Abstract

Epigenetic signals comprise DNA methylation and histone tail modification (including lysine methylation). They are essential for development and involved in disease processes. After discussing some general patterns of DNA methylation observed in many species, I will present new data concerning the mechanism of DNA methylation by the Dnmt3a/3L de novo DNA methyltransferase which include its multimerisation and targeting by histone tail modifications. We developed peptide array based approaches to determine the specificity of protein lysine methyltransferases and identified several novel non-histone substrate proteins for the G9a and SET7/9 enzymes. These results contribute to the general view that protein lysine methylation is a widespread post-translational modification not restricted to histone proteins and chromatin. Finally, I will discuss the application of peptide arrays for studying the binding of reading domains and antibodies to hypermodified histone tails.