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Evolution of developmental regulatory system in plants based on large scale phylogenetic analyses utilizing whole genome shotgun sequence data

A comparison of eumetazoan genomes revealed that their common ancestor had complex sets of genes similar to those used in extant bilateral metazoan development. In contrast, the evolution of developmental genes in another major lineage of multicellular land organisms, the land plants, has remained a mystery due to a lack of genomic data for non-flowering plants. By incorporating the accumulated genomic sequence data for the lycopod *Selaginella moellendorffii* and the moss *Physcomitrella patens*, we analysed the phylogenetic relationships of homologues of 826 *Arabidopsis thaliana* genes that function in development and identified putative orthologues to each gene. Here we show that *S. moellendorffii* and *P. patens* retain 88% and 86% of putative orthologues, respectively, including those involved in flowering plant specific development. Eighty-one percent of putative orthologues was shared in all the land plants. However, we also found flowering plant and vascular plant specific putative orthologues. Furthermore, lineage-specific expansions and contractions especially in cytoskeleton-, epigenetic gene regulation-, light signalling-, and phytohormone-related gene families were conspicuous. These data suggest that divergence in the number of putative orthologues amongst various land plant lineages contributed to the divergence of development in land plants.

Trees and alignments are available through http://moss.nibb.ac.jp/treedb and the discussion can be found at http://wiki.genomics.purdue.edu/index.php/Selaginella

CV

Education: 1991-1995, The University of Tokyo, Japan
PhD thesis: 1995-2000, Graduate School of Science, The University of Tokyo, Japan (Biological Sciences)
Postdoc: 2000-2005, National Institute for Basic biology
Assistant Professor: 2005- Kanazawa University
Group Leader: 2006- Informatics Evolution group, ERATO HASEBE Reprogramming Evolution project, Japan Science and Technology Agency

Selected publication

Sakakibara K, Nishiyama T, Deguchi H, Hasebe M. (2008)
Class 1 KNOX genes are not involved in shoot development in the moss *Physcomitrella patens* but do function in sporophyte development.
Evol Dev. 10:555-566

T. Nishiyama, et al. (2004) Chloroplast Phylogeny Indicates that Bryophytes are Monophyletic. Mol. Biol. Evol. 21:1813-1819

T. Nishiyama, et al. (2003) Comparative genomics of *Physcomitrella patens* gametophytic transcriptome and *Arabidopsis thaliana*: implication for land plant evolution. Proc. Natl. Acad. Sci. USA 100: 8007-8012

T. Nishiyama, et al. (2000) Tagged Mutagenesis and Gene-trap in the Moss, *Physcomitrella patens* by Shuttle Mutagenesis. DNA Res. 7: 9-17