

## Evolution of cytokinin biosynthesis in land plants

Keiko Sakakibara<sup>1</sup>, Tomoaki Nishiyama<sup>2,3</sup>, Hironori Deguchi<sup>1</sup> and Mitsuyasu Hasebe<sup>3,4,5</sup>

<sup>1</sup> Department of Biological Science, Graduate School of Science, Hiroshima University, Higashi-Hiroshima, Japan

<sup>2</sup> Division of Functional Genomics, Advanced Science Research Center, Kanazawa University, Kanazawa, Japan

<sup>3</sup> Exploratory Research for Advanced Technology, Japan Science and Technology Agency

<sup>4</sup> Division of Evolutionary Biology, National Institute for Basic Biology, Okazaki, Japan

<sup>5</sup> School of Life Science, The Graduate University for Advanced Studies, Okazaki, Japan

[bara@hiroshima-u.ac.jp](mailto:bara@hiroshima-u.ac.jp)

Cytokinins are plant hormones that play important roles in the regulation of cell division and differentiation in various land plants including mosses. Their biosynthesis, receptors and signal transduction pathways have been extensively studied in flowering plants, especially in *Arabidopsis thaliana*. A key step of cytokinin biosynthesis is catalyzed by isopentenyltransferase (IPT). Two types of IPT genes, transfer RNA (tRNA) IPT genes and ATP/ADP IPT genes were identified in flowering plants. Nine IPT genes were found in *A. thaliana* genome, two of which are tRNA IPT genes (*AtIPT2* and *AtIPT9*), and the other seven are ATP/ADP IPT genes. Cytokinin biosynthesis in *A. thaliana* depends mostly on the activity of ATP/ADP IPT genes and tRNA IPT genes contribute little for the cytokinin biosynthesis.

To investigate evolutionary origin of cytokinin biosynthesis, we searched IPT genes from the whole genome shotgun sequence data of a moss *Physcomitrella patens* and a lycophyte *Selaginella moellendorffii* and inferred the phylogenetic relationships of IPT genes. Flowering plant IPT genes were divided into two groups: the plant I group contains *AtIPT9* and the plant II group contains all the other eight *AtIPT* genes. *P. patens* and *S. moellendorffii* IPT genes belong to the plant I group, but we could not find any plant II genes in neither *P. patens* nor *S. moellendorffii*. This result suggests that ATP/ADP IPT genes of plant II group have increased in the number and diverged in the flowering plant lineage, which is likely related to the evolution of complex developmental regulations.