

Preface

This book provides descriptions of the most common techniques used in breast cancer research with a special emphasis on the study of the normal breast as the basis for understanding the pathological processes in this organ.

The authors have poured their 37 years of experience in the field of breast cancer research into this book and described the process of handling and interpreting the complex organ that is the human breast using original data and unique material collected over the years.

Chapter 1 discusses the normal architecture of the human breast using the whole mount preparations and provides the parameters of how to identify each single structure in the tissues of nulliparous and parous women.

Chapter 2 describes possible sources of normal breast tissue, from autopsy specimens to core needle biopsies, and the morphological characteristics of each source when the normal tissue is studied. The pros and cons of each source, depending on the study planned in this organ, are also outlined.

Chapter 3 is an introduction to laser capture microdissection (LCM) in both fresh tissue and paraffin-embedded material. A detailed analysis of the extraction of DNA and RNA and the quality required for molecular studies is described and analyzed.

In Chap. 4, the technique of tissue microarray (TMA) is described and guidelines for the preparation of TMA for breast cancer as well as normal breast tissue are provided. There is original information on the limitations and quality expected for TMA of normal breast tissue arrays.

Chapter 5 discusses the role of tissue culture in the understanding of breast cancer with a historical perspective, followed by a description of the cell lines frequently used in any breast cancer research laboratory. Space is dedicated to analysis of the phenotypes commonly used for detecting malignant transformation in vitro and the use of cell lines for testing epigenetic targeting processes.

Chapter 6 provides novel information on detection of stem cells in paraffin-embedded tissue and data on how the use of immunocytochemical markers of stemness can provide prognostic indication of tumor behavior.

Chapter 7 provides a comparative analysis of the use of flow cytometry and immunofluorescence techniques compared with immunocytochemistry. The value of

in situ hybridization is also explored with a critical approach to the use of these techniques in breast cancer laboratories.

Chapter 8 is dedicated to the use of the in vivo model for studying breast cancer with extensive description of the xerograph model and the use of the tail vein and intra-auricular injection of neoplastic cells for studying metastasis.

Chapter 9 describes the use of RNA sequencing in breast tissue and the methodology for purification of small amounts of RNA when the tissue obtained is from normal core biopsies.

Finally, in Chap. 10, the latest techniques for the study of epigenetic changes in the human breast are described. This chapter provides a new path for studying epigenetic changes induced by physiological processes in the normal breast, providing a methodology on how to analyze the data and their interpretation.

Altogether, the authors have established the methodological basis for studying the human breast in its normal and pathological conditions, providing a valuable reference for those researchers who are pursuing a deeper understanding of the human breast.

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