Chapter 3: The catalytic mechanism of a recombinant bovine GLYAT

Enzymatic characterisation and elucidation of the catalytic mechanism of a recombinant bovine glycine N-acyltransferase

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Erratum: In this paper it is reported that Glu\textsuperscript{226} of bovine GLYAT is the catalytic residue. However, this residue was incorrectly numbered and should be Glu\textsuperscript{227} of the bovine GLYAT reference sequence (NP_803479). This mistake has been brought to the attention of Drug Metabolism and Disposition.
Enzymatic Characterization and Elucidation of the Catalytic Mechanism of a Recombinant Bovine Glycine N-Acetyltransferase

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ABSTRACT:

Glycine conjugation, a phase II detoxification process, is catalyzed by glycine N-acetyltransferase (GLYAT; E.C. 2.3.1.13). GLYAT detoxifies various xenobiotics, such as benzoic acid, and endogenous organic acids, such as isovaleric acid, which makes GLYAT important in the management of organic acidemias in humans. We cloned the open reading frame encoding the bovine ortholog of GLYAT from bovine liver mRNA into the bacterial expression vector pC227 Bl. The recombinant enzyme was expressed, partially purified, and enzymatically characterized. Protein modeling was used to predict Glu256 of bovine GLYAT to be catalytically important. This was assessed by constructing an E226Q mutant and comparing its enzyme kinetics to that of the wild-type recombinant bovine GLYAT. The Michaelis constants for benzoyl-CoA and glycine were determined and were similar for wild-type recombinant GLYAT, E226Q recombinant GLYAT, and GLYAT present in bovine liver. At pH 8.0, the E226Q mutant GLYAT had decreased activity, which could be compensated for by increasing the reaction pH. This suggested a catalytic mechanism in which Glu256 functions to deprotonate glycine, facilitating nucleophilic attack on the acetyl-CoA. The recombinant bovine GLYAT enzyme, combined with this new understanding of its active site and reaction mechanism, could be a powerful tool to investigate the functional significance of GLYAT sequence variations. Eventually, this should facilitate investigations into the impact of known and novel sequence variations in the human GLYAT gene.

Introduction

Humans and other animals are constantly exposed to various toxic substances. Homeostasis is maintained by the detoxification and elimination of these toxins. Detoxification is commonly divided into phase I and phase II detoxification enzyme systems (Liska, 1998). Phase I detoxification enzymes convert toxic compounds to secondary metabolites that are frequently more chemically reactive and thus more toxic than the original compounds. Phase II detoxification enzymes decrease the toxicity of the secondary metabolites by means of conjugation to soluble carrier molecules such as glycine or glutathione. The resulting conjugates are usually less toxic, more water-soluble, and more readily excreted in urine than the secondary metabolites. In humans, impaired detoxification has been associated with diseases such as cancer and with adverse reactions to pharmaceutical drugs (Campbell et al., 1988; Liska, 1998; Wallig, 2004).

Glycine N-acetyltransferase (GLYAT; E.C. 2.3.1.13) is a phase II detoxification enzyme found in the liver and kidney mitochondria of mammals (Schachter and Taggart, 1954). GLYAT is a member of the GGT-related N-acetyltransferase (GNAT) superfamily, one of the largest and most functionally diverse superfamilies of enzymes known (Vetting et al., 2005). GLYAT uses glycine and an acyl-CoA as substrates, forming free CoA and an acylglycine as products (Dyda et al., 2000; van der Westhuizen et al., 2000; Vetting et al., 2005). The acylglycines are less toxic than the un conjugated organic acids and are more readily excreted into urine by the kidneys (Tanaka and Isselbacher, 1967; Dufy et al., 1995). Examples of xenobiotic metabolites that are detoxified by conjugation to glycine include salicylic acid, benzoic acid, and methylbenzoic acid, a metabolite of the industrial solvent xylene (Campbell et al., 1988; Dufy et al., 1995). Studies have shown that in humans, metabolism of aspirin to its glycine conjugate may be impaired by exposure to xylene, which is detoxified via the same pathway (Campbell et al., 1988). Organic acids of endogenous origin, including isovaleric acid, 3-methylcrotonic acid, tiglic acid, and hexanoic acid, are also detoxified by conjugation to glycine. For this reason, glycine conjugation is of key importance to the management of inherited organic acidemias in humans (Kelvraa and Gregersen, 1986; Ogier de Bauaney and Saudubray, 2002). For example, isovaleric acidemia is treated by means of glycine supplementation, which enhances formation and excretion of isovalerylglucine (Tanaka et al., 1966; Tanaka and Isselbacher, 1967). Isovaleric acidemia is only one of a large group of human diseases known as CoA sequestration, toxicity, or redistribution (CARTOR) disorders (Mitchell et al., 2008), which represent a...
major segment of biochemical genetics. One of the primary mechanisms of pathogenesis in CASTOR disorders is depletion of free CoA, which derail cellular metabolism. GLYAT converts the accumulated acyl-CoA to acylglycines and free CoA, restoring levels of free CoA and carnitine (Salumaa, 1991). Significant interindividual variation in glycine conjugation capacity has been demonstrated using human liver samples (Temellini et al., 1993). The basis for this variability is not understood, but genetic variations in the coding sequence may be a factor. Six nonsynonymous single-nucleotide polymorphisms have been identified in the open reading frame of the human GLYAT gene. However, it is not yet understood whether, or how, these variations influence enzyme function (Yamamoto et al., 2009; Lind Caradenas et al., 2010).

Because of the large number of compounds metabolized by GLYAT, the human ortholog is of clinical interest. However, we have not yet been able to express an enzymatically active recombinant human GLYAT. Here, we report the bacterial expression and enzymatic investigation of a recombinant bovine GLYAT. Bovine GLYAT is an enzyme expressed in bovine liver and kidney mitochondria, with a molecular mass ranging to be between 33 and 36 kDa (Nandi et al., 1979; van der Westhuizen et al., 2000). Investigations of human and bovine GLYAT have shown that these enzymes are similar in terms of molecular mass, reaction kinetics, and substrate specificity (Bartlett and Gompertz, 1974; Kelly and Vessey, 1993; Lin Cardenas et al., 2010). The alignment generated by GenTHREADER was used with the structural model of the bovine GLYAT, combined with molecular modeling and site-directed mutagenesis, was used to investigate the catalytic mechanism used by GLYAT. The data suggest that residue Glu<sup>209</sup> of bovine GLYAT serves as a general base catalyst. The identification of this catalytic residue provides the first insights into the catalytic mechanism and active site location of the GLYAT enzymes.

Materials and Methods

Sequence Analysis and Molecular Modeling. The bovine GLYAT amino acid sequence (NP_847470) was submitted to the GenTHREADER server (Jones, 1999) for identification of potential structural homologs. An uncharacterized protein from <i>Drosophila melanogaster</i>, with Protein Data Bank (PDB) code 1SQH, was identified as the best homolog and was used for molecular modeling. Although this protein is only 13% identical to bovine GLYAT, it is structurally very similar to other GNAT enzymes and was used as template structure because of the exceptional conservation of structure in the GNAT superfamily of acyltransferases, despite there being virtually no sequence similarity between some members of the superfamily (Venting et al., 2005). The alignment generated by GenTHREADER was used with the structure of 1SQH as input for model generation using MODELLER 9.3 (Eswar et al., 2005). For side-chain modeling, SCWRL 3.0 (Dunbrack Lab, Fox Chase Cancer Center, Philadelphia, PA) was used (Wang et al., 2008). The molecular model was superimposed with the structures of N-acetyltransferase (PDB code 1C9W), dopamine N-acetyltransferase (PDB code 2Q4V), and Esat (PDB code 2GHE) using the matchmaker algorithm of University of California, San Francisco, Chimera (UCSF Chimera) (Pettersen et al., 2004). UCSF Chimera was used to generate images of the molecular model. The bovine GLYAT amino acid sequence was also submitted to a Basic Local Alignment Search Tool (BLAST) (www.ncbi.nlm.nih.gov) search, and the homologs were aligned using CLUSTAL X 2.0.10.

Cloning of the Bovine GLYAT Open Reading Frame into the Bacterial Expression Vector pColdIII. Total RNA was isolated from bovine liver tissue using the RNeasy Mini Kit (QIAGEN, Valencia, CA). Cloned avian myeloblastosis virus reverse transcriptase (Invitrogen, Carlsbad, CA) was used to generate cDNA from the bovine liver mRNA. The open reading frame of bovine GLYAT was amplified from the cDNA using oligonucleotide primers (5'-GCC GCA TAT GAT TGT CCT GCT GC-3' and 5'-CAT CTC GAG TCA CAG ACG TTC AC-3') that contained NdeI and XhoI restriction endonuclease recognition sites to facilitate cloning into pColdIII (Takara Bio USA, Madison, WI). Oligonucleotide primers were obtained from Invitro Biotechnical Industries (Portoria, South Africa). The pColdIII vector was modified to encode a C-terminal hexahistidine tag after the XhoI site. The recombinant plasmid was sequenced to confirm that bovine GLYAT had been cloned without any sequence alterations.

Construction of the E226Q Mutant Recombinant Bovine GLYAT. Site-directed mutagenesis using a mega-primer method (Aljan and Lein, 1993) was used to generate the E226Q mutant coding sequence for the E226Q bovine GLYAT. The mutant oligonucleotide primer 5'-CCA GAC GAG ACA GAT GGC GAT GAT G-3' was used with the reverse primer 5'-CTT CTC GAG GTC CTA GCT TCA GTG 3' to generate a 240-base pair ampiclon. This ampiclon was gel purified and was used in a site-directed mutagenesis reaction with the forward primer 5'-GCC GCA TAT GAT CCT GCT GC-3' to generate a full-length mutated GLYAT coding sequence. The mutated ampiclon was gel purified, digested with NdeI and XhoI, and cloned into pColdIIl Expression and Affinity Purification of Wild-Type and E226Q Recombinant Bovine GLYAT. The pColdIII-bovine GLYAT plasmid was introduced into Origami cells (Novagen, Madison, WI) by electroporation. Expression of the recombinant GLYAT was performed as follows. The cells in 50 ml of overnight culture in Luria Bertani medium, containing 100 mg/ml ampicillin, were harvested by centrifugation at 4000g for 5 min. The cells were resuspended in 200 ml of Luria broth medium containing 50 mg/ml ampicillin. The cultures were incubated at 37°C for 15 h. NADH-1-thio-β-β-galactosidase was added to a final concentration of 0.5 mM. The cultures were incubated at 37°C for 24 h with vigorous shaking. Cells were then harvested by centrifugation at 4000g for 20 min. The cell pellets were resuspended in 5 ml of BagBlaster protein extraction reagent (Novagen) containing 30 µl lysozyme (Novagen) and 25 µl BSA (Boehringer Mannheim). The cultures were incubated at room temperature for 3 min. Insoluble material was removed by centrifugation at 12,000g for 20 min at 4°C. The cleared lysates were processed through Proteo-Ni-TEC 2000 columns (Macherey-Nagel, Düren, Germany) equilibrated with buffer LEW (Macherey-Nagel). The columns were washed with 10 µl of buffer LEW containing 20 mM imidazole. The bound protein was eluted from the columns in 9 µl of buffer ELB (Macherey-Nagel) and was added to Vivaspin ultrafiltration devices (GE Healthcare, Chalfont St. Giles, Buckinghamshire, UK). The proteins were concentrated to approximately 500 µl by centrifugation in a fixed-angle centrifuge at 8000g for 15 min. The proteins were then washed by adding 10 µl of 50 mM Tris-HCl pH 8.0, and repeating the centrifugation to again concentrate the solution to approximately 500 µl. Protein expression and purification were monitored by means of SDS-polyacrylamide gel electrophoresis (PAGE) analysis and Coomassie Brilliant Blue staining (Laemmli, 1970).

Preparation of an Extract Containing Bovine Liver Mitochondrial GLYAT. To prepare an extract containing bovine liver mitochondrial GLYAT, 100 g of liver tissue was homogenized in 400 ml of 0.13 M KCl. The homogenate was centrifuged for 10 min at 6000g. The supernatant was centrifuged again at 9000g for 10 min to isolate mitochondria, which were then lysed by three cycles of freezing and thawing in 10 ml of 0.13 M KCl. The lysates were clarified by centrifugation at 35,000g for 2 h. The GLYAT enzyme was further enriched from these lysates by collecting the fraction soluble between 40 and 66% ammonium sulfate. The precipitate was dissolved in 4 ml of 50 mM Tris-HCl pH 8.0, and was dialyzed overnight against 1000 ml of 50 mM Tris-HCl pH 8.0 (van der Westhuizen et al., 2000). This crude mitochondrial GLYAT preparation is referred to as "bovine liver GLYAT" in the remainder of this article.

Enzyme Assays for Determination of <i>K<sub>v</sub></i> Parameters. Reaction mixtures were 500 µl in volume and contained, in addition to enzyme, 25 mM Tris-HCl, pH 8.0, 0.1 mM DTNB [5,5'-dithiobis(2-nitrobenzoic acid)], and varying concentrations of substrates (Kelvna and Gregersen, 1986). The glycine concentration was varied from 2.5 to 30 mM, and the benzoyl-CoA concentration was varied from 5 to 50 µM. The assays were performed at 30°C, and the change in absorbance at 412 nm over the first 4 min was measured using a UVikon XS spectrophotometer (NorthStar Scientific, Bardey, Leeds, UK) (van der Westhuizen et al., 2000). The absorbance change at 412 nm is the result of reduction of DTNB by the liberated thiol group of CoA, forming 2-nitro-5-thiobenzoate. 2-Nitro-5-thiobenzoate is a yellow species that absorbs at 412 nm with an extinction coefficient of 13.6 mM<sup>-1</sup>cm<sup>-1</sup> (Ellman, 1959).

To each reaction, 1 unit of GLYAT activity was added. A unit of GLYAT activity was defined as a change in ΔA<sub>412</sub> of 0.24 units in 4 min, using cytoxes
with a 1-cm light path, 20 mM glycine, and 100 µM benzoyl-CoA. The amount of enzyme used per assay was defined in this way because the enzymes used were generally used to determine the amount of E226Q recombinant GLAT. Because the same amount of enzyme is used in each assay in a particular experiment, pH is the only variable that influences activity. Reactions that contain all components except enzyme were also performed for control purposes. The reactions were monitored at 412 nm in 96-well plates on a BioTek plate reader and the accompanying Gen5 software (Bio-Tek Instruments, Winooski, VT). Measurements were made every 30 seconds and recorded on nanomoles per minute. Reactions were performed in triplicate, and the data were plotted on a logarithmic scale for the x-axis. Data were plotted using GraphPad Prism 4.02 (GraphPad Software Inc., San Diego, CA).

Results
Prediction of the Catalytic Importance of Glu226 of Bovine GLAT. To investigate the catalytic mechanism of bovine GLAT, a candidate for the catalytic residue had to be identified. A BLAST search using the bovine GLAT amino acid sequence as query was performed. After removing sequences of significantly different length from bovine GLAT, a multiple sequence alignment was performed (Fig. 1A). The bovine GLAT sequence was then used to construct a molecular model. By investigating the superposition of the GLAT model with GNAT enzymes for which the catalytic residues are known, a putative catalytic residue was identified. The Glu226 residue of bovine GLAT coincided spatially (Fig. 1B) with the catalytic residue, His120, of serotonin N-acetyltransferase (Scheibner et al., 2002). Similar results were obtained when this superposition was done using other GNAT enzymes for which catalytic mechanisms are known (Fig. 1B). The Glu226 residue of bovine GLAT was also conserved in the top 40 GLAT homologs obtained by a BLAST search, suggesting the residue to be functionally significant (Fig. 1A shows part of the multiple alignment).

Expression and Purification of Recombinant Bovine GLAT Enzymes. Both the wild-type and E226Q recombinant bovine GLAT were expressed at high levels from the bacterial expression vector pColdIII. Most of the recombinant bovine GLAT, both of the wild-type and the E226Q mutant, was insoluble (Fig. 2A; GLAT is indicated by an arrow). Soluble wild-type and E226Q recombinant GLAT was obtained by means of nickel-affinity chromatography and ultrafiltration (Fig. 2B). The lower bands in Fig. 2B (indicated by the arrow) represent soluble recombinant bovine GLAT enzymes and some copurifying proteins. Expression of the recombinant bovine GLAT enzymes with hexahistidine tags containing serine-glycine linkers of different lengths, to enhance the flexibility and accessibility of the tag, did not improve purification. Expression with the tags of different length did, however, result in size differences being observed for the lower bands in Fig. 2B, indicating that these bands represent the recombinant bovine GLAT enzymes (results not shown). The recombinant bovine GLAT proteins were not subjected to further purification, as the copurified proteins did not seem to interfere with any subsequent investigations.

Kinetic Properties of the Recombinant Bovine GLAT Enzymes. To characterize the wild-type and E226Q recombinant bovine GLAT enzymes, Michaelis constants were determined using glycine

Fig. 1. Prediction of a putative catalytic glutamate residue for bovine GLAT. A, part of a multiple alignment of sequences with significant similarity to bovine GLAT, demonstrating that the Glu226 residue is conserved. Homologous are results of a BLAST search and GenBank accession numbers are shown to the left of the alignment. B, a part of a structural superposition of the structures of SNAT, SSAAT, and East with the bovine GLAT model. The catalytic residue side chains of the GNAT enzymes are shown. The bovine GLAT Glu226 residue is indicated on both the multiple alignment and the molecular model. The small molecule to the right is CoA-Ser, a substrate bound to SNAT. This image was generated using UCSF Chimera.
and benzoyl-CoA and were compared to those for GLYAT extracted from bovine liver mitochondria. Nonlinear regression was used to analyze the kinetic data, and Lineweaver-Burk plots were used to visually represent the data (Fig. 3). The $K_M$ values for benzoyl-CoA were similar for the bovine liver GLYAT and the recombinant bovine enzymes, at approximately 16 mM (Table 1). The $K_M$ values for glycine for bovine liver GLYAT and wild-type recombinant GLYAT were also similar, at approximately 2 mM. However, the $K_M$ value for glycine of the E226Q mutant was higher, at approximately 7 mM (Table 1). The apparent $K_M$ values (at 200 mM glycine) were also determined for bovine liver GLYAT and wild-type recombinant bovine GLYAT, using propropionyl-CoA, isovaleryl-CoA, benzoyl-CoA, and octanoyl-CoA. These values were also comparable for the two enzymes (Table 2).

**The pH Dependence of Bovine GLYAT Enzymes**

The catalytic importance of the Glu226 residue of bovine GLYAT was investigated by determining the pH dependence of wild-type and E226Q mutant recombinant bovine GLYAT enzymes and comparing it to that of GLYAT extracted from bovine liver mitochondria. Increasing pH resulted in increased reaction rates for all three enzymes. Both the bovine liver GLYAT and wild-type recombinant bovine GLYAT enzymes had relatively low activity at pH 6.0, and activity increased with pH to a maximum at pH 7.5. As the pH increased further from 7.5 to 9.6, no significant increase in enzyme activity was observed (Fig. 4). The activity of the E226Q mutant GLYAT enzyme increased as the pH was increased from 6.0 to 9.6. In a representative experiment, the activity of the E226Q mutant bovine GLYAT was approximately 6% of the activity of the wild-type recombinant bovine GLYAT, at pH 8.0. At higher pH values, the activity of the mutant was increased significantly, with the E226Q mutant being approximately 111% as active as the wild-type recombinant GLYAT, at pH 9.6 (Fig. 4). This effect was consistently observed using different preparations of the enzymes. Because the recombinant bovine GLYAT enzymes were only partially purified, SDS-PAGE had to be used to compare the recombinant bovine GLYAT content of the wild-type and E226Q recombinant GLYAT preparations. This method worked well but is not completely accurate, which explains the difference between the activities of the wild-type and E226Q mutant recombinant GLYAT at pH 9.6.

**Discussion**

The purpose of this study was to generate and enzymatically characterize a recombinant bovine GLYAT and to initiate investigations of the catalytic mechanism of the enzyme. It is important to understand the molecular and biochemical characteristics of the GLYAT family of enzymes, because these enzymes metabolize a
wide range of endogenous and xenobiotic compounds and may present as yet unknown targets for the therapeutic manipulation of inherited metabolic disorders or exposure to toxins. A recombinant bovine GLYAT was used in this study because it could be expressed in an enzymatically active form in Escherichia coli. Our attempts to express enzymatically active human GLYAT in bacteria have thus far been unsuccessful. This perhaps correlates with the observation that GLYAT isolated from human liver is less active and less stable than GLYAT isolated from bovine liver (Nandi et al., 1979; Mawal and Qureshi, 1994; van der Westhuizen et al., 2000). However, the reaction kinetics and substrate specificity of the human and bovine GLYAT enzymes are similar, and we started investigations of the GLYAT domain architecture, catalytic mechanism, and functional residues, using the bovine ortholog (Schachter and Taggart, 1954; Bartlell and Gregersen, 1974; Nandi et al., 1979; Kelvraa and Gregersen, 1986; Mawal and Qureshi, 1994; van der Westhuizen et al., 2000).

Our results show that recombinant bovine GLYAT, expressed in E. coli, has enzymatic properties similar to those of GLYAT present in an extract of bovine liver mitochondria. The $K_m$ values for several acyl-CoA substrates and glycine were determined and found to be similar for those two enzymes (Tables 1 and 2). In the literature, there is great variation in the $K_m$ values reported for bovine liver GLYAT. The $K_m$ values for benzoyl-CoA range from 9 to 310 $\mu$M, and those for glycine range from 2 to 15 $\mu$M (Schachter and Taggart, 1954; Bartlell and Gregersen, 1974; Nandi et al., 1979; Gregersen et al., 1986; Kelley and Vessey, 1986, 1993, 1994; Kelvraa and Gregersen, 1986; Mawal and Qureshi, 1994; van der Westhuizen et al., 2000). The $K_m$ values we determined for the bovine liver GLYAT and recombinant bovine GLYAT (approximately 16 $\mu$M for benzoyl-CoA and 2 $\mu$M for glycine) fall within the range reported in the literature.

The similarity of recombinant bovine GLYAT to bovine liver GLYAT, in terms of $K_m$ parameters, suggested that the recombinant enzyme could be a valuable tool for investigation of the catalytic residues of bovine GLYAT. When glycine was omitted from the enzyme assays, no activity could be observed, confirming that the enzyme preparations were not contaminated with any proteins that nonspecifically hydrolyze benzoyl-CoA.

### Table 1

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<th>$K_m$ values for wild-type and E226Q mutant recombinant bovine GLYAT and GLYAT from bovine liver ($n = 3$)</th>
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<td>Enzyme type</td>
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Based on the pH dependence of the human and bovine GLYAT enzymes, as reported in the literature, we anticipated that a general base catalyst is involved in the reaction (Schachter and Taggart, 1954; Bartlell and Gregersen, 1974; Nandi et al., 1979; Mawal and Qureshi, 1994). Our hypothesis, based on molecular modeling and the similarity of GLYAT to the GNAT superfamily of acyltransferases, was that the residue Glu226 of bovine GLYAT served as a general base catalyst in the GLYAT reaction.

The $K_m$ values we determined for the wild-type and E226Q recombinant bovine GLYAT enzymes were assayed at pH 8.0, there was a difference of approximately 20-fold in activity between the two enzymes. This suggests that the mutation may simply modify the enzyme. The $K_m$ values for both wild-type and E226Q recombinant bovine GLYAT, meaning that both substrates were saturating.

The loss of catalytic activity displayed by the E226Q mutant GLYAT is not sufficient evidence to conclude that our biochemical analyses and prediction of the catalytic importance of Glu226 of bovine GLYAT are valid. This is because the mutation may simply have altered some structural component of the enzyme, lowering the catalytic rate. Because our objective was to demonstrate that Glu226 serves as a general base catalyst, the pH dependence of the mutant and wild-type enzymes was investigated. The wild-type recombinant bovine GLYAT and bovine liver GLYAT reached maximal activity at pH 7.5, and further increases in pH did not have a significant effect.

However, the activity of the E226Q mutant increased significantly as pH increased from 6.0 to 9.6. At pH 9.6, the E226Q mutant had activity comparable to that of the wild-type recombinant bovine GLYAT and bovine liver GLYAT. When interpreted in light of the similarity of the kinetic parameters of the wild-type and mutant enzymes (suggesting that the mutant is structurally intact), it was concluded that the loss of catalytic activity displayed by the E226Q mutant GLYAT is not sufficient evidence to conclude that our biochemical analyses and prediction of the catalytic importance of Glu226 of bovine GLYAT are valid. This is because the mutation may simply have altered some structural component of the enzyme, lowering the catalytic rate. Because our objective was to demonstrate that Glu226 serves as a general base catalyst, the pH dependence of the mutant and wild-type enzymes was investigated. The wild-type recombinant bovine GLYAT and bovine liver GLYAT reached maximal activity at pH 7.5, and further increases in pH did not have a significant effect.
amino group of glycine is important, because it is chemically impossible for the protonated amine to act as a nucleophile, and that Glu226 seems to be involved in the process.

For acyl-transfer reactions, there is an alternative mechanism to the ternary-complex, direct transfer mechanism, commonly known as the ping-pong mechanism (Dyda et al., 2000; Bendsen and Deno, 2005). The literature supports our analyses that bovine GLYAT employs a general base-catalyzed, ternary-complex mechanism. First, the reaction kinetics support a ternary-complex mechanism but not a ping-pong mechanism (Nandi et al., 1979; van der Wees thuizen et al., 2000). Second, GLYAT is insensitive to thiol-modifying reagents, such as iodoacetamide and N-ethylmaleimide, which would inactivate the active site cysteine residue of a ping-pong enzyme (Nandi et al., 1979). Finally, GLYAT is homologous to the GNAAT superfamily of acyltransferases, of which members studied to date all employ direct transfer mechanisms.

Based on our analyses, we propose the ternary-complex, base-catalyzed reaction mechanism, as depicted in Fig. 5, for bovine GLYAT. In brief, the glycine amino group is deprotonated by the Glu226 residue to increase its nucleophilic character. The nucleophilic amine then attacks the thioester, forming a tetrahedral intermediate that collapses to form the CoA and acylglycine products. We speculate that this mechanism should be conserved among the GLYAT enzymes of different species, based on the conservation of the Glu226 residue in the homologs of bovine GLYAT (Fig. 1). If our interpretation is valid, this may provide the first insight into the active site of the human ortholog of bovine GLYAT, an enzyme of increasing clinical relevance. Conclusive evidence for the ternary-complex, base-catalyzed mechanism we propose for bovine GLYAT awaits the determination of a crystal- or NMR structure of a GLYAT enzyme, preferably with bound substrates or an inhibitor. Repeating the photoaffinity labeling of GLYAT, performed by Lau et al. (1977), combined with mass spectrometric identification of the labeled residues, would be another means of investigating the GLYAT active site.

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References


Catalytic mechanism of GLYAT

Fig. 5. A schematic representation of the general base-catalyzed, ternary-complex mechanism proposed for bovine GLYAT. A, for nucleophlic attack to occur, the glycine amino group must be deprotonated by Glu226. B, a tetrahedral intermediate is formed after nucleophilic attack by the amino group of glycine on the thioester carbonyl group. C, finally, the tetrahedral intermediate collapses, forming the peptide product and CoA. ChemDraw 10.8 (CambridgeSoft, Cambridge, MA) was used to produce this schematic.

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