The bacterial degradation pathways for the nematocide 1,3-dichloropropene rely on hydrolytic dehalogenation reactions catalyzed by cis- and trans-3-chloroacrylic acid dehalogenases (cis-CaaD and CaaD, respectively). X-ray crystal structures of native cis-CaaD and cis-CaaD inactivated by (R)-oxirane-2-carboxylate were elucidated. They locate four known catalytic residues (Pro-1, Arg-70, Arg-73, and Glu-114) and two previously unknown, potential catalytic residues (His-28 and Tyr-103). The Y103F and H28A mutants of these latter two residues displayed reductions in cis-CaaD activity confirming their importance in catalysis. The structure of the inactivated enzyme shows covalent modification of the Pro-1 nitrogen atom by (R)-2-hydroxypropanoate at the C3 position. The interactions in the complex implicate Arg-70 or a water molecule bound to Arg-70 as the proton donor for the epoxide ring-opening reaction and Arg-73 and His-28 as primary binding contacts for the carboxylate group. This proposed binding mode places the (S)-enantiomer, but not the (R)-enantiomer, in position to covalently modify Pro-1. The absence of His-28 (or an equivalent) in CaaD could account for the fact that CaaD is not inactivated by either enantiomer. The cis-CaaD structures support a mechanism in which Glu-114 and Tyr-103 activate a water molecule for addition to C3 of the substrate and His-28, Arg-70, and Arg-73 interact with the C1 carboxylate group to assist in substrate binding and polarization. Pro-1 provides a proton at C2. The involvement of His-28 and Tyr-103 distinguishes the cis-CaaD mechanism from the otherwise parallel CaaD mechanism. The two mechanisms probably evolved independently as the result of an early gene duplication of a common ancestor.

The cis- and trans-3-chloroacrylic acid dehalogenases (cis-CaaD and CaaD) catalyze the cofactor-independent hydrolytic dehalogenation of, respectively, the cis- and trans-isomers of 3-chloroacrylic acid (I and 2, Scheme 1) to produce malonate semialdehyde (5) and HCl (1–3). Both reactions may be initiated by the attack of water at C3 to form an enzyme-stabilized enediolate intermediate (3). Subsequent ketonization of 3 with protonation at C2 generates a chlorohydrin intermediate (4), which can collapse by direct expulsion of the chloride to afford 5 (1, 4, 5). Alternatively, ketonization of 3 can result in chloride loss and the formation of the enol intermediate, 6, which tautomerizes to afford 5. The two enzymes are found in bacterial pathways that convert the cis- and trans-isomers of 1,3-dichloropropene, used as nematocides, to acetaldehyde (7) and carbon dioxide (6).

The cis- and trans-3-chloroacrylic acid dehalogenases have low sequence identity (~20%) and different oligomerization states (1–3). CaaD is a heterohexamer consisting of three 75-residue α-chains and three 70-residue β-chains, whereas cis-CaaD forms a homotrimer of three identical 149-residue polypeptide chains, which can be considered as the fusion product of a CaaD α- and β-chain (2, 3, 5). As a result, the two enzymes have been classified in two different families in the tautomerase superfamily, with each being related to 4-oxalocrotonate tautomerase (7–9). Yet, the differences in catalytic efficiency are only modest, and major elements of the catalytic mechanisms are conserved. In both, a glutamate residue (Glu-114 in cis-CaaD and αGlu-52 in CaaD) is proposed to function as a general base catalyst to activate a water molecule for attack at C3 (of I or 2) and the N-terminal proline (Pro-1 in cis-CaaD and βPro-1 in CaaD) is believed to provide a proton at C2. Two

The abbreviations used are: cis-CaaD and CaaD, cis- and trans-3-chloroacrylic acid dehalogenase, respectively; Fp and Fc, observed and calculated structure factor amplitudes, respectively; MSAD, malonate semialdehyde decarboxylase; r.m.s.d., root-mean-square deviation.
arginine residues (Arg-70 and Arg-73 in cis-CaaD and αArg-8 and αArg-11 in CaaD) are proposed to interact with the C1 carboxylate group, aligning the substrate in the active site and drawing electron density away from C3 (1, 3–5). Such an interaction would generate a partial positive charge at C3 and facilitate the addition of water. The conservation of key functionalities suggests that the two enzymes are related by divergent evolution from a common ancestor.

Nevertheless, recent kinetic and mechanistic work has uncovered two subtle differences. First, the activation of the water molecule likely requires additional residues in cis-CaaD (1). Mutation of Glu-114 to a glutamine produces a partially active mutant protein, whereas the αE52Q mutant of CaaD has no detectable activity, even after a prolonged incubation period. Second, only cis-CaaD is irreversibly inhibited by the (R)-oxirane-2-carboxylate (8) due to covalent modification of Pro-1 (10). The (S)-enantiomer is a weak competitive inhibitor of cis-CaaD and both enantiomers competitively inhibit CaaD (10) (Structure 1).

To delineate the structural basis for the isomer-specific dehalogenation reaction and the stereospecificity of the inactivation reaction, crystal structures of the native cis-CaaD and cis-CaaD inactivated by (R)-8 were obtained. They confirm the trimeric nature of cis-CaaD and pinpoint the roles of Pro-1, Arg-70, Arg-73, and Glu-114. The assisting roles of His-28 and Tyr-103 in activation of, respectively, the substrate and water molecule for catalysis, suggested by the crystallographic observations fully support the proposal that cis-CaaD and CaaD form two separate evolutionary lineages that followed the independent duplication of a 4-oxalocrotonate tautomerase-like sequence.

EXPERIMENTAL PROCEDURES

Materials—All reagents, buffers, and solvents were obtained from Sigma-Aldrich, Fisher Scientific, Spectrum Laboratory Products (New Brunswick, NJ), or EM Science (Cincinnati, OH), unless noted otherwise. A literature procedure was used for the synthesis of (R)-8 (11). The sources for the components of Luria-Bertani media, the enzymes and reagents used in the molecular biology procedures, and the strains used for cloning and overproducing cis-CaaD and the mutant proteins have been reported elsewhere (1, 10). The Amicon concentrator and the YM10 ultrafiltration membranes were obtained from Millipore Corp. (Bedford, MA). Oligonucleotides for DNA amplification and sequencing were synthesized by Genosys (The Woodlands, TX).

General Enzymology Methods—General procedures for cloning and DNA manipulation were performed as described elsewhere (12). The wild-type cis-CaaD and the mutant proteins were purified to homogeneity, as assessed by SDS-PAGE, according to a published procedure (1, 10). Protein was analyzed by SDS-PAGE on gels containing 15% polyacrylamide (13). The gels were stained with Coomassie Brilliant Blue. Protein concentrations were determined by the method of Waddell (14). The native molecular masses of the mutant proteins were determined by gel filtration on a Superose 12 column (Amersham Biosciences) using the Waters 501/510 high-pressure liquid chromatography system.

Crystallization and Structure Determination of Inactivated cis-CaaD—cis-CaaD was covalently inactivated by incubating the enzyme with a 25-fold excess of (R)-8 for 4 h, after diluting the protein solution to 0.5 mg/ml to prevent overheating. Crystals of inactivated cis-CaaD were obtained from 2-μl hanging drops consisting of equal amounts of protein solution (10 mg/ml) and well solution containing 1.6 M potassium sodium phosphate and 100 mM HEPES buffer, pH 7.5. Thin hexagonal shaped crystals of 1.5 μm grew in a few days. A diffraction data set to 2.1-Å resolution was collected in-house on a MacScience image plate system using CuKα radiation from a rotating anode generator. The data were processed using DENZO and SCALEPACK (15). The crystals belong to the space group P63 with cell constants a = b = 59.5 Å, and c = 57.9 Å. The asymmetric unit contains one monomer of 149 residues, of which the 22 C-terminal residues were not resolved in the electron density map.

Molecular replacement solutions were obtained with the program AMORE available in CCP4 (16, 17). A search model was constructed using the atomic coordinates of one heterodimer subunit (composed of an α and a β chain) from the Pseudomonas pavonaceae 170 heteroxameric CaaD (PDB code 150Y) (5). All residues were changed to alanines except for the proline and glycine residues. Rotation and translation func-
Structures of Native and Inactivated cis-CaaD

Table 1: Data collection and refinement statistics

<table>
<thead>
<tr>
<th>Data statistics</th>
<th>Native cis-CaaD</th>
<th>Inactivated cis-CaaD</th>
</tr>
</thead>
<tbody>
<tr>
<td>Space group</td>
<td>P2₁̄ 3</td>
<td>P6₁</td>
</tr>
<tr>
<td>No. chains/asymmetric unit</td>
<td>3</td>
<td>1</td>
</tr>
<tr>
<td>Unit cell (Å)</td>
<td>141.4</td>
<td>141.4</td>
</tr>
<tr>
<td>Resolution (Å)</td>
<td>0.76</td>
<td>0.76</td>
</tr>
<tr>
<td>R̂ (sym) (%) overall (outer shell)</td>
<td>19.2 (2.1)</td>
<td>19.8 (2.5)</td>
</tr>
<tr>
<td>Completeness (%) overall (outer shell)</td>
<td>99.9 (100.0)</td>
<td>99.9 (100.0)</td>
</tr>
<tr>
<td>l/σ overall (outer shell)</td>
<td>0.83</td>
<td>0.83</td>
</tr>
<tr>
<td>Reflections total (unique)</td>
<td>165,665 (23,148)</td>
<td>61,304 (6,850)</td>
</tr>
</tbody>
</table>

Refinement

<table>
<thead>
<tr>
<th>Total atoms/water/SO₄</th>
<th>3,470/159/17</th>
<th>975/61/0</th>
</tr>
</thead>
<tbody>
<tr>
<td>R/Re-f free (%)</td>
<td>19.2/35.9</td>
<td>19.8/35.5</td>
</tr>
<tr>
<td>R/Fo (sym) (%) overall (outer shell)</td>
<td>93.9/35.9</td>
<td>96.0/35.5</td>
</tr>
<tr>
<td>Ramachandran plot (%) (favored/allowed/generously allowed/disallowed)</td>
<td>93.9/35.9</td>
<td>96.0/35.5</td>
</tr>
</tbody>
</table>

a Rsym = 2Σ|Fo − Fc|/ΣFo, where I is the observed intensity and σ(I) the average intensity.

b R free = R on the basis of 5% of the data withdrawn from the cross-validation test.

tions were calculated using the data between 10- and 4-Å resolution. The molecular replacement yielded the position and orientation of a single monomer in the asymmetric unit. Refinement of the solutions by AMORE gave a correlation coefficient of 0.19 and an R-factor of 43.6%. The electron-density maps at this stage were not interpretable, but density was observed extending from some alamines of the search model. A σA-weighted map (18) calculated from the refined solutions from AMORE was used in a density-modification and phase-extension procedure using the prime-and-switch method available in the program RESOLVE (19). This improved the overall figure of merit from 0.24, after calculation of the starting map, to 0.52 in the final cycle of the density modification procedure. The resulting σA-weighted maps from RESOLVE showed improved electron density for the amino acid side chains and allowed identification of the N-terminal proline residue in the monomer of cis-CaaD. Manual building of side chains and missing main-chain atoms were subsequently alternated with simulated annealing and minimization runs in CNX (Accelrys Inc.). The program RESOLVE was used to obtain the most unbiased maps for model building, until σA-weighted 2Fo −Fc maps were of superior quality. The structure was built using QUANTA (Accelrys Inc.) and XtalView (20). Coordinates for the covalent adduct were based on 2-hydroxypropanoate and improved electron density for the amino acid side chains and allowed identification of the N-terminal proline residue in the monomer of cis-CaaD. Manual building of side chains and missing main-chain atoms were subsequently alternated with simulated annealing and minimization runs in CNX (Accelrys Inc.). The program RESOLVE was used to obtain the most unbiased maps for model building, until σA-weighted 2Fo −Fc maps were of superior quality. The structure was built using QUANTA (Accelrys Inc.) and XtalView (20). Coordinates for the covalent adduct were based on 2-hydroxypropanoate and minimized in QUANTA (Accelrys Inc.), and its parameters were generated using the Hic-Up server (21). The quality of the final model was analyzed with PROCHECK (22). A summary of the data collection statistics, the refinement statistics, and geometric quality of the models is given in Table 1. Docking of 1 and 2 in the active sites of cis-CaaD and CaaD, respectively, was carried out manually using the program XtalView (20).

Construction, Expression, and Characterization of the H28A, Y103F, and Y103F/E114Q Mutants of cis-CaaD—The three mutant genes were generated by overlap extension PCR (23) using the plasmid pCC5 (1) as the template. The oligonucleotides, 5’-ATACATGGCGGTTTATATGTGTATT-3’ and 5’-CATGGAATCCCTAGTGCCCGAGGTCCACCAT-3’ were used as the forward and reverse external primers, respectively. The forward primer contains an NdeI restriction site (in bold), and the reverse primer has a BamHI restriction site (in bold). For the H28A mutant, the internal PCR primers were oligonucleotides 5’-ATACACCCGGGAGCTCCAG-3’ and 5’-CATGGAATCCCTAGTGCCCGAGGTCCACCAT-3’. For the Y103F mutant, the internal PCR primers were oligonucleotides 5’-CATGGAATCCCTAGTGCCCGAGGTCCACCAT-3’ and 5’-TGCGTCACATGGCGGTTTATATGTGTATT-3’. For the Y103F/E114Q mutant, the internal PCR primers were oligonucleotides 5’-TGCGTCACATGGCGGTTTATATGTGTATT-3’ and 5’-TGCGTCACATGGCGGTTTATATGTGTATT-3’. The codons used to introduce the mutations are underlined. The amplification mixtures contained the appropriate synthetic primers, the deoxynucleotide triphosphates, the appropriate template DNA
Structures of Native and Inactivated cis-CaaD

FIGURE 1. Stereo views of (A) the monomeric and (B) the trimeric structure of cis-CaaD. The catalytic Pro-1 is shown in ball-and-stick (A) and Corey-Pauling-Koltun (B) representation. The figures were made using MOLESCRIPT and RASTER3D (24, 25).

RESULTS AND DISCUSSION

Structure of the Native cis-CaaD—The native cis-CaaD crystal structure was solved to 2.75-Å resolution by molecular replacement methods and refined to $R$ and $R_{free}$ values of 23.3% and 26.3%, respectively. The asymmetric unit contains three monomers. Each monomer consists of a four-stranded $\beta$-sheet that is formed by the anti-parallel interaction of a pair of two-stranded parallel $\beta$-sheets (Fig. 1A). Two $\alpha$-helices, each spanning the two strands of the parallel $\beta$-sheets, lie anti-parallel to each other in the concave side of the $\beta$-sheet plane. Hence, each monomer is made up of two $\beta$-$\alpha$-$\beta$ structural motifs that are characteristic of the tau-tomerase superfamily (7-9).

The three monomers in the asymmetric unit superimpose with root-mean-square deviation (r.m.s.d.) values of $\sim$0.4 Å for 129 equivalent $C_\alpha$ atoms (out of a total of 149 amino acids). Each of the three monomers forms an independent barrel-like trimer by rotation around one of the crystallographic 3-fold rotation axes in the crystal (Fig. 1B). Interactions between the monomers are mediated by the edges of the four-stranded $\beta$-sheets and are mainly hydrophobic in nature. Each $\beta$-sheet further contributes polar residues that interact with each other and with three water molecules in

$\beta$-sheet further contributes polar residues that interact with each other and with three water molecules in...
the central cavity of the trimer. Additional monomer–monomer interactions are provided by two small /H9252 -hairpin structures near the termini of the central /H9252 -sheet and the two C-terminal /H9251 -helices (Fig. 1, A and B).

**Active Site of Native cis-CaaD—** cis-CaaD contains three active sites with the catalytically important N-terminal proline buried in the interior of a monomer on one side of the trimer (Fig. 1B). The Pro-1 nitrogen interacts with one of the oxygen atoms of a sulfate ion, or possibly a phosphate ion, that is bound in the active site cavity (Fig. 2A). Both ions were present in the crystallization solution. The prolyl nitrogen atom interacts with one of the sulfate/phosphate oxygen atoms. The other three oxygen atoms of the sulfate/phosphate ion have electrostatic and hydrogen-bonding interactions with two arginines, Arg-70 and Arg-73, a positively charged histidine, His-28, and Thr-34 (not shown). The prolyl nitrogen atom further interacts with one of the side-chain oxygen atoms of the catalytic base, Glu-114, which is stacked between Leu-119 and Trp-101’ from a neighboring monomer.

The same oxygen atom of Glu-114 interacts with the side-chain hydroxyl group of Tyr-103’, also from a neighboring monomer. The other carboxylate oxygen of Glu-114 interacts with the backbone carbonyl oxygen of Leu-38, suggesting that the side chain of Glu-114 is protonated. As such, Glu-114 cannot function as the water-activating catalytic base in the hydration reaction catalyzed by cis-CaaD. Such a protonation state of the glutamate, however, could be an artifact of the low pH at which the native enzyme was crystallized.

**Comparison of cis-CaaD with Tautomerase Superfamily Members—** cis-CaaD represents one of the five presently known families identified as constituents of the tautomerase superfamily (1, 2, 7–9, 26, 27). The other four families, represented by their title enzymes, are the 5-(carboxymethyl)-2-hydroxymuconate isomerase (28), 4-oxalocrotonate tautomerase (26, 29), macrophage migration inhibitory factor (30), and malonate semialdehyde decarboxylase (MSAD) families (27). cis-CaaD has been classified in a separate tautomerase family, the cis-CaaD family, because of the absence of significant sequence identity with known members of the other four families (1). The trans-specific CaaD, however, belongs to the 4-oxalocrotonate tautomerase family.

Like 5-(carboxymethyl)-2-hydroxymuconate isomerase, macrophage migration inhibitory factor, and MSAD, cis-CaaD is a trimer constructed from monomers containing two adjacent /\beta/ -/\alpha/-/\beta/ structural motifs, which run in opposite directions (31–33). A structural alignment shows that the monomer structures of the four enzymes superimpose with r.m.s.d. values of 1.2 Å for 39 C_/\alpha_/ atoms out of a total of 114–147 amino acids. These C_/\alpha_/ atoms are located in the four /\beta/-strands and the second /\alpha/-helix that build the central core of the monomers. The low number of matching C_/\alpha_/ atoms reflects the structural differences found in the loop that connects the first and second /\beta/-/\alpha/-/\beta/ structural motif, and the C terminus. Of the four, the

5 The unprimed and primed residues come from different monomers of cis-CaaD.
monomers of cis-CaaD and MSAD are structurally the most similar: in a pairwise alignment 97 out of 129 (MSAD) and 147 (cis-CaaD) Cα atoms align with an r.m.s.d. value of 1.3 Å. A structural alignment further shows that the two connected β-α-β structural motifs in cis-CaaD, and the α- and β-chains of CaaD align with r.m.s.d. values of 0.9 Å for 50 Cα atoms out of a total of 55–62 amino acids. Thus, even though CaaD and cis-CaaD belong to different families of the tautomerase superfamily, cis-CaaD and CaaD are structurally very similar.

Structure of cis-CaaD Inactivated by (R)-8—It has previously been shown that cis-CaaD is inactivated by the active site-directed irreversible inhibitor, (R)-8 (10). In contrast, the (S)-enantiomer of 8 is only a weak competitive inhibitor with a $K_i$ value of 9.2 ± 0.8 mM (10). Mass spectral analysis of cis-CaaD inactivated by (R)-8 showed that the sole site of modification on the enzyme is Pro-1, and that the increase in molecular mass for the inactivated cis-CaaD is consistent with covalent modification by a 2-hydroxypropanoate species. The crystal structure of the inactivated cis-CaaD was determined to 2.1 Å resolution by the molecular replacement method using the atomic coordinates for one heterodimer subunit in the heterohexameric CaaD and refined to $R$ and $R_{free}$ values of 20.2% and 23.0%, respectively.

The electron-density map of the inactivated cis-CaaD clearly established a covalent linkage between the Pro-1 nitrogen and C3 of the ring opened (R)-8 and allowed an unambiguous determination of the nature of the covalent adduct (Fig. 2B). Electron density extends from Pro-1 with an angle that is consistent with a tetrahedral conformation at the prolyl nitrogen, indicating a single bond between the prolyl nitrogen and the C3 atom of the adduct. The prolyl nitrogen is within hydrogen bonding distance (2.8 Å) of the backbone carbonyl oxygen of Leu-38, showing that the prolyl nitrogen is protonated and thus positively charged. Attack at C3 of (R)-8 by Pro-1 places a hydroxyl group at C2 (10). Accordingly, the electron-density map shows electron density consistent with an oxygen atom attached to the second carbon atom (C2) of the adduct, that is at hydrogen bonding distance (3.0 Å) from a water molecule bound to Arg-70. Additional electron density, consistent with a carbonylate group, extends toward the side chains of His-28 and Arg-73. On the basis of these observations, it is concluded that Pro-1 attacked the C3 position of (R)-8 to result in the attachment of (R)-2-hydroxypropanoate to the prolyl nitrogen.

The Active Site of cis-CaaD Inactivated by (R)-8—The (R)-2-hydroxypropanoate carbonylate group occupies a similar position as the sulfate/phosphate ion in the native structure and makes similar interactions (Figs. 2A and 3A). It makes two hydrogen bonds (~3.0 Å) with the side-chain guanidinium group of Arg-73 and one hydrogen bond with the backbone nitrogen of Arg-70. In addition, it forms a hydrogen bond (2.7 Å) with the ε-nitrogen of His-28. The 2-hydroxyl group of the adduct interacts with the water molecule bound to the side chain of Arg-70 and the hydroxyl group of Thr-34 (not shown). The catalytic base Glu-114 makes a hydrogen bond (2.5 Å) with the side-chain guanidinium group of Arg-70 and the hydroxyl group of Tyr-103 (Fig. 3A) and is rotated with respect to its position in the native structure of cis-CaaD. As a result, the other carbonylate oxygen atom of Glu-114 does not interact anymore with the backbone carbonyl group of Leu-38 but instead interacts with a water molecule located approximately at the position of Leu-119 in the native structure. Leu-119 is one of the 22 C-terminal residues that are

---

**FIGURE 3.** Detailed overviews of the active sites of inactivated cis-CaaD and CaaD. A, close-up stereo view of the active site of inactivated cis-CaaD showing the interaction of the carboxylate of the (R)-2-hydroxypropanoate adduct with the two arginines (Arg-70 and Arg-73) and histidine (His-28). B, close-up stereo view of the active site of inactivated CaaD (S) showing the interaction of the carboxylate group of the 3-oxopropanoate adduct with the two arginines (αArg-8 and αArg-11). Dark-colored chains represent the β-chains of the heterohexameric CaaD, whereas the light-colored chains represent the α-chains. In both figures, residues are labeled by their chain color, except Pro-1, which is labeled in black. The figures were made using MOLSCRIPT and RASTER3D (24, 25).
not visible in the electron-density maps of the inactivated cis-CaaD structure. It remains unclear whether the unstructured C terminus of the inactivated enzyme is due to inactivation of the enzyme by (R)-8 or to a crystallization artifact. Despite this, and given the pH at which the inactivated enzyme was crystallized (pH 7.5), Glu-114 is likely not protonated and in a position to activate the nucleophilic water molecule (see below).

**Differences between the cis-CaaD and CaaD Active Sites—**The cis-CaaD active site shows two significant differences compared with that of CaaD inactivated by 3-bromopropiolate (PDB entry 1S0Y, Fig. 3B) (5). The first difference is the presence of a new residue, His-28, involved in the binding of the carboxylate group of the covalent adduct. Significantly, His-28 is conserved in the four sequences included in the cis-CaaD family (1). In CaaD, the equivalent position is occupied by a threonine (βThr-27). Second, the active site of cis-CaaD has a tyrosine residue (Tyr-103’) that directly interacts with Glu-114. Although the tyrosine is not conserved and is present in only two of the four cis-CaaD family sequences (1), its proximity to Glu-114 and the Pro-1 nitrogen suggests that it may have a catalytic role, e.g. assisting Glu-114 in the activation of the catalytic water molecule. Indeed, mutation of Tyr-103’ has an effect on enzyme activity (see below). Moreover, the presence of His-28 and Tyr-103’ in cis-CaaD, but not in CaaD, could account for the individual substrate specificities.

**Structural Basis for the Substrate Specificity of cis-CaaD—**A comparison of the structures of cis-CaaD and CaaD offers an explanation for their different substrate specificities (Fig. 4). In cis-CaaD, the carboxylate group of the substrate is bound by the His-28/Arg-70/Arg-73 cluster, such that the rest of the substrate in the active site is oriented toward the surface of the enzyme (Fig. 4A). In CaaD, the carboxylate group of the substrate is bound by the αArg-8/αArg-11 pair, with the remainder of the substrate projecting deeper into the active site (Fig. 4B). Thus, the presence of an additional carboxylate-binding residue (His-28) in cis-CaaD results in differences in the orientation of the substrate in the active site with respect to CaaD.

The substrate-binding pockets fit the shape of their respective substrates (cf. 1 and 2), the pocket of cis-CaaD being more U-shaped, whereas the pocket of CaaD is more elongated in shape. One of the residues responsible for this shape difference is Tyr-103’ (αVal-41 in CaaD). In CaaD, αVal-41 creates a hydrophobic region allowing the 3-chloro moiety of the substrate to bind between αPhe-39 and αPhe-50. In the presence of additional carboxylate-specificity (His-28) in cis-CaaD, the carboxylate group of the substrate is bound by the αArg-8/αArg-11 pair, with the remainder of the substrate projecting deeper into the active site (Fig. 4A). Thus, the presence of an additional carboxylate-binding residue (His-28) in cis-CaaD results in differences in the orientation of the substrate in the active site with respect to CaaD.

**Differences in the cis-CaaD and CaaD Active Sites—**The cis-CaaD active site shows two significant differences compared with that of CaaD inactivated by 3-bromopropiolate (PDB entry 1S0Y, Fig. 3B) (5). The first difference is the presence of a new residue, His-28, involved in the binding of the carboxylate group of the covalent adduct. Significantly, His-28 is conserved in the four sequences included in the cis-CaaD family (1). In CaaD, the equivalent position is occupied by a threonine (βThr-27). Second, the active site of cis-CaaD has a tyrosine residue (Tyr-103’) that directly interacts with Glu-114.

Although the tyrosine is not conserved and is present in only two of the four cis-CaaD family sequences (1), its proximity to Glu-114 and the Pro-1 nitrogen suggests that it may have a catalytic role, e.g. assisting Glu-114 in the activation of the catalytic water molecule. Indeed, mutation of Tyr-103’ has an effect on enzyme activity (see below). Moreover, the presence of His-28 and Tyr-103’ in cis-CaaD, but not in CaaD, could account for the individual substrate specificities.

**Structural Basis for the Substrate Specificity of cis-CaaD—**A comparison of the structures of cis-CaaD and CaaD offers an explanation for their different substrate specificities (Fig. 4). In cis-CaaD, the carboxylate group of the substrate is bound by the His-28/Arg-70/Arg-73 cluster, such that the rest of the substrate in the active site is oriented toward the surface of the enzyme (Fig. 4A). In CaaD, the carboxylate group of the substrate is bound by the αArg-8/αArg-11 pair, with the remainder of the substrate projecting deeper into the active site (Fig. 4B). Thus, the presence of an additional carboxylate-binding residue (His-28) in cis-CaaD results in differences in the orientation of the substrate in the active site with respect to CaaD.
CaaD in an orientation similar to that proposed for 2, then the linear acetylene molecule would be directed into the active site. In this proposed binding mode, the two arginine residues of CaaD would interact with the 2-carbonyl oxygen as well as one or both carboxylate oxygens of 9. If 9 binds to cis-CaaD in a comparable mode to that proposed for 1, the linear acetylene molecule would now be directed into the U-shaped cavity. Such an orientation would not be a favorable one and may preclude efficient binding and catalysis. The presence of Tyr-103 might also interfere with the binding of 9.

**Mutagenesis of His-28 and Tyr-103**—To investigate the importance of Tyr-103’ and His-28 for the dehalogenation reaction, the H28A, Y103F, and Y103F/E114Q mutants of cis-CaaD were made and purified. Determination of their kinetic parameters and comparison with the wild type and E114Q-cis-CaaD activities showed that His-28 is essential for catalytic activity, because the H28A mutant has no detectable activity in the kinetic assay. Glu-114 is more important than Tyr-103’ as assessed by their $k_{cat}$ values (Table 2), but neither one is as critical as His-28. However, the Glu-114/Tyr-103’ pair is necessary as indicated by the observation that the Y103F/E114Q mutant has no detectable activity in the kinetic assay. Thus, it can be concluded that the three residues His-28, Tyr-103’, and Glu-114 are important for the cis-CaaD-catalyzed dehalogenation of 1.

To assess the relative importance of the six active site residues identified to date (Pro-1, His-28, Arg-70, Arg-73, Tyr-103’, and Glu-114) to cis-CaaD activity, the reactions catalyzed by the individual mutant proteins (P1A, H28A, R70A, R73A, Y103F, and E114Q) and the double mutant protein (Y103F/E114Q) were examined by $^1$H NMR spectroscopy at 17 or 22 h, Y103F, and E114Q) and the double mutant protein (Y103F/E114Q) resulted in a trace of product, the R70A-catalyzed reaction showed only a 1% product at 22 h. In contrast, the R70A-catalyzed reaction showed only a trace of product, the R73A reaction mixture generated 0.2% product at 22 h. The reaction mixture containing the double mutant protein (Y103F/E114Q) resulted in 6% product (at 17 h). The NMR analysis, which is consistent with the kinetic data reported here and elsewhere (1), suggests that Pro-1, Arg-70, and Arg-73 are the most essential catalytic residues in cis-CaaD. Hence, substrate activation and protonation at C2 may be more critical for the dehalogenation reaction than the activation of water.

**Mechanism of Inactivation of cis-CaaD by (R)-8**—It has previously been shown that inactivation of cis-CaaD by (R)-8 requires Pro-1, Arg-70, and Arg-73 (10). In contrast, the E114Q mutant protein is alkylated by (R)-8 indicating that Glu-114 is not essential for the inactivation reaction. These observations are consistent with a mechanism for covalent modification involving the nucleophilic attack of Pro-1 at C2 or C3 of (R)-8 concomitant with the formation of a hydrogen bond between the oxirane oxygen and a nearby proton donor or protonation of the oxirane oxygen by a proton source (10).

The present crystal structure of the inactivated cis-CaaD establishes the C3 position of (R)-8 as the site of nucleophilic attack by Pro-1. The structure also shows that the carboxylate group of the adduct interacts with the side chains of His-28, Arg-73, and the backbone nitrogen atom of Arg-70 (Fig. 3A). The side chain of Arg-70 interacts only indirectly, via a water molecule, with the hydroxyl and carboxylate groups of the inhibitor. These observations suggest that Arg-73 and His-28 are predominantly involved in the binding of the carboxylate group and that Arg-70 may facilitate ring opening by direct interaction with the epoxide oxygen or by placing a water molecule in position to interact with the epoxide oxygen. Furthermore, the interactions of Arg-70 and the His-28/Arg-73 pair with the covalent adduct suggest that prior to inactivation (R)-8 was positioned in the active site with the oxirane oxygen near Arg-70 and the C3 atom proximal to Pro-1 (Scheme 3A). If the (S)-enantiomer of 8 binds to cis-CaaD with similar interactions between the carboxylate group and Arg-73 and His-28, the C3 carbon atom would be directed away from Pro-1 and toward Arg-70 (Scheme 3B). This binding mode precludes alkylation of Pro-1 but could result in competitive inhibition, which has been observed experimentally (10).

The proposed binding mode also provides a reasonable explanation for the fact that CaaD is not inactivated by either enantiomer of 8. CaaD lacks His-28 (or an equivalent) in the active site so that the carboxylate group of 8 might interact with both arginines (in this case, αArg-8 and αArg-11), similar as observed in the crystal structure of inactivated CaaD (Fig. 3B). Because both arginines are now involved in binding the carboxylate group, this would prevent one of the arginines from functioning as the required proton donor assisting in the ring opening reaction of the epoxide moiety. Such a binding mode could again lead to competitive inhibition, which has been observed experimentally. This analysis implicates His-28 as a critical residue that makes cis-CaaD, but not CaaD, subject to irreversible inhibition.

**Mechanism of the Dephalogenation of 1**—The crystallographic observations and mutagenesis results described above along with work discussed elsewhere (1) identify and establish the relative importance of Pro-1, His-28, Arg-70, Arg-73, Tyr-103’, and Glu-114 in the cis-CaaD catalytic mechanism (Scheme 4). The mechanism can be broken down into three components:

### Table 2

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>$k_{cat}$</th>
<th>$K_m$</th>
<th>$k_{cal}/K_m$</th>
</tr>
</thead>
<tbody>
<tr>
<td>cis-CaaD</td>
<td>1.7 ± 0.1</td>
<td>55 ± 6</td>
<td>3.1 × 10^4</td>
</tr>
<tr>
<td>E114Q</td>
<td>0.020 ± 0.006</td>
<td>4.3 ± 0.2</td>
<td>4.6 × 10^4</td>
</tr>
<tr>
<td>Y103F</td>
<td>0.13 ± 0.002</td>
<td>2.4 ± 1.1</td>
<td>5.4 × 10^4</td>
</tr>
</tbody>
</table>

* The steady-state kinetic parameters were determined in 20 mM Na2HPO4 buffer (pH 9.0) at 23 °C. Errors are standard deviations. There was no detectable activity for the H28A or the Y103F/E114Q mutant proteins.
activation of water by Glu-114 and Tyr-103'; activation and alignment of substrate by His-28, Arg-70, and Arg-73; and protonation at C2 by Pro-1. Our results show that the individual contributions of the residues in substrate activation and protonation are more important to catalysis than those involved in the activation of water.

The structures of the native and inactivated enzyme suggest that Tyr-103' is in a position to assist Glu-114 in the activation of a water molecule for attack at C3 of 1. A specific role cannot be assigned to Tyr-103', but three possibilities exist. Tyr-103' can position the water molecule or the carboxylate group of Glu-114, assist in activation of the water molecule (as shown in Scheme 4), or any possible combination. All of these roles are consistent with the diminished $k_{cat}$ of the Y103F mutant protein, but the function of Glu-114 is clearly more important than that of Tyr-103' in water activation. Removing both residues does, however, severely compromise cis-CaaD activity.

The structures also suggest that the His-28/Arg-70/Arg-73 cluster assists in the binding and activation of the substrate by interacting with the oxygen atoms of the C-1 carboxylate group. The three residues likely polarize the carboxylate group, which results in a partial positive charge at C3, which, in turn, facilitates the addition of water. The specific interactions between the His-28/Arg-70/Arg-73 cluster and the carboxylate group are not known, but they may parallel those observed in the His-28/Arg-70/Arg-73 cluster and the carboxylate group of cis-CaaD active site and the low sequence identity would further suggest that the two enzymes diverged quite some time ago. Two scenarios can be envisioned: in one, cis-CaaD evolved from a direct ancestor of CaaD, whereas in the other, CaaD and cis-CaaD evolved independently. A gene duplication event of a small gene encoding the $\beta$-$\alpha$-$\beta$ structural motif followed by co-evolution of the two genes could give rise to CaaD. cis-CaaD could then have diverged from these two genes (and thus from the direct ancestor of CaaD), by a second duplication event of the two genes followed by gene fusion. In this scenario, the two enzymes have a single evolutionary lineage. Alternatively, cis-CaaD might have evolved from an independent gene duplication event of the small gene followed by gene fusion. In this scenario, CaaD and cis-CaaD evolved independently. The presence of His-28 and Tyr-103' in the cis-CaaD active site and the low sequence identity between CaaD and cis-CaaD implicate the second scenario, which is consistent with our previously reported phylo-
genetic analysis (1). Hence, the last common ancestor of CaaD and cis-CaaD was probably a small gene encoding the $\beta$-$\alpha$-$\beta$ structural motif.

REFERENCES