ABSTRACT

Rice (*Oryza sativa*), a member of Gramineae family, is a major crop plant that feeds almost half of the global human population. In recent years, this plant has emerged as a model system for functional genomics studies among the monocot plants. The availability of its complete genome sequence, easy transformation protocols and various mutant lines have been instrumental in unravelling the genetic and epigenetic molecular mechanisms that regulate gene expressions and various developmental pathways including reproductive development in rice. However, despite these advances, one of the important epigenetic regulators, the process of DNA methylation, has largely remained unexplored partly because of increased complexity in higher plant organization. With the view to get a clearer picture of the role of this regulatory process and to be able to understand the roles of its molecular components in modulating gene expression patterns, we selected an early land plant *Physcomitrella patens* as the second model organism for the present study. *P. patens* is a simple moss plant with fully sequenced genome. This study in the two model organisms has provided significant insight into the conservation and diversity among the methylation machinery components and their evolutionary relationships in land plants.

The objective of this Ph.D. work was to first establish conclusively the role of DNA methylation in regulating growth, development and differentiation in both, *Physcomitrella* and *O. sativa* and then to identify and characterize the core component of the DNA methylation machinery, cytosine DNA methyltransferases, in these plants. As a first step in this direction, the effect of global hypomethylation induced by cytidine analog, zebularine, on growth and development of *O. sativa* and *Physcomitrella* was examined. Thereafter, a genome-wide *in silico* study was undertaken to identify the genes encoding cytosine

methyltransferases in these plants. A comprehensive structural and phylogenetic analysis of rice and moss methyltransferase gene families was then carried out. This was followed by expression analysis of genes during different developmental stages and in response to abiotic stress conditions. Thereafter, putative functions of the genes were speculated by studying *in vivo* subcellular localization patterns of methyltransferase-GFP fusion proteins in onion epidermal cells and moss protonema cells. Finally, functional characterization of selected rice methyltransferase genes (*OsCMT2*, *OsMET1-2*, *OsDRM2*, *OsDRM3* and *OsDNMT2)* was undertaken using gene silencing and overexpression strategies.

The concise review of literature presented at the beginning of the thesis is aimed to discuss and highlight the evolutionary relatedness among the methyltransferase genes in eukaryotes and the pivotal roles played by cytosine DNA methylation in plant development. The experimental procedures used in this study and the results thus obtained have been summarized in separate sections. The new and recent findings and their relevance to the current research scenario has been discussed and significant conclusions have been drawn. References cited throughout this study and the research publications earned through this work have been compiled at the end.

This research not only enhances our understanding of the evolution and functional conservation/diversification of DNA methylation and components of the methylation machinery, but it also provides evidence for the role of methyltransferases in modulating various developmental pathways regulating growth and development in both, *O. sativa* and *Physcomitrella patens*.