Plant Physiology's Best Paper Award 2000

It is always extremely difficult to select recipients for awards because invariably there are more worthy candidates than there are awards. It is fortunate that the burden of deciding between the many excellent nominees for *Plant Physiology's* first Best Paper Award was borne collectively by the Editorial Board. Based on their consensus, it is my pleasure to announce the winner of this year's Award: Dr. Thomas Girke for research he performed while a postdoctoral fellow in the laboratory of Dr. John Ohlrogge at Michigan State University. This work was published in the December 2000 issue of *Plant Physiology* (Girke et al., 2000).

Thomas, who is now doing research at Dow Agro-Sciences in San Diego, followed a nontraditional career path into plant molecular biology. He first studied nursing in Germany and worked for several years as a nurse on a psychiatric ward. After deciding to pursue a career in research, he received his PhD from the Botanisches Institut of the University of Hamburg in 1998. From his PhD research in the laboratory of Dr. Ernst Heinz, Thomas Girke also produced a landmark publication in which he demonstrated for the first time targeted gene disruption and homologous recombination resulting in a biochemical phenotype in a multicellular plant, namely the moss *Physcomi*trella patens (Girke et al., 1998). The gene disruption resulted in a dramatic alteration of the fatty acid pattern in the knockout plants. The large increase in linoleic acid and the concomitant disappearance of γ -linolenic and arachidonic acid in all knockout lines suggested that the new cDNA coded for a $\Delta 6$ desaturase. This paper has been one of the most highly cited Plant Journal papers from 1998.

Thomas's background in the molecular biology of lipid biosynthesis made him a valued member of a research effort launched in the combined laboratories of John Ohlrogge and Christoph Benning at Michigan State University. The purpose of this research initiative was to elucidate which genes in the Arabidopsis genome are expressed in seeds. Given the agricultural importance of *Brassica* seed oils (such as canola), and the fact that Arabidopsis is the leading model for dicot plant biology, it is surprising that relatively few molecular biological studies of Arabidopsis had focussed on its seeds. The contribution of Girke et al. (2000) goes a long way in filling the gaps in our knowledge concerning the molecular biology of Arabidopsis seeds.

With the advent of the genomics revolution, biologists are moving away from the study of a single or a few genes to much more encompassing investigations. Microarrays are one of several new tools that provide a less myopic examination of gene activity. Our understanding of 25,000 Arabidopsis genes should include information on the tissues in which each gene is expressed. Such information, coupled with analysis of gene expression under different physiological conditions and in mutants, reveals the modus operandi for each gene, and this will eventually lead to a better description of the gene's function. To learn more about which Arabidopsis genes are expressed specifically in seeds, White et al. (2000) sequenced 11,000 expressed sequence tags from a developing seed cDNA library. The unique clones selected from this set of expressed sequence tags became the basis of the microarrays discussed by Girke et al. (2000). In this paper, Thomas and his colleagues provide many fascinating insights concerning metabolic routes for the conversion of photosynthate into oil in developing Arabidopsis seeds. The paper carries enormous mechanistic information and the authors barely touched upon them all. Many scientists undoubtedly will continue to mine the data provided in this paper.

Given Thomas's famous wanderlust—he has traveled extensively through Asia and other parts of the world, including a trek to the bottom of the Grand Canyon and back in one day—we feel certain that he can put the award money to good use. Congratulations, Thomas!

LITERATURE CITED

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Natasha V. Raikhel Editor-in-Chief of *Plant Physiology*