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Introduction

Breast cancer is the second most common malignancy worldwide and is the most common aggressive malignant neoplasm in premenopausal women. The progression of this cancer, treatment options, and the response to treatments largely depend on genetic variation of the breast epithelium and on the surrounding microenvironment. Recent studies also highlight the hierarchy of mammary stem/progenitors cells that are selectively susceptible to tumorigenic stimuli unfolding the early events in breast carcinogenesis. A major challenge in the field is disease recurrence due to intrinsic or acquired resistance to commonly used therapeutic agents, elucidation of its mechanism, and exploration of ways to circumvent drug resistance. This special issue of *Gene Expression* addresses these issues and focuses on four timely topics in breast cancer.

The article on Gene Expression Profiling, by Wesolowski and Ramaswamy, reviews the latest development in breast cancer classification in the light of advancements in cDNA microarray and quantitative reverse transcriptase polymerase chain reaction. Expression profiling that led to gene expression signature of primary breast tumors has significantly advanced molecular subtyping of breast cancer. Since the discovery of intrinsic molecular breast cancer types, several gene microarrays were commercially developed as clinically useful prognostic and predictive tools that could lead to novel strategies for treatment of breast cancer patients.

The article by Taylor, Lee, and Schiemann reviews the recent advances on the dual and paradoxical role of TGF-β pathway that facilitates tumor metastasis. TGF-β pathway has been in the forefront of different signaling pathways as it plays a key role in linking tumor microenvironment to tumor progression. The authors discuss the major "driver role" of TGF-β1 in breast tumor metastasis, as well as its role in the regulation of differentiation and proliferation of fibroblasts in the mammary tumor microenvironment and in angiogenesis at the late stage of tumorigenesis.

Bruno and Smith give an overview of another important and extensively studied area in the last decade regarding the role of stem/progenitor cells in tumorigenesis. In this article, the authors have highlighted the hierarchy of mammary progenitor cells in mammary gland development and susceptibility to tumorigenesis using mouse models.

The last article deals with the emerging role of mircroRNAs in acquiring resistance to drugs commonly used in breast cancer therapy. Majumder and Jacob have reviewed this fast moving field with particular emphasis on the role of two microRNAs, miR-221 and miR-222, in conferring resistance to antiestrogen agents. Deregulation of specific microRNAs leads to alteration in cell cycle regulatory pathways, multidrug-resistant pathway, and pathways regulating epithelial-mesenchymal transition, all leading to tumor recurrence and metastasis.

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