
Preface

Cervical cancer (CxCA) is one of very few types of cancer that have experienced remarkable progress in scientific, clinical, and socioeconomic areas. The discovery of the first high-risk human papillomavirus (HPV) types by Zur Hausen's group in the early 1980s opened the doors to research on the viral origin of cervical cancer. Some 30 years later, it is generally accepted that high-risk HPV types represent the major etiologic agents of CxCA. Cytological screening and HPV genotyping in women have become routine in many countries. Because of the sexually transmittable nature of HPVs, men are being enrolled in large-scale screening programs as well. In addition, two effective HPV vaccines have been developed and implemented by many countries, and novel vaccination modalities or immunotherapies are in clinical trials. In brief, our knowledge base and know-how with regard to all aspects of CxCA have grown considerably over the last three decades.

In order to adequately represent the most relevant procedures and technologies that continue to advance the field of HPV-mediated carcinogenesis of the cervix and other anatomical regions of squamocolumnar transition (anorectum, penis, and oropharynx), we have compiled a series of protocols into two parts with the first part covering HPV types, pathogenesis of CxCA, prevention, and novel potential drug targets, and the second part exploring pathology, genomics, modeling of CxCA, and experimental therapeutic strategies. Part I is subdivided into four major sections containing protocols for the detection and genotyping of high-risk HPV types; for studying the molecular pathogenesis of CxCA; for analyzing the impact of current immune responses to HPV infections; and for the identification of novel drug targets. In the second half, readers will find essential protocols for the histopathological detection, typing, and staging of CxCA; for performing genomic analysis of CxCA; and for modeling human CxCA in the culture dish or in mice and testing novel therapeutic avenues.

Each protocol in the *Methods in Molecular Biology* series is, on average, fourteen pages long and organized into six sections, i.e., a brief "Summary," an "Introduction," "Materials" and "Methods" sections, a "Notes" section, and "References." The "Notes" section is particularly useful as it highlights potential problem areas and ways to troubleshoot them, some variations in procedures, as well as assay sensitivity and timescale.

With this collection of close to 30 protocols, which faithfully cover the spectrum of techniques and strategies currently in use across the globe, we hope to provide a valuable resource to both bench scientists and clinicians who step into the realm of high-risk HPVs and CxCA for the first time or who wish to learn novel approaches or expand their toolbox for the study of CxCA.

We wish to extend our warmest thanks to Professor John M. Walker (Series Editor), who has provided amazing guidance and support during the realization of this project, and to all contributors of protocols for their hard work and patience.

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Cervical Cancer

Methods and Protocols

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2015, XIV, 413 p. 70 illus., 42 illus. in color., Hardcover

ISBN: 978-1-4939-2012-9

A product of Humana Press