Cancer Metastasis Rev (2014) 33:835
DOI 10.1007/s10555-014-9509-1

Preface

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Published online: 28 October 2014

The development, progression, and metastasis of cancer is a multifactorial and polygenic cellular process involving coordinated interplays of regulatory gene products with roles in the nucleus, the cytoplasm, and in distinct cellular sub-compartments. The cancerous phenotypic outcome of such regulatory processes is primarily driven by epigenetic control and functional manifestation of regulatory genes, in addition to other mechanisms. Central to this process is the ability of cancer cells to sense extracellular milieu and integrate resulting signaling onto chromatin remodeling complexes which, in turn, play a fundamental role in governing gene expression. The chromatin remodeling complexes could either stimulate or repress gene transcription depending upon the functional specialization of their interacting enzymes and coregulatory factors—namely, coactivators or corepressors. Further, the process of epigenetic regulation of gene expression is regulated by signaling-dependent dynamic changes in the posttranslational modifications of these coregulators. This thematic issue of *Cancer and Metastasis Reviews* brings together the most exciting molecular facets and significance of one such family of chromatin remodelers—the metastatic tumor antigens or metastasis-tumor antigen or metastasis-associated protein (MTA) in cancer.

Since the identification of MTA1—the first discovered member of the MTA family of genes by Toh, Pen, and Nicholson on September 16, 1994—the field has witnessed a monumental growth of the roles and clinical significance of the MTA proteins in human cancer. To celebrate two decades of scientific progress and global interest in MTA proteins in cancer laboratories around the world, the journal invited original contributors and experts of MTA research and oncology thought leaders to summarize for the first dedicated volume on the MTA family of chromatin remodelers the significant advances in MTA biology in cancer medicine.

Our contributors highlight non-redundant functions of MTA proteins and how lack of colocalization of MTA proteins within the same NuRD complex might confer some degree of target specificity and, hence, functionality. Further, we discuss the underlying basis of a dual coregulatory activity of MTA1—a property not demonstrated for other MTA family members. Paramount in the activities of MTA proteins is the role played by signaling-dependent posttranslational modifications and dynamic reversal of these modifications by epigenetic enzymes and chromatin landscape. The MTA proteins contribute to the multiple cancer-relevant cellular processes, including transformation, growth, invasion, epithelial-mesenchymal transition, survival, DNA-damage response, angiogenesis, inflammation, and metastasis.

The expert reviews also provide a comprehensive status and clinical significance of MTA proteins in breast cancer; gynecological malignancies such as ovarian, endometrial, and cervical cancer; prostate cancer; non-hormonal cancer; hepatocellular carcinoma; head and neck cancer; esophageal and gastric cancer; colon cancer; non-small-cell lung cancer; osteosarcoma; and lymphomas. Because the significance of MTA-containing chromatin remodeling complexes in gene expression is not limited to cancer cells, we also summarize physiological functions of MTA proteins in normal cells and non-cancerous pathologic conditions. Our expert contributors also shed light on the potential clinical applications of MTA proteins in human cancer as well as therapeutic targeting of these regulatory proteins for the development of anticancer strategies. The editor hopes that these MTA reviews will provide the journal's readers with an update on the status of the MTA family of regulatory proteins in cancer.

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