A Spin Label Substrate Analogue as Active Site-directed Modifying Agent
TRYPHTOHAN 140 OF ASPARTATE AMINOTRANSFERASE*

Ana Iriarte and Marino Martinez-Carrion
From the Department of Biochemistry, Medical College of Virginia, Virginia Commonwealth University, Richmond, Virginia 23298

The interaction of cytoplasmic aspartate aminotransferase with the spin probe substrate analogue potassium nitrosodisulfonate (NDS) has been investigated using the α-subform of the pig heart enzyme. Electron paramagnetic resonance studies show that NDS binds to the enzyme. Scatchard plots with different concentrations of NDS are linear and show the presence of two binding sites/dimer (Kd = 0.7 mM). Substrates or substrate analogues display enzyme-bound NDS. NDS is also a competitive substrate inhibitor (K0.5 = 0.72 mM) when tested in assays for transaminase activity. Treatment of the enzyme with 0.2 mM NDS at pH 7.5 results in an inactivation that follows pseudo-first order and saturation kinetics with a maximum inactivation rate of 0.04 min⁻¹ and Kinear of 1.2 mM. The NDS rate of inactivation is pH-independent, and substrates and substrate analogues protect the enzyme. These results are consistent with a role for NDS acting as an active site-directed reagent.

The absorption spectrum of NDS-treated apo- or holoenzyme shows an increase in absorbance in the 320-nm region that parallels the loss in activity and a decrease in the 280/260-nm absorbance ratio. The amino acid composition of NDS-modified enzyme shows only a loss of tryptophyl residues (1/subunit). Peptide fractionation of tryptic digests of the NDS-modified enzyme revealed only one extra peptide with absorption at both 220 and 320 nm. Both the amino acid composition and partial sequence of this peptide indicate that it corresponds to residues 130-153 in the cytoplasmic aspartate aminotransferase sequence. This protein fragment includes Trp 140 residue which, in the 2.8-Å x-ray maps of the enzyme's active site region, appears located in front of the pyridine ring of pyridoxal phosphate (Metzler, D. E., Jansonius, J. N., Arnone, A., Martinez-Carrion, M., and Manning, J. M. (1982) Fed. Proc. 41, 2432-2433).

The reaction mechanism and protein structure of the pyridoxal-P-dependent enzyme aspartate aminotransferase (EC 2.6.1.1) from pig heart have been extensively studied. Amino acid groups participating in the catalytic process or in coenzyme and substrate interactions have been investigated using reagents with specificity toward a given type of functional group, affinity labels of substrates, or of derivatives of the coenzyme. The first of such residues to be located was the lysyl (Lys 258) residue whose ε-amino group forms a Schiff base linkage to the coenzyme pyridoxal-P (1-3).

Chemical modification with tetraniometane also affected cysteinyl residues by photodestruction of the enzyme in the presence of methylene blue (10, 11) and, apparently, the oxidation of this residue (identified as Cys 390) facilitated nitration of tyrosine. Inactivation of aspartate aminotransferase with various dicarbonyl reagents by modification of arginyl (Arg 292) residues (7-9) and the destruction of some histidyl residues by photodestruction of the enzyme in the presence of methylene blue (10, 11) have been reported. The properties of the enzyme modified in this way suggested the possibility that these groups might be binding sites for the carbonyl groups (7-9, 11) of the substrates or participate in proton removal from the substrate (12). Another guanidinium group forms an ion pair with the phosphate group of the enzyme (13) but has not been chemically modified.

The arrangements of these above mentioned groups in the active site region are now being detected by x-ray diffraction methods (13, 14). Several other residues which appear in the active center region have not yet been tagged by chemical modification procedures, and their role in the enzyme's functions remains undefined. Of particular interest is the presence of a tryptophan residue, Trp 140, which appears to be located in front of the pyridine ring with its indole side chain within van der Waals contact with the coenzyme (14). In solution, this proximity appears to reflect on a fluorescence quenching for the tryptophan (15-17) and circular dichroism perturbations of the aromatic amino acid region (18) upon binding of coenzyme by apoenzyme. Identification of this residue in solution through chemical modification procedures has not been fruitful, and it appears desirable to selectively alter Trp 140 and investigate its potential role in enzyme function. To this end, the chemical reagent of choice is known from studies with model compounds (19, 20) and with different types of proteins (21, 22) to be a specific oxidizing agent mainly for tyrosine and tryptophan groups. Another important consideration which led us to the selection of NDS as the modifier agent is its reported behavior as an analogue of oxalacate when used as an active site probe for citrate synthase (23). This suggested the possibility that it could act as a more specific active site probe in enzymes employing oxalacate as

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1The abbreviations used are: NDS, potassium nitrosodisulfonate; HPLC, high performance liquid chromatography; TPCK, L-1-tosylamido-2-phenylethyl chloromethyl ketone.
substance or inhibitor such as in aspartate aminotransferase. In this publication, we describe the effect of the free radical NDS diaminon acting as an irreversible inactivator of cytoplasmic aminotransferase with selective modifications of Trp 140.

**EXPERIMENTAL PROCEDURES**

The α-form of cytoplasmic aspartate aminotransferase was isolated from pig hearts as previously described (24). Potassium nitrosodisulfonate (Fremy's salt) was obtained by Alfa Inorganics (Venton Corp.) and stored in a desiccator over calcium oxide in the presence of ammonium carbonate in a separate dish to provide an anaerobic atmosphere (19). The concentrations of NDS solutions were measured optically at 545 nm (ε = 20.8 M⁻¹ cm⁻¹) (25), 2 Methyl-αL-aspartate, L-aspartate, oxalacetate, α-ketoglutarate, N-acetyl-L-tyrosine ethyl ester, N-acetyl-L-tryptophan ethyl ester, NADH, and malate dehydrogenase were purchased from Sigma. TPCK-treated trypsin was obtained from Worthington. All solvents for high performance liquid chromatography were spectrophotometric grade obtained from Aldrich. Amino acid analyzer reagents and buffers were obtained from Durrum.

**Electron Paramagnetic Resonance Studies**—Spectra of 0.05 mM samples of NDS solutions were obtained in borosilicated glass capillaries by using a Varian E-9 spectrometer. Binding of NDS to the enzyme was measured by comparison of the peak-to-peak amplitude of the three lines in the paramagnetic resonance spectra of the sample containing the probe plus enzyme in 0.05 mM phosphate buffer, pH 7.5, with that of a comparable solution of NDS in the same buffer. Three or more spectra were taken at different times, and the peak-to-peak amplitude value extrapolated to the time of NDS addition to the sample containing the enzyme, since the amplitude of the three lines of the spectra decreases with time under these conditions.

**Treatment of Aspartate Aminotransferase with NDS**—Enzyme modifications were carried out at 25 °C in 0.05 mM potassium phosphate buffer, pH 7.5. The concentration of enzyme was 1 mg/ml and the concentration of NDS ranged from 0.2-4 mM. Modification reactions were initiated by adding a suitable volume of freshly prepared solution of reagent to the enzyme in the phosphate buffer along with any other compound being studied. All reagents were neutralized before they were added to the enzyme solution. Aliquots were withdrawn from the reaction mixtures at various time intervals and the activity monitored by spectrophotometric assay as previously described (26). When 80% inactivation had occurred, the modifier was removed from the sample by passing the modified enzyme through a Sephadex G-25 column (2 x 25 cm) equilibrated and eluted with 0.05 mM potassium phosphate buffer (pH 7.5).

Protein concentrations were calculated from the absorbance at 280 nm (ε = 140,000 M⁻¹ cm⁻¹) for a molecular weight of 94,000. All of the absorption spectra and absorbance measurements were carried out with a Cary model 210 recording spectrophotometer.

**Trypsin Digest**—Protein samples (5 mg/ml) were dialyzed against 0.1 M Tris/HCl buffer, pH 8.0, and digested by heating in a boiling water bath for 5 min in the presence of 1 mM dithiothreitol and 10 mM EDTA. After cooling, the sample was carbamomyethylated by adding a 50-fold molar excess of recrystallized iodoacetic acid. After incubation for 2 h at room temperature, the solution was dialyzed overnight against deionized water at 5 °C. The pH was adjusted to 8.0 with ammonia bicarbonate and hydrolyzed with TPCK-trypsin. Aliquots of freshly prepared 1 mg/ml solution of TPCK-trypsin in 1 mM HCl were added to give a total amount of trypsin equal to 1% by weight of the amount of protein being digested. The digestion was performed for 5 h at 37 °C.

**Peptide Mapping by High Performance Liquid Chromatography**—Peptide mapping was performed by reverse-phase high performance liquid chromatography as described by Schroeder et al. (27) using a Varam model 5000 liquid chromatograph. Five nmol of protein digest were analyzed on a Varmco Micro Pak MCH 10 C-18 column (0.46 cm × 30 cm) at room temperature. The column was equilibrated with 54.4 mM sodium phosphate at pH 2.86. The sample was applied in 100 μl of this buffer and eluted with a gradient of this buffer and acetonitrile as second solvent. The percentage of acetonitrile, initially at zero, was increased to 12% during the first 13 min, then increased to 25% during the next 65 min, and, finally, to 62% during the final 30 min. The flow rate was 1 ml/min. Peptides were detected by their absorbance at 220 and 320 nm with a variable wavelength monitor. Peptide peaks were collected directly from the detector cell through microbore tubing into acid-cleaved tubes in 1-Ml fractions. The fractions were dried in a Savant Speed-Vac Concentrator and subjected to further analysis.

**Amino Acid Analysis and Peptide Mapping**—The amino acid analyses were carried out in a Durrum MBF amino acid analyzer after acid hydrolysis of the sample in 6 N HCl containing 0.1% phenol for 24 h at 110 °C in sealed evacuated tubes. Tryptophan content was determined after hydrolysis by methanolic sulfuric acid for 22 h at 110 °C according to Simpson et al. (28) or spectrophotometrically (29). Sulfhydryl groups were determined with 5,5'-dithiobis-(2-nitrobenzoic acid) according to the procedure of Ellman (30) in 6 M guanidine hydrochloride. The titration was done by the addition of 0.4 mM 5,5'-dithiobis-(2-nitrobenzoic acid) to 0.004 mM enzyme in 0.3 M Tris-chloride, pH 8.0, 1 mM EDTA using a molar absorptivity of the compound at a wavelength of 412-420 nm has been reported for thionitrobenzoate in guanidine hydrochloride (31).

Manual Edman degradations were performed by the method of Tarr (32). Generally 1-2 nmol of protein were used. The phenylthiohydantoin derivatives were identified by HPLC using an Altex Ultrasphere ODS column, and the elution from the column was performed with a gradient of 5% tetrahydrofuran in 5.75 mM acetic acid, pH 5.02, and 90% acetonitrile in 10% tetrahydofuran as the second solvent. The percentage of this second solvent was increased from 0 to 40% over 30 min at a flow rate of 1.3 ml/min. The phenylthiohydantoin derivatives were detected at 254 nm.

**RESULTS**

**Binding of NDS to Aspartate Aminotransferase**—A comparison of the electron paramagnetic spectra of 0.2 mM NDS in buffer with that in buffer plus 0.21 mM aspartate aminotransferase (assuming 94,000 for enzyme molecular weight) indicated that the amplitude of the three lines is decreased considerably by the addition of the enzyme (Fig. 1). Such an observation is indicative of binding of a small molecule of NDS to a large macromolecule (23). Comparison of the amplitude of each line with that of the corresponding line in the absence of enzyme used as standard allows the estimation of the per cent bound and unbound NDS. The peak-to-peak line amplitude of NDS in solution containing the enzyme decreases with time, indicating that NDS is being reduced by oxidizable groups in the enzyme. This decrease in signal with time necessitated the recording of three or more spectra over a period of 10 min followed by plotting the peak-to-peak line amplitude as a function of time and extrapolation to the time of NDS addition. The extrapolated line amplitude was used in binding calculations. The enzyme was titrated using different concentrations of NDS to determine the dissociation constant (K_D) of the probe-enzyme complex and the number of binding sites/enzyme molecule. A Scatchard plot of the data (Fig. 2) was linear, indicating two specific binding sites/enzyme dimer. A value of 0.7 mM was obtained for the dissociation constant (K_D) of NDS from these two sites.

As it has been reported (33), treatment of the enzyme with N-ethylmaleimide in the presence of the substrate pair L-glutamate (70 mM) and α-ketoglutarate (2 mM) (sacalytic modification) modifies three sulfhydryl groups/subunit and the modification of one of them (identified as Cys 390) reduces aminotransferase activity to less than 5% of the initial value. Yet, this N-ethylmaleimide treatment does not prevent the loss of NDS probe signal. These results indicated that the decrease in signal observed in the EPR spectrum of NDS in the presence of enzyme is not primarily due to oxidation of accessible cysteinyl residues.

**Displacement of NDS from Aspartate Aminotransferase by Substrates and Analogues**—The addition of different ligands such as substrates and analogues to the NDS-enzyme system displaced appreciable amounts of bound NDS (Table 1). Furthermore, the presence of substrates in the sample not only displaces the probe from the enzyme complex but also protects against destruction of the probe signal. For example,
Transaminase Active Site Tryptophan

Fig. 1. Paramagnetic resonance spectra of NDS (0.2 mM) in the absence (A) and presence (B) of aspartate aminotransferase (0.21 mM). Modulation amplitude 0.5 gauss; gain $2.5 \times 10^5$.

Fig. 2. Scatchard plot of the paramagnetic resonance data for NDS binding to cytoplasmic aspartate aminotransferase obtained as explained in the text.

under the conditions given in the legend of Table I, 6.5% destruction of NDS signal was observed over a 6-min period in the absence of other ligands. When 50 mM a-ketoglutarate was added, only 2.6% signal decay occurred over the same period of time. This behavior suggests that the reduction of NDS by oxidizable amino acid residues in the enzyme takes place mainly when NDS is bound to the enzyme.

Similar results regarding NDS displacement from the binding site and protection against signal destruction were obtained when the enzyme was previously incubated with the substrates or even when the ligands were added to the NDS-enzyme system if a correction is made for the per cent signal lost during the period of observation.

Inactivation of Aspartate Aminotransferase by Incubation with NDS—Incubation of aspartate aminotransferase with NDS produces a loss of enzymatic activity which follows first order kinetics (Fig. 3). Less than 1% of the initial activity remains after a 10-h incubation with 2 mM NDS. Activity is not restored by dialysis, gel filtration, or treatment with thiol compounds or pyridoxal-P. The inactivation exhibited saturation kinetics as can be observed upon plotting the first order inactivation rate constants as a function of reciprocal NDS concentration. As shown in the inset in Fig. 3, extrapolation of the line to the abscissa gives a $K_{inact}$ (reagent concentration yielding one-half the maximum rate of inactivation) of 1.2 mM. The maximum rate of inactivation calculated from the same plot was 0.04 min$^{-1}$.

The loss in activity is not caused by modification or loss in the coenzyme pyridoxal-P. In fact, under the same experimental conditions, the apoenzyme's rate of inactivation is identical with that of the holoenzyme (data not shown). Furthermore, the pyridoxal-P content of enzyme modified to a 20% residual activity was found to be 90% that of native enzyme. On the other hand, as shown in Fig. 4, NDS can act as a competitive inhibitor ($K_I = 0.725$ mM) of aspartate aminotransferase when assayed at a fixed concentration of L-aspartate (10 mM) at different concentrations of a-ketoglutarate (0.05-0.25 mM) and in the presence of 2-5 mM NDS. The value obtained from these data agrees with the $K_I$ for the dissociation of NDS from the probe-enzyme complex calculated from the direct binding data.

All of the substrates and analogues tested protected the

<table>
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<tr>
<th>Substrate or analogue</th>
<th>Concentration (mM)</th>
<th>NDS bound</th>
<th>Percentage of NDS displaced</th>
<th>NDS (%)</th>
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<td>None</td>
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<td>0.053</td>
<td>51</td>
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* Similar results were obtained by previous addition of the ligands and a correction made for the percent signal lost during the period of observation before addition of the ligands.

Table I
Displacement of NDS bound to aspartate aminotransferase by substrates and analogues

Each sample (100 pl) contained 0.08 $\times 10^{-8}$ M enzyme, 0.7 mM NDS, and the indicated concentrations of substrates in 50 mM potassium phosphate buffer, pH 7.5. Five or more EPR spectra of 0.05-ml samples were obtained over a period of 10 min. The value obtained for the line amplitude after extrapolation to the time of NDS addition was used for the calculation of the concentration of bound NDS and expressed as a percentage of the concentration in the absence of ligands (NDS-enzyme system).
enzyme against inactivation, the best being \( \alpha \)-ketoglutarate and \( \alpha \)-methylaspartate (Fig. 5).

**Spectral Changes in the Modified Enzyme**—The absorption spectra of aspartate aminotransferase modified by incubation with 0.2 mM NDS after removal of the excess of reagent by dialysis are compared to those of untreated enzyme in Fig. 6. At high pH, native enzyme absorbs at 360 nm as modified enzyme does, although it is decreased slightly in magnitude. The ultraviolet absorption spectra show an increase in absorbance in the region of the 250-nm absorption minimum, suggesting the breakdown of tryptophan (34) that appears as a maximum at 245 nm in the difference spectrum shown in the inset of Fig. 6. On the other hand, an increase in absorbance is observed in the 320-nm region. The rate of increase in absorbance at 320 nm was closely correlated with the loss in activity (Fig. 7). This absorbance increment at 320 nm is not due to the formation of a derivative of the coenzyme pyridoxal-P because it remains after removal of pyridoxal-P and appears in apoenzyme modified under identical conditions. Its appearance must be related to the modified amino acid residue(s) responsible for the inactivation of the enzyme. Furthermore, incubation of the holoenzyme with NDS, but in the presence of 50 mM \( \alpha \)-ketoglutarate, protects the enzyme against both inactivation and increase in absorbance at 320 nm. Samples in the absence and presence of the protective ligand were incubated for 4 h at 25 °C in 0.05 M potassium phosphate buffer, pH 7.5, and passed through a Sephadex G-25 column to remove the excess of NDS and stop the reaction.

As has been described (19, 20), NDS oxidizes specifically both tyrosine and tryptophan residues free or incorporated in a protein. NDS treatments of model compounds, N-acetyl-L-tyrosine ethyl ester and N-acetyl-L-tryptophan ethyl ester,
FIG. 6. Absorption spectra of the pyridoxal form of cytoplasmic aspartate aminotransferase before (solid curve) and after incubation with 0.2 mM NDS (dashed curve) to 25% residual activity. Difference spectrum is shown in the inset.

FIG. 7. Time course for inactivation ( ), absorption increment at 320 nm ( ), and NDS reduction ( ) resulting from incubation of aspartate aminotransferase (0.021 mM) with a 10-fold molar excess of NDS in 50 mM potassium phosphate buffer, pH 7.5, at 25 °C. At various time intervals, aliquots of 1 µl were withdrawn and determined for enzyme activity. Absorption and electron paramagnetic spectra were recorded in aliquots of 1 ml and 50 µl, respectively, at different times. A₀ and A₀ denote absorbance (320 nm) and line amplitude of the EPR spectra of NDS for the indicated periods; Aₐ, Aₐ₀, and Aₐ₋ₐ₀ denote the same parameters at initial and final values.

were carried out in order to detect possible changes in absorption spectra. The spectrum of the tryptophyl derivative most closely resembled the one from the modified enzyme with a broad increase in absorbance around 320 nm which progressed with length of incubation. The spectrum from tyrosyl derivative incubated with NDS under similar conditions also showed an absorbance increment at 320 nm, yet the main characteristics were the appearance of two new absorption maxima at 300 and 390 nm. These latter maxima are absent in NDS-treated aspartate transaminase.

pH Dependence for Inactivation of Aspartate Aminotransferase with NDS—The inactivation of aspartate aminotransferase with a 10-fold molar excess of NDS was followed in a series of buffered solutions from pH 5.6-9. The experiments could not be performed at lower pH values because of the instability of NDS at acidic pH. The rates of inactivation were essentially independent upon the hydrogen ion concentration over the pH range studied.

Loss of Amino Acid Residues Accompanying the Inactivation of Aspartate Aminotransferase by NDS—The amino acid composition of native and modified aminotransferase with a 10-fold molar excess of NDS to 25% residual activity was determined after hydrolysis for 22 h at 110 °C in methane sulfonic acid in order to avoid the destruction of tryptophyl residues. No appreciable loss of the theoretically susceptible tyrosine is observed and only a decrease in the number of tryptophyl residues is detected when compared with the composition of a sample of native enzyme treated in a similar way. It has been reported (21) that 3 mol of NDS must be consumed/mol of indole residue oxidized. Hence, the destruction of approximately 1.3 Trp residues/subunit agrees with both the stoichiometry of the amount of NDS reduced per mol of enzyme (6 ± 0.5/dimer) (Fig. 8) and the changes in the absorption spectrum concurrent with the modification.

Isolation and Characterization of the Tryptic Peptide(s) Containing the Modified Residue(s)—Treatment of the enzyme for 4 h with a 10-fold molar excess of NDS results in destruction of 70-75% of its original activity. These samples,
denatured and alkylated as described under "Experimental Procedures." were digested with TPCK-trypsin and the resulting peptide fragments were separated by HPLC chromatography. Peptide elution was monitored at both 220 and 320 nm in order to identify the fragment that includes the modified amino acid. This wavelength was chosen because kinetic data showed that the increase of enzyme absorbance in this region during incubation with NDS correlated with loss in activity (Fig. 7). Tryptic digests of samples from native enzyme were analyzed in a similar manner. The chromatograms obtained are shown in Fig. 9. For the modified enzyme, only one peptide showed absorbance at both wavelengths. This peptide, having a retention time of 61 min, is also associated with a new 220 nm absorbing peak which is not present in controls of native enzyme digests. The relative amplitude of this peak in the chromatograms from modified enzyme varies with the extent of the inactivation at the time the reaction was stopped. Samples of enzyme incubated for the same period of time but in the presence of 50 mM a-ketoglutarate (65% activity after a 4-h incubation), which protects the enzyme from inactivation, showed that the relative amplitude of the 61-min peak in the HPLC chromatograms was significantly decreased.

The 61-min fractions were repurified by HPLC with a different chromatographic system using a linear gradient from 0.1% trifluoroacetic acid to 70% acetonitrile in 0.1% trifluoroacetic acid over 100 min and at a flow of 1 ml/min. The elution profile showed again only one peak with absorbance at 320 nm. The fractions containing the peak were pooled and concentrated. The peptide was subjected to amino acid analysis in 6 N HCl for 24 h at 110 °C. From the amino acid analysis of this fraction, a 50-55% recovery of the total amount of digest applied to the HPLC column was obtained. The amino acid composition of the peptide, as shown in Table II, indicates that it corresponds to the tryptic fragment that includes residues 130-153 in the amino acid sequence of cytoplasmic aminotransferase (35) which has the following sequence: Asp-Thr-Pro-Val-Tyr-Val-Ser-Ser-Pro-Thr-Trp-Glu-Asn-His-Asp-Gly-Val-Phe-Thr-Thr-Ala-Gly-Phe-Lys.

The first 2 residues in the NH2-terminal region of the peptide were identified by manual Edman degradation. Aspartic acid was found as the NH2-terminal residue and threonine as the second amino acid. This confirms the identity of the peptide with that including residues 130-153 in the amino acid sequence of native transaminase since it is the only tryptic fragment in the complete sequence that has this composition and those 2 amino acid residues in the NH2-terminal sequence. This peptide includes tryptophan 140.

**DISCUSSION**

As reported for citrate synthase (23), the free radical NDS also binds to cytoplasmic aspartate aminotransferase. However, in citrate synthase, NDS appears to act solely as a reversibly binding analogue of substrate oxalacetate, but, in the aminotransferase, binding leads to inactivation. In this sense, it appears to act as an active site-directed modifying...
agent which is extremely efficient because, as a substrate analogue, it is site specific and, thus, effective at low concentrations. In turn, the low concentrations of modifier employed render it ineffective as a general modifier of tyrosyl and tryptophyl residues for which this agent is known to be an avid oxidizer in aqueous solution. Evidence supporting our conclusion that there is interaction of NDS with the active site region of aspartateaminotransferase is (a) the NDS radical is displaced by different substrates and analogues such as dicarboxylic acids inhibitors as observed from the binding data obtained by EPR and (b) NDS is also a substrate-competitive inhibitor. Furthermore, the affinity for the binding site (Kd = 0.7 mM) is similar to the one displayed by substrates such as oxalacetate and α-ketoglutarate and by other dicarboxylic acids inhibitors such as succinate. The irreversible inactivation of the enzyme seems to be due to active site modifications because inactivation follows the reversible complex formation between reagent and active site of the enzyme with Kd, K0 values for NDS all in the 0.7–1.2 mM range. Finally, the first order inactivation kinetics, the rate saturation with respect to NDS concentration, and the protective effect of different substrates and analogues against loss of activity are consistent with an active site-specific modification.

The results of the present study show that the loss in activity of aspartateaminotransferase by incubation with NDS is accompanied by destruction or modification of a tryptophyl residue. Comparison of the amino acid composition of native and modified enzyme shows that other amino acid residues theoretically susceptible to NDS oxidation, especially tyrosine and cysteine, as well as the coenzyme are not appreciably affected. Several lines of evidence support the result gleaned from amino acid analysis. It has been reported that NDS is a stable free radical which, after oxidizing tyrosine and tryptophan residues, free or incorporated in proteins, induces the appearance of characteristic changes in the absorption spectra. The spectral changes observed during incubation of the enzyme with NDS (appearance of an absorption peak at the 320-nm region) follow the same time course as the loss in enzyme activity and the decrease in the 280/260-nm absorbance ratio. Similar spectral changes upon oxidation of tryptophyl residues with different reagents have been reported in the literature. In addition, we found a stoichiometric ratio of 6 ± 0.5 mol of NDS consumed/mol of enzyme (Mn = 94,000) for complete enzyme inactivation. Thus, the stoichiometry of the reaction is close to 3 mol of NDS consumed/mol of subunit which is in close agreement with the value of 3 mol of NDS reduced in the modification of each tryptophyl residue in studies on isolated molecules and on some proteins. By contrast, in the oxidation of tyrosine by NDS, be it free, peptide-bound, or incorporated into a protein, 2 mol of NDS/mol of tyrosine were reported to be consumed.

The amino acid composition and partial sequence of the tryptic peptide which contains the residue modified during the inactivation allow its identification in the known amino acid sequence of cytoplasmic aminotransferase. This tryptic peptide in the native enzyme includes tryptophan 140 which has been located by x-ray crystallographic studies in the active site region of the enzyme near the lower portion of the pyridine component of pyridoxal-P. The inactivation of aspartateaminotransferase by NDS probably proceeds by a two-step process. The reagent first binds to the substrate binding site as a noncovalent Michaelis complex. The protective effect of different substrates supports this view. Binding is the likely result of the two sulfonates mimicking the carboxylate groups of the substrates in their association with specific residues in the active center of the enzyme. As candidates for carboxylate groups binding sites, lysyl, histidyl, and arginyl residues have been suggested. NDS could bind to the enzyme through one or both sulfonate groups through electrostatic interactions with positively charged amino acid side chains in such manner that the potentially reactive nitroso group of the reagent could be placed within striking range of Trp 140. The second step of inactivation would proceed with the oxidation of the indole ring with possible formation of the 5-hydroxyindole and/or the 4,5-indolequinone derivatives, both of which have been reported as products of the oxidation of indole derivatives by free NDS radical.

A variety of ionizable amino acids has been located in the vicinity of pyridoxal-P in this transaminase. Some of these residues, including Arg 292 and Lys 258, have also been assigned roles in the active center through chemical modification studies. On the other hand, the implication of tryptophan residue as influencing the pyridoxal-P region had only been inferred through physical studies including enzyme tryptophan fluorescence quenching and circular dichroism of the aromatic region, and, more recently, x-ray crystallography. Other pyridoxal-P-dependent enzymes also appear to contain buried tryptophyl residues capable of influencing the electronic structure of pyridoxal-P and, through a circumstantial association of ideas, tryptophan and pyridoxal-P have been implicated in cause-effect relationships between these two aromatic groups in pyridoxal-P enzymes in general.

Little is known regarding the role of tryptophyl residues in enzymatic active centers. A wealth of information appears to center on physical observations such as fluorescence studies of the behavior of rotational freedom and exposure or movement of tryptophans in many enzymes upon binding of ligands. Also, perturbations induced through modifications of tryptophyl residues with reagents such as bromosuccinimide have been informative in pointing out probable roles of this residue in structure-function relationships in proteins. On the other hand, we are unaware of specific examples in which a tryptophyl residue may be directly implicated in an enzyme-active center with an assigned function in an enzyme reaction mechanism. In crystalline aspartate transaminase, free holoenzyme the Trp 140 lies in front of the pyridoxal-P coenzyme, at about a 70° angle and van der Waals contact with the pyridine ring. Modification without insertion of a bulky modifier and without significant change in the overall charge of the modified indole can now be accomplished by using NDS. What is the role of the apparent interactions of indole and pyridine rings in the active center? The indole could assist in the electron delocalization process in the well known reaction sequence of transamination. Furthermore, the forward movement of the pyridine upon formation of external aldimines with substrates should be accompanied by parallel displacements of the indole ring of Trp 140. If, in any way, the new indole derivative produced by NDS oxidation impedes this movement, it could affect catalytic events and possibly even the complex stereochemistry of exposure of external aldimines to added reducing agents such as NaBH₄. These challenging questions and many others now appear to be testable both in solution and in crystals of aspartate transaminase since enzymes differing only in the nature of the indole at Trp 140 can be prepared. Since the aminotransferase enzyme is well known because of the ease with which events at the active center in the reaction sequence can be followed by a variety of spectroscopic means, the answer to many questions regarding a possible role of tryptophan appears to be an attainable goal.
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