer-omics into function"* is dedicated to this aspect and shall provide a trans-disciplinary forum for researchers working at the interfaces between basic cell biology, tumorigenesis, and personalized medicine.

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