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Expression profiling modeling of epigenetic factors in human diseases: a leap for future diagnostic

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Epigenetic has emerged as one of the most promising areas that address some of the gaps in our current knowledge in the development of many human diseases. Epigenetic mechanisms include DNA methylation, chromatin alterations, histone modification, and microRNA. Cardiovascular diseases and cancer remain among the leading causes of mortality and morbidity worldwide. They are associated with multiple genetic and environmental factors that can only explain a small part of their variability. In the last decade, the research investigating epigenetic mechanisms in many human diseases has flourished and witnessed significant progress. It paved the way for a new era of integrated research linking the genome and the environmental changes. In this project, we examined epigenetic changes in several histone modifications and chromatin remodeling factors in cancer and cardiovascular disorders using a plethora of specific expression arrays for epigenetic factors followed by rigorous predictive modeling analysis. Our study resulted in identifying several novel epigenetic factors that regulate the process of gene expression and the possible expression pattern implicated in the two disease models used (cancer and cardiovascular disorders). These findings will establish novel epigenetic targets and paradigm that consequently will provide insights into the molecular mechanism and the interplay between genetic and epigenetic factors in these diseases. Moreover, these data will serve as a primer for new approaches that can lead to innovative therapeutic tools.

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