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Translational Research in Breast Cancer

Biomarker Diagnosis, Targeted Therapies and Approaches to Precision Medicine

Springer

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Preface

Breast cancer is the most frequently diagnosed cancer and the leading cause of cancer death among females, accounting for 23% of the total cancer cases and 14% of the cancer deaths worldwide. Breast cancers are genetically heterogeneous, which can be generally classified into four categories with distinct patterns of molecular profile and different treatment strategies. Besides, about 5–10% of cases are inherited mainly due to the germline mutations of BRCA1 and BRCA2, which are key DNA repair regulators, and thus lead to the DNA repair-targeting therapy with PARP inhibitors. Unraveling the biological heterogeneity of breast cancer in its natural history and its responsiveness to therapy from one patient to another will help to translate new approaches for breast cancer prevention and treatment and improve the quality of care offered to breast cancer patients.

There is a broad consensus that cancer is a genetic disease and that accumulation of molecular alterations in the genome of somatic cells is the basis of cancer progression. In breast cancer, the accumulated mutations often result in the amplification of growth signal followed by the activation of PI3K/AKT/mTOR pathway and RAS/MEK/ERK pathway and thus cause the agitation of downstream transcription, metabolic reprogramming, etc., leading to the increase of breast cancer stem cell self-renewal and acceleration of cell cycle or less apoptosis. The understanding of genomic changes and oncogenic signaling cascade of breast cancer has inspired the development of targeting treatments, such as the clinical trials in PI3K, AKT, and mTORC1 inhibitors.

On the other hand, breast cancer, like other cancers, occurs because of an interaction between an environmental (external) factor and the genetically susceptible host. The immuno-environment has been demonstrated as a barrier of the clinical cancer. Overcoming the restriction of immune checkpoints is an essential step for cancer development. Therefore, recovering these checkpoints may prevent cancer progression. In addition, stromal cells such as tumor-associated macrophages (TAMs) promote tumorigenesis by limiting immuno-response or directly promoting cancer metastasis. The knowledge has been translated into successful approaches of immuno-therapies such as the application of anti-PD1 and anti-PDL1 strategies for malignancy treatment.

Together, elucidating the molecular landscape of breast cancers has facilitated the development of diagnostic, prognostic, and predictive biomarkers for clinical oncology. In addition, a burst of knowledge in cancer biology, immunology, genomics, metabolism, and so on has broken new grounds for designing innovative therapeutic approaches and selecting appropriate treatments according to the precise information of an individual cancer patient. The present book is an endeavor to convey a comprehensive knowledge of the translational efforts in breast cancer and address the latest approaches of precision medicine based on the understanding of breast cancer.

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