Alanine Aminotransferase Homologs Catalyze the Glutamate:Glyoxylate Aminotransferase Reaction in Peroxisomes of Arabidopsis¹

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Plant peroxisomal glyoxylate aminotransferases play central roles within the photo respiratory pathway. Genes encoding glyoxylate aminotransferases have been isolated from several animals and microbes, but only recently have plant homologs been identified. Three Arabidopsis homologs of alanine (Ala):glyoxylate aminotransferase 2 (AGT2) contain a putative type 1 peroxisomal targeting signal (PTS1), but the metabolic significance of these AGT2 homologs is unknown. GGT1 and GGT2 are Ala aminotransferase (AlaAT) homologs from Arabidopsis that represent another type of glyoxylate aminotransferase. These proteins are class I aminotransferases, each containing a putative PTS1. GGT1 and GGT2 are members of a small family of AlaATs in Arabidopsis. When expressed as recombinant proteins in Escherichia coli, GGT1 and GGT2 displayed biochemical characteristics very similar to one another, and to the Arabidopsis protein purified from leaves. Four aminotransferase activities were specifically associated with GGT1 and GGT2, using the substrate pairs glutamate (Glu):glyoxylate, Ala:glyoxylate, Ala:2-oxoglutarate, and Ala:pyruvate. GGT1 and GGT2 may have partially redundant functions; transcripts of both genes were detected in many of the same tissues. Although Glu:glyoxylate aminotransferase (GGT) activity has been observed in several locations in different plants and algae, including the cytoplasm and mitochondria, our subcellular fractionation data indicate that GGT activity was exclusively peroxisomal in Arabidopsis. Thus, glyoxylate aminotransferase reactions in plant peroxisomes appear to be catalyzed by at least two distinct types of aminotransferases: an AGT1 homolog with GGT activity (A.H. Liepman, L.J. Olsen [2001] Plant J 25: 487–498), and a pair of closely related, potentially redundant AlaAT homologs with GGT activity.

¹ This work was supported in part by the University of Michigan Cellular Biotechnology Training Program (fellowship no. NIH–GM08353 to A.H.L.) and by the Rackham School of Graduate Studies (fellowship to A.H.L.).

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Article, publication date, and citation information can be found at www.plantphysiol.org/cgi/doi/10.1104/pp.011460.

photorespiration, genes encoding several enzymes of this pathway may consume a significant proportion of the energy generated by photosynthesis in C₃ plants (Ogren, 1984; Husic et al., 1987; Buchanan et al., 1995). We demonstrated previously that an AGT1 homolog with SGT activity is localized to peroxisomes, mitochondria, or both organelles, depending upon dietary habit (Danpure, 1997), whereas AGT2 is a class II aminotransferase localized exclusively to mitochondria in animals (Takada and Noguchi, 1980; Noguchi and Mori, 1981; Ogawa et al., 1990; Lee et al., 1995). Animals contain two structurally distinct types of AGTs: AGT1 and AGT2. AGT1 is a class IV aminotransferase that is localized to peroxisomes, mitochondria, or both organelles, depending upon dietary habit (Danpure, 1997), whereas AGT2 is a class II aminotransferase localized exclusively to mitochondria in animals (Takada and Noguchi, 1980; Noguchi and Mori, 1981; Ogawa et al., 1990; Lee et al., 1995). We demonstrated previously that an AGT1 homolog with SGT activity is located in peroxisomes, where it is involved in the photorespiratory pathway in Arabidopsis. Kinetic analysis of Arabidopsis AGT1 suggests that this protein mainly uses the substrates Ser and glyoxylate. Although AGT1 catalyzes an AGT reaction in vitro, its high Kₘ value for Ala glycolate and various amino acids, in conjunction with studies of photorespiration mutants, have demonstrated that peroxisomal glyoxylate aminotransferases occupy central roles in photorespiration (Kisaki and Tolbert, 1969; Somerville and Ogren, 1980; Chang and Huang, 1981; Betsche, 1983; Liang and Huang, 1983; Yu et al., 1984).

Although genes encoding glyoxylate aminotransferases have been isolated in various animals and microbes (Nishiyama et al., 1990; Chistoserdova and Lidstrom, 1994; Lee et al., 1995; Hagashita et al., 1996), genes encoding plant homologs had not been characterized until recently (Liepman and Olsen, 2001). Animals contain two structurally distinct types of AGTs: AGT1 and AGT2. AGT1 is a class IV aminotransferase that is localized to peroxisomes, mitochondria, or both organelles, depending upon dietary habit (Danpure, 1997), whereas AGT2 is a class II aminotransferase localized exclusively to mitochondria in animals (Takada and Noguchi, 1980; Noguchi and Mori, 1981; Ogawa et al., 1990; Lee et al., 1995).
indicates that Ala may not be a physiological substrate for this enzyme (Liepman and Olsen, 2001).

Recent studies of Arabidopsis glyoxylate aminotransferases were preceded by a number of studies in which these enzymes were purified and characterized from a variety of plants (Rehfield and Tolbert, 1972; Noguchi and Hayashi, 1981; Nakamura and Tolbert, 1983; Paszkowski and Niedzielska, 1989; Roberts and Lees, 1997). There has been some confusion regarding the identities of these aminotransferases because of varying degrees of enzyme purity and the ability of these enzymes to catalyze reactions with multiple amino donor:acceptor combinations. Previous reports suggest that enzymes possessing GGT and AGT activities also catalyze Glu:pyruvate aminotransferase (GPT) and Ala:2-oxoglutarate aminotransferase (AKT) reactions (Noguchi and Hayashi, 1981; Biekmann and Feierabend, 1982; Paszkowski and Niedzielska, 1989; Orzechowski et al., 1999). GPT and AKT activities are typically attributed to Ala aminotransferases (AlaATs; EC 2.6.1.2). Much of the previous research on plant AlaATs has been characterization of chromatographically purified preparations from many different plant and algal sources. These studies indicate that all AlaATs possess AKT and GPT activities, and that a subset of the AlaATs also catalyzes GGT and AGT reactions.

Plants contain multiple AlaAT isoforms, localized to various subcellular locations including peroxisomes, mitochondria, and the cytosol. Between two and six forms of AlaAT have been observed in plant tissues (Gazeu-Reyjal and Crouzet, 1976; Noguchi and Hayashi, 1981; Biekmann and Feierabend, 1982; Penther, 1991; Son et al., 1991; Otter et al., 1992; Watson et al., 1992; Orzechowski et al., 1999). In general, it appears that AlaATs with glyoxylate aminotransferase activity are localized to peroxisomes, whereas those lacking glyoxylate aminotransferase activity are extraperoxisomal (see also Biekmann and Feierabend, 1982; Noguchi and Fujiwara, 1982; Yokota et al., 1985).

The presence of several AlaAT isoforms localized within different subcellular compartments in plants suggests that these enzymes may play roles in a number of metabolic pathways. Some isoforms appear to be expressed constitutively and play roles in general amino acid metabolism (Penther, 1991; Otter et al., 1992). There is also evidence that other isoforms may have more specialized roles. Several groups have observed light-dependent expression of plant AlaAT isoforms, indicating potential involvement in photorespiration (Noguchi and Fujiwara, 1982; Penther, 1991; Son et al., 1991; Otter et al., 1992; Son and Sugiyama, 1992). A cytosolic AlaAT isozyme in Panicum miliaceum, with increased expression during greening, is found in both mesophyll and bundle sheath cells, and has been implicated in the transfer of C₃ units between these cell types (Son et al., 1991; Son and Sugiyama, 1992). An AlaAT lacking glyoxylate aminotransferase activity is induced by hypoxia in barley (Hordeum vulgare), corn (Zea mays), and P. miliaceum roots (Good and Muench, 1992; Muench and Good, 1994; Muench et al., 1998). Elevated levels of Ala are observed in oxygen-deficient roots (Hoffman et al., 1986); Ala production may be an effective mechanism used by plants to conserve nitrogen and carbon atoms that would be lost by ethanol glycolysis (Good and Muench, 1992; Muench et al., 1998). In rice (Oryza sativa), an AlaAT gene is expressed in the starchy endosperm tissue of maturing seeds, where it may serve a key role in amino acid conversion for seed storage protein production (Kikuchi et al., 1999).

We have previously identified AGT1, the peroxisomal glyoxylate aminotransferase that catalyzes the AGT reaction of photorespiration (Liepman and Olsen, 2001). At least one additional distinct glyoxylate aminotransferase within the photorespiratory pathway has been implicated in biochemical and genetic studies (Somerville and Ogren, 1980; Nakamura and Tolbert, 1983; Yu et al., 1984). The objectives of this study were to identify the gene(s) encoding Arabidopsis GGT and to determine the subcellular localization and substrate specificity of this enzyme. Here, we report the identification of a pair of Arabidopsis genes encoding closely related GGTs belonging to a small group of AlaATs in Arabidopsis. We also describe kinetic and transcript expression analyses of these multispecific aminotransferases and the subcellular distribution of GGT activity in Arabidopsis. Although genes encoding AlaATs have been isolated from a number of plants and other organisms (Son and Sugiyama, 1992; Muench and Good, 1994, Muench et al., 1998; Kikuchi et al., 1999), this is the first report, to our knowledge, describing the identification of genes encoding a GGT from any organism.

RESULTS

Arabidopsis AGT2 Homologs

Although GGT activity is well documented in plants, the identity of the enzyme that catalyzes this reaction is unknown. It was demonstrated previously that purified enzyme preparations from various plants that contained GGT activity also contained AGT activity. In animals, there are two structurally distinct aminotransferases that catalyze the AGT reaction, AGT1 and AGT2 (Noguchi et al., 1978). Because the Arabidopsis AGT1 homolog did not catalyze the AGT reaction with physiologically relevant kinetics (Liepman and Olsen, 2001) and did not display any GGT activity (A.H. Liepman and L.J. Olsen, unpublished data), a logical candidate for a plant AGT/GGT could be an AGT2 homolog. Three Arabidopsis AGT2 homologs (At2g38400, At3g08860, and At4g39660) were identified using rat (Rattus norvegicus) AGT2 to query the databases (Fig. 1).

All three Arabidopsis AGT2 homologs are class II aminotransferases, and have predicted molecular
weights of approximately 52 kD. Based on sequence alignment and comparison with solved structures of other class II aminotransferases, residues G264, D290 or E291, K320, and R450 of Arabidopsis AGT2 homolog At4g39660 correspond to the conserved residues involved in enzymatic catalysis and binding of the cofactor PLP. Pair-wise comparison of these sequences with each other indicates that the Arabidopsis AGT2 homologs are 60% to 71% identical and 89% to 93% similar to one another. The Arabidopsis AGT2 homologs are 37% to 40% identical and 72% to 74% similar to the rat sequence (Lee et al., 1995). Expressed sequence tags (ESTs) of these genes are much lower in abundance in the databases compared with known photorespiratory genes (e.g. AGT1 and hydroxypyruvate reductase). These ESTs were present in some mixed tissue libraries, but, interestingly, all three Arabidopsis AGT2 genes appear to be expressed in developing seed tissues. ClustalW analysis indicates that all of the AGT2-like sequences are more closely related to one another than any representative is to AGT1 or to AlaAT sequences (Fig. 1A).

Figure 1. Sequence analysis of Arabidopsis aminotransferases. A. Unrooted tree containing members of the AGT1, AGT2, and AlaAT families was constructed using the ClustalW 1.75 program at the Genebee server (http://www.genebee.msu.su/clustal/advanced.html). The origin of the unrooted tree is indicated with a black circle. Default settings were used for tree construction, except that Kimerua’s correction was enabled. The AGT2 homologs from Arabidopsis are designated by their Arabidopsis Genome Initiative (AGI) locus numbers (At2g38400, At3g08860, and At4g39660). The mammalian homologs closest to each type of Arabidopsis aminotransferase are shown. RnAGT2, rat AGT2 (accession no. Q64565); HsAGT1, human (Homo sapiens) AGT1 (accession no. 178273); HsAlaAT, human AlaAT (accession no. P24298); AtAGT1, Arabidopsis AGT1 (AGI locus At2g13360); AtGGT1, Arabidopsis GGT1 (AGI locus At1g23310); AtGGT2, Arabidopsis GGT2 (AGI locus At1g70580); AtAlaATc, cytosolic isozyme of Arabidopsis alanine aminotransferase (AGI locus At1g7290); and AtAlaATm, mitochondrial isozyme of Arabidopsis alanine aminotransferase (AGI locus At1g72330). B, Arabidopsis AGT2 homologs were aligned with rat AGT2 (RnAGT2) to produce a consensus sequence (cons.) using the ClustalW algorithm. Asterisks denote residues identical in all four sequences; dots indicate residues similar in at least two of the sequences. Black circles have been placed above putative aminotransferase consensus residues; K320 of At4g39660 is the predicted pyridoxal-5’-phosphate (PLP) cofactor-binding site. A solid bar above the carboxyl terminus of the three Arabidopsis AGT2 homologs indicates the putative PTS1.
Although mammalian AGT2s are localized exclusively to mitochondria, each Arabidopsis AGT2 homolog contains a PTS1, suggesting peroxisomal localization (Fig. 1B). TargetP analysis predicts that each Arabidopsis AGT2 homolog is mitochondrial, although this program does not specifically recognize peroxisome-targeting signals (Emanuelsson et al., 2000).

To determine whether an Arabidopsis AGT2 homolog catalyzes GGT or AGT transaminations, the coding sequence of At4g39660 was subcloned into the bacterial expression vector pET-28. Recombinant At4g39660 was expressed in the soluble fraction at relatively high levels in Escherichia coli. Lysates of bacteria expressing this construct contained no additional GGT, AGT, SGT, AKT, or GPT activity, compared with empty vector controls (data not shown). The failure to detect any aminotransferase activity associated with the expression of this cDNA could indicate that this protein does not catalyze any of the reactions assayed, or that the protein was improperly folded in E. coli, resulting in its inactivity. Gross misfolding of the enzyme is probably not the cause of the observed lack of activity because the recombinant protein was soluble and not in inclusion bodies.

**Purification and Identification of Arabidopsis GGT**

Because the reverse genetics approach was unsuccessful in identifying an enzyme catalyzing GGT/AGT reactions, GGT activity was chromatographically purified from Arabidopsis leaf tissue. A gel depicting the progress of the protein purification is shown in Figure 2; the final purification factor was greater than 50-fold (Table I).

A protein of approximately 55 kD copurified with the GGT activity peak at each step of the purification. After hydroxylapatite chromatography, this protein was excised from a Coomassie Blue-stained gel and subjected to trypsin digestion and matrix-assisted laser-desorption ionization time of flight (MALDI-TOF) analysis. The spectrum obtained for the tryptic fragments of the purified protein was used to query the nr database, resulting in the identification of a pair of putative AlaATs from Arabidopsis with high degrees of peptide coverage. GGT1, the most likely candidate, containing peptides corresponding to 19 of 19 predicted peaks (covering 41% of the predicted protein sequence; Table II; Fig. 3A), matched AGI locus At1g23310. Another candidate, GGT2, containing peptides corresponding to 16 of 19 peaks (covering 37% of the predicted protein sequence), corresponded to AGI locus At1g70580. No other proteins contained peptides corresponding to more than four peaks, including both of the other two predicted Arabidopsis AlaAT homologs in the Arabidopsis genome, AGI loci At1g72330 and At1g72290.

Analysis of the GGT1 and GGT2 sequences revealed that these proteins are 93% identical and 99% similar at the amino acid level. GGT1 and GGT2 are also closely related to the two other Arabidopsis AlaAT isozymes and to human AlaAT (Figs. 1A and 3B). The high degree of sequence conservation between GGT1 and GGT2 is probably because of a segmental duplication of the region of Arabidopsis chromosome I containing these two genes (AGI, 2000). Each of the predicted proteins is 481 amino acids in length, contains a protein family class I aminotransferase signature, and a conserved variant of the PTS1 (Olsen, 1998), suggesting peroxisomal localization. The other two putative Arabidopsis AlaATs (also segmentally duplicated) are predicted to be mitochondrial (AtAlaATm, AGI no. At1g72330) and cytosolic (AtAlaATc, AGI no. At1g17290) isozymes. For each of the putative organellar isozymes, the targeting information is appended as carboxyl- or amino-terminal extensions. The PTS1 sequence of the two putative peroxisomal isozymes resides on short carboxyl-terminal extensions, not present on the other isozymes, whereas the putative mitochondrial isozyme contains a long amino-terminal extension.

![Figure 2. Purification of GGT activity from Arabidopsis leaves. GGT activity was chromatographically purified from Arabidopsis leaves after ammonium sulfate precipitation as described in “Materials and Methods.” Samples containing approximately equal amounts of GGT activity were separated by SDS-PAGE and silver stained. The size of molecular mass standards (in kD) are indicated along the left side. The purification factor relative to the initial soluble fraction is indicated below the corresponding lane of the gel. Note that the large subunit of Rubisco obscures the GGT1 band before the Q-Sepharose purification step.](image-url)
Table I. Purification of GGT activity from Arabidopsis

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<th>Sample</th>
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<th>Total Activity</th>
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<td>45% to 60% (w/v) (NH₄)₂SO₄</td>
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Expression of Arabidopsis GGT1 and GGT2

The sequences of GGT1 and GGT2 were both used to search for corresponding Arabidopsis ESTs. Over 70 ESTs, including several potential full-length clones corresponding to GGT1, were identified. These GGT1 ESTs were present in Arabidopsis cDNA libraries produced from mixed tissues, aboveground organs, green siliques, roots, flower buds, and leaves of salt-treated plants (Newman et al., 1994; Asamizu et al., 2000). Only two potential EST sequences corresponding to GGT2 were discovered, including a single potential full-length cDNA. Many additional cDNAs encoding AlaAT homologs from other organisms including Chlamydomonas reinhardtii, rice, P. miliaceum, barley, corn, human, rat, trypanosome (Trypanosoma brucei), yeast (Saccharomyces cerevisiae), Caenorhabditis elegans, and Drosophila melanogaster are also present in the databases. Reverse transcriptase (RT)-PCR analysis with gene-specific primers demonstrated that GGT1 and GGT2 transcripts are detected in Arabidopsis seedlings grown in the light or in darkness (Fig. 4). GGT1 and GGT2 transcripts were also detected in mature leaves and green siliques of Arabidopsis; however, only GGT2 transcripts were detected in roots, where GGT1 transcripts were not observed. Although GGT1 transcripts were observed in 2- and 4-d-old plate-grown seedlings grown in continuous light or darkness, GGT2 transcripts were not detected in 4-d-old dark-grown seedlings. The transcript expression patterns observed for GGT1 and GGT2 were similar to that of AGT1 (Fig. 4), a photosynthetic gene (Liepman and Olsen, 2001).

Enzymatic Activity of Arabidopsis GGT1 and GGT2

The EST 70G6T7 was obtained from the Arabidopsis Biological Resource Center (Ohio State University, Columbus) because it contained the entire predicted coding sequence of GGT1, including 5’- and 3’-untranslated regions (UTRs). The 1,714-bp cDNA contained a 1,443-bp coding sequence that is flanked by 147 nucleotides of 5’-UTR and 124 nucleotides of 3’-UTR, and is predicted to encode a polypeptide of 53.3 kD. An in-frame stop codon, located one codon upstream of the predicted start codon, suggests that this cDNA contains the complete coding sequence of GGT1. To determine the activity of the enzyme encoded by this cDNA, the coding sequence of GGT1 was subcloned into the bacterial expression vector pET-28. Recombinant GGT1 was soluble when expressed in E. coli. Lysates of bacteria expressing this construct contained significantly increased levels of GGT, GPT, and AKT activity compared with empty vector controls (Fig. 5). AGT activity was also detectable, but GGT1 did not catalyze SGT or AspAT reactions (data not shown).

RT-PCR primers to amplify the coding sequence of GGT2 were designed using the sequence of the putative full-length cDNA (accession no. AY035130). The RT-PCR product was sequenced and corresponded perfectly to bases 107 to 1,688 of the putative full-length GGT2 cDNA. The 1,581-bp RT-PCR product contained 1,443 bp of coding sequence flanked by 19 nucleotides of 5’-UTR and 119 nucleotides of 3’-UTR, and was predicted to encode a

<table>
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<th>Peaks Observed</th>
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*Observed peaks in bold indicate diagnostic peaks predicted for GGT1 but not for GGT2.
protein of 53.4 kD. An in-frame stop codon, located four codons upstream of the predicted start codon, indicates that this cDNA contains the complete coding sequence of **GGT2**. Recombinant GGT2 was soluble when expressed in *E. coli*; lysates of bacteria expressing this construct exhibited significantly increased activity.

Figure 3. Sequence analysis of Arabidopsis alanine aminotransferases. A, Two peroxisomal Arabidopsis AlaAT homologs (**AtGGT1**, AGI locus no. At1g23310; and **AtGGT2**, AGI locus no. At1g70580) were aligned with the putative cytosolic Arabidopsis AlaAT isozyme (**AtAlaATc**, AGI locus no. At1g17290), the putative mitochondrial Arabidopsis isozyme (**AtAlaATm**, AGI locus no. At1g23310), and human AlaAT (**HsAlaAT**, accession no. P24298) to produce a consensus sequence (cons.) using the ClustalW algorithm. Asterisks denote residues identical in all five sequences; dots indicate residues similar in at least three of the sequences. Black circles indicate the four residues that best conform to the aminotransferase signature; K291 is the predicted PLP cofactor-binding site of GGT1. A solid bar above the carboxyl terminus of GGT1 and GGT2 indicates the putative PTS1. Residues in bold in the GGT1 sequence correspond to tryptic fragments identified with MALDI-TOF analysis of purified protein with GGT activity from the hydroxylapatite fraction. B, Pair-wise sequence similarity and identity between Arabidopsis and human AlaAT homologs. Percent similarity between two sequences is shown above the diagonal line; percent identity is shown below the diagonal line.
GGT1 and GGT2, Peroxisomal Ala Aminotransferases in Arabidopsis

Subcellular Localization of GGT Activity

Plant AlaATs are localized in multiple cellular locations including the cytosol, peroxisomes, and mitochondria. GGT activity has been found in peroxisomes and the cytosol of various plant species, and also within algal mitochondria. To determine the subcellular localization of GGT activity in Arabidopsis, extracts of young seedlings were subjected to Suc gradient fractionation. Fractions were assayed for organellar marker enzyme activities, including catalase as a peroxisomal marker, fumarase as a mitochondrial marker, and chlorophyll to indicate chloroplasts. Fractions were also assayed for GGT activity. Peak GGT activity cofractionated with the catalase peak, very little GGT activity cofractionated with the mitochondrial and chloroplast peaks (Fig. 6). The GGT activity observed in Arabidopsis peroxisomes is likely the sum of the contributions from

To compare the enzymatic activity of these two nearly identical aminotransferases, recombinant GGT1 and GGT2 were chromatographically purified to near homogeneity (Fig. 5). Both purified recombinant proteins catalyzed GGT, GPT, and AKT reactions (Fig. 5B; Table III). These purified aminotransferases had very similar features for the amino acid substrates Glu and Ala, as well as the 2-oxoacid substrates glyoxylate, pyruvate, and 2-oxoglutarate. The purified recombinant aminotransferases also had similar kinetic characteristics compared with the protein purified from Arabidopsis leaves (Table III). Because aminotransferase reactions proceed via a bimolecular ping-pong mechanism (Velick and Vavra, 1962; Henson and Cleland, 1964; Nakamura and Tolbert, 1983; Leegood et al., 1995) or thermodynamic reasons (Smith, 1985), B, Lysates of bacteria (approximately 100 μg of protein) expressing the empty pET-28 vector, or this pET vector containing the AtGGT1 or AtGGT2 cDNA, were separated by SDS-PAGE and stained with Coomassie Brilliant Blue. Total cellular protein was collected before induction with isopropyl-β-D-thiogalactopyranoside (IPTG; pre), or 4 h after induction with IPTG (post). Recombinant AtGGT1 and AtGGT2 were chromatographically purified as described in “Materials and Methods”; approximately 11 μg of purified recombinant GGT1 and 18 μg of purified GGT2 are shown. The presence (+) or absence (−) of various aminotransferase activities in the whole-cell lysates or purified protein preparations is indicated below the gels. The activity of purified recombinant AtGGT1 and AtGGT2 for each aminotransferase reaction relative to the GGT reaction is shown below each purified protein. Because the recombinant proteins were at different concentrations, a specific activity of 15.5 units GGT activity mg protein−1 was set as 100% relative activity for AtGGT1, whereas a specific activity of 26.9 units GGT activity mg protein−1 was set as 100% relative activity for AtGGT2.

Expression, purification, and enzymatic characterization of AtGGT1 and AtGGT2. A, Four aminotransferase reactions catalyzed by GGT1 and GGT2: GGT, GPT, AKT, and AGT. Transaminations involving glyoxylate are thought to be irreversible because of low affinity of glyoxylate aminotransferases for Gly (Nakamura and Tolbert, 1983; Leegood et al., 1995) or thermodynamic reasons (Smith, 1985). B, Lysates of bacteria (approximately 100 μg of protein) expressing the empty pET-28 vector, or this pET vector containing the AtGGT1 or AtGGT2 cDNA, were separated by SDS-PAGE and stained with Coomassie Brilliant Blue. Total cellular protein was collected before induction with isopropyl-β-D-thiogalactopyranoside (IPTG; pre), or 4 h after induction with IPTG (post). Recombinant AtGGT1 and AtGGT2 were chromatographically purified as described in “Materials and Methods”; approximately 11 μg of purified recombinant GGT1 and 18 μg of purified GGT2 are shown. The presence (+) or absence (−) of various aminotransferase activities in the whole-cell lysates or purified protein preparations is indicated below the gels. The activity of purified recombinant AtGGT1 and AtGGT2 for each aminotransferase reaction relative to the GGT reaction is shown below each purified protein. Because the recombinant proteins were at different concentrations, a specific activity of 15.5 units GGT activity mg protein−1 was set as 100% relative activity for AtGGT1, whereas a specific activity of 26.9 units GGT activity mg protein−1 was set as 100% relative activity for AtGGT2.

Materials and Methods

Gene-specific RT-PCR analysis of AtGGTs. RT-PCR with gene-specific primers was used to examine AtGGT transcript presence in total RNA samples prepared from 2- and 4-d-old dark-grown (D2 and D4) and light-grown (L2 and L4) Arabidopsis seedlings, as well as mature leaves, green siliques (sil), and roots. RT-PCR products were separated on 1.5% (w/v) agarose gels and visualized with ethidium bromide in UV light. The cDNA lanes in the left represent PCR reaction products using the indicated cDNAs as the template and the same gene-specific primers as were used in the corresponding RT-PCR reactions. The positions of molecular mass standards (in bp) are indicated to the right of each gel. No RT-PCR product corresponding in size to the cDNA control was observed in control reactions lacking RT; the larger band seen with ATG1 primers and root mRNA is probably because of amplification of the genomic sequence in the absence of transcript. All reactions were repeated at least twice, with similar results.
GGT1 and GGT2 because both catalyze this reaction. It was not possible to determine the individual contribution of each enzyme to the total activity in peroxisomes using activity assays; however, GGT1 probably catalyzes most of the activity based on the comparative EST abundance of these genes. These subcellular fractionation data are consistent with a solely peroxisomal localization of GGT activity in Arabidopsis. The lack of GGT activity outside of the peroxisomes also suggests that the two other AlaAT isozymes of Arabidopsis do not catalyze this transamination, but may be specific for the GPT/AKT reaction.

**DISCUSSION**

Two peroxisomal glyoxylate aminotransferases are central to the photorespiratory pathway; one catalyzes the SGT transamination, the other catalyzes GGT and AGT transaminations (Fig. 7). Until recently, the identity of the corresponding enzymes was unknown. We previously demonstrated that a peroxisomal AGT1 homolog catalyzes the SGT reaction in Arabidopsis (Liepman and Olsen, 2001). The isolation and characterization of two Arabidopsis AlaATs with glyoxylate aminotransferase activity (GGT1 and GGT2) are presented here.

The amino acid sequences of GGT1 and GGT2 are 99% similar, probably because of a segmental duplication of the region of chromosome I containing these genes (AGI, 2000). GGT1 and GGT2 are also closely related to putative mitochondrial and cytosolic AlaAT isozymes in Arabidopsis. GGT1 and GGT2 both catalyze at least four aminotransferase reactions (Fig. 5), the two glyoxylate transaminations GGT and AGT, and the reversible AKT/GPT transamination that is characteristic of AlaATs. Kinetic analyses of GGT1 and GGT2 indicate that the amino acid substrates Glu and Ala, and the 2-oxoacids glyoxylate, 2-oxoglutarate, and pyruvate, are all possible in vivo substrates of these enzymes (Table III). Where the concentrations of these metabolites have been measured in plant cells, the $K_m$ values of GGT1 and GGT2 for these substrates fall well within the observed ranges (Winter et al., 1993, 1994). The similar transcript expression patterns (Fig. 4) and enzymatic activities of GGT1 and GGT2 indicate that these enzymes may serve partially redundant functions in Arabidopsis.

GGT activity was localized exclusively to Arabidopsis peroxisomes (Fig. 6). The discovery of two peroxisomal AlaAT isozymes in Arabidopsis is consistent with observations with spinach (*Spinacia oleracea*) leaves; however, in spinach, one form catalyzed the GGT reaction and the other did not (Noguchi and Hayashi, 1981).

Animals contain two forms of glyoxylate aminotransferases: AGT1 and mitochondrial AGT2. Because an AGT1 homolog catalyzes the SGT reaction of photorespiration in Arabidopsis (Liepman and Olsen, 2001), a logical candidate for another peroxisomal glyoxylate aminotransferase was an AGT2 homolog. The Arabidopsis genome contains three AGT2 homologs, each with a putative PTS1 (Fig. 1). The localization of AGT2 appears to be limited to mitochondria in animals, where its physiological role remains unclear (Takada and Noguchi, 1980; Noguchi and Mori, 1981; Ogawa et al., 1990; Lee et al., 1995).

When expressed in *E. coli*, one of the Arabidopsis AGT2 homologs did not appear to catalyze any of the glyoxylate aminotransferase or AlaAT activities assayed. It was not possible to determine whether this lack of activity resulted from enzymatic inactivity or

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**Table III. Kinetic parameters of purified Arabidopsis GGTs**

<table>
<thead>
<tr>
<th>Reaction</th>
<th>Amino Acid $K_m$ (mM)</th>
<th>2-Oxoacid Concentration</th>
<th>2-Oxoacid $K_m$ (mM)</th>
<th>Amino Acid Concentration</th>
</tr>
</thead>
<tbody>
<tr>
<td>Arabidopsis GGT*</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GGT</td>
<td>3.00</td>
<td>5</td>
<td>0.27</td>
<td>10</td>
</tr>
<tr>
<td>GPT</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>AKT</td>
<td>7.16</td>
<td>2.5</td>
<td>0.27</td>
<td>20</td>
</tr>
<tr>
<td>Recombinant GGT1b</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GGT</td>
<td>1.97</td>
<td>5</td>
<td>0.21</td>
<td>10</td>
</tr>
<tr>
<td>GPT</td>
<td>–</td>
<td>–</td>
<td>0.31</td>
<td>10</td>
</tr>
<tr>
<td>AKT</td>
<td>4.76</td>
<td>2.5</td>
<td>0.31</td>
<td>20</td>
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<tr>
<td>Recombinant GGT2c</td>
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<td></td>
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<td></td>
</tr>
<tr>
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<td>GPT</td>
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<td>–</td>
<td>0.36</td>
<td>10</td>
</tr>
<tr>
<td>AKT</td>
<td>3.56</td>
<td>2.5</td>
<td>0.51</td>
<td>20</td>
</tr>
</tbody>
</table>

*Purified from Arabidopsis leaves. bPurified from lysate of *E. coli* expressing pET-GGT1. cPurified from lysate of *E. coli* expressing pET-GGT2.
if the recombinant enzyme was active but does not catalyze the assayed reactions. Plants containing mutations in one or more of these genes may provide another means to examine the physiological significance of these enzymes. If one or more of these Arabidopsis AGT2 homologs is peroxisomal, as suggested by the PTS1 in each sequence (Fig. 1), it is highly unlikely that such double mutant plants could be isolated with their screening method. GGT1 and GGT2 transcripts are present in etiolated and light-grown Arabidopsis seedlings (Fig. 4), and GGT activity has been observed in etiolated cucumber (Cucumis sativus), where it increases in response to greening (Noguchi and Fujiwara, 1982). These observations suggest that these proteins may be active in additional pathways other than photorespiration; thus, mutations in one or both of these genes could prove lethal. It will be interesting to investigate the phenotypes of plants with disruptions within the GGT1 and GGT2 genes. Using single and double mutant plants, it should be possible to define the

Figure 6. Localization of GGT activity to Arabidopsis peroxisomes by subcellular fractionation. Extracts of 2-week-old light-grown Arabidopsis seedlings were separated by Suc density centrifugation. A, Each fraction was assayed for GGT activity and the peroxisomal marker enzyme catalase as described in "Materials and Methods." B, Gradient fractions were also assayed for the mitochondrial marker fumarase, chloroplast marker chlorophyll, and Suc content. The specific activity (μmol min⁻¹ mg⁻¹ total protein) of each enzyme is shown (catalase × 10⁴, fumarase × 10⁶, and GGT × 10⁷); chlorophyll is expressed as mg chlorophyll mg⁻¹ protein. Fraction 1 is from the bottom of the gradient; fraction 12 is the top.

Figure 7. The photorespiratory peroxisomal glyoxylate aminotransferases, and other possible aminotransferase reactions in plant peroxisomes. Photorespiration involves reactions and metabolite exchange between chloroplasts, peroxisomes, and mitochondria. Key aminotransferases catalyzing some of these reactions in peroxisomes are indicated. Numbered enzyme key: 1, Rubisco; 2, phosphoglycerate phosphatase; 3, glycolate oxidase; 4, Gly decarboxylase/Ser transhydroxymethyltransferase; 5, hydroxyproline reductase; and 6, glycine kinase. PGA, 3-Phosphoglycerate; P-glycolate, 2-phosphoglycerate; RuBP, ribulose 1,5-bisphosphate.
precise roles of each GGT. If double mutants have no GGT activity, this would rule out the possibility that one or more of the Arabidopsis AGT2 homologs also catalyzes this reaction.

Because of their relatively high degree of sequence conservation, Arabidopsis AlaATs may be good targets for directed evolution experiments to alter substrate specificity. Several groups have successfully changed the substrate specificity of bacterial Asp AT (Yano et al., 1998; Graber et al., 1999; Oue et al., 1999). Many AlaATs, including presumably the mitochondrial and cytosolic isozymes of Arabidopsis, are specific for the reversible AKT/GPT transamination, and do not accept glyoxylate as an amino acceptor (Rech and Crouzet, 1974; Gazeu-Reyjal and Crouzet, 1976; Good and Muench, 1992). In addition to AKT and GPT transaminations, Arabidopsis GGT1 and GGT2 also catalyze GGT and AGT reactions. Although these aminotransferases are closely related to the other AlaATs in Arabidopsis, there are several regions where the sequences diverge. Thus, it may be possible to alter the substrate specificity of Arabidopsis AlaATs to add new 2-oxoacid substrates to the range of these enzymes, without significantly changing the overall affinity of these proteins for their native substrates.

The two commonly described glyoxylate transaminations of the photorespiratory pathway are the SGT and GGT reactions (Fig. 7). Arabidopsis GGT1 and GGT2 both catalyze an AGT reaction in addition to the GGT reaction, consistent with the work of a number of groups (Noguchi and Hayashi, 1981; Nakamura and Tolbert, 1983, Yu et al., 1984), but the physiological significance of the AGT reaction for photorespiration has been disputed (Betsche, 1983; Yu et al., 1984). Estimates based upon whole-leaf labeling analysis suggested that Ala contributed 3 times more amino groups to photorespiratory Gly formation than Glu did (Betsche, 1983), whereas another study involving feeding metabolites to purified peroxisomes concluded that Glu contributed more to glyoxylate transamination than did Ala (Yu et al., 1984). It is noteworthy that both Glu and Ala concentrations in the cytosol of leaves exposed to light are very high (3–90 mm; Winter et al., 1993, 1994), and that the $K_m$ values of GGT1 and GGT2 for these substrates fall near the lower limit of this range (Table III). The concentrations of Glu and Ala in the cytosol, however, may not reflect the concentrations of these metabolites inside peroxisomes because the peroxisomal membrane is not freely permeable to these amino acids (Liang and Huang, 1983). Thus, the relative glyoxylate aminotransferase activity in planta with Glu and Ala may depend upon other factors determining the supply of these substrates, including metabolite transport and the activity of other anabolic and catabolic pathways.

Although the photorespiratory pathway has been the subject of many detailed investigations and the proposed target for metabolic engineering strategies to increase crop productivity, genes encoding some of the enzymes within the pathway have only recently been identified. Future studies to more thoroughly define the physiological roles of these enzymes should benefit from the recent generation of plants with disruptions in these genes. Such studies, along with additional efforts to identify and characterize genes encoding the remaining unidentified photorespiratory enzymes, are necessary for a complete understanding of this physiologically significant pathway.

MATERIALS AND METHODS

Purification of Arabidopsis GGT

All purification steps were carried out at 4°C, unless otherwise noted. Five grams of Arabidopsis leaf tissue was pulverized in liquid nitrogen with a mortar and pestle. Frozen leaf powder was homogenized in a ground-glass homogenizer containing 15 mL of extraction buffer (50 mM MES-NaOH [pH 6], 0.2 mM PLP, 10% [v/v] glycerol, and 0.1% [v/v] Triton X-100). The plant extract was clarified twice by centrifugation at 29,000g for 10 min. Finely powdered ammonium sulfate was added incrementally to the cleared extract to bring the solution to 45% (w/w) saturation. Precipitated proteins were pelleted by centrifugation for 10 min at 29,000g and discarded. The supernatant was brought to 60% (w/v) saturation with ammonium sulfate. Precipitated proteins were recovered by centrifugation for 10 min at 29,000g. The 45% to 60% (w/v) pellet was resuspended in 2.5 mL of extraction buffer, and desalted using a PD-10 column (Pharmacia Biotech, Piscataway, NJ) before SP-Sepharose FF (Pharmacia Biotech) chromatography. GGT displayed very low affinity for SP-Sepharose media, and was eluted with 50 mM MES-NaOH (pH 6), 10% (v/v) glycerol, and 0.2 mM PLP. Fractions containing GGT activity were pooled and concentrated using a Centricon YM-30 centrifugal concentrator device. The buffer was exchanged for 50 mM Tris-HCl (pH 8), 10% (v/v) glycerol, and 0.2 mM PLP (buffer A) using a PD-10 column. The sample was applied to a Q-Sepharose FF (Pharmacia Biotech) column and eluted with a linear ammonium sulfate gradient (0–150 mM) in buffer A. Fractions containing peak GGT activity were pooled, concentrated, and buffer exchanged for buffer B (50 mM Tris-HCl [pH 7.1], 10% [v/v] glycerol, and 10 mM potassium phosphate). The sample was applied to a hydroxylapatite (Bio-gel HTP, Bio-Rad Laboratories, Hercules, CA) column, and eluted with a linear gradient of potassium phosphate (10–200 mM) in buffer B.

MALDI-TOF Analysis

After the hydroxylapatite chromatography step, a Coomassie Blue-stained protein band of approximately 54 kD co-fractionating with peak GGT activity throughout the purification procedure was excised from an acrylamide gel after SDS-PAGE. An in-gel trypsin digestion was performed using 500 ng of modified porcine trypsin (Promega, Madison, WI) as described (Phadke et al., 2001). Sample preparation and MALDI-TOF analysis followed the procedure of Phadke et al. (2001) with the following modification: Peptide mass fingerprints were searched against the Arabidopsis proteins of the National Center for Biotechnology Information Database (4/19/01 version) using the MS-Fit program (Protein Prospector package; Clausner al., 1999; http://prospect.ucsf.edu/), with a mass accuracy of 50 ppm. For the search, trypsin digestion with a maximum of two missed enzymatic cleavages, unmodified Cys, modification by acrylamide, peptide N-terminal Glu to pyro-Glu, Met oxidation, and protein N-terminal acetylation were considered.

Primer Sequences

The following sequences correspond to primers used for cloning procedures and RT-PCR. Sequences in bold indicate restriction sites designed to facilitate specific cloning steps described below: A14g39960-NcoI,
RT-PCR Analysis

Arabidopsis seedlings were grown on germination plates (Olsen et al., 1993). Total RNA was collected and 4 d after germination from whole etiolated seedlings and seedlings grown under continuous light. Total RNA was also collected from mature Arabidopsis leaves, siliques, and roots using the RNeasy plant mini-kit (Qiagen, Valencia, CA). RNA was analyzed on agarose:formaldehyde gels (Liepman and Olsen, 2001) and quantitated spectrophotometrically. RT-PCR analysis was conducted using the Access RT-PCR system and manufacturer’s recommended conditions (Promega). One hundred nanograms of total RNA from the specified tissues was used as template. RT-PCR products corresponding in size to the cDNA products from one experiment that was repeated at least two times with similar results.

Constructs

The EST 229N617 was selected and obtained from the Arabidopsis Biological Resource Center EST collection (Newman et al., 1994) because it appeared to contain the complete coding sequence of an Arabidopsis AGT2 homolog. The pZL2 vector (Life Technologies/Gibco-BRL, Cleveland) was used to introduce a unique NcoI restriction site containing the start codon position of AGT2. The NcoI/ HindIII fragment of pZL2-AGT2 was subcloned into the corresponding sites of the pET-28 vector (Novagen) to produce pET-AGT2. Both strands of cDNA clones of AGT1 and AGT2 from Arabidopsis were fully sequenced and the sequences deposited in GenBank: AGT1 (accession no. AF479639) and AGT2 (accession no. AF479640).

Recombinant AGT1 and AGT2 Expression and Purification from Escherichia coli

BL21(DE3) cells were transformed with pET-AGT1, pET-AGT2, or the pPET empty vector, and grown on Luria-Bertani (LB) plates supplemented with kanamycin. Single colonies were inoculated to 3 mL of LB with kanamycin selection. One hundred microliters from the overnight culture was used to inoculate 250 mL of fresh LB media. Cells were shaken at 37°C until an OD600 of approximately 0.5 was reached before the addition of 500 µM IPTG to induce protein expression. After the addition of IPTG, cultures were supplemented with 50 µM pyridoxine hydrochloride and shaken at 25°C. Four to 12 h after induction, cells were harvested by centrifugation at 4,068 g for 10 min. To test for protein expression and enzyme activity, bacterial whole-cell lysates were made from 1.5 mL aliquots of cells collected before and after induction with IPTG. Whole-cell lysates were prepared by resuspending the cells at a concentration of 5 OD600, mL⁻¹ in cold lysis buffer (50 mM Tris-HCl [pH 7.1], 10 mM EDTA, 10 mM NaCl, 0.1 mM PPL, 10% [v/v] glycerol, 0.1% [v/v] β-mercaptoethanol, and 0.1% [v/v] Triton X-100). Cells were broken mechanically by repeated cycles of freezing and thawing in liquid nitrogen. AGT1 and AGT2 were purified from the soluble fraction of E. coli lysates prepared from 250-mL cultures as described above for the Arabidopsis leaf protein. Satisfactory purifications of AGT1 and AGT2 required only Q-Sepharose FF and hydroxyapatite chromatography.

Enzyme Assays

GGT, GPT, AGT, and AKT activities were measured spectrophotometrically in quartz cuvettes with a UV1601 Spectrophotometer (Shimadzu, Columbia, MD) at 25°C. GGT activity was measured at 340 nm using an assay modified from Huang et al. (1976) by coupling the reductive amination of 2-oxoglutarate produced by GGT to the oxidation of NADH, catalyzed by excess bovine liver glutamic dehydrogenase (G2501, Sigma, St. Louis). To assay GGT activity, protein extract (5–10 µL) was added to a 1-mL reaction mixture containing 60 mM potassium phosphate (pH 7.5), 5 mM glycine, 0.17 mM NADH, and 2.2 units mL⁻¹ glutamic dehydrogenase. GPT activity was measured using conditions identical to the GGT assay except that 3 mM pyruvate replaced glyoxylate as the amino acceptor. AKT activity was measured at 340 nm by coupling the reduction of pyruvate to the oxidation of NADH, catalyzed by excess rabbit muscle lactate dehydrogenase (Sigma). To assay AKT activity, protein extract (5–10 µL) was added to a 1-mL reaction mixture containing 70 mM Hepes-NaOH (pH 7.5), 2.5 mM 2-oxoglutarate, 0.17 mM NADH, and 5 units mL⁻¹ lactate dehydrogenase, AGT, SGT, and ASpAT activities were assayed as described by Liepman and Olsen (2001) and Rehfield and Tolbert (1972). Although the AGT assay allowed for clear detection of AGT activity, increasing concentrations of glyoxylate inhibited the assay, limiting its utility for kinetic studies (Rehfield and Tolbert, 1972; Roberts and Lees, 1997). For each aminotransferase assay, the reaction was initiated by adding amino acid to a final concentration of 10 to 20 mM to the sample cuvette; water was added instead of amino acid in the reference cuvette. All assays were linear over the time course of the measurements. For kinetic measurements, substrate concentrations ranged from 0.5 to 100 mM for amino acids, and 0.025 to 5 mM for 2-oxoacids. Arabidopsis GGTs displayed typical Michaelis-Menten kinetics within these substrate ranges. Kₘ values were calculated from (at least) triplicate data points using nonlinear regression software (PRISM, GraphPad Software, San Diego). One unit of activity corresponds to the amount of enzyme converting 1 µmol Glu to 2-oxoglutarate per minute under assay conditions.

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Subcellular Fractionation

Subcellular fractionation was performed as previously described (Liepman and Olsen, 2001). GGT activity in Suc gradient fractions was assayed as described above except that 0.1% (v/v) Triton X-100 was included in the assay mixture to disrupt organellar membranes and ensure access to matrix proteins. Gradient fractions were analyzed for protein concentration, Suc content, and organellar marker enzymes as previously described (Liepman and Olsen, 2001).

ACKNOWLEDGMENTS

We thank Mr. Nikhil Phadke for excellent technical assistance with MALDI-TOF analysis. We also thank Drs. Marianne Laporte, Eran Pichersky, and Steven Clark and Ms. Tanya Johnson for insightful discussions.

Received July 18, 2002; returned for revision September 6, 2002; accepted September 30, 2002.

LITERATURE CITED

Collard H, Muench NE, Tolbert NE (1964) Kinetic studies of glutamic oxaloacetic transaminase from the scots pine (Pinus sylvestris L.) seedling. Planta 103: 250–258


