Higher plant plastids and cyanobacteria have folate carriers related to those of trypanosomatids*

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Running Title: FBT Family Transporters

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Cyanobacterial and plant genomes encode proteins with some similarity to the folate and bioppterin transporters (FBTs) of the trypanosomatid parasite *Leishmania*. The Synechocystis slr0642 gene product and its closest Arabidopsis homolog, the At2g32040 gene product, are representative examples. Both have twelve probable transmembrane domains, and the At2g-32040 protein has a predicted chloroplast transit peptide. When expressed in *Escherichia coli* pabA pabB or folE mutants that are unable to produce or take up folates, the slr0642 protein and a modified At2g32040 protein (truncated and fused to the N-terminus of slr0642) enabled growth on 5-formyltetrahydrofolate or folic acid, but not on 5-formyltetrahydrofolate triglutamate, demonstrating that both proteins mediate folate monoglutamate transport. Both proteins also mediate transport of the antifolate analogs methotrexate and aminopterin, as evidenced by their ability to greatly increase the sensitivity of *E. coli* to these inhibitors. The full-length At2g32040 polypeptide was translocated into isolated pea chloroplasts and, when fused to green fluorescent protein, directed the passenger protein to the envelope of *Arabidopsis* chloroplasts in transient expression experiments. At2g32040 transcripts were present at similar levels in roots and aerial organs, indicating that the protein occurs in non-green plastids as well as chloroplasts. Insertional inactivation of At2g32040 significantly raised the total folate content of chloroplasts and lowered the proportion of 5-methyltetrahydrofolate, but did not discernibly affect growth. These findings establish conservation of function among FBT family proteins from three kingdoms of life.

Tetrahydrofolate (THF)¹ and its derivatives (collectively termed folates) are essential cofactors for one-carbon transfer reactions in almost all organisms (1, 2). Bacteria and plants synthesize folates *de novo*, but higher animals do not and so need a dietary supply (1, 3, 4). Folates consist of a pteridine, p-aminobenzoate (pABA), and one or more glutamate residues (Fig. 1A). All these moieties are synthesized and assembled into folates in the cytosol of bacteria, but in plants the pathway is split among three subcellular compartments. The pteridine is made in the cytosol and the pABA is made in plastids; both then enter mitochondria, where they are coupled together and glutamylated to yield folate (Fig. 1B). Much of the folate produced exits the mitochondria to supply folate pools in the cytosol, plastids, and vacuoles (13-17). This compartmentation of the synthesis pathway and its end products entails various transmembrane fluxes of folates and their precursors (Fig. 1B). While pABA can cross membranes by simple diffusion (18), folate and pteridine fluxes are likely to be carrier-mediated, as in animals (19-22) and bacteria (23-25). Plants therefore presumably have several as yet undiscovered organelar folate or pteridine transporters (Fig. 1B).

Multiple transporters that act on folates as well as antifolates such as methotrexate or aminopterin have been characterized in mammals. These transporters include the reduced folate carrier, which catalyzes exchange with organic anions, folate receptors, which mediate folate entry via endocytosis, folate efflux pumps of the ATP-binding cassette family, and a protein from the mitochondrial carrier family (19-21).

High-affinity folate and pteridine transporters are also known from the trypanosomatid *Leishm-
ania, a parasitic protist that is auxotrophic for folate and pteridine (26). These carriers are a biopterin transporter (BT1) and two folate transporters (FT1, FT5), all three being similar proteins with about twelve putative transmembrane helices (27-29). Together, they define a small family (the FBT family) that is a distant member of the major facilitator superfamily (30). BT1 is the only carrier yet known to act on pteridines; it also has low-affinity folate transport activity (22).

Besides proteins from trypanosomatids, the FBT family (also known as the BT1 family, Pfam03092) includes a highly conserved protein from cyanobacteria and nine Arabidopsis proteins. In this study we used heterologous expression in E. coli mutants to probe the functions of a representative cyanobacterial FBT protein and its closest Arabidopsis homolog. Having demonstrated that both have folate and antifolate transport activity, we investigated the subcellular location of the Arabidopsis protein, the expression of its gene, and the effect of ablating this gene.

**EXPERIMENTAL PROCEDURES**

**Chemicals and Reagents**—Folates and pteridines were from Schircks Laboratories (Jona, Switzerland), p-Aminobenzoyleglycine (pABA-Glu) was HPLC-purified before use. Percoll and [5,6-^3^H]UTP (35 Ci/mmol) were from Amersham Biosciences (Piscataway, NJ). [^3^H]Leucine (59 Ci/mmol) was from PerkinElmer (Boston, MA). E. coli Strains—Strain BN1163 (pabA1, pabh::Kan, rpsL704, ilvG-, rfb-50, rph-1) was supplied by B. Nichols (University of Chicago, Chicago, IL) and strain NM1200 by N. Majdalani (NCBI, Bethesda, MD). The NM1200 strain was constructed by P1 transduction of the Mini-λ prophage carrying the Red gam, beta, and exo genes under the P_L promoter (31) in MG1655 (E. coli K12, E. coli Genetic Stock Center). The folE gene was deleted by targeted homologous recombination using electroporated linear DNA and strain NM1200 as described (32). Briefly, the kanamycin cassette was amplified from plasmid pUC4K with primers FolE-5' and FolE-3' (see Supplemental Table I), which respectively included the start and stop codon of folE and 47-bp 5' and 3' flanking sequences. After inducing the recombination system at 42°C for 15 min, strain NM1200 was transformed with the PCR product. Clones with the desired replacement of the folE gene were selected on LB plates containing 300 µM thymidine and 30 µg/ml kanamycin. The kanamycin resistance locus was then transferred by P1 transduction to strain K12, to give strain P1-7B. Deletion of the folE gene was confirmed by PCR and sequencing. P1-7B was maintained on LB medium containing 300 µM thymidine and 30 µg/ml kanamycin.

**Plants and Growth Conditions**—Arabidopsis (ecotype Columbia) plants were grown at 23-28°C in 12-h days (photosynthetic photon flux density 80 µeinsteins m^-2 s^-1) in potting soil irrigated with water. When roots were required, plants were grown hydroponically (33).

**Expression Constructs**—Synechocystis slr0642 and Arabidopsis At2g32040 amplicons preceded by a Shine-Dalgarno sequence were cloned between the NotI and SstI sites of pLOI707HE (34), which contains the lac promoter, the lacIq repressor gene, and the tet marker. Templates were Synechocystis sp. PCC 6803 genomic DNA (from W. Vermaas, Arizona State University, Tempe, AZ) and an At2g32040 cDNA (GenBank™ BT003363, from the Arabidopsis Biological Resource Center). The following PCR primers were used (see Supplemental Table I): for Synechocystis Slr0642, Slr1-5' and Slr1-3'; for the mature At2g32040 construct, At-t1-5' and At-t1-3'; for the chimeric At2g32040 construct (with codons 1-128 replaced by codons 1-37 of slr0642), Slr1-5' and Slr-c1-3' to amplify the slr0642 fragment, At-c1-5' and At-t1-3' to amplify the At2g32040 fragment, and Slr1-5' and At-t1-3' to splice the fragments. The complete slr0642 amplicon was cloned into pGEM®-T Easy (Promega), excised with NotI and SstI and then cloned into pLOI707HE; other amplicons were cut with NotI and SstI and cloned straight into pLOI707HE. For the vector minus insert control, pLOI707HE was digested with NotI and SstI, end-polished with T4 polymerase and religated. Constructs were made in E. coli strain DH5a, sequence-verified, then introduced into E. coli strains BN1163 and P1-7B, both harboring pACYC-RIL (Stratagene), which contains three rare E. coli tRNA genes and the cat marker. Transformants were grown on LB plates containing tetracycline 10 µg/ml, kanamycin 30-50 µg/ml, chloramphenicol 20 µg/ml, and (for P1-7B only) thymidine 300 µM.

**Folate Uptake Tests**—BN1163 cells harboring pACYC-RIL and a pLOI707HE construct were streaked on minimal medium plates containing M9
salts (35), 0.1 mM CaCl₂, 0.5 mM MgSO₄, trace elements (36), and 0.4% (w/v) glucose, supplemented with antibiotics as above and 0.5 mM IPTG. To this medium was added 3.6 µM pABA, or 11 µM (6R,6S)-5-formyl-THF (5-CHO-THF), folic acid, or (6R,6S)-5-formyl-THF triglutamate. P1-7B cells harboring pACYC-RIL and a pLO1707-HE construct were streaked on LB medium containing 0.1% (w/v) Na-ascorbate and 1 mM dithiothreitol, appropriate antibiotics, and IPTG, minus or plus 11 µM 5-CHO-THF, dihydropteroate, hydroxymethyldehydropterin, or dihydropterin-6-aldehyde. Tests with the two latter compounds were made in a 10-l vessel flushed with N₂ at 25 ml/h.

Antifolate Uptake Tests—Solid or liquid minimal media were supplemented with antibiotics, IPTG, and pABA as described above. For tests on solid medium, cells were streaked on plates containing a central 1-cm disk of Whatman no. 1 paper soaked with 10 µl of dimethylsulfoxide alone or containing 100 mM methotrexate or 80 mM aminopterin. For tests in liquid medium, cells from an overnight culture were inoculated to give an A₆₀₀ reading of 0.05 in 1.5 ml of fresh medium supplemented with various amounts of methotrexate or aminopterin. Growth was evaluated by measuring A₆₀₀ after incubating at 37°C for 9.5 h with shaking at 220 rpm.

Transient Expression of Green Fluorescent Fusion Protein in Arabidopsis Protoplasts—The entire At2g32040 sequence was amplified using primers At-gfp-5’ and At-gfp-3’, digested with Sall and NcoI and cloned in frame upstream of the green fluorescent protein (GFP) gene in pTH2 (37). Protoplasts were prepared from cell cultures, transformed, and cultured as described at 22°C for up to 48 h (7, 38). Transformation efficiencies were typically 5-20%. Samples were analyzed by epifluorescence microscopy as described (11).

Chloroplast Import Assays—The full length At2g32040 sequence and a version lacking the first 88 residues were respectively amplified using forward primer At-ifi-5’ or At-it-5’, and reverse primer At2g32040 sequence was amplified using primers At-gfp-5’ and At-gfp-3’, digested with SalI and NcoI and cloned in frame upstream of the green fluorescent protein (GFP) gene in pTH2 (37). Protoplasts were prepared from cell cultures, transformed, and cultured as described at 22°C for up to 48 h (7, 38). Transformation efficiencies were typically 5-20%. Samples were analyzed by epifluorescence microscopy as described (11).

Chloroplast Folate Analyses—Chloroplasts were purified from leaf discs of 4-week old Arabidopsis plants as described (42, 43). Folic acid was extracted from samples (~1 mg chlorophyll), deglutamylated, affinity-purified, and determined by HPLC electrochemical detection as described (41).
RESULTS

FBT Family Genes in Cyanobacteria and Plants—Blast searches of GenBank™ confirmed and extended the delineation of the FBT family given in the Pfam database. Homologs of the Leishmania FT and BT1 transporters were found only in trypanosomatids, apicomplexans, cyanobacteria, and plants. Cyanobacterial genomes have a single FBT gene specifying a highly conserved (≥56% identity) protein. In contrast, plant genomes encode several diverse FBT proteins, there being nine in Arabidopsis. Multiple alignment and phylogenetic analysis showed that one of these, At2g32040, clustered with cyanobacteria while the others fell into two groups of four each (see Supplemental Fig. 1, A and C). The At2g32040 protein shares 52-54% identity with the cyanobacterial proteins, but differs in having a ~90-residue N-terminal extension with the features of a plastid targeting peptide (44) (see Supplemental Fig. 1C). The cyanobacterial and plant proteins have twelve predicted transmembrane α-helices, as illustrated in Supplemental Fig. 1B for the Synechocystis slr0642 protein.

Since trypanosomatids and apicomplexans have apparently acquired numerous genes from photosynthetic organisms (45, 46), and plants acquired many genes from cyanobacteria (47), the cyanobacterial protein is potentially the archetype of the FBT family. We accordingly chose a representative cyanobacterial FBT protein, Synechocystis slr0642 (henceforth slr0642) for further study along with its close plant relative, Arabidopsis At2g32040 (henceforth At2g32040).

Folate Uptake by E. coli Expressing slr0642 or At2g32040—Folates cannot normally cross the inner membrane of E. coli cells, preventing rescue of folate synthesis mutants by supplied folates (48). We therefore evaluated folate transport activity by expressing FBT constructs in a pabA pabB mutant, which is auxotrophic for pABA, and testing for growth on minimal medium with or without 5-CHO-THF or folic acid (the two most stable folates) in place of pABA. [The mutant also harbored a plasmid bearing genes for three rare E. coli tRNAs (argU, ileY, leuW, corresponding to AT-rich codons). This plasmid was found to be needed to express At2g32040 constructs.] The N-terminal extension that contains the predicted targeting peptide was removed from At2g32040 constructs, basing the truncation point (after residue 88) on alignments with slr0642 (see Supplemental Fig. 1C) and with orthologous plant sequences derived from ESTs (not shown). Since the truncated At2g32040 protein had a more hydrophilic N-terminal region than slr0642, and this region may affect membrane targeting or translation in E. coli (49), we also constructed a chimeric version in which residues 1-40 of the truncated protein were replaced by residues 1-37 of slr0642.

After two passages on minimal medium plus or minus folate, the growth of mutant cells harboring the empty pLOI707HE vector ceased (Fig. 2A). In contrast, cells expressing slr0642 continued to grow when given folates (Fig. 2A), showing that the latter are transported. The truncated At2g32040 did not confer the ability to grow on folates but the chimeric version was effective (Fig. 2A). Cells expressing slr0642 or chimeric At2g32040 did not grow when 5-CHO-THF triglutamate replaced the monoglutamyl form (not shown), indicating that both transporters, like most other folate carriers, prefer monoglutamates. (Note, however, that the triglutamate approaches in size the exclusion limit of the outer membrane porins of E. coli, which may also have impeded uptake.) Cells cured of their plasmids were not rescued by folates, confirming that the transport trait is plasmid-encoded.

Although 5-CHO-THF and folic acid are relatively stable, some spontaneous breakdown is inevitable, releasing pABA-Glu. To rule out the possibility that the growth seen on folates was due to such release we confirmed that pABA-Glu did not support growth of mutant cells expressing slr0642 or chimeric At2g32040 (not shown). As E. coli cannot normally take up pABA-Glu but can utilize it once absorbed (50), this result further shows that neither protein is able to transport pABA-Glu.

The results from the pabA pabB mutant were corroborated using a second mutant – a folE deletant, which lacks the first enzyme of the pteridine branch of folate synthesis (GTP cyclohydrolase I). This deletant could grow on rich medium supplemented with 5-CHO-THF when expressing slr0642 or chimeric At2g32040 but not when harboring the empty vector (Fig. 2B). The folE deletant could not be used to test slr0642 or At2g32040 for transport of dihydropterotate or dihydropterins (hydroxymethyl)dipterin, dihydropterin-6-aldehyde) as these compounds supported growth of deletant cells harboring the empty vector (not shown).
**Antifolate Uptake**—The antifolates aminopterin and methotrexate are close structural analogs of folic acid, differing only in one and two groups, respectively (Fig. 1A). *E. coli* normally has little capacity to take up these compounds, and they are inhibitory only at high concentrations (50, 51). We therefore tested antifolate transport activity by evaluating growth of cells exposed to antifolate gradients on plates (Fig. 3A) or to various levels of antifolates in liquid medium (Fig. 3, B and C). Expression of slr0642 or the chimeric At2g32040 construct imparted large increases in sensitivity that were qualitatively obvious on plates and were quantified as 30- to 100-fold in liquid culture. The truncated At2g32040 protein was again ineffective.

**Subcellular Localization of At2g32040**—This was investigated first by transient expression of an At2g32040::GFP fusion construct in *Arabidopsis* protoplasts. Consistent with the presence of a putative plastid targeting peptide, expression of the fusion protein resulted in green fluorescence that colocalized with the red autofluorescence of chlorophyll; the green fluorescence was strongest at the chloroplast margins, suggesting that the protein is concentrated in the envelope (Fig. 4A). Expression of GFP alone gave green fluorescence throughout the cytoplasm (Fig. 4A).

Import assays with isolated pea chloroplasts substantiated these results (Fig. 4B). After the import reaction with the full-length protein, chloroplasts contained a labeled product that was smaller than the full-length protein and was protected from attack by thermolysin, as expected for a translocated protein. In contrast, a truncated version lacking the predicted targeting peptide was not processed and was thermolysin-sensitive, indicating that it had not been taken up. [The latter protein (calculated molecular mass 51 kDa) behaved in SDS-PAGE as a 51-kDa species as expected, but the full-length protein (calculated mass 61 kDa) migrated as a 72-kDa species (Fig. 4B). Other FBT family proteins likewise migrate anomalously (52). Thus, while the migration of the imported protein as a 67-kDa band (Fig. 4B) implies that the point we chose to truncate At2g32040 is not identical to the normal processing site, electrophoretic anomalies preclude quantifying the discrepancy.]

**Expression of At2g32040 in Arabidopsis Organs**—Quantitative RT-PCR analysis indicated that the At2g32040 gene is constitutively expressed throughout the plant at a low level. ( Sequencing of the RT-PCR product obtained from root and young leaf RNA confirmed that it corresponded to At2g32040 mRNA.) Thus, the abundance of At2g32040 transcripts varied rather little among major organs, from 5 to 14 × 10^6 copies/250 ng total RNA (Fig. 5A), which corresponds to a frequency between 1 in 20,000 and 1 in 60,000 mRNAs (assuming that mRNA is 1% of total RNA and has an average size of 1.5 kb). Ubiquitous, low-level expression is also reported for At2g32040 in the GENEVESTIGATOR *Arabidopsis* microarray database (53). The presence of At2g32040 transcripts in roots as well as aerial organs implies that the protein is expressed in non-green plastids as well as chloroplasts.

**Identification and Analysis of a T-DNA Insertion Mutant**—To explore the function of At2g32040 *in vivo*, an *Arabidopsis* line bearing a T-DNA insertion in the coding region of the gene was identified in the Salk collection (40). This mutant has a single T-DNA insertion in exon 1 at codon 24 (Fig. 5, B and C), as determined from the flanking DNA sequence and co-segregation of kanamycin resistance with the T-DNA. The insertion creates at least two in-frame stop codons and so is predicted to result in a complete knockout.

Homozygous mutant plants did not differ noticeably from their wild type siblings in growth rate, morphology, leaf color, or fertility. As At2g32040 is located in the plastid (Fig. 4), we compared the folate profiles of chloroplasts from wild type and mutant plants (Fig. 6). As in pea (15-17), total folate levels in wild type chloroplasts were low, about 50 pmol/mg protein or 150 pmol/mg chlorophyll, which is equivalent to a stromal concentration of ~2 μM (taking stromal volume as 66 μl/mg chlorophyll, Ref. 54). The most prominent folate forms were 5-methyl- and 5,10-methenyl-THF. (The acidic HPLC mobile phase used in the analysis converts 10-formyl-THF to 5,10-methenyl-THF, so that the 5,10-methenyl-THF measured includes 10-formyl-THF plus any preexisting 5,10-methenyl-THF.) Relative to wild type, mutant chloroplasts contained significantly (*p* < 0.05) more 5,10-methenyl-THF and total folate per unit protein (Fig. 6A) and, when data were expressed on a percent basis, a significantly lower proportion of 5-methyl-THF (Fig. 6B).
DISCUSSION
We report here the functional expression of an FBT family protein in *E. coli*, an advance that should help studies of transport mechanisms. Expressing the *Synechocystis* slr0642 protein in *E. coli* was straightforward, but success with *Arabidopsis* At2g32040 required the presence of a plasmid bearing rare AT-rich codons, and modification of the protein. Deleting its N-terminal extension did not suffice; it was necessary also to replace the N-terminus of the truncated protein with the corresponding sequence from slr0642, a region that may affect membrane insertion or translation in *E. coli*. This modification altered only the initial part (the first third) of predicted transmembrane helix number 1, which part is not involved in substrate binding in other major facilitator superfamily proteins (55, 56).

As shown in Supplemental Fig. 1C, there is remarkably high sequence conservation between the cyanobacterial carrier and At2g32040 that extends over the entire protein except the region between transmembrane helices 6 and 7, a large loop that separates the two halves of the molecule. The residues that are conserved both in these proteins and the *Leishmania* FT1, FT5, and BT1 carriers are likewise spread throughout the sequence except for helices 6 and 7 and the region between them (see Supplemental Fig. 1C). In this interstitial region the *Leishmania* sequences are predicted to have two additional transmembrane α-helices, an uncommon configuration in the major facilitator superfamily (57).

Folate transport was evaluated via bacterial growth, which is a sensitive way to detect transport activity but not to assess its rate or substrate specificity. For example, growth on 5-CHO-THF or folic acid lagged behind that on pABA, but this does not necessarily imply that the uptake rate of either folate limited growth. Both 5-CHO-THF and folic acid need enzymatic conversion to metabolically active forms (5,10-methenyl-THF and THF, respectively) before use (1, 58), so conversion rates could have been limiting. Moreover, 5-CHO-THF inhibits folate-dependent enzymes (58) and may have slowed growth on this account. Respecting substrate specificity, growth tests could not show whether or not slr0642 and At2g32040 act on dihydropteridines because *E. coli* cells took such compounds up unaided. These proteins thus remain unconfirmed candidates for the pteridine transport activities observed or inferred in cyanobacteria and chloroplasts (59-61).

Although *E. coli* is suspected to have a cryptic gene (*abgT*) – not normally expressed – that can allow transport of folate analogs and perhaps folates (51), three arguments exclude activation and selection of this or any other *E. coli* gene as an explanation for our data. First, curing transport-proficient cells of the expression plasmid abolished folate transport capacity. Second, the antifolate uptake results of Fig. 3 could not have involved selection because transport-proficient cells were *ipso facto* unable to divide. Third, when cells harboring empty expression vector underwent prolonged incubation on folate media, the growth of colonies was far too infrequent to compromise the folate uptake experiments of Fig. 2, where all cells expressing an active FBT carrier grew.

The subcellular localization and expression pattern of At2g32040 imply that it has a housekeeping function in green and non-green plastids alike. That this function is folate transport is supported by the finding that ablating At2g32040 caused a 23% rise in chloroplast total folate and a 34% fall in the proportion of 5-methyl-THF. That these changes were not more marked implies that there are other chloroplast folate transporters, and there is indeed recent evidence for a second one in *Arabidopsis* (62).

Since At2g32040 acts on 5-CHO-THF, folic acid, and antifolates it is clearly not highly specific and so can presumably transport the monoglutamyl form of any folate found in plastids. In this connection it is noteworthy that plastid folate transport fluxes include not only net import, but also an exchange with the cytosol, driven by methionine synthesis. Plastids synthesize homocysteine and contain an isoform of methionine synthase, which converts homocysteine to methionine using 5-methyl-THF as methyl donor (63). However, plastids cannot make 5-methyl-THF due to lack of the enzyme that produces it from 5,10-methylene-THF and so must import it from the cytosol (64) in exchange (not necessarily *via* the same carrier) for other folates in a shuttle reaction. Since stoichiometric, not catalytic, amounts of 5-methyl-THF are needed for methionine synthesis, this methyl group shuttle must greatly exceed the net import of folates into plastids.
Finally, this work establishes conservation of folate transport function among FBT family proteins from species representing three kingdoms of life—monera (*Synechocystis*), plants (*Arabidopsis*), and protists (*Leishmania*). Given the evidence for lateral transfer of genes from cyanobacteria to plants (47), and from cyanobacteria or plants to trypanosomatids and apicomplexans (45, 46), it seems likely that the FBT family arose in cyanobacteria and passed to the other groups, the evolutionary driver being the selective advantage conferred by folate transport. Whatever the case, these folate carriers that function across kingdom boundaries may offer new options for engineering folate production in bacteria and plants (1, 65). Such carriers might be used, for example, to enhance folate export from bacteria or folate sequestration in storage compartments in plant cells.

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FOOTNOTES

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† The abbreviations used are: pABA, p-aminobenzoic acid; pABA-Glu, p-aminobenzyolglutamate; FBT, folate-biopterin transporter; GFP, green fluorescent protein; RT-PCR, reverse transcription-polymerase chain reaction; THF, tetrahydrofolate; 5-CHO-THF, 5-formyltetrahydrofolate.

FIGURE LEGENDS

FIG. 1. Structure of folates, and compartmentation of folate biosynthesis in plants. A, folic acid. Aminopterin and methotrexate differ from folic acid in having an amino instead of an oxo group at C4, and N10 is methylated in methotrexate. The pteridine ring of folic acid is fully oxidized; in natural folates it is reduced to dihydro- or tetrahydro- forms. A γ-linked polyglutamyl tail of up to about six residues is usually attached to the first glutamate. B, distribution of folate biosynthesis steps between cytosol, mitochondria, and plastids, and inferred carrier-mediated transport steps for folates (open symbols) and pteridines (gray symbol). Note that polyglutamylation of folates also occurs in the cytosol and plastids (7). DHN, dihydronopterin; DHNTP, dihydronopterin triphosphate; DHM, dihydromonapterin; HMDHP, hydroxymethyl DHN; DHP, dihydropterate; DHP, dihydrofolate; THF, tetrahydrofolate, ADC, aminodeoxochorismate; pABA, p-aminobenzoate.

FIG. 2. Folate uptake tests in E. coli expressing Synechocystis slr0642 or modified Arabidopsis At2g32040. A, strain BN1163 (a paba pabB mutant) harboring pACYC-RIL was transformed with pLOI707HE with no insert (V), or containing slr0642 (slr), the truncated At2g32040 protein (At-t), or a
chimeric At2g32040 protein with residues 1-128 replaced by residues 1-37 of slr0642 (At-c) (see Supplemental Fig. 1C). Six independent clones of each construct were streaked on minimal medium plus IPTG alone (control) or containing 3.6 µM pABA or 11 µM 5-CHO-THF. Clones were streaked once on pABA-supplemented plates, thrice in succession on the others. Incubation was at 37°C. The pABA plates were photographed 1 day after streaking, others after 3 days. Similar results were obtained when 11 µM folic acid replaced 5-CHO-THF except that growth was slightly slower. B, strain P1-7B (a folE deletion) harboring pACYC-RIL was transformed with V, slr, and At-c constructs as above. Four independent clones of each construct were streaked on LB medium plus 0.1% (w/v) Na-ascorbate, 1 mM dithiothreitol and IPTG alone (control) or containing 11 µM 5-CHO-THF. Plates were incubated for 2 days at 37°C.

FIG. 3. Antifolate uptake tests in E. coli expressing Synechocystis slr0642 or modified Arabidopsis At2g32040. Strain BN1163 harboring pACYC-RIL was transformed with pLOI707HE with no insert (V), or containing slr0642 (slr), the truncated At2g32040 protein (At-t), or the chimeric At2g32040 protein (At-c). A, clones were streaked radially on minimal medium plates containing IPTG and 3.6 µM pABA, with a central 1-cm filter paper disk impregnated with 10 µl of dimethylsulfoxide alone (control) or containing 100 mM methotrexate or 80 mM aminopterin. Plates were photographed after 2 days. B and C, growth (absorbance at 600 nm) after 9.5 h in liquid minimal medium containing IPTG, 3.6 µM pABA, and various concentrations of methotrexate (B) or aminopterin (C). Data are means of triplicate cultures; S.E. values were ≤ 9% of the means in all cases.

FIG. 4. Evidence that the At2g32040 protein is targeted to chloroplasts. A, transient expression in Arabidopsis protoplasts of GFP fused to the C-terminus of At2g32040 (upper frames) or GFP alone (lower frames). GFP (green pseudo-color) and chlorophyll (red pseudo-color) fluorescence were observed with an epifluorescence microscope. B, protein import into isolated pea chloroplasts. Full-length (FL) and truncated (T) versions of At2g32040 were translated in vitro in the presence of [3H]leucine. The translation products were incubated for 15 min in the light with Mg2+-ATP and chloroplasts (CP), which were then purified, or first treated with thermolysin (TH) to remove adsorbed proteins. Proteins were separated by SDS-PAGE and visualized by fluorography. Samples were loaded on the basis of equal chlorophyll content, next to aliquots of the respective translation products. The molecular masses (kDa) shown in the figure were estimated from the positions of standards run on the same gel.

FIG. 5. Expression of the At2g32040 mRNA in Arabidopsis organs, and structure of the T-DNA-mutated At2g32040 gene. A, levels of At2g32040 mRNA in Arabidopsis organs, determined by real-time RT-PCR. Young leaves were harvested at 21 days, and mature leaves, stems, and siliques at 35 days. Roots were from hydroponically grown plants, harvested at 35 days. Data are means of three determinations for independent tissue samples, and S.E. B, structure of the At2g32040 gene, with introns as solid lines and exons as boxes. The positions of the T-DNA insertion, of the start and stop codons, and of the primers used to identify wild type and mutant segregants are indicated. C, agarose gel analysis of the PCR products obtained from pooled genomic DNA from two wild type or three homozygous mutant plants using the primer pairs indicated. The approximate size of the products (bp) is indicated.

FIG. 6. Chloroplast folate profiles of wild type and At2g32040 mutant Arabidopsis. Chloroplasts were purified by Percoll gradient centrifugation. Folates were analyzed in deglutamylated samples by HPLC with electrochemical detection. Data are presented per unit protein in A, and as percent of total chloroplast folate in B. 5-CH3-THF, 5-methyl-THF; 5-CHO-THF, 5-formyl-THF; 5,10=CH-THF, 5,10-methenyl-THF; 10-CHO-DHF, 10-formyldihydrofolate (formed during isolation from 10-formyl-THF). Data are means and S.E. from six wild type and five mutant chloroplast preparations. Asterisks indicate differences between mutant and wild type that are significant at p < 0.05 by Student’s t-test; percent data were arcsine transformed before the t-test.
Fig. 1
Fig. 2
Fig. 3

A
Control  Methotrexate  Aminopterin

B
Methotrexate

C
Aminopterin

Fig. 3
Fig. 4
Fig. 5

A

Copies x 10^4 / 250 ng total RNA

Roots  Silique  Stems  Young Leaves  Mature Leaves

B

ATG  TAA

At-s-5'  At-s-3'

T-DNA

SalkLBb1

C

| At-s-5' / At-s-3' | SalkLBb1 / At-s-3' |
|-------------------|--------------------|
| **WT**            | **KO**             |
| 930               | 350                |
Fig. 6
SUPPLEMENTAL TABLE I

*Synthetic oligonucleotides used in this study*

Restriction sites are underlined. Start codons are in green. Stop anticodons are in red. Shine-Dalgarno sequences are in blue. Recoded regions (replacing codons used rarely in *E. coli*) are in magenta. The SP6 promoter sequence is italicized.

| Names            | Sequences (5' → 3')                                      |
|------------------|----------------------------------------------------------|
| Slr1-5'          | GCGGCCGCCACAGGAAACAGCTATGCTTGTTGCTATGTCCATG             |
| Slr1-3'          | GAGCTCTAGGACGCTGGAAACTT                                  |
| Slr-c1-3'        | TGCTACAGCCAGTAACTCCAACTG                                 |
| At-t1-5'         | TAATTAGCGGCCGCAAGGAAACAGCTATGGAAAGGGCGACCGCGATACTACTTAT |
| At-t1-3'         | TGCAGAGCTCTTAAATTGGACTTCATCT                             |
| At-c1-5'         | GGAGTTACTGGCTGATCAATGTTGT                               |
| At-gfp-5'        | ATTAGCGTCGACATGGCGAGTCGCTCCTCTCTCT                    |
| At-gfp-3'        | ATAAGCCCATGGAATTGGACTTCATCTCAACGT                        |
| At-ifl-5'        | CCGGAATTCATGGCGAGTCGCTCTCTCT                             |
| At-ifl-5'        | CCGGAATTCATGGCGAGACAGAGATAC                              |
| At-i-3'          | GCATAAGCAAGCTTNTTAATTGGACTTCATCTCAAC                   |
| At-rt-5'         | CAGTCCTTGCTCAGGCTTCAT                                     |
| At-rt-3'         | TGCTTCCATTCTTCTTGACT                                    |
| At-rt-probe      | ATGCCGGTTCTGTGTAGCAGCGAGA                               |
| At-SP6std-5'     | ATTTAGGTGACACTATAAGGGAAGGCAAGCTGGATGGCGAGTCGCTCCTCTCTT |
| At-std-3'        | TTTTTTTTCTATGAAAGGCTGCT                                  |
| At-s-5'          | ACGTAACCAGATTTTCCC                                      |
| At-s-3'          | AATCCTCAAATGGCAATTCTG                                    |
| SalkLBb1         | GCGTGACCAGGCTGCTCAACT                                    |
| FolE-5'          | TGCCCCACGCGAGGCGAGGCCACACCTGCGAGGAAATCATAATGAAAACAGCTATG |
| FolE-3'          | GAACAAAAATCGAGCGTACGTTGCGCTCCCATGTTCTGCTGCTTTTAATCAGTGTATTAGAAA-AACATCGAGGC |
Supplemental Figure 1

A

B
| H9  | H10  |
|-----|------|
| BT1 |       |
| FT1 |       |
| FT5 |       |

**Synechocystis**

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**Synechococcus**

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**Nostoc**

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**BT1**

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**FT1**

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|       |

**FT5**

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**Synechocystis**

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**Synechococcus**

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**Nostoc**

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**BT1**

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**FT1**

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|       |

**FT5**

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**Synechocystis**

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**Synechococcus**

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**Nostoc**

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**BT1**

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**FT1**

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|       |

**FT5**

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**Synechocystis**

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**Synechococcus**

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**Nostoc**

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Phylogeny, predicted membrane topology, and alignment of FBT family proteins. A, unrooted phylogram of the FBT proteins of *Leishmania*, *Arabidopsis*, and representative cyanobacteria, constructed using neighbor-joining and 1,000 bootstrap iterations. Asterisks mark branchpoints with bootstrap values >90%. Note that the Arabidopsis At2g32040 sequence (*boxed*) clusters with the cyanobacterial proteins. The phylogram was built using Phylip using the alignment shown below with gaps ignored. B, topology model of the *Synechocystis* slr0642 protein. The model is based on the structures of the lactose transporter LacY (1pv7) (55) and the glycerolphosphate/phosphate transporter GlpT (1pw4) (56) from *E. coli*, which – like FBT proteins – are members of the major facilitator superfamily. Since there is low sequence similarity between the three proteins, structural alignments (66), hydropathy profiling (TMHMM) (67), analysis of the amphipathic properties of α-helices, and secondary structure predictions (PSIPRED) (68) were combined with sequence information to generate the model. C, alignment of the FBT proteins of *Leishmania*, *Arabidopsis*, and cyanobacteria, made using ClustalW with manual optimization. Identical residues are shaded in black, similar residues in gray. Dashes are gaps introduced for optimal alignment. Predicted transmembrane helices (*H1-H12*) are overlined. In the At2g32040 sequence the residue (Val89) that was changed to the initiation methionine in the truncated version is *highlighted in red* and the residue at which the N-terminal region was exchanged with that of the slr0642 protein (Ala129) is *highlighted in blue*. 
Higher plant plastids and cyanobacteria have folate carriers related to those of trypanosomatids
Sebastian M. J. Klaus, Edmund R. S. Kunji, Gale G. Bozzo, Alexandre Noiriel, Rocio Diaz de la Garza, Gilles J. C. Basset, Stephane Ravanel, Fabrice Rebeille, Jesse F. Gregory III and Andrew D. Hanson

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