et al.
et al. 2013). Variation in the amount of DNA methylation is associated with changes in gene expression and biological processes, including cancer progression and aging (Ballestar et al. 2005; Kouzarides 2007). DNA methylation occurs through the action of DNA methyltransferases (DNMTs), which transfer a methyl group to cytosine residues in DNA, resulting in the formation of 5-methylcytosine (5mC). This modification is essential for the regulation of gene expression, cell differentiation, and development (Bird 1986; Jones and Baylin 1998).

DNA methylation is often accompanied by histone modifications, such as acetylation, deacetylation, methylation, and demethylation, which can alter chromatin structure and gene expression (Workman and Kingston 2006). These modifications are mediated by various enzymes, including histone deacetylases (HDACs), histone acetyltransferases (HATs), histone methyltransferases (HMTs), and histone demethylases (HDMs) (Jenuwein and Allis 2001; Reinberg 2002).

In addition to epigenetic modifications, genetic mutations can also alter gene expression and lead to disease (Cancer Genome Atlas et al. 2013). Mutations in tumor suppressor genes and oncogenes can lead to uncontrolled cell proliferation and the development of cancer (Fearon and Vogelstein 1990; Hanahan and Weinberg 2011). The integration of epigenetic and genetic alterations provides a more comprehensive understanding of disease etiology and can lead to the development of new therapeutic strategies (Loda et al. 2005; Bigner et al. 2000).

Therefore, a comprehensive approach to cancer research should consider both genetic mutations and epigenetic modifications, as these alterations often work in concert to drive disease progression and resistance to therapy (Esteller 2001; Caldas 2004). The integration of these approaches has already led to the identification of new therapeutic targets and the development of more effective treatments for cancer (Jänne et al. 2013; Kufe et al. 1998).

In conclusion, the understanding of the complex interplay between genetic mutations and epigenetic modifications is crucial for the development of targeted therapies and the improvement of cancer outcomes. This knowledge has the potential to revolutionize cancer research and treatment and is essential for the future of oncology.