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Title	Molecular identification of genes involved in histone : related epigenetic mechanisms in early land plant <i>Marchantia polymorpha</i>
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## SUMMARY

Histone is the core component of nucleosome and modification on histone tails is one of the most pivotal epigenetic regulatory mechanisms. Acetylation/deacetylation on lysine residues of histone is carried out by two groups of proteins: histone acetyltransferases (HATs) and histone deacetylases (HDACs), and proved to be tightly linked to activation of gene expression. However, the study of histone genes or genes involved histone acetylation/deacetylation in non-flowering plants has never been addressed before.

In this study, the liverworts: *Marchantia polymorpha* was used as a subject to study how histone genes and genes related to histone acetylation were involved in early land plants.

To take advantage of sequenced *Marchantia* genome information, a total of 28 histone proteins were identified in *Marchantia* genome including 8 H2A, 6 H2B, 8 H3 and 4 H4. Sequence analyses indicated that all histone proteins would be functional in *Marchantia*. A non-flowering specific amino acid substitution pattern was observed between MpH3.1 and MpH3.3 proteins, and an amino acid substitution at position of H4 was also identified between AtH4 and MpH4 proteins. Expression analyses by real-time qPCR of *Marchantia* H3 genes suggested that expression levels of two *MpH3.3* genes were significant higher than those of other H3 genes in all tested tissue samples.

8 and 12 *Marchantia* genes representing 4 HAT and 3 HDAC families, respectively, were found in *Marchantia* genome. Sequence analyses of MpHATs and MpHDACs including functional domain analyses and subcellular predication suggest that they would be functional and localized in different organelles. Phylogenetic analyses identified two new classes of RPD3/HDA1 and SIRT family HDACs that were only presented in non-flowering plants and green algae. The substantial diversification of HATs and HDACs that has occurred since the divergence of chlorophytes, bryophytes and angiosperms suggests a surprising extent of evolutionary diversification in these core chromatin components.

This thesis also provides the study of expression pattern of *Marchantia* histone acetyltransferases and histone deacetylases encoding genes. All *MpHATs* and *MpHDACs* were constitutively expressed in different tissues of *Marchantia*. Their expressions were regulated by exogenous hormones and abiotic stresses to different extent suggesting that *MpHATs* and *MpHDACs* may play important roles in plant defense responses.

Overall in this course of study, the molecular identification of histone genes and genes related to histone acetylation in early land plant, *Marchantia polymorpha* was reported and it could shed lights on the functions of histone proteins and histone acetylation in plants.