The epigenetic regulation plays an important role in normal development and maintenance of tissue-specific genes expression in humans, and the disturbance of these patterns leads to changes involved in tumor formation. Global epigenetic changes and genes’ promoter-specific methylation patterns have been observed in many cancer types as playing an essential role in carcinogenesis. More recently, epigenetic changes have been observed in early stages of tumor development and together with the genetic alterations have been defined as abnormalities, necessary for cancer initiation and progression.

Different cancer types not only express distinct methylation patterns but also share common epigenetic changes that are very important in early detection, progression, and prognosis as well as the design of new therapeutic tools against cancer cells.

The technology available to detect these epigenetic changes is evolving rapidly and provides more understanding of these processes in normal and cancerous cells. Several of these technologies are discussed in this book.

Recent studies identified several factors that may play a significant role in the initiation of the epigenetic changes in cancer. Some of the genetic and environmental factors that have been shown to be involved in these processes are also being discussed.

All these epigenetic alterations can be used in clinical practice as biomarkers of early cancerous lesions or markers of progression and prognosis.

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