A glutathione S-transferase (GST) with activity toward 1,2-epoxy-2-methyl-3-butene (isoprene monoxide) and cis-1,2-dichloroepoxyethane was purified from the isoprene-utilizing bacterium *Rhodococcus* sp. strain AD45. The homodimeric enzyme (two subunits of 27 kDa each) catalyzed the glutathione (GSH)-dependent ring opening of various epoxides. At 5 mM GSH, the enzyme followed Michaelis-Menten kinetics for isoprene monoxide and cis-1,2-dichloroepoxyethane, with \( V_{\text{max}} \) values of 66 and 2.4 \( \mu \text{mol min}^{-1} \text{mg}^{-1} \) of protein \(^1\) and \( K_m \) values of 0.3 and 0.1 mM for isoprene monoxide and cis-1,2-dichloroepoxyethane, respectively. Activities increased linearly with the GSH concentration up to 25 mM. \(^1\)H nuclear magnetic resonance spectroscopy showed that the product of GSH conjugation to isoprene monoxide was 1-hydroxy-2-glutathionyl-2-methyl-3-butene (HGMB). Thus, nuclease attack of GSH occurred on the tertiary carbon atom of the epoxide ring. HGMB was further converted by an NAD\(^+\) dependant dehydrogenase, and this enzyme was also purified from isoprene-grown cells. The homodimeric enzyme (two subunits of 25 kDa each) showed a high activity for HGMB, whereas simple primary and secondary alcohols were not oxidized. The enzyme catalyzed the sequential oxidation of the alcohol function to the corresponding aldehyde and carboxylic acid and followed Michaelis-Menten kinetics with respect to NAD\(^+\) and HGMB. The results suggest that the initial steps in isoprene metabolism are a monoxygenase-catalyzed conversion to isoprene monoxide, a GST-catalyzed conjugation to HGMB, and a dehydrogenase-catalyzed two-step oxidation to 2-glutathionyl-2-methyl-3-butenedioic acid.

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**MATERIALS AND METHODS**

**Organisms and growth conditions.** *Rhodococcus* sp. strain AD45 was grown on isoprene in batch culture or in continuous culture, using a mineral medium supplemented with 20 mg of yeast extract per liter as described before (32). Reaction mixtures consisted of 50 mM Tris-HCl buffer (pH 8.5) containing 5 mM substrate and 5 mM GSH unless stated otherwise. The dimensionless Henry coefficients that were used for the calculation of activities are 0.001 for cis-1,2-dichloroepoxyethane, 0.007 for epoxypropane, 0.02 for 1,2-epoxyhexane, and 0.02 for 1,2-epoxy-2-methyl-3-butene (32). The dimensionless Henry coefficients of epithiopropane (0.06), 1,2-epoxybutane (0.008), 2,3-epoxybutane (0.01), epifluorohydrin (0.007), epichlorohydrin (0.006), and epibromohydrin (0.004) were determined as described before (30).

The formation of GSH-isoprene monoxide conjugates was monitored by removing samples from a reaction mixture containing 10 mM GSH and 5 mM isoprene monoxide. The samples were quenched by mixing with 1 volume of 1 M formic acid and analyzed for the presence of GSH-isoprene monoxide conjugates by high-pressure liquid chromatography (HPLC). Dehydrogenase activities were measured in 100 mM glycine-NaOH buffer (pH 10.0) to which 1 mM NAD\(^+\) and 7.5 mM GSH-isoprene monoxide conjugate was added from a 0.5 M stock solution, unless stated otherwise. The activity was monitored by following the production of NADH at 340 nm. Activities are expressed in units per milligram of protein. One unit is defined as the activity that catalyzes the conversion of 1 \( \mu \)mol of substrate per min.

**Purification of the GST.** Isoprene-grown cells were harvested from a continuous culture that was operated at a dilution rate of 0.026 h\(^{-1}\) (32) and resuspended in 10 mM Tris-HCl buffer (pH 7.5). All further steps were carried out at 0 to 4°C. Cells were washed twice with this buffer before they were resuspended in 10 mM Tris-HCl buffer containing 1 mM \( \beta \)-mercaptoethanol, 1 mM EDTA, and 3 mM Na\(_2\)MoO\(_4\) (TEMA buffer). After sonication, a cell extract was obtained by centrifugation (40,000 \( \times \) g, 60 min).

Solid (NH\(_4\))\(_2\)SO\(_4\) was added to the extract to 40% saturation. The mixture was
pH 7.0) containing 1 mM EDTA, 1 mM p-mercaptoethanol, 1.5 mM NaN₃, and 10% glycerol (PEMAG buffer) and subjected to column (Pharmacia). Retained protein was eluted with a 20-ml linear decreasing gradient of 1.5 to 0 M (NH₄)₂SO₄ in buffer A (flow rate, 0.5 ml min⁻¹; fraction volume, 0.5 ml). Activity eluted at 0.1 to 0.85 M (NH₄)₂SO₄. Approximately 25% of the activity that was thus collected eluted as pure protein, as judged by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE). The other 75% was further purified by applying it a second time to the Resource Iso column. The pooled purified enzyme was dialyzed against TEMA buffer and stored at 4°C.

Purification of the dehydrogenase. In the first step of the purification protocol, cell extract was subjected to anion-exchange chromatography using a DE52 column (diameter, 3 cm; height, 10 cm; Sigma). The protein was eluted with a 500-ml linear gradient of 0 to 0.3 M NaCl in TEMA buffer containing 10% glycerol (flow rate, 1 ml min⁻¹; fraction volume, 4 ml). Activity eluted at 0.2 to 0.25 M NaCl. Active fractions were pooled and concentrated by ultrafiltration with an Amicon diaflow membrane (10-kDa exclusion pore) fitted in an Amicon chromatography system (Pharmacia Biotech). The buffer system consisted of TEMA buffer (buffer A) and TEMA buffer with 0.45 M NaCl (buffer B). Retained protein was eluted with a three-step increasing linear gradient: 0 to 15% TEMA buffer (flow rate, 0.8 ml min⁻¹; fraction volume, 2 ml). Activity eluted at 90 to 105 mM NaCl, and active fractions were pooled.

Solid (NH₄)₂SO₄ was added to a concentration of 1.5 M, and the protein was applied to a Resource Iso column (1 ml; Pharmacia Biotech). Retained protein was eluted with a 28-ml linear decreasing gradient of 1.5 to 0 M (NH₄)₂SO₄ in buffer A (flow rate, 0.5 ml min⁻¹; fraction volume, 0.5 ml). Activity eluted at 0.2 to 0.25 M NaCl. Active fractions were pooled and concentrated by ultracentrifugation with an Amicon diaflow membrane (10-kDa exclusion pore) fitted in an Amicon chromatography system (Pharmacia). The solution was dialyzed against TEMA buffer to remove (NH₄)₂SO₄, and the protein was applied to a Resource Iso column (1 ml; Pharmacia Biotech). Retained protein was eluted with TEMA buffer (flow rate, 1 ml min⁻¹; fraction volume, 4 ml). Activity eluted at 0.1 to 0.15 M NaCl. Active fractions were pooled and dialyzed against TEMA buffer containing 1.5 M (NH₄)₂SO₄ and applied to a Resource Iso column (Pharmacia). Retained protein was eluted with a 20-ml linear decreasing gradient of 1.5 to 0 M (NH₄)₂SO₄ in TEMA buffer (flow rate, 0.5 ml min⁻¹; fraction volume, 0.5 ml). Activity eluted at 1.1 to 0.95 M (NH₄)₂SO₄.

Estimation of molecular mass. Molecular masses of the native enzymes were estimated by gel filtration on a Superose 12 HR 10/30 column equilibrated with TEMA buffer containing 100 mM NaCl. Immunoglobulin G (160 kDa), bovine serum albumin (67 kDa), ovalbumin (43 kDa), and soybean trypsin inhibitor (20.1 kDa) were used as reference proteins.

Molecular masses of denatured enzymes were determined by SDS-PAGE. Phosphorylase a (94 kDa), bovine serum albumin (67 kDa), ovalbumin (43 kDa), carbonic anhydrase (30 kDa), soybean trypsin inhibitor (20.1 kDa), and a-lactalbumin (14.4 kDa) were used as reference proteins.

Amino acid analysis and N-terminal amino acid sequence determination. Determination of amino acid composition and N-terminal amino acid sequence determination were performed by Eurosequence BV (Groningen, The Netherlands).

For N-terminal sequence analysis, approximately 50 μg of pure protein was applied to SDS-PAGE and electroblotted on a polyvinylidene difluoride membrane (Immobilon-P, Millipore). The N-terminal sequence was determined by Edman degradation using an automated sequenator (model 477A; Applied Biosystems). The amino acid composition was determined after the protein was hydrolyzed with 5.7 N HCl at 165°C for 2 h. The hydrolysate was applied to an HP Aminopac equipped with a Shandon Hyperpress OD column (2.1 by 200 mm).

Homology search. The amino acid analysis program at EMBL (Heidelberg, Germany) was used to search the SwissProt database for proteins with a homologous amino acid composition (19). The BLAST program (5) was used to search the SwissProt database for proteins that show sequence similarity with the N-terminal sequences. Multiple sequence alignments were generated with Clustal W version 1.7 (29). Conserved amino acids are indicated according to the following scheme: P, A, G, S, T; Q, N, E, D, R, K; I, L, M, V, F, Y, W, C, H. All used programs were offered as services on the Worldwide Web.

HPLC-MS analysis of GST conjugates. GST-epoxide conjugates present in the supernatants were analyzed by reversed-phase HPLC using a Merck Hitachi L-6200A system equipped with a Lichrosorb 5C18 column (20 by 4.6 mm) or a Lichrospher 100 RP-18 column (250 by 4.6 mm). Ultraviolet detection (280 nm), XIC detection (200 mm)

RESULTS

Purification and biochemical properties of the GST. Previously, we observed that only in extracts of isoprene- and isoprene monoxide-grown cells of Rhodococcus sp. strain AD45 could a GST activity with epoxides be detected (32). We purified this enzyme to homogeneity from cells grown on isoprene in continuous culture. No binding or retardation of the protein was observed upon affinity chromatography with GSH-coated agarose. Therefore, the enzyme was purified by (NH₄)₂SO₄ precipitation followed by anion-exchange chromatography and hydrophobic interaction chromatography (Table 1). The purification protocol reproducibly yielded pure protein, as judged by SDS-PAGE (Fig. 1). The protein was purified 13-fold, implying that the GST represents approximately 8% of the total protein in isoprene-grown cells. This is in agreement with the presence of a prominent protein band of the same electrophoretic mobility in cell extracts of isoprene-grown cells (Fig. 1).

Gel filtration indicated that the native protein had a molecular mass of 46 ± 4 kDa. Since the band obtained with SDS-PAGE represented a polypeptide of 27 ± 2 kDa, the enzyme is probably a homodimer (Fig. 1).

The enzyme was not affected by the addition of 1 mM MnCl₂, CoCl₂, CuSO₄, MgSO₄, RbCl₂, or ZnSO₄. Since the activity was not also influenced by the addition of 5 mM EDTA, we concluded that the enzyme does not require divalent cations for optimal activity. Preincubation of the enzyme with N-ethylmaleimide, p-chloromercuribenzoate, or HgCl₂, which react with sulhydrl groups in proteins, did not have a significant effect on activity. Activity was also not influenced by the addition of 1 mM β-mercaptoethanol. The enzyme could be stored at 4 or −20°C for 3 months with less than 20% loss of activity.

The N-terminal amino acid sequence and amino acid composition (Table 2) were determined to investigate whether the enzyme was related to one of the many GSTs that have been characterized. The N-terminal sequence obtained was Met-Ile-Thr-Val-Tyr-Gly-Tyr-Val-Pro-Ala-Trp-Gly-Ile-Pro-Asp-Ile-Ser-...
composition or the N-terminal sequence was compared to those of proteins present in the SwissProt database. However, GSTs typically contain one and often two tyrosine residues between positions 4 and 8 in the N-terminal part of the protein (8, 34). This feature is shared by the enzyme of strain AD45 since it contains tyrosine residues at positions 5 and 7. These tyrosine residues are involved in activation of the sulfhydryl group of bound GSH in all GSTs except the theta class. The latter proteins, to which many bacterial GSTs belong, appear to use a serine residue that is located in the N-terminus of the polypeptide. In the enzyme of strain AD45, this may be the function of the serine at position 17 (8, 35).

**Substrate range and kinetics of the GST.** The activities of the GST at different pH values and with various epoxides were measured with on-line GC. Optimal activity was observed at pH 8.5 to 9.0 (Fig. 2). All epoxides tested were substrates for the enzyme, and the relative activities are shown in Table 3. The highest conversion rates were observed with the physiological substrate isoprene monoxide. Other terminal epoxides and epipropiolane were converted at rates of 25 to 37% of that of isoprene monoxide. Another good substrate was the cis-1,2-dichloroepoxyethane accurately detectable, although the rate of conversion was much lower.

The enzyme followed Michaelis-Menten kinetics with isoprene monoxide and cis-1,2-dichloroepoxyethane as substrates. At 5 mM GSH, a $V_{\text{max}}$ of 66 U mg of protein$^{-1}$ and a $K_m$ of 0.1 mM were found with isoprene monoxide as a substrate. With cis-1,2-dichloroepoxyethane, these values were 2.4 U mg of protein$^{-1}$ and 0.1 mM, respectively. Activity with isoprene monoxide was linearly dependent on the GSH concentration up to 25 mM, above which the nonenzymatic reaction of GSH with isoprene monoxide was too high to allow accurate determination of enzyme-catalyzed reaction rates. From these data, we calculated that the specificity constants ($k_{\text{cat}}/K_m$) for GSH are $1.1 \times 10^4$ and $4.1 \times 10^4$ M$^{-1}$ s$^{-1}$ with isoprene monoxide and cis-1,2-dichloroepoxyethane, respectively, as the substrates.

**Identification of the reaction product of GSH and isoprene monoxide.** To identify the product formed from isoprene monoxide, we incubated the substrate with twofold excess GSH and analyzed samples by HPLC. The elution profiles showed that the amount of GSH decreased about 50% during conversion, indicating that GSH reacted stoichiometrically with isoprene monoxide (Fig. 3). The major product (compound 1) formed during the degradation of isoprene monoxide eluted at 17 min, and a minor product (compound 2) eluted at 18 min. The ratio between compound 1 and compound 2 was estimated to be 10:1 (Fig. 3 and 6). Analysis with HPLC-MS at 70-V nozzle voltage showed that compound 1 had a molecular ion with $m/z$ 392, which is consistent with the theoretical value for a conjugate of isoprene monoxide and GSH. The presence of such a conjugate was confirmed by the observation of a protonated dimet ($m/z$ 783). At higher nozzle voltage (170 V), collision-induced fragmentation is expected. Indeed, we observed loss of the isopropoy moiety from the cysteinyl sulfur, regenerating GSH and producing an ion with $m/z$ 308 ($M^+$ − 84). The other ions observed showed a typical peptide fragmentation pattern (11) from the conjugate generating ions with $m/z$ 392 (M$^+$), 263 (Y$^{2-}$), 130 (B$_1$), and 76 (Y$^{3-}$) and for the dealkylated compound with $m/z$ 308 (M$^+$), 291 (Z$_2$), 233 (B$_2$), 179 (Y$^{2-}$), and 162 (Z$_3$).

For compound 2, analyzed at a nozzle voltage of 70 V, a molecular ion with $m/z$ 392 (M$^+$) was also observed, indicating

![FIG. 1. Cell extract of *Rhodococcus* sp. strain AD45 grown on isoprene in continuous culture (lane 1), purified GST (lane 2), and purified dehydrogenase (lane 3). Each lane contained approximately 20 μg of protein.](image)

### Table 1. Purification of the GST and dehydrogenase from *Rhodococcus* sp. strain AD45

<table>
<thead>
<tr>
<th>Step</th>
<th>Total protein (mg)</th>
<th>Total activity (U)</th>
<th>Sp act (U mg of protein$^{-1}$)</th>
<th>Purification factor</th>
<th>Yield (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>GST</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>Cell extract</td>
<td>188</td>
<td>959</td>
<td>5.1</td>
<td>1</td>
<td>100</td>
</tr>
<tr>
<td>(NH$_4$)$_2$SO$_4$</td>
<td>233</td>
<td>932</td>
<td>4.0</td>
<td>0.8</td>
<td>97</td>
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<tr>
<td>Resource O</td>
<td>60</td>
<td>786</td>
<td>13.1</td>
<td>2.6</td>
<td>82</td>
</tr>
<tr>
<td>Resource Iso</td>
<td>8.9</td>
<td>594</td>
<td>66.7</td>
<td>13.1</td>
<td>62</td>
</tr>
<tr>
<td>Dehydrogenase</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cell extract</td>
<td>336</td>
<td>1,001</td>
<td>2.9</td>
<td>1</td>
<td>100</td>
</tr>
<tr>
<td>DES2</td>
<td>96</td>
<td>932</td>
<td>6.3</td>
<td>2.2</td>
<td>93</td>
</tr>
<tr>
<td>Sephacryl S-300</td>
<td>42</td>
<td>786</td>
<td>8.0</td>
<td>2.8</td>
<td>79</td>
</tr>
<tr>
<td>Blue Sepharose</td>
<td>15</td>
<td>198</td>
<td>13.3</td>
<td>4.6</td>
<td>20</td>
</tr>
<tr>
<td>Resource Iso</td>
<td>18.0</td>
<td></td>
<td></td>
<td></td>
<td>6.2</td>
</tr>
</tbody>
</table>
The Ha protons of the isoprene moiety shifted downfield after spectrum of isoprene monoxide showed that in the conjugates atom to the isoprene moiety. Comparison with the 1H NMR Rhodococcus methyl-3-butene. (ii) The chemical shift of the resonances of substituted carbon atom rather than protons located on a sulfur-ination energies did not give a clear indication of the structure of this product due to the small amounts present and poor separation at higher column loading. It is likely that compound 2 represents the product formed by substitution of GSH at the less-favored carbon atom in the epoxide ring (see below).

Since no ions arising from fragmentation in the isoprene moiety of compounds 1 and 2 were observed, it was necessary to use NMR to determine whether GSH was linked via a thioether bond to the C-1 or C-2 carbon atom of the isoprene moiety. Thus, the product of the GST-catalyzed reaction of GSH with isoprene monoxide was subjected to 1H NMR analysis, and the spectra were compared with those of related compounds (Fig. 4). Isoprene monoxide is a chiral compound, and since it was used as a racemic mixture, two diastereomeric products would be formed by GSH conjugation. It was found that isoprene oxidation by strain AD45 favors mainly the generation of the (R) enantiomer of isoprene monoxide (enantiomeric excess = 95%) (33). Therefore, we also used isoprene monoxide produced by strain AD45 to synthesize the conjugate with GSH.

With the conjugates formed with racemic isoprene monoxide and with biologically prepared isoprene monoxide, the signals produced by the GSH moiety could easily be identified by comparison with literature values (7, 20, 38) and by comparison with the 1H NMR spectrum of GSH (Table 4). The largest change in chemical shift of the protons of the GSH moiety was observed for the Cys H$_{\alpha}$ protons (Table 4), indicating that the GSH moiety is covalently linked via the sulfur atom to the isoprene moiety. Comparison with the 1H NMR spectrum of isoprene monoxide showed that in the conjugates the H$_{\alpha}$ protons of the isoprene moiety shifted downfield after conjugation with GSH, indicating opening of the epoxide ring. Therefore, the expected reaction product was 1-glutathionyl-2-hydroxy-2-tsubstituted carbon atom rather than protons located on a sulfur-substituted carbon atom as in 1-glutathionyl-2-hydroxy-2-methyl-3-buten-1,2-dihydroxy-2-methyl-3-buten-1,2-dichloroepoxyethane 4.

The methyl group of the isoprene monoxide moiety in HGMB that was synthesized with racemic isoprene monoxide produced two signals with similar intensities (each represent-

![Fig. 2](image_url)  
**FIG. 2.** Effect of pH on enzyme activity of the GST (A) and the dehydrogenase (B) of *Rhodococcus* sp. strain AD45. Activity was determined at different pH values in 50 mM potassium phosphate ( ), 50 mM Tris-HCl ( ), 50 mM sodium carbonate ( ), or 50 mM glycine-NaOH.

**TABLE 3.** Substrate specificity of the GST from *Rhodococcus* sp. strain AD45

<table>
<thead>
<tr>
<th>Substrate</th>
<th>% of activity*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Isoprene monoxide</td>
<td>100</td>
</tr>
<tr>
<td>Epoxethane</td>
<td>37</td>
</tr>
<tr>
<td>Epoxopropane</td>
<td>32</td>
</tr>
<tr>
<td>1,2-Epoxybutane</td>
<td>26</td>
</tr>
<tr>
<td>1,2-Epoxyhexane</td>
<td>25</td>
</tr>
<tr>
<td>cis-2,3-Epoxybutane</td>
<td>13</td>
</tr>
<tr>
<td>Epithropane</td>
<td>34</td>
</tr>
<tr>
<td>Epifluorohydron</td>
<td>28</td>
</tr>
<tr>
<td>Epichlorohydron</td>
<td>31</td>
</tr>
<tr>
<td>Epibromohydron</td>
<td>25</td>
</tr>
<tr>
<td>cis-1,2-Dichloroepoxyethane</td>
<td>4</td>
</tr>
</tbody>
</table>

* All activities were determined in 50 mM Tris-HCl buffer (pH 8.5) with 5 mM GSH except for epifluorohydron, epichlorohydron, and epibromohydron, in which case 50 mM Tris-HCl (pH 8.0) was used to reduce the chemical reaction rate between these substrates and GSH. Activities are expressed as percentages of the activity found, at the same pH, with isoprene monoxide.

**Purification of the HGMB-dependent dehydrogenase.** Experiments were performed to study the metabolism of HGMB. When NAD$^+$ and HGMB were added to extracts of isoprene-grown cells, rapid formation of NADH was observed. The enzyme catalyzing this activity was purified from isoprene-grown cells that were harvested from a continuous culture (Table 1). The 6.2-fold increase of the specific activity that was observed upon purification indicates that the dehydrogenase represented approximately 16% of the total soluble protein. SDS-PAGE analysis indeed showed that the dehydrogenase was one of the major proteins present in crude extracts of strain AD45 grown on isoprene, although the content may be less than 16% (Fig. 1). The similar intensities of the bands representing the GST and the dehydrogenase indicate that some dehydrogenase was inactivated during the purification procedure, which is in agreement with the low yield.

Optimal activity was observed in a glycine-NaOH buffer at pH 9 to 10 (Fig. 2). No NADH formation was observed when GSH, methanol, ethanol, glycerol, 2-methylbutanol, 3-methylbutanol, 1-hydroxy-3-methyl-3-buten-1,2-dihydroxy-2-methyl-3-buten-1,2-dichloroepoxyethane were not substrates for the enzyme. We also tested whether the conjugates of GSH with other 1,2-epoxyalkanes would be substrates of the enzyme. When the conjugate of GSH and epoxopropane was added as a substrate, NADH formation was detected at a rate that was eightfold lower than that with HGMB. The conjugates of GSH with 1,2-epoxybutane and 1,2-epoxyhexane were not substrates for the enzyme. HGMB oxidation followed Michaelis-Menten kinetics for both NAD$^+$ and HGMB. The $K_m$ for NAD$^+$ was 0.07 mM at 7.5 mM HGMB. The $K_m$ for HGMB was 1.4 mM, and the $V_{max}$ was 18 $\mu$g of protein $^{-1}$.

Analysis of the N-terminal amino acid sequence of the protein by Edman degradation yielded the 23 residues as shown in Fig. 5. Significant homology was found with enzymes of the short-chain dehydrogenase/reductase (SDR) family (Fig. 5), with the highest score for the 3-oxoacyl-acyl carrier protein...
reductase, an enzyme that is involved in fatty acid biosynthesis and that requires NADP⁺ for activity. The N-terminal sequence of proteins of the SDR family typically contains a GXXXGXXG motif that is involved in the binding of the NAD⁺ or NADP⁺ (21). This motif is also present in the enzyme of strain AD45, but the last glycine residue is replaced by an alanine.

Identification of the product of the reaction that is catalyzed by the dehydrogenase. A sample removed from a dehydrogenase assay containing NAD⁺ and HGMB in a 1:1 molar ratio was analyzed by HPLC-MS (Fig. 6). NADH generation was accompanied by a decrease of HGMB and the generation of a product eluting at 21 min (compound 3). Strikingly, no decrease of compound 2 was observed, emphasizing the high specificity of the enzyme for HGMB (compound 1). Mass spectrometry analysis of compound 3 showed the presence of a molecular ion with m/z 406 and collision-induced fragments with m/z 331 (B2), 303 (A2, weak), 277 (Y2), 174 (I2), 130 (B1), and 76 (Y1). Furthermore, a fragment was observed with m/z 259, which is consistent with loss of the carboxyl function in the isoprene moiety from the A2 fragment. From these data, it was concluded that the hydroxyl function in HGMB is oxidized to a carboxyl function to yield 2-glutathionyl-2-methyl-3-butenoic acid.

In the presence of excess HGMB, the formation of a small amount of another product was observed. The compound eluted at 18.5 min and yielded a molecular ion with m/z 390. This is consistent with the molecular ion of the theoretical product of the oxidation of the hydroxyl function in the conjugate to a carbonyl function. From these data we conclude that the dehydrogenase catalyzes the two-step NAD⁺-dependent oxidation of HGMB. Initially, HGMB is oxidized to 1-oxo-2-glutathionyl-2-methyl-3-butene, which is then oxidized to 2-glutathionyl-2-methyl-3-butenoic acid.

DISCUSSION

A wide range of enzymes, such as hydrolases, reductases, isomerases, metalloglutathione S-transferases, lyases, and carboxylases, are involved in microbial metabolism of epoxides (3, 6, 7, 9, 13, 16, 17, 28, 36). In this paper, we report the purification and characterization of a GST that catalyzes the GSH-dependent metabolism of epoxides in the isoprene-utilizing bacterium Rhodococcus sp. strain AD45. The enzyme had activity with a broad range of epoxides. The best substrate was isoprene monoxide, which is the primary oxidation product of isoprene. The enzyme followed Michaelis-Menten-type kinetics for epoxides but had a very low affinity for GSH, even compared to other bacterial GSTs. With only a few exceptions, all known bacterial GSTs belong to the theta class (34), and the...
and 1,2-epoxyhexane accumulated, which indicated that strain that in 1,2-epoxyhexane-exposed cells, the conjugate of GSH the physiological cofactor of the enzyme. Previously we showed high pH optimum raised the question of whether GSH is really
more than a theta class GST (9).

mologous to extradiol dioxygenases and glyoxalase I, rather
activity, FosA is a metalloglutathione
strain AD45, which does not need divalent metal ions for
doxypropylphosphonic acid. However, unlike the GST of
action of GSH and fosfomycin to form 1-glutathionyl-2-hy-
epoxypropylphosphonic acid) resistance and catalyzes the re-
FosA. This protein is involved in bacterial fosfomycin (1,2-
GST for which a similarly high pH optimum was observed is
due is not significantly lowered by interactions with residues in
the active site of the enzyme. To our knowledge, the only other
affinity for GSH of these enzymes is often low compared to
GSH Isoprene monoxide 1-Hydroxy-2-methyl-3-butene

<table>
<thead>
<tr>
<th>H</th>
<th>HGMB</th>
<th>GSH</th>
<th>Isoprene monoxide</th>
<th>1-Hydroxy-2-methyl-3-butene</th>
</tr>
</thead>
<tbody>
<tr>
<td>Glutamate</td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>$H_a$</td>
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<td>3.5 (1, NR)</td>
<td>3.6 (1, dd)</td>
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</tr>
<tr>
<td>$H_b$</td>
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<td>2.0 (2, m)</td>
<td>1.9 (2, m)</td>
<td></td>
</tr>
<tr>
<td>$H_c$</td>
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<td>2.4 (2, m)</td>
<td>2.3 (2, m)</td>
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<td></td>
</tr>
<tr>
<td>$H_a$</td>
<td>3.55 (1, s)</td>
<td>3.6 (2, s)</td>
<td>3.6 (2, s)</td>
<td></td>
</tr>
<tr>
<td>Isoprene moiety</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>$H_a$</td>
<td>3.45 (1) (NR)</td>
<td>3.5 (2, NR)</td>
<td>2.8 (2, dd)</td>
<td>3.3 (2, dd)</td>
</tr>
<tr>
<td>$H_b$</td>
<td>5.65 (1, dd)</td>
<td>5.7 (1, dd)</td>
<td>5.6 (1, m)</td>
<td>5.6 (1, m)</td>
</tr>
<tr>
<td>$H_c$</td>
<td>5.05 (1, dd)</td>
<td>5.1 (2, dd)</td>
<td>5.3 (2, m)</td>
<td>4.9 (2, m)</td>
</tr>
<tr>
<td>$H_{ne}$</td>
<td>1.15 (1, 5, s)</td>
<td>1.2 (0, 4, s)</td>
<td>1.3 (3, s)</td>
<td>0.8 (3, d)</td>
</tr>
<tr>
<td>$H_{ne}$</td>
<td>1.20 (1, 5, s)</td>
<td>1.25 (2, 6, s)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

* Spectra were recorded in D$_2$O at room temperature. Chemical shifts were measured relative to sodium 4,4-dimethyl-4-silapentane-1-sulfonate and assigned with 0.05-ppm accuracy. The protons are assigned with reference to Fig. 5. NR, not resolved. Multiplicity of the H protons could not be resolved due to overlap of spectral lines.

$^b$ Singlet $H_a$ (Gly) protons gave two signals due to an increased rotational barrier in the conjugate compared to unmodified GSH.

affinity for GSH of these enzymes is often low compared to
GSHs of other classes (24).

Another unusual feature of the enzyme of strain AD45 is the high pH optimum that coincides with the pK$_a$ values of the cysteine residue of GSH in aqueous solution. These data suggest that unlike with most GSTs, the pK$_a$ of the cysteine residue is not significantly lowered by interactions with residues in the active site of the enzyme. To our knowledge, the only other GST for which a similarly high pH optimum was observed is FosA. This protein is involved in bacterial fosfomycin (1,2-epoxypropylphosphonic acid) resistance and catalyzes the reaction of GSH and fosfomycin to form 1-glutathionyl-2-hydroxypropylphosphonic acid. However, unlike the GST of strain AD45, which does not need divalent metal ions for activity, FosA is a metalloglutathione S-transferase that is homologous to extradiol dioxygenases and glyoxalase I, rather than a theta class GST (9).

The low affinity of the GST of strain AD45 for GSH and the high pH optimum raised the question of whether GSH is really the physiological cofactor of the enzyme. Previously we showed that in 1,2-epoxyhexane-exposed cells, the conjugate of GSH and 1,2-epoxyhexane accumulated, which indicated that strain AD45 indeed contains an enzyme that covalently couples GSH to epoxides (32). We have checked extracts of isoprene-grown cells of strain AD45 for the presence of other enzymes that have activity for aliphatic epoxides. However, no activity for isoprene monoxide was detected in assays for epoxide hydrolase, epoxide isomerase, or epoxide hydrogenase (32). Furthermore, the GST identified here was one of the two most prominent proteins in isoprene-grown cells of strain AD45.

The GST catalyzes the reaction of GSH and isoprene monoxide to form a stable conjugate. The major product is the conjugate in which the GSH moiety is covalently linked to the tertiary carbon atom of the isoprene monoxide moiety to yield HGMB. This shows that the enzyme catalyzes the nucleophilic attack of GSH to the sterically most hindered carbon atom in the epoxide ring.

Epoxide carboxylation was shown to be a key step in the metabolism of epoxides in both gram-positive and gram-negative epoxyp propane-utilizing organisms (3, 4). In these organisms carboxylation is catalyzed by a multiprotein complex that catalyzes epoxide ring opening and the formation of a carbon-carbon bond. Simultaneously, transhydrogenation occurs in which NADPH is oxidized and NAD$^+$ is reduced. Strikingly, 2-methyl-1,2-epoxypropane, which contains a methyl group rather than a hydrogen substituent at the C-2 carbon atom, is a mechanism-based inactivator of epoxide carboxylase activity (2). Reaction of this compound with the carboxylase is thought to result in a covalently modified active site that cannot react further due to the absence of an extractable hydrogen at the C-2 position. Isoprene monoxide does also not contain an extractable hydrogen at C-2, and therefore isoprene monoxide conversion would not be possible by the carboxylation route. In strain AD45, this problem appears to be addressed by a GST-catalyzed conjugation to GSH to yield HGMB. Hence, the GST described here represents a novel type of catabolic epoxide-converting enzyme.
Degradation of HGMB in strain AD45 proceeds by a dehydrogenase that catalyzes the two-step oxidation of the alcohol function to yield 2-glutathionyl-2-methyl-3-butenoic acid with the concomitant reduction of NAD$^+$ to NADH. In contrast to the GST, the dehydrogenase has a very narrow substrate range and seems to be optimized for the oxidation of the HGMB. The toxicity of 1,2-epoxyhexane (32) can now be explained considering the broad substrate range of the GST. The conjugate of 1,2-epoxyhexane and GSH that is formed by this enzyme is not a substrate for the dehydrogenase and will accumulate. Hence, intracellular GSH concentrations will decrease and isoprene monoxide conversion will be inhibited.

The initial steps in the degradation pathway of isoprene in Rhodococcus sp. strain AD45 are summarized in Fig. 7. Degradation starts with oxidation of the methyl-substituted double bond by a monoxygenase to yield 1,2-epoxy-2-methyl-3-butene (32). After conversion by the GST and the two oxidation steps by the dehydrogenase, 2-glutathionyl-2-methyl-3-butenoic acid is generated.

FIG. 6. NAD$^+$-dependent HGMB conversion by the dehydrogenase of Rhodococcus sp. strain AD45. HPLC elution profiles of assays without dehydrogenase (A) and with dehydrogenase (70 μg/ml) (B). The assay mixture consisted of 0.4 mM NAD$^+$ and 0.4 mM HGMB in 50 mM glycine-NaOH (pH 10). Activity was monitored by following the generation of NADH at 340 nm, and samples for HPLC-MS analysis were removed at 60 min. Compounds 1 (HGMB) and 2 were identified as conjugates of GSH and isoprene monoxide. Compound 3 was identified as 2-glutathionyl-2-methyl-3-butenoic acid.

FIG. 7. Initial steps in isoprene degradation by Rhodococcus sp. strain AD45.

It remains to be elucidated how further degradation proceeds. Currently, we are investigating the genetics of isoprene degradation which may be helpful in understanding the complete metabolic pathway for isoprene.

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REFERENCES