

Do We Need Another Model Plant?

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Without any doubt, plant biology has profited enormously from the concentration of resources on a single model plant, *Arabidopsis thaliana*. In the eighties there were many good reasons to choose this “useful weed” (Meyerowitz, 1989), namely its relatively small genome, its rapid life cycle and its small size. Having all the highly elaborated techniques at hand now to analyse this model plant and facing an increasing public demand for applied biology, namely on crop plants, we have to ask if it is worthwhile investing public money and scientific careers into the establishment of mosses, namely *Physcomitrella patens*, as another model plant species.

It has been argued (Goldberg, 1988) that dominance of the gametophyte, i.e., haploidy of the major tissues and simplicity of the body plan are strong arguments that genetic dissection of *Physcomitrella* could make a significant contribution to understanding the evolution of plant developmental processes. And it is often overlooked that milestones of biological research like the first description of sex chromosomes in plants, the continuity of chromosomes during the mitotic cycle and non-Mendelian inheritance as well as the introduction of UV-mutagenesis to genetic research were first introduced by scientists working on bryophytes (citations in Reski, 1998). Whereas those findings were made in the first half of the last century, the most recent milestone, the discovery of efficient gene targeting by homologous recombination in *Physcomitrella* by Schaefer and Zrýd (1997) was less than ten years ago.

The whole field has advanced very quickly since then. For basic as well as for applied research several genes have been knocked-out by efficient homologous recombination. Tagged mutant populations were established as well as huge amounts of expressed sequence tags generated. We now know that *Physcomitrella* has more protein-encoding genes than *Arabidopsis*, a huge portion of them associated with secondary metabolism, and that mosses conserved genes and pathways not known from seed plants. In-depth analyses of these genes by the world-wide community will substantially add to our understanding of plant evolution and diversity.

For example, it will be fascinating to see how a haploid genome of a size more than four times bigger than that of *Arabidopsis* maintained its integrity over about 450 million years, and to analyse if highly efficient homologous recombination is one of the answers to this question. We may learn if and how this so far uniquely efficient process can be transferred

to seed plants, completely changing the way we produce, understand and use transgenic plants in the future.

This special issue of PLANT BIOLOGY celebrates the fact that a proposal from colleagues from University of California at Berkeley (USA), Washington University (USA), National Institute for Basic Biology Okazaki (Japan), Leeds University (UK), and University of Freiburg (Germany) to fully sequence the *Physcomitrella* genome was granted by the Joint Genome Institute (JGI) of the US Department of Energy. The first megabasepairs are already publicly available and the first draft of the complete moss genome will be released by the end of this year. It will be the fourth complete plant genome after *Arabidopsis*, rice and poplar, and the first sequenced genome of a non-seed plant.

Arabidopsis (dicots) and rice (monocots) are evolutionarily separated by about 100 million years, but the last common ancestor of mosses and seed plants lived about 450 million years ago. Obviously, work on mosses never can substitute work on seed plants, not only because mosses do not flower. Nevertheless, as genomics and functional genomics tools are becoming more and more powerful, it is the right time to widen our perspective and to study plant biodiversity and plant evolution in its full context. In line with this argumentation we do not simply need another model plant, but we need more resources into research on model species in the different groups of algae, in mosses, liverworts, hornworts, ferns, and in gymnosperms. These all contribute in one way or another to current plant life and we can not afford to neglect them in the future.

The arguments in favour of mosses remain nonetheless valid: Few cell types, simplicity of the tissue, and a simple body plan make them ideal candidates to combine molecular and cell biological tools to unravel basal plant developmental processes. In fact, they appear as prime candidates for a holistic approach on plant development and patterning: Moss systems biology as a long-term goal.

To date, the international moss community is less than five percent the size of the international *Arabidopsis* community, making progress often slow and painful. May this special issue of PLANT BIOLOGY convince more scientists to join in.

References

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