

*Arabidopsis* but not the Columbia version. The researchers mapped the feeding phenotype and identified a new quantitative trait locus: TASTY. Unexpectedly, the susceptible strain had increased glucosinolate content and myrosinase activity, both of which scientists consider to be involved in insect defense. The group also found no relation between TASTY and other traits known to affect insect feeding, such as trichome density, flowering time and leaf surface wax. *TS*

## Plant biotechnology gets the internet treatment

What are biotechnology and genetic engineering? How do you make a GMO? What kinds of GMOs are already on the market? The answers to these – and many other – questions can be found on a new web site that is devoted to providing ‘trustworthy and up-to-date information on agricultural biotechnology and thereby to contribute to an open debate’ [www.checkbiotech.org]. Among the facilities offered by the site is a free electronic newsletter that can be delivered to subscribers on a daily or weekly basis via e-mail. Although it is independently operated, the site is sponsored by Syngenta, one of the world’s leading agribusinesses [www.syngenta.com]. *NC*

Comment

## Do plants have more genes than humans? Yes, when it comes to ABC proteins

Joachim Messing in his recent ‘Comment’<sup>1</sup> discussed the remarkable similarity in gene count between the human<sup>2,3</sup> and *Arabidopsis thaliana* genomes<sup>4</sup>. No one knows why the number of open-reading-frames (ORFs) in the *Arabidopsis* genome (25 500)<sup>4</sup> is only slightly less than that estimated for the human genome (31 500)<sup>2,3</sup> – specifically, how humans can get by with so few genes – but we can answer Messing’s opening question ‘Do plants have more genes than humans?’ in the affirmative in at least some cases. The ATP-binding cassette (ABC) proteins are a case in point, many of which are

## Cash boost to land reclamation

In collaboration with European colleagues, a team at the University of Southampton (UK) has recently received £100 000 for a three-year study to identify the genes that enable certain plants to accumulate and tolerate toxic metals. Although several plants have the ability to tolerate high levels of metals such as nickel and cadmium, they are generally small and slow growing. Identifying the genes involved in metal tolerance should lead to the development of larger, faster-growing ‘super’ plants, with the ultimate goal of using them to clean-up some of the estimated 4 million ha of European land that is contaminated by harmful heavy metals. [http://www.soton.ac.uk/~pubaffrs/0163.htm] *NC*

## China’s entry into GM

China will increase efforts to develop GM crops for commercial purposes according to Xu Guanhua, minister of the Ministry of Science and Technology (MOST) at a press conference on 30 May 2001. Although farmers cultivated >40 million hectares of genetically engineered crops worldwide in 1999, in China, the government approved only one transgenic variety of pest-resistant cotton for commercial purposes.

There are many examples of promising GM products still in the experimental stages in Chinese laboratories, including pest and disease resistance in rice, potatoes and maize. (*Financial Times Information*, 31 May 2001) *TS*

## Plight of the bumblebee

Many important crops – not to mention more humble plants – rely on insects to pollinate them and ensure the arrival of the next generation. Thus, any decline in insect numbers has attendant ecological and economic problems. This is a particular problem for bumblebees in the UK, whose numbers have declined over the past 50 years, largely because of changes in farming methods. Using DNA-marking techniques, Dave Goulson of the University of Southampton (UK) will study bumblebees and assess which land-management practices result in increases in their numbers. Hopefully, such information will help to prevent further decline in this important pollination agent. [http://www.soton.ac.uk/~pubaffrs/0161.htm] *NC*

**Nigel Chaffey**  
nigel.chaffey@bbsrc.ac.uk

**Trevor Stokes**  
tstokes@artsci.wustl.edu

modularly constructed membrane proteins containing idiotypic nucleotide-binding folds (NBFs). By compiling the first complete inventory of the ABC protein superfamily from *Arabidopsis*<sup>5</sup> (http://www.arabidopsisabc.net) – the first complete inventory of ABC proteins from any multicellular organism – we have determined that the genome of this plant encodes 129 ABC proteins, which fall into 13 subfamilies (Fig. 1). This gene count far outstrips those for the human genome and for any other animal genome sequenced to date. The human genome is estimated to encode a mere 51 ABC proteins (http://www.humanabc.org); those of *Caenorhabditis elegans* (19 000 ORFs; http://www.proteome.com/databases/WormPD/WormPDsearch-long.html) and *Drosophila melanogaster* (13 600 ORFs; http://flybase.bio.indiana.edu) only 58 and 55, respectively.

The results from *Arabidopsis* are equally impressive when viewed in another way – through the transport physiologist’s eye. Of the total ABC protein ORFs identified in *Arabidopsis*, ~103 probably encode membrane transporters – proteins possessing membrane spans contiguous with one or two NBFs (Ref. 5 and http://www.arabidopsisabc.net) Taking this into account, when the rough equivalence of the total transporter gene complement of *Arabidopsis* (700 ORFs) is compared with those of animals such as *C. elegans* (650 ORFs) and *Drosophila* (600 ORFs)<sup>4</sup>, it is evident that *Arabidopsis* allocates nearly twice as many of its transporter genes to ABC transporters as do *C. elegans* or *Drosophila*.

The forces, evolutionary or otherwise, responsible for the disproportionate

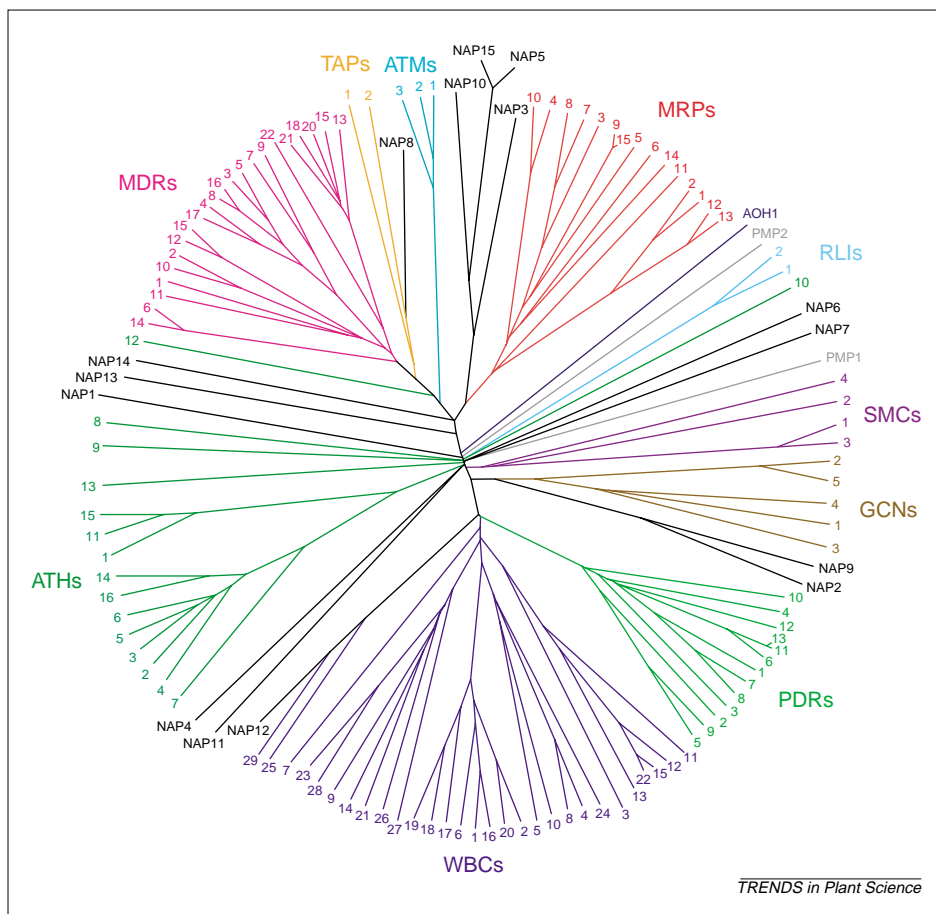


Fig. 1. Phylogeny of *Arabidopsis* ABC proteins. The 13 subfamilies identified are shown in different colors. These are four subfamilies of full-molecule transporters (the MDRs, MRPs, PDRs and AOH), five subfamilies of half-molecule transporters (the WBCs, ATHs, ATMs, TAPs and PMPs) and four subfamilies of proteins lacking transmembrane spans (the RLIs, GCNs, SMCs and NAPs) (see Ref. 5 for further details).

allocation of coding sequences to ABC proteins – and of the total transporter gene complement to ABC transporters – in *Arabidopsis*, and presumably other plants, can only be speculated. However, given the inherently greater capacity of transporters, such as ABC transporters, which are directly energized by ATP, versus  $H^+$ -coupled secondary transporters, for establishing steep concentration gradients across membranes under the conditions that prevail *in vivo*<sup>6</sup> and the fact that most characterized eukaryotic ABC transporters (albeit a small fraction of those that are now known to exist) have been implicated in the transport of secondary metabolites, organic xenobiotics and other complex amphiphiles<sup>6,7</sup>, several factors come to mind. Most notable of these is the extraordinary metabolic versatility of plants. More than 100 000 secondary metabolites have been identified in plants<sup>4</sup>, most of which would be toxic to

the cells that produce them, even at pharmacological concentrations, if they were not transported across membranes out of the compartments in which they are synthesized against steep concentration gradients<sup>6,7</sup>. Furthermore, although the capacity of green plants for photosynthesis greatly augments their metabolic versatility, this process and its photo-oxidative consequences, places even greater demands on the cellular detoxification machinery. As if this were not enough to contend with, plants not only manufacture their own secondary products but also have to suffer those of other organisms, for example allelochemicals and microbial metabolites and chemicals associated with humans and their various environmentally destructive activities. In combination, all these factors, plus the sessile lifestyle of plants – their inability to exercise speedy avoidance behaviors – and their frequent lack of specialized excretory structures, necessitate cellular detoxification

mechanisms of exquisite range and sophistication.

It is probably no coincidence that members of another gene superfamily implicated in secondary metabolism and xenobiotic detoxification, the cytochromes P450, are also disproportionately represented in plants compared with animals. The *Arabidopsis* genome encodes 286 putative cytochromes P450 (Ref. 4), three- to fourfold more than the numbers predicted from the genome sequences of *C. elegans* (73 ORFs) and *Drosophila* (94 ORFs).

Gene and protein head counts are not an end in themselves but instead constitute component toolboxes for meaningful functional analyses and intraorganismal and interorganismal comparisons. This is especially true of the *Arabidopsis* ABC protein superfamily. The amenability of *Arabidopsis* to transcriptomic, proteomic and reverse genetic approaches, combined with its possession of such an extended and hierarchical family of ABC proteins, will probably lead to completely new insights into the mechanistic basis of a wide range of processes.

Rocío Sánchez-Fernández

Philip A. Rea\*

Plant Science Institute, Dept of Biology,  
University of Pennsylvania, Philadelphia,  
PA 19104, USA.

T.G. Emyr Davies

Julian O.D. Coleman

IACR-Rothamsted, Harpenden,  
Hertfordshire, UK AL5 2JQ.

\*e-mail: parea@sas.upenn.edu

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