Properties of the quinoprotein aldehyde dehydrogenase from
'Acetobacter rancens'

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The membrane-bound aldehyde dehydrogenase from 'Acetobacter rancens' CCM 1774, solubilized from the
membrane fraction by treatment with surfactants and subsequently purified to homogeneity, was characterized
with respect to the M, of the dimeric enzyme (145000), pH optimum (5.1), pI value (5.3), substrate specificity
towards straight-chain aldehydes, substrate inhibition and the effects of various inhibitors and ions. Methanol
extracts of the membrane fraction and of the purified enzyme showed properties identical with pyrroloquinoline
quinone as revealed by spectrophotometric methods and reactivity with apoquinoprotein glucose dehydrogenase.
Pyrroloquinoline quinone could not be liberated by EDTA treatment. The enzyme activity of an apoenzyme could
be partly restored by addition of membrane extracts containing pyrroloquinoline quinone adducts. The solubilized,
purified quinoprotein aldehyde dehydrogenase and the membrane-bound enzyme differed in substrate binding,
substrate inhibition, pH optimum and linkage to a c-type cytochrome which acts as electron acceptor in membrane
fractions. Since double-reciprocal plots of initial reaction rates with various concentrations of aldehyde or electron
acceptor showed intersecting lines, different inhibition patterns were obtained for the two forms of the enzyme,
a ping-pong kinetic behaviour with the two reactants was excluded. The kinetic mechanism was suggested to be
changed after solubilization from a random-order type to a compulsory-order type, and is thus atypical for
quinoproteins reported so far.

Introduction

'Acetobacter rancens' CCM 1774 can use n-alkanes as a
source of carbon and energy (Hommel & Kleber, 1984a).
Hexadecane is predominantly oxidized via monoter-
minal attack to palmitic acid. Aldehydes are considered
to be metabolic intermediates in microbial alkane
utilization, being oxidized to fatty acids by aldehyde
dehydrogenase. For most enzymes involved in hydrocar-
bon metabolism pyridine-nucleotide-dependency and
induction by growth substrate have been reported
(reviewed by Sorger & Aurich, 1978).

'A. rancens' possesses two constitutive aldehyde dehy-
drogenases: a cytoplasmic NADP*-dependent enzyme
that is highly specific towards short-chain aldehydes
(Hommel et al., 1988) and a membrane-bound dye-linked
enzyme. Their relative specific activity is influenced by the
carbon source, e.g. glucose or n-hexadecane, with the
activity of the membrane-bound enzyme being enhanced
to a greater extent by hydrocarbons (Hommel & Kleber,
1984b).

The membrane-bound aldehyde dehydrogenase was
purified by Hommel & Kleber (1984c). This hydropho-
bic enzyme was very unstable and could be stabilized
only slightly in the presence of high surfactant concen-
trations and by addition of benzaldehyde (Hommel et al.,
1985).

Amevama & Adachi (1982) characterized the dye-
linked aldehyde dehydrogenase from acetic acid bacte-
ria; this enzyme is a quinoprotein, a novel class of
dehydrogenases that possess pyrroloquinoline quinone as
prosthetic group (Duine et al., 1987).

The present paper describes the chemical and kinetic
properties of the purified membrane-bound aldehyde
dehydrogenase from 'A. rancens'.

Methods

Organism and culture conditions. 'A. rancens' CCM 1774, obtained
from the Czechoslovak Collection of Micro-organisms, Brno, Czechoslovakia, was used throughout this study. [Inverted commas indicate

Abbreviations: PQQ, pyrroloquinoline quinone, [2,7,9-tricarboxy-
1H-pyrrolo(2,3-f) quinoline-4,5-dione]; PMS, phenazine methosul-
phate; pCMB, p-chloromercuribenzoate; DCFIP, 2,6-dichlorophenol-
indophenol; AldDH(acc), quinoprotein aldehyde dehydrogenase
(aldehyde:pyrroloquinoline quinone oxidoreductase; EC 1.2.99.3).
that the organism is not in the Approved Lists of Bacterial Names (Skerman et al., 1980), has not been validly published since 1 January 1980, and therefore does not have nomenclatural standing.) Culture conditions were as described by Hommel & Kleber (1984b).

Preparation of crude extracts, solubilization and purification. All procedures were done at 0 to 4 °C. Sodium/potassium phosphate buffer (PB) was used throughout. Crude extracts were obtained by ultrasonication and membranes by differential centrifugation (Hommel & Kleber, 1984b). Membranes in PB (10 mM, pH 6-1) were solubilized by two consecutive detergent treatments: (i) with a Brij 35: protein ratio of 0.8 mg mg⁻¹; after centrifugation at 130000 g for 1 h at 4 °C the precipitate was dissolved in PB and solubilized (ii) at a Triton X-100:protein ratio of 4 mg mg⁻¹ at a protein concentration of 2.5 mg ml⁻¹. The centrifugation was repeated and benzaldehyde (final concentration 2.5 mM) was added to the supernatant to lessen the otherwise rapid inactivation.

The supernatant was applied to a DEAE-Sepharose CL-6B column (2.6 × 7.6 cm) previously equilibrated with PB (10 mM, pH 6-1 containing 5% w/v, Triton X-100 and 2.5 mM-benzaldehyde) and eluted with a linear gradient of 0 to 150 mM-PB at a flow rate of 16 ml cm⁻² h⁻¹. Active fractions appearing at a conductivity of 5-2 mS were collected and concentrated by ultrafiltration (XM 50, Amicon). The concentrated enzyme was applied to a Sepharose 4B column (4 × 28 cm) equilibrated with 1 mM-PB and eluted with the same buffer (2.5 ml cm⁻² h⁻¹). Active fractions were applied to a hydroxyapatite-cellulose column (2.6 × 10 cm) and eluted (10 ml cm⁻² h⁻¹) by a discontinuous gradient of 1 to 150 mM-PB. Active fractions eluting at 62 mS were concentrated by ultrafiltration as above.

Cytochrome c-thiol-Sepharose. Glutathione was linked to CNBr-activated Sepharose (Cuantrecasas & Anfinsen, 1971) as described by Brocklehurst et al. (1974). The thiol-Sepharose was washed with NaHCO₃ buffer (0-1 M, pH 8-3, containing 0.5 M-NaCl) and sodium acetate buffer (0-1 M, pH 4-0, containing 0.5 M-NaCl) and finally suspended in PB (0-1 M, pH 6-1). The packed column was equilibrated with PB (10 mM, pH 6-1). Cytochrome c (horse heart) (1-7 mg per g of gel) was circulated for 15 h. After washing with 3 column vols of PB the circulation of cytochrome c was repeated. The cytochrome c-thiol-Sepharose column was washed and equilibrated with PB (pH 6-1, containing 5% w/v, Triton X-100 and 2.5 mM-benzaldehyde). Samples were applied to the column, washed with 5 column vols of buffer and eluted by stepwise increase of ionic strength of the buffer (0-01, 0-1, 1 M). The flow rate was 20 ml cm⁻² h⁻¹. Under these conditions the aldehyde dehydrogenase was eluted specifically at 0.55 mS conductivity. No further purification was obtained.

Lysosome treatment. Bacteria grown on n-hexadecane (0.5 g wet wt) were suspended in 10 ml PB (0.1 M, pH 7-5) and treated with lysosome (2 mg) for 30 min at room temperature followed by disintegration of spheroplasts and protoplasts with glass beads in the presence of RNAase and DNAase (1 mg each). Membranes were sedimented at 130000 gₘ, for 60 min at 4 °C, and the pellet was resuspended in 50 mM-PB (pH 6-1) containing sucrose (10% w/v) and resedimented as above. This centrifugation was repeated twice. The final membrane pellet was suspended in buffer containing 25% w/v sucrose. Of this suspension 0.3-5 ml containing 3 mg protein, was layered on top of a discontinuous sucrose gradient (4.2 ml, 30 to 50% w/v, sucrose) and centrifuged for 7 h at 80000 gₘ. The gradient was then fractionated and analysed.

Measurement of enzyme activities. All tests were done at 25 °C. The oxidation of aldehydes by aldehyde dehydrogenase was measured as reported by Hommel & Kleber (1984b). NADH dehydrogenase and NAD⁺ oxidase were estimated according to Matsushita et al. (1978). Dye-linked membrane-bound glucose and alcohol dehydrogenases were assayed spectrophotometrically at 600 nm by following the oxidation of DCPIP. The assay mixture consisted of DCPIP (40 µM), Trit/HCl (20 mM, pH 7-6), FMS (0-4 µM), and glucose (16 mM) or ethanol (66 mM), respectively.

Determination of Mₜ. The Mₜ of the homogeneous native enzyme was determined (i) by electrophoresis using the method of Hedrick & Smith (1968) with acrylamide concentrations from 4-11% w/v in the presence of Triton X-100 (1% w/v) with BSA oligomers as Mₜ standards, and (ii) by gel-filtration on a Sephadex G-200 superfine column (0.9 × 60 cm) in PB (0.1 M, pH 7.5, containing 1% w/v Triton X-100) as described by Andrews (1964) with myoglobin, pepatin, ovalbumin, BSA, and lactate dehydrogenase as Mₚ standards. The Mₜ of the subunits was determined by SDS-PAGE using the system of Weber & Osborn (1969) with BSA, ovalbumin, pepatin, chymotrypsin A (bovine), trypsin, cytochrome c (horse heart) and RNAse as standards.

Staining for enzyme activity in gels was done as in Hommel & Kleber (1984b). Protein was stained with Coomassie brilliant blue G 250.

Determination of isoelectric point. Isoelectric focussing in polyacrylamide gels was done according to Vestenberg & Svensson (1966). After electrophoresis for 7 h at 250 V, activity staining was done as above and the pl value was estimated from the pH gradient of reference rods and from the following standards: amyloglucosidase, glucose oxidase, human serum albumin, insulin and cytochrome c.

Extractions of prosthetic group and generation of apoenzyme. Membrane suspensions or enzyme fractions concentrated by ultrafiltration using a XM-50 membrane were extracted by addition of methanol (Ameyama et al., 1981). The methanol extract was evaporated to dryness, dissolved in PB (10 mM, pH 6-1) and extracted five times with chloroform to remove surfactants. The buffer containing the prosthetic group was designated methanol extract.

The remaining membrane fractions and proteins treated with methanol showed no enzyme activity and were considered to be apoenzyme.

Analytical methods. Protein was determined according to Dully & Griewe (1975) with BSA as standard. 3-Deoxy-d-manno-2-octulosonic acid was determined as described by Osborn et al. (1972). The concentration of aldehydes was estimated enzymically (Bergmeyer, 1962).

Absorption spectra were recorded with a Perkin-Elmer M-336 spectrophotometer (d = 1 cm) at 25 °C. Fluorescence spectra of the prosthetic group were measured with a MPF-4 spectrofluorimeter (d = 0.5 cm) in 10 mM-PB (pH 6-1, 25 °C); excitation and emission wavelengths were 370 and 480 nm, respectively.

Kinetic parameters. The apparent Kₐ (Kₐ'ₚ) and V values were determined by measuring the initial velocities in the presence of seven non-saturating concentrations of the first substrate, at a fixed saturating concentration of the second substrate. The Michaelis and inhibitor constants (Kₐ, Kₐ'ₚ for the aldehydes and Kₐ, Kₐ'ₚ for ferricyanide, respectively) were determined by the two-substrate method. In kinetic experiments each point represents the mean of at least five independent measurements. Standard deviations were less than 5%. Linear correlations were fitted by regression. Results were used with 0.98 ≤ r ≤ 1.

Chemicals. All chemicals were of reagent-grade quality or better. Aldehydes were distilled under nitrogen prior to use. Chloral was redistilled immediately before application. The proteins and enzymes were obtained from Serva, Boehringer and AWD (Dresden, GDR). PQO and apquinoprotein glucose dehydrogenase were gifts of Professor J. A. Duine, Delft University, The Netherlands.
Results

Localization

Outer and cytoplasmic membranes were separated by density gradient centrifugation of membrane fractions of bacteria grown on n-hexadecane. Aldehyde dehydrogenase, alcohol dehydrogenase and glucose dehydrogenase showed maxima similar to those of the marker enzymes of cytoplasmic membranes, NADH dehydrogenase and NADH oxidase (Matsushita et al., 1978). The outer membrane marker 3-deoxy-d-manno-2-octulosonic acid exhibited only low aldehyde dehydrogenase activities (less than 10% of those of the cytoplasmic membrane) and no NADH oxidase and NADH dehydrogenase activities. Aldehyde dehydrogenase was purified 2.7-fold. No enzyme activity was measurable at the top of gradient. Using cells grown on glucose or on other water-soluble substrates separation of membranes failed.

Purification, Mᵣ, and isoelectric point

Membrane-bound aldehyde dehydrogenase from ‘A. rancens’ was purified 173-fold (Table 1). The specific activity of the final enzyme preparation was about 2000 nkat (mg protein)⁻¹. The activity of the purified enzyme was reduced to 50% after 4 d in the presence of the stabilizing agents Triton X-100 and benzaldehyde (Hommel et al., 1985). Therefore, the purification procedure was also accompanied by a decrease in enzyme activity, which resulted in low yields.

SDS-PAGE revealed two aldehyde dehydrogenase subunits, with Mᵣ values of 66000 and 78000 (mean of five determinations). In some estimations a minor band (less than 5% of the total protein) of Mᵣ 48000 was detected. It was thus concluded that native aldehyde dehydrogenase is composed of two dissimilar subunits. Electrophoresis under non-denaturating conditions in the presence of Triton X-100 gave an apparent Mr of 70000 (mean of seven determinations) for the active enzyme. This indicates dissociation of the enzyme into its subunits in the presence of Triton X-100. The Mr, determined by gel-filtration on Sephadex G-200 superfine in the presence of Triton X-100 was 145000 (± 7000).

The Pl of the active enzyme in the presence of Triton X-100 was 5.3.

Investigation of the prosthetic group

Absorption spectra and fluorescence studies of the purified enzyme and the methanol extracts revealed the presence of PQQ by comparison with literature values (Ameyama et al., 1981; Anthony & Zatman, 1967; Dekker et al., 1982) and with authentic PQQ which was treated in the same way as the methanol extracts.

Reconstitution experiments were done with the apoenzyme generated by methanol extraction. After incubation of the apoenzyme with buffer containing PQQ enzyme activity was partly restored. Optimal restoration (about 50%) of activity was obtained after preincubation for 60 min in the presence of Mg²⁺. The concentration-dependent reactivation exhibited saturation kinetics which could be linearized by double reciprocal plots. Shorter incubation periods also yielded good results (10% of initial activity). Activity could also be partly restored by addition of extracts containing PQQ.

Similar activation plots were obtained for glucose dehydrogenase apoquinoprotein with methanol extracts of the quinoprotein aldehyde dehydrogenase [AldDH(acc)].

Attempts to obtain apoenzyme by dialysis following the protocol of Duine et al. (1979) failed.

Cytochrome binding

The difference spectrum of the membrane fraction showed cytochrome reduction during incubation with either ethanal or glucose (Fig. 1). The peaks with

<table>
<thead>
<tr>
<th>Step</th>
<th>Protein (mg)</th>
<th>Total activity (nkat)</th>
<th>Specific activity (nkat (mg protein)⁻¹)</th>
<th>Yield (%)</th>
<th>Purification (ifold)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Crude extract</td>
<td></td>
<td></td>
<td>(5-3)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Membrane fraction</td>
<td>321</td>
<td>3600</td>
<td>11-2</td>
<td>100</td>
<td>1</td>
</tr>
<tr>
<td>Solubilization</td>
<td>18-7</td>
<td>4070</td>
<td>217</td>
<td>113</td>
<td>19-4</td>
</tr>
<tr>
<td>DEAE-Sepharose</td>
<td>5-4</td>
<td>2700</td>
<td>500</td>
<td>75</td>
<td>45</td>
</tr>
<tr>
<td>Sepharose 4B</td>
<td>1-1</td>
<td>677</td>
<td>615</td>
<td>19</td>
<td>55</td>
</tr>
<tr>
<td>Hydroxyapatite</td>
<td>0-08</td>
<td>155</td>
<td>1938</td>
<td>4-3</td>
<td>173</td>
</tr>
</tbody>
</table>

Table 1. Purification of membrane-bound aldehyde dehydrogenase from ‘A. rancens’
absorption maxima at 553 and 554 nm and at 523 and 528 nm can be assigned respectively as \( \alpha \) and \( \beta \) absorption peaks characteristic of reduced c-type cytochrome, e.g. cytochrome c-553 (Ameyama et al., 1987). Appropriate difference spectra were not obtained with the purified enzyme. Both the purified and the membrane-bound enzyme were able to transfer electrons to horse heart cytochrome c. Furthermore, the purified enzyme bound to cytochrome c-thiol-Sepharose.

Effects of salts and inhibitors on enzyme activity

The effect of selected salts and inhibitors on both aldehyde dehydrogenases was examined by incubating them with each of the compounds at 25 °C for 3 min prior to assaying enzyme activity. The results were compared to reference assays in the absence of the effectors. Both forms of AldDH(acc) were activated 1.5-fold by 0.05 mM-MgSO\(_4\), -MnSO\(_4\) and (to a minor extent) -CaSO\(_4\). At a concentration of 5 mM, MgSO\(_4\) and MnSO\(_4\) activated 3.1- and 2.3-fold, respectively. This activation was reversed by 5 mM-EDTA, whereas EDTA itself had no effect on either enzyme form. A 1.9-fold activation of both aldehyde dehydrogenases was obtained with 5 mM-NH\(_4\)Cl. Salts of univalent cations (e.g. KCN and NaN\(_3\)) had no effect on the membrane-bound enzyme. However, there was a slight activation of the purified enzyme by KCN and NaN\(_3\). Thiol reagents (pCMB, AgNO\(_3\), Hg\(_2\)Cl\(_2\), NaAsO\(_3\)) and iodoacetic acid (all 0.05 mM) were potent irreversible inhibitors of both enzyme forms.

Kinetic properties

For the purified AldDH(acc) substrate inhibition became apparent at concentrations of aldehydes above 5 \( \times \) \( K_{m}^{app} \) (ethanal), 1 \( \times \) \( K_{m}^{app} \) (propanal, butanal, pentanal) and 3 \( \times \) \( K_{m}^{app} \) (other aldehydes), while the membrane-bound enzyme was not affected by any substrate at concentrations up to 5 \( \times \) \( K_{m}^{app} \) (data not shown). Below these concentrations the initial velocity followed Michaelis–Menten kinetics. Plots of the apparent \( pK_{m} \) values versus the number of carbon atoms in the aldehydes gave a straight line from ethanal to dodecanal with the membrane-bound AldDH(acc) and to dodecanal with the purified enzyme (Fig. 2a). With the solubilized enzyme the highest \( V \) was measured with
Quinoprotein aldehyde dehydrogenase

Table 2. Comparison of kinetic constants and derived quotients of kinetic constants

The constants shown are for the oxidation reactions of the membrane-bound and the purified AldDH(acc) with the substrates ethanal, hexanal and octanal under the conditions described in Methods.

<table>
<thead>
<tr>
<th>Kinetic constants (mM)</th>
<th>Kinetic quotients</th>
</tr>
</thead>
<tbody>
<tr>
<td>Aldehyde</td>
<td></td>
</tr>
<tr>
<td>Ethanal</td>
<td></td>
</tr>
<tr>
<td>Hexanal</td>
<td></td>
</tr>
<tr>
<td>Octanal</td>
<td></td>
</tr>
<tr>
<td>(a) Membrane-bound enzyme</td>
<td></td>
</tr>
<tr>
<td>Ethanal</td>
<td>0.96</td>
</tr>
<tr>
<td>Hexanal</td>
<td>0.064</td>
</tr>
<tr>
<td>Octanal</td>
<td>0.028</td>
</tr>
<tr>
<td>(b) Purified enzyme</td>
<td></td>
</tr>
<tr>
<td>Ethanal</td>
<td>0.348</td>
</tr>
<tr>
<td>Hexanal</td>
<td></td>
</tr>
</tbody>
</table>

Quotient was calculated according to Cleland (1970).
† Quotient was calculated according to Dalziel (1957).

butanal (Fig. 2b). The K_{app} values for ferricyanide of both enzymes were constant irrespective of the aldehydes tested: 0.362 ± 0.018 mM [membrane-bound AldDH(acc)] and 0.552 ± 0.023 mM [purified AldDH(acc)].

Kinetic constants (Table 2) were estimated from replots of slopes and intercepts of double reciprocal plots with intersecting lines on the abscissa, which exclude ping-pong mechanisms. The kinetic constants suggested rapid equilibrium conditions, since K_{a} ≈ K_{a} and K_{f} ≈ K_{f}. The quotients calculated according to Dalziel (1957) and Cleland (1970) for the purified enzyme gave a value of 1, typical of a random-order mechanism. Quotients calculated for the membrane-bound enzyme were < 1 (according to Dalziel, 1957) and > 1 (according to Cleland, 1970), which exclude such a mechanism for this enzyme.

For further characterization of the reaction mechanism inhibition studies were done: the two products, and the substrate analogues acetic acid, butanoic acid, hexanoic acid and decanoic acid esters, did not inhibit the enzyme reaction (data not shown). No inhibitory analogue was found for ferricyanide.

The use of chloral hydrate, a substrate analogue that acts as a competitive inhibitor of ethanal (cf. Table 3) and of other aldehydes (data not shown) allowed discrimination between random-order and other sequential reaction mechanisms (Fromm, 1975). The inhibition patterns for the membrane-bound AldDH(acc) (Table 3) were consistent with a compulsory-order mechanism, in which the aldehyde binds to the enzyme first (Fromm, 1975). In intact membranes electron transfer to ferricyanide should occur, as already demonstrated, via c-type cytochrome, which is obviously impossible for the purified enzyme. Results of inhibition studies with the purified enzyme agreed with a random-order mechanism.

Table 3. Inhibition of AldDH(acc) by chloral hydrate

<table>
<thead>
<tr>
<th>Inhibition by chloral hydrate</th>
<th>Membrane-bound enzyme</th>
<th>Purified enzyme</th>
</tr>
</thead>
<tbody>
<tr>
<td>Substrate</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ethanal</td>
<td>Competitive Nonlinear*</td>
<td></td>
</tr>
<tr>
<td>Ferricyanide</td>
<td></td>
<td>Noncompetitive</td>
</tr>
<tr>
<td>K (mM)</td>
<td>13 (30)†</td>
<td>20 (15)†</td>
</tr>
<tr>
<td>Mol inhibitor bound per mol active centre†</td>
<td>1.21</td>
<td>0.94</td>
</tr>
</tbody>
</table>

* Analysis by the method of Baici (1981) showed partially noncompetitive inhibition.
† Estimated according to Chou & Talalay (1981).

Discussion

Sucrose density-gradient centrifugation after lysozyme treatment revealed AldDH(acc) to be located in the cytoplasmic membrane. This location would allow electron transfer via a c-type cytochrome to the respiratory chain with oxygen acting as terminal acceptor (Hommel & Kleber, 1984b). Aldehyde dehydrogenase in 'A. rancens' is a hydrophobic integral membrane protein, as shown by its solubilization at a Triton X-100:protein
ratio of 4, its instability in the solubilized form and its specific lipid requirement for phosphatidylglycerol (Hommel et al., 1985).

The $M$, of AldDH(acc), a dimeric enzyme with two dissimilar units, is 145000, which is in the range reported by Ameyama & Adachi (1982) and Adachi et al. (1980). By comparing the $M$, obtained under denaturing and non-denaturing conditions it may be suggested that the monomer of $M$, 70000 (in the presence of Triton X-100) is the enzymatically active subunit; this is in agreement with Fukaya et al. (1989) who cloned the gene encoding the $M$, 75000 subunit from Acetobacter polyoxogenes. The $M$, of the minor band agrees with that (48000) of cytochrome c-553 (Ameyama et al., 1987). However, there is no evidence for its presence in the purified enzyme.

Spectrophotometric investigations of methanol extracts showed differences from highly purified PQQ; these are due to formation of reversible adducts with, e.g., methanol and water, which react with PQQ (Duine et al., 1987). The reconstitution experiments are in accordance with the proposed classification of aldehyde dehydrogenases of acetic acid bacteria as quinoproteins (Ameyama & Adachi, 1982). In reconstitution experiments with extracts from different enzyme preparations, saturation kinetics were obtained in each case. Reconstitution was strongly stimulated by Mg$^{2+}$, as was that of the glucose dehydrogenase apoquinoprotein. This agrees with the stimulation of enzyme activity by Mg$^{2+}$, which has been suggested to promote and stabilize binding of PQQ (Adachi et al., 1980; Duine et al., 1987). In contrast to other microbial quinoenzymes (e.g. Dokter et al., 1986), PQQ could not be liberated from the AldDH(acc) by EDTA treatment or dialysis.

The solubilization and purification procedure resulted in alterations in pH optimum without influencing the $pK$ values, and in changes of substrate inhibition. From the dependence of $pK_{\text{app}}$ on the chain-length of aldehydes, it can be concluded that substrate binding by both enzymes was strongly influenced by hydrophobic interactions (Schöpp & Aurich, 1973), as described for the aldehyde dehydrogenase from Acinetobacter calcoaceticus (Bergmann, 1981).

The kinetic properties indicate that the quinoprotein aldehyde dehydrogenase from 'A. rancens' is quite different from other quinoprotein dehydrogenases described so far. The proposed kinetic mechanisms, i.e. compulsory-order for the membrane-bound and random-order for the purified enzyme, are not in accordance with investigations on purified quinoproteins, e.g. quinoprotein glucose dehydrogenase from Acinetobacter calcoaceticus (Geiger & Görsch, 1986; Dokter et al., 1986) and quinoprotein methanol dehydrogenase from Hyphomicrobiurn X (Duine & Frank, 1980) for which ping-pong mechanisms have been elucidated. Furthermore, the inhibition experiments do not agree with a covalent coupling of substrate to PQQ as shown for methanol dehydrogenase (Duine et al., 1987); suicide inhibition by chloral hydrate did not occur, nor was enzyme activity diminished after prolonged incubation with substrates. The results confirm the direct transfer of reduction equivalents from substrate to PQQ, generating PQQH$_2$ and product.

Quinoproteins described so far have been studied in a highly purified form and appropriate conclusions have been drawn with respect to in vivo reactions (Duine et al., 1987). Most microbial PQQ enzymes are membrane-bound or at least associated with membrane structures (Ameyama et al., 1987; Duine et al., 1986). The specific lipid requirements may influence the behaviour of the purified enzyme.

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References


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