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EDITORIAL COMMENT

Genomics of metastatic progression

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Metastatic potential of transformed cells is the hallmark of malignancy and is the basis of pathological diagnosis of tumors. Characterization of the metastatic potential of cancer cells is still a hot topic in cancer research despite of a pletora of studies published in the past decade. Although these studies provided meaningful information on the basic alterations at expression levels, these data are frequently controversial. Controversies exist between cellular systems, preclinical models and clinicopathological studies. The data indicate that in vitro systems are dependent on the effects of the specific artificial conditions, that preclinical models are affected significantly by the „foreign" stroma signatures of the host and that the clinicopathological studies are greatly dependent on the histopathological specifics of the cancer. Furthermore, all these variabilities are further complicated by the specificities of the array platforms used throughout these studies.

Against all of these odds, the validity of these types of approaches is justified by the clinical utility of various genomic tests in breast cancer, the 70-gene prognostic signature (Mammaprint) and the 21-gene recurrence signature (OncotypeDX). However, even in breast cancer there are several other signatures available purported to predict metastatic potential, ranging from 17 to 442 genes. Unfortunately, none of the identified „prognostic" signatures of other cancer types obtained FDA approval for genomic testing in clinical situations, suggesting that they were not properly validated in the preclinical or clinical processes.

We have decided to critically analyze these studies, because we believe that these types of analysis could provide important data for further studies in this field. We have invited leading experts of prognostic genomics both from experimental and clinical fields to interpret the past and outline tasks for the future.

The major focus in the literature is on breast cancer, the neoplasm for which the greatest effort in the search of genomic signatures has been invested. This issue has approached melanoma, lung cancer, sarcomas, and also endothelial cells, as partners of tumor progression. We also address, perspectives in proteomic strategies.

We are convinced that the Journal of Clinical Experimental Metastasis, the official Journal of the Metastasis Research Society, is the proper media for this kind of evaluation, and we hope that this special issue will be a valuable resource for further studies in this continuously developing field.

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