The ATP-Binding Cassette Transporters: Structure, Function, and Gene Family Comparison between Rice and Arabidopsis

Michal Jasinski, Eric Ducos, Enrico Martinoia, and Marc Boutry*

Unité de Biochimie Physiologique, Institut des Sciences de la Vie, Université catholique de Louvain, Croix du Sud 2–20, B–1348 Louvain-la-Neuve, Belgium (M.J., E.D., M.B.); and Laboratory of Molecular Plant Physiology, Institute of Plant Biology, Zurich University, CH–8008 Zurich, Switzerland (M.J., E.M.)

Cells are separated from their external environment by a membrane barrier, which ensures that certain ions, metabolic intermediates, and macromolecules, such as proteins, remain within the cell. However, life is not possible without the exchange of material and information with the external environment. Therefore, during evolution, efficient transport systems have been developed to allow interaction with the environment, and they ensure that essential ions and metabolites enter the cell and other compounds leave it.

Many molecules are transported against a concentration gradient, requiring the use of energy. For several transport systems, this energy is directly provided by ATP hydrolysis. Well known examples of ATP-powered transport systems are cation pumps, such as the Ca\textsuperscript{2+}/H\textsuperscript{+}, H\textsuperscript{+}/H\textsuperscript{+}, Na\textsuperscript{+}/H\textsuperscript{+}, and H\textsuperscript{+}/K\textsuperscript{+}/H\textsuperscript{+}-ATPases. The ATP-binding cassette (ABC) transporters, which constitute another major class of ATP-powered transporters, are less well characterized, and the physiological function of many is still unknown.

Here, we will review the structure and catalytic mechanism of these enzymes, tackle their mysterious capacity to transport a variety of substrates with unrelated structures, compare the Arabidopsis and rice (Oryza sativa subsp. japonica) gene family composition, and finish by mentioning examples of the physiological roles of ABC transporters in plants. Some of these topics have been reviewed in detail (Theodoulou, 2000; Sanchez-Fernandez et al., 2001; Martinoia et al., 2002; Rea et al., 2002).

STRUCTURAL CHARACTERISTICS OF ABC TRANSPORTERS

The ABC transporter family is very large (79 members in Escherichia coli, 29 in Saccharomyces cerevisiae, and 131 in Arabidopsis) and its members are found in all organisms. The encoded enzymes couple ATP hydrolysis to the transport, across various membranes, of a great variety of substrates, including lipids, heavy metal ions, inorganic acids, glutathione conjugates, sugars, amino acids, peptides, secondary metabolites, and xenomolecules, used as drugs (Higgins, 1992; Rea et al., 1998).

The ABC genes have been divided into several clusters or subfamilies corresponding to phylogenetic pathways and structural features. The names used to define the subfamilies are often historic and related to the function of drug resistance, although some members are clearly not involved in drug transport and may, for example, function as a channel or channel regulator. The three best characterized subfamilies are the pleiotropic drug resistance (PDR), multidrug resistance (MDR), and multidrug resistance-associated protein (MRP) subfamilies.

MOTIFS AND DOMAINS

ABC proteins have a characteristic modular structure consisting of a double set of two basic structural elements, a hydrophobic transmembrane domain (TMD) usually made of six membrane-spanning α-helices, and a cytosolic domain, the latter containing a region involved in ATP binding and known as the nucleotide-binding domain (NBD; for review, see Higgins, 1992).

Although most prokaryotic ABC proteins are encoded as separate TMD and NBD subunits or as one-half-size (one TMD and one NBD) transporters, in the majority of eukaryotic ABC transporters, all four domains (two TMDs and two NBDs) are contiguous on a single polypeptide, constituting a full-length transporter in the “forward” TMD1-NBD1-TMD2-NBD2 orientation in the MDR subfamily or the “reverse” NBD1-TMD1-NBD2-TMD2 orientation in the PDR subfamily (Fig. 1A). In the MRP subfamilies...
ily, the arrangement is in the forward orientation, but some MRPs (e.g. MRP1) have five α helices (sometimes designated as TMD0) at the N terminus.

THE THREE-DIMENSIONAL STRUCTURE

Deciphering the molecular mechanism of the coupling between ATP hydrolysis and substrate transport represents a major challenge requiring the solution of the protein atomic structure. Despite the tremendous problems involved in the crystallization and x-ray analysis of membrane proteins, several recent successes have been reported. The structure of several NBDs has been determined in bacterial ABC transporters as, in this case, these soluble subunits are synthesized independently from the membrane subunits and are thus more amenable to crystallization and x-ray diffraction analysis.

A high-resolution structure of two E. coli entire ABC transporters has been determined: MsbA (Chang and Roth, 2001) and BtuCD (Locher et al., 2002) involved in lipid and vitamin B12 transport, respectively. There are some discrepancies between these structures, as well as between the structures obtained for soluble NBDs. For instance, although there is a consensus for the structure of a single NBD, there are divergences concerning the interactions between a pair of NBDs. These are largely separated in MsbA and are closely interacting in BtuCD. This might be related to a crystallization artifact joining together two one-half-size transporters in a non-native conformation. Alternatively, these two conformations might represent two different states of the catalytic cycle. The BtuCD model shows that a single NBD does not constitute an independent functional structure by itself, but that both NBDs interact, with the ABC signature of one NBD interacting with the other motifs from the other NBD to constitute an ATP-binding site. Thus, there are two ATP-binding sites lying at the interface between the two NBD subunits. A similar interaction was found in Rad50, an enzyme involved in DNA repair and sharing a common ancestor with ABC NBDs (Hopfner et al., 2000). In contrast to the BtuCD study, Rad50 was crystallized in the presence of ATP. Comparison of the two structures suggests that ATP binding induces a closer interaction of the signature motif of one NBD with the other NBD. This proposed interaction is also in agreement with older biochemical observations reporting cooperativity of ATP binding and hydrolysis. A recent 22 Å projection structure of the mouse

Figure 1. Topology and putative catalytic mechanism of ABC transporters. A, Topology. The TMD, with the predicted membrane spans (zig-zag), and the NBD, containing the nucleotide binding fold, are shown for the three main types of full-size ABC transporters. B, Putative catalytic mechanism. The figures schematize an ABC transporter with its four domains, two of which (TMDs) are embedded in the membrane. A substrate (S) coming from the cytosol or already within the membrane binds to a substrate binding site in one of the TMDs (this site has not yet been localized precisely and might, as a matter of fact, be one among several binding sites) (I→II). This is followed by ATP (T) binding to the nucleotide-binding site localized at the interface between both NBDs (note that only one of the two nucleotide binding sites is represented) (II→III). ATP binding and hydrolysis is accompanied by a structural rearrangement that allows the substrate to access to, and to be translocated through, a membrane path (III→IV). Upon ADP (D) and phosphate dissociation, the protein returns to the initial state (IV→I). This still putative model is based on that proposed for the bacterial BtuCD (Locher et al., 2002) except for the substrate path, which is inverted. Alternatively, the central cavity might represent the substrate-binding site (discussed in the text).
P-glycoprotein, an MDR-type ABC transporter, confirmed the close association between the two NBDs (Lee et al., 2002).

Because of the large structural variety of substrates transported by ABC carriers, the membrane domains, which are involved in substrate binding and translocation, are poorly conserved at the primary structural level and are expected to differ markedly at the three-dimensional level. In the E. coli BtuCD and MsbA structures mentioned above, a large central cavity was found between the two TMDs within the membrane; this is lined with hydrophobic residues, has two openings toward the membrane, and might represent the translocation pathway (Locher et al., 2002).

The BtuCD structure and others, as well as many biochemical data, provide some clues about the catalytic cycle. The following succession of events can be proposed (Fig. 1B). The transported substrate, coming from the cytosol if it is hydrophilic or directly from the inner membrane leaflet if it is hydrophobic or amphiphilic, binds to a site in the membrane domain. This promotes the binding of ATP at the NBD site. ATP hydrolysis (and possibly ATP binding) is accompanied by a structural rearrangement of the NBD that extends to the membrane domains and induces translocation of the substrate through the inner path toward the other face of the membrane. Finally, the transporter returns to its initial configuration upon ADP and phosphate dissociation.

MULTISUBSTRATE TRANSPORTERS

One surprising observation regarding ABC transporters was the wide range of structurally and functionally unrelated compounds that are transported, raising the question of how a single protein can bind and transport such a remarkably diverse collection of substrates. The modular construction of ABC transporters and the presence of two homologous TMD-NBD units raise the possibility that each can contribute to the binding and transport of different classes of compounds. Such a conclusion was drawn from transport kinetic data. For instance, Arabidopsis AtMRP2 and AtMRP3 can simultaneously transport endogenous substrates, such as chlorophyll catabolites, and a model glutathionated compound, S-(2, 4-dinitrophenyl) glutathione, neither of which interferes with the transport of the other (Lu et al., 1998; Tommasini et al., 1998). However, detailed studies of AtMRP2 transport multispecificity, using the above-mentioned chlorophyll catabolites and S-(2, 4-dinitrophenyl) glutathione, together with other substrates for plant MRPs, such as glucuronide 17β-estradiol, glutathionated metolachlor, and glutathione, showed more complex relationships at the binding site and transport levels that were difficult to explain on the basis of only two binding sites, leading to the proposal that AtMRP2 has several substrate binding sites (Klein et al., 1998; Liu et al., 2001).

For some mammalian ABCs, binding sites for drugs have been proposed on the membrane-spanning domains. Many drug substrates of multidrug transporters are lipophilic or amphiphilic molecules. On the basis of their preferential partitioning in the membrane, it has been proposed that some drugs directly access ABC transporters within the membrane bilayer.

Neyfakh (2002) recently proposed that the large membrane chamber mentioned above might actually contain multisubstrate binding sites. Substrates would establish a number of van der Waal’s interactions with surrounding hydrophobic residues. The size of the binding pocket is large enough to accommodate different substrates interacting with different residues forming the pocket walls. Considering the fact that most of the ABC transporter substrates are not genuinely hydrophobic and do possess polar, besides hydrophobic, functionalities, Neyfakh (2002) proposes that these molecules can interact with a few charged and polar residues located within the walls of the membrane cavity. The major interest of this hypothesis is that it gives a simple explanation for the multiple structurally dissimilar substrates of ABC transporters. Clearly, molecular information about substrate binding and transport must await the detailed three-dimensional structure determination of several ABC transporters. This should uncover a common mechanism for the coupling of ATP hydrolysis and substrate translocation. In addition, the determination of the three-dimensional structure of ABC translocators crystallized with their substrates, together with site-directed mutagenesis, should unravel the mystery of multiple substrates.

THE PLANT ABC GENE FAMILY

Several transporters have been characterized in plants and, in some cases, their physiological roles have been identified. However, the great majority of plant ABC transporters remain uncharacterized. The Arabidopsis ABC gene family alone contains 131 members, including 54 full-size transporters (consisting of two hydrophobic and two hydrophilic domains; Sanchez-Fernandez et al., 2001; Martinoa et al., 2002) and, therefore, it is still too early to draw a general picture of their roles. It might turn out that the diversity of their roles equates with the size of the gene family. The recent sequencing of 93% of the rice genome (Goff et al., 2002) has allowed us to retrieve putative ABC genes and to analyze how the ABC gene family has evolved since monocots and dicots diverged. We limited this analysis to the full-size transporters, for which biochemical and physiologica data are available.

We identified 45 rice sequences that putatively encode full-size ABC transporters. As in Arabidopsis, almost all of these (44) belong to the three main PDR, MDR, and MRP subfamilies. We also found one gene
homolog to PXA/PDE/CTS (Zolman et al., 2001; Footitt et al., 2002; Hayashi et al., 2002). We did not find any rice sequence homologous to AtAOH1, the unique Arabidopsis representative of the so-called ABC1 subfamily, which is highly represented in the human genome.

To simplify the comparison, phylogenetic trees were obtained separately for the PDR, MDR, and MRP subfamilies (Fig. 2). It is clear that most of the rice ABC genes identified have at least one Arabidopsis homolog with which they share more than 60% amino acid identity. This is reflected by the observation that Arabidopsis and rice genes are found together in many branches within a subfamily. Furthermore, some of the exceptions might disappear when the sequence of the remaining 7% of the rice genome is deciphered. Therefore, we can conclude that the overall organization of the full-size ABC genes is similar in Arabidopsis and rice and thus predates the separation between monocots and dicots. However, because there are rice branches in which no Arabidopsis gene was found, we have to consider that, in some branches, rice or Arabidopsis genes have been lost during evolution.

On the other hand, inspection of the various branches within each subfamily shows that the number of genes within a subfamily branch is not the same for both species, indicating that gene duplication or deletion occurred after monocots and dicots diverged. For instance, five rice genes were identified in the branch in which the single AtPDR9 is found, whereas only one rice MRP gene was found in the same branch as the four Arabidopsis genes AtMRP1, 2, 12, and 13. In the absence of any biochemical data on most of these genes and their encoded products, the reason for this asymmetry is not clear. A larger number of genes might lead to enzymes with more specialized functions related to species evolution or simply to a higher expression level. It could also be that a single gene with a broad expression is replaced with multiple genes in the rice genome.

**Figure 2.** Phylogenetic trees showing the predicted relationships between plant MDR, MRP, or PDR ABC transporters. CLUSTAL W 1.82 (Thompson et al., 1994) was used to align full-length ABC transporters sequences belonging to the MDR, MRP, or PDR subfamilies. Distance matrix, bootstrap values (1,000 replicates) and phylogenetic trees were calculated with CLUSTAL W. Accession numbers of the ABC transporters sequences from rice are reported in Table I. MDR and MRP Arabidopsis sequences were recovered according to the NCBI accession numbers described by Sanchez-Fernandez et al. (2001). PDR sequences are named as described by Martinoia et al. (2002), offering a more exhaustive list. Accession numbers BAB85651, BAB62040, AAF23176, AAD10836, CAA71179, CAA94437, CAC40990, and BAB92011, correspond, respectively, to the proteins TaMDR1 (wheat, *Triticum aestivum*), CjMDR1 (Coptis japonica), OsMDR1 (Oryza sativa), OsMRP1 (rice, *Oryza sativa*), and OsPDR1 (rice, *Oryza sativa*). Arabidopsis (At) ABC transporters are in green, Rice (Os) ABC transporters are in red, and other species and bootstrap values are in black.
by several genes, each having a more restricted expression or a tighter regulation at the transcriptional or posttranscriptional level. This kind of evolution is expected to provide the plant with more flexibility. For instance, the plant kingdom is characterized by a large diversity in secondary metabolite production. Therefore, adapted transporters might have been required to transfer these metabolites into the external medium or the adequate internal compartment.

It is interesting to note that in some branches, rice and Arabidopsis homologs are very closely related (e.g., 78% identity between AtMDR14 with OsMDR10), whereas this is not the case in other branches (e.g., 57.4% identity between AtMDR22 and OsMDR17). It is tempting to speculate that the highly conserved homologs are required for basic functions that have to be fulfilled in both plants, whereas the more distantly related homologs might have evolved more rapidly and adapt to plant specialization. For instance, AtMDR11 mentioned above is proposed to be involved in auxin transport, which might be considered as an essential function. The high identity shared with the rice OsMDR11 and OsMDR12 is in the same range as that observed between rice and Arabidopsis genes encoding plasma membrane H\(^+\)-ATPases, which belong to a highly functionally conserved transporter family (Arango et al., 2002).

Generally, intron organization confirms the general subdivision within each tree (see “Supplementary Material”). For instance, MDR genes cluster into two main subdivisions: OsMDR3 to OsMDR9, all closely related, and OsMDR10 to OsMDR16, more distant among themselves. OsMDR1 and OsMDR2, on the one hand, and OsMDR17, on the other hand, are more individualized. In the MRP subfamily, OsMRP1 singles out by still possessing 26 introns, whereas all the other OsMRPs have no more than 12 introns. The other genes are divided into two clusters with OsMRP2 to OsMRP7, on the one hand, and OsMRP8 to OsMRP11, on the other hand. Finally, the PDR tree is too compact and the intron organization is too conserved to clearly identify clusters. In agreement with this, the PDR subfamily is that for which the highest global identity was found.

FUNCTIONS OF PLANT ABC TRANSPORTERS

Compared with our extensive knowledge of the organization and sequences of the ABC gene family, functional data are still sketchy. Multiple functions, such as MDR, described for ABC transporters in other taxa, triggered research into plant homologs. Possible roles, such as cross-resistance to toxic compounds, including herbicides, have been postulated for plant ABC proteins. Two main events started the plant ABC odyssey, these being the cloning and characterization of Arabidopsis AtPGP1 encoding a homolog of human MDR1 and MDR3 (Dudler and Herzig, 1992), and biochemical studies on the uptake of a glutathione S-conjugate into barley vacuoles associated with an ABC transporter (Martinoia et al., 1993). Since then, rapid progress in the identification and characterization of plant ABC transporter genes has resulted in the discovery of a large diversity of functions for the plant ABC family (for review, see Rea et al., 1998, 2002; Rea, 1999; Davies and Coleman, 2000; Theodoulou, 2000; Sanchez-Fernandez et al., 2001; Martinoia et al., 2002). Several examples of characterized plant MDR-, MRP-, and PDR-type ABC transporters are described below.

THE MDR SUBFAMILY

Genome sequencing revealed 22 MDR-like genes in Arabidopsis (Sanchez-Fernandez et al., 2001) and 17 in rice (Fig. 2). At this point, it is worth mentioning that because they show sequence homology with human MDR1, all ABC-type proteins are described as MDRs, despite the fact that, in several cases, their physiological role might be unrelated to drug resistance. This is, for instance, the case for STE6 from Saccharomyces cerevisiae, which codes for a transporter of the sex pheromone peptide (Kuchler et al., 1989).

One of the two MDR clusters mentioned above contains 17 closely related genes (\(\geq\)54.1 identity), eight from Arabidopsis, seven from rice, and two from other species: CjMDR1, which was isolated from alkaloid-producing cultured cells of Coptis japonica (Yazaki et al., 2001), and TaMDR1, which is induced in wheat root apices by aluminum (Sasaki et al., 2002). The other cluster contains more divergent MDRs, including some isoforms that seem to be species specific, because no close homolog was found in the other species (i.e. OsMDR15 and OsMDR16).

Except for the Arabidopsis AtPGP1 gene mentioned above, few MDRs have been characterized in detail at the functional level. AtPGP1 is expressed in several plant organs, including the apical regions of shoots and roots, and it has been suggested that AtPGP1 might export a signal (peptide hormone) from the shoot apical region. In situ immunofluorescence and subcellular fractionation methods have shown that AtPGP1 is localized in the plasma membrane. It has been suggested to be involved in hypocotyl cell elongation (Sidler et al., 1998).

AtPGP1 (called AtMDR1 in Sanchez-Fernandez et al., 2001 and in this paper) is the closest homolog to AtMDR1 (called AtMDR11 in Sanchez-Fernandez et al., 2001 and in this paper). Interestingly, Noh et al. (2001) observed epinastic cotyledons with AtMDR1 knockout plants. Double AtPGP1 and AtMDR1 knockouts exhibit a more pronounced phenotype, with a dwarf phenotype and twisted leaves. These authors proposed that AtMDR1, probably in conjunction with AtPGP1, is required for the transport of auxin from the apical meristematic regions, where auxin synthesis takes place, to basal tissues.
THE MRP SUBFAMILY

This subfamily was originally identified in drug-resistant human lung cancer cell lines (MRP1; Cole et al., 1992). MRPs are able to transport glutathione and glucuronide conjugated to toxic compounds out of the cytosol and have been studied in yeast, in which YCF1 has been shown to be a vacuolar glutathione conjugate pump conferring cadmium resistance (Szczypka et al., 1994; Li et al., 1996). Finally, the observation of the uptake of glutathione S-conjugates of N-ethylmaleimide and metolachlor into barley vacuoles (Martinoia et al., 1993) triggered the identification of plant MRPs. In Arabidopsis and in rice, 15 and 12 MRP genes, respectively, have been identified. In contrast to MDR transporters, MRPs are defined by a hydrophobic N-terminal extension. Biochemical studies of the transport properties of AtMRP1, AtMRP2, and AtMRP3 provided evidence for their role in the export from the cytosol of exogenous or endogenous compounds (Lu et al., 1997; Lu et al., 1998; Tommasini et al., 1998). To date, vacuolar localization has only been demonstrated for AtMRP2. During the cellular detoxification process, potentially toxic compounds are modified and transformed in more hydrophilic compounds by conjugation to glutathione, Glc, glucuronide, or malonyl moieties (Kreuz et al., 1996) and transported into the vacuole by plant MRPs (Martinoia et al., 2000).

Although AtMRP1, AtMRP2, and AtMRP3 are all glutathione conjugate transporters, AtMRP2 and AtMRP3 can also transport chlorophyll catabolites, whereas AtMRP1, the closest homolog of AtMRP2, cannot (Lu et al., 1998). This clearly suggests that intraspecies and a fortiori interspecies sequence homology is not necessarily linked to the identical function.

In animals, some ABC proteins have channel activity or regulate heterologous channels. This is the case for the cystic fibrosis transmembrane conductance regulator and the sulfonylurea receptor. Studies on ion flux in guard cells using ion channel regulators that alter ion conductance, e.g. glibenclamide, suggested the presence in plants of cystic fibrosis transmembrane conductance regulator- or/and sulfonylurea receptor-like proteins involved in stomata movement (Leonhardt et al., 1997, 1999). Recently, AtMRP5, expressed in the vascular bundle and epidermis, especially in guard cells, has been suggested to function as an ion channel regulator (Gaedeke et al., 2001) because in contrast to wild-type plants, stomata in a knockout AtMRP5 mutant did not open upon glibenclamide addition.

THE PDR SUBFAMILY

Starting from the observation of drug resistance in the yeast, *S. cerevisiae*, another ABC transporter subfamily was identified and designated as PDR. The yeast *PDR5* gene was originally isolated as coding for a transporter mediating resistance to cycloheximide (Balzi et al., 1994), but *PDR5* has now been shown to mediate resistance to a wide range of structurally and functionally unrelated compounds (Kolaczkowski et al., 1996) and is considered a functional homolog of human *MDR1*, despite the structural differences (Fig.
1). The Arabidopsis and rice genomes contain 15 PDR-like genes (Fig. 2). Compared with the other two subfamilies, the PDR subfamily displays the least divergence.

None of the Arabidopsis PDR genes has been characterized in detail. However, data from other plant species are available. Smart and Fleming (1996) isolated a homolog of yeast PDR5, designated as TUR2, from the aquatic plant, great duckweed (Spirodela polyrhiza). The SpTUR2 transcript is up-regulated by abscisic acid and by environmental stresses, including low temperature, high salt, or cycloheximide. Another member of this subfamily, NpABC1, has been identified in wild tobacco. In vitro and in situ immunodetection showed NpABC1 to be localized in the plasma membrane. NpABC1 is expressed in the leaf epidermis. In leaf tissues and in cell culture, its expression is strongly enhanced by scclareol, an antifungal diterpene produced at the leaf surface of Nicotiana species, and, in parallel with NpABC1 induction, cells acquire the ability to excrete a labeled scclareol analog. These data suggest that NpABC1 is involved in the secretion of secondary metabolites that play a role in plant defense (Jasinski et al., 2001). Recently, SpTUR2, mentioned above, was shown to confer resistance to scclareol in Arabidopsis; however, resistance was not extended to other drugs tested (van den Brüle et al., 2002). This led the authors to suggest that in contrast to the fungal PDR transporters, which are characterized by a large substrate spectrum, plant PDR transporters might have a much higher substrate specificity.

Recently, another member of the PDR subfamily, NtPDR1 from cultivated tobacco, has been identified and its expression shown to be induced by various microbial elicitors (Sasabe et al., 2002), which is further support for the idea that some PDR genes might be involved in plant defense. In the same branch as NpABC1, NtPDR1, and SpTUR2, a single Arabidopsis gene, AtPDR9, and five rice genes have been identified (Fig. 2).

OTHER SUBFAMILIES

Several other subfamilies of ABC transporters have been identified in Arabidopsis (described in detail in Sanchez-Fernandez et al., 2001). One-half-size ABC transporters with a single TMD-NBD module are as numerous as the full-size transporters (two TMD-NBD modules). Among these, a large group (29 members) of WBC-type transporters has been identified by homology with the White, Scarlet, and Brown ABC transporters from Drosophila, which transport pigment precursors (Sanchez-Fernandez et al., 2001). However, these are currently poorly characterized, except for Arabidopsis STA1, which is localized in mitochondria, is involved in the maturation of cytosolic Fe/S proteins, and represents a functional ortholog of yeast Atm1p (Kushnir et al., 2001).

Finally, 26 putative soluble ABC proteins containing one or two NBDs, but no TMD, have been predicted in Arabidopsis (Sanchez-Fernandez et al., 2001) and are expected to work in association with other proteins. Only one has been studied, AtABC1, which is a plastid protein with a single NBD. Disruption of the gene results in reduced responsiveness to far-red light and the accumulation of protoporphyrin IX, suggesting that AtABC1 transports this precursor and is involved in intercompartmental communication of light signaling (Moller et al., 2001).

CONCLUSION

Because of the large variety of substrates translocated and, as a consequence, their multiple physiological roles, ABC transporters have been at the center of interest for many years. Major questions for the future concern their structure-function relationships, which will require the elucidation of their three-dimensional structures and multisubstrate binding properties and of the membrane transport pathway.

Although the general organization of the ABC gene family is conserved between rice and Arabidopsis, there are differences at a more detailed level. In the phylogenetic tree, some branches are specific to or more subdivided in either species, possible related to functional specialization. Therefore, this observation...
shows the interest to combine experimental approaches on several species.

The prediction of a large number of ABC proteins in Arabidopsis and in rice, the largest number reported to date, implies the versatility of these enzymes and their importance in plants. Being immobile, plants have been forced to develop a sophisticated enzymatic machinery to cope with the environment, and the ABCs appear to be an important part of this machinery. In contrast to the situation in other organisms, studies of plant ABC proteins are still at an early stage, and new information on members of the plant ABC family is impatiently awaited.

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