



Epigenetic and Transcriptional Mechanisms in Gynecological Cancers Development, Progression, and Resistance to Treatment

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Message from the Guest Editor

Newer genome-wide methods have identified a group of genes and enzymes whose regulation is epigenetically altered during the disease progression. DNA methyltransferases (DNMTs) and histone deacetylases (HDACs) are one of the key enzymes mediating epigenetic regulation of gene expression. Its improper function results in DNA hypermethylation and/or histone deacetylation in gene promoter regions that is associated with a reduction or silencing of transcription. DNMT and HDAC inhibitors induce DNA demethylation and histone acetylation, respectively, leading to reactivation of silenced genes and dramatic morphological and functional changes in cancer cells. The potential reversibility of epigenetic mechanisms makes them attractive candidates for the prevention and/or treatment. Detecting the epigenetic signature specific for particular gynaecological cancers could be useful in identifying potential biomarkers for disease detection, classification, monitoring, as well as could facilitate personalized treatment.





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Message from the Editor-in-Chief

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