Preface

The tissue microarray (TMA) method presents as a modern high technology, although its roots go back to the 80s when researchers first started to combine several small pieces of tissues into so-called sausage blocks. In this respect, the TMA invention was not firstly characterized by technical improvements, but its true novelty was to link clinical data to the tissues that were combined on one slide. The very high number of tissues that can be included into one TMA, the small size and regular shape of the tissue spots, the preservation of integrity of the donor tissue blocks, and the highly organized array pattern that allows for reliable allocation of clinical data to individual tissue spots made it a discrete technique with unique features.

When the TMA technology was developed 12 years ago, its benefit was controversially debated. While many researchers welcomed the method enthusiastically, there were concerns by others that results obtained from the small tissue cores used for TMA making would not be sufficiently representative of the donor tissues. Meanwhile, the increasing use of this technology has imposingly demonstrated its tremendous utility in research. In fact, basically all clinically relevant associations between molecular markers and clinical endpoints could be reproduced using only one single 0.6 mm core per tissue sample so that TMAs have nowadays become a standard tool allowing for a new dimension of tissue analysis. Rather than just representing an efficient and economic alternative to expensive and time-consuming conventional large section tissue analysis, TMAs enable the analysis of whole populations of tissues with a previously unreached statistical power.

In the era of microarrays that were typically made from spotted cDNAs or oligonucleotides, selection of the term “tissue microarray” for the new emerging tissue analysis technique was probably not optimal. It has led to tremendous efforts to develop automated devices to manufacture, scan, and analyze TMAs rapidly. However, TMAs – in sharp contrast to DNA arrays that comprise homogeneous spots of nucleic acids – represent a miniaturized kind of histopathology. All the critical issues connected with “classical” tissue analysis, e.g., fixation artifacts, antigen retrieval strategies, tissue heterogeneity, differentiation between normal and neoplastic cells, or intra- and interobserver differences in the analysis of specific cytologic structures, are still the same in a TMA than in a conventional large tissue section.

The aim of this book is not only to introduce the world of TMA making and TMA applications, but also to provide insights into the inherent and complex aspects of the most popular assays used for in-situ tissue analysis. Various applications of the TMA technology and the various kinds of sources for TMAs, including, for example, human, animal, and plant tissues; cell lines, or xenografts, make it an attractive technique not only for pathologists, but also for molecular biologists, physicians, and other researchers in the various areas of life sciences.

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