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New opportunities from clinical multigene panel sequencing for the molecular stratification of metastatic colorectal cancer

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Abstract

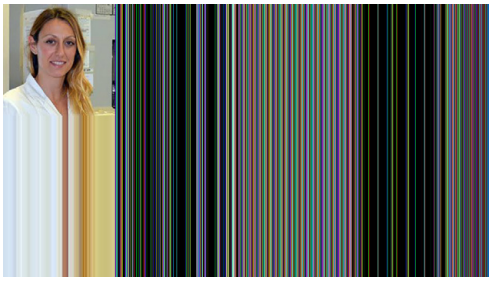
Colorectal carcinoma (CRC) is one of the most commonly diagnosed cancers worldwide. The metastatic disease contributes to the high mortality rate reported for such tumors. Significant benefit on overall survival was brought about the introduction of monoclonal antibodies anti-EGFR and anti-VEGF used in combination with chemotherapy in metastatic CRC (mCRC). While anti-VEGF treatment does not require biomarker-based selection criteria, the potential efficacy of anti-EGFR antibodies is neglected to patients with activating mutations in KRAS and NRAS (RAS) genes, that became a clinical routine.

Recently, different molecular classification of CRC patients mostly based on omics approaches has been proposed. Although these might have implications for prognostic or therapy decisions, their immediate transfer to routine diagnostic/clinical settings is seriously challenging in terms of methodology, turnaround time, costs and mindset. As a consequence, to date, only few molecular biomarkers, such as RAS or BRAF, are routinely used in the standard clinical management of mCRC patients, but in the era of personalized therapy, we should be able to reach beyond the concept "one gene-one drug".

With the aim of responding to the clinical demand of RAS testing, many new rapid, sensitive and economic approaches have been implemented over the years, among them the NGS platforms.

Introduction

Francesca Belardinilli has a PhD in Biotechnology and since November 2012 has joined the laboratory of Molecular Oncology. She has technical skills in molecular, cellular biology and statistics. Her most important expertise is in the molecular genetics of Breast, Lung and Colorectal cancer. In particular, she is currently investigating the biological and clinical role of mutations observed in colorectal tumours, as well as their frequencies and associations.



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