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STUDIES OF A HALOPHILIC NADH DEHYDROGENASE

I. PURIFICATION AND PROPERTIES OF THE ENZYME

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SUMMARY

- I. An NADH dehydrogenase obtained from an extremely halophilic bacterium was purified 570-fold by a combination of gel filtration, chromatography on hydroxyapatite, and ion-exchange chromatography on OAE-Sephadex.
- 2. The purified enzyme appeared to be FAD-linked and had an apparent molecular weight of 64 000.
- 3. Even though enzyme activity was stimulated by NaCl, considerable activity (43% of the maximum activity observed in the presence of 2.5 M NaCl) was observed in the absence of added NaCl.
- 4. The enzyme was unstable when incubated in solutions of low ionic strength. The presence of NADH enhanced the stability of the enzyme.

INTRODUCTION

We previously described the oxidation of NADH by crude extracts prepared from an extremely halophilic bacterium (designated as strain AR-I) and showed that high concentrations of NaCl were required for maximum activity of the enzyme¹. These studies suggested that the salt requirement could not be fully explained in terms of charge neutralization² since, in addition to certain anomalous cation effects, anions were found to markedly affect the ability of monovalent cations to activate the enzyme. Furthermore, the requirement for NaCl could be satisfied by mM concentrations of Mg²⁺ salts or μ M concentrations of polyamines such as spermine³. These observations were subsequently confirmed by others⁴⁻⁶ and it was proposed that the requirement for high concentrations of NaCl, in the case of a membrane-bound menadione reductase obtained from *Halobacterium cutirubrum*, reflected the ability of certain ions to stabilize hydrophobic interactions⁷.

 $Abbreviations: NADH \ dehydrogenase, \ reduced \ NAD: \ 2,6-dichlorophenolindophenol \ oxidoreductase; \ DCIP, \ 2,6-dichlorophenolindophenol; \ TES, \ N-tris-(hydroxymethyl)-methyl-2-amino-ethanesulfonic acid; \ QAE, \ diethyl-(2-hydroxypropyl)aminoethyl.$

In order to study these various ionic effects in a system uncomplicated by the presence of a multi-enzyme system, particularly one enriched with respect to the hydrophobic components associated with bacterial membranes, an attempt was made to separate and purify the reduced-NAD:2,6-dichlorophenolindophenol oxido-reductase, EC 1.6.99.3 (NADH dehydrogenase) component from the electron-transport chain of strain AR-I.

Although enzymes from halophilic bacteria are extremely labile in solutions of low ionic strength⁸, certain observations suggested that several techniques used to purify nonhalophilic enzymes might be applicable to purification of the NADH dehydrogenase from AR-I. For example, the bulk proteins from several extremely halophilic bacteria contain large amounts of glutamic and aspartic acids9 resulting in relatively acidic proteins. On the assumption that the NADH dehydrogenase from AR-I was likewise acidic, chromatography on hydroxyapatite seemed potentially useful since carboxyl groups were reported responsible for protein-hydroxyapatite interaction¹⁰. In addition, polyamines, such as spermine, stabilized NADH dehydrogenase activity in solutions of low ionic strength³ suggesting that ion-exchange chromatography, if carried out in the presence of a suitable stabilizing agent, could be used to purify the enzyme. Subsequently, NADH was found to be a more effective stabilizing agent than spermine. Finally, the NADH dehydrogenase from AR-I, like certain other enzymes obtained from extremely halophilic bacteria¹¹, was reactivated by the addition of optimal concentrations of NaCl following inactivation by exposure to solutions of low ionic strength.

The present paper describes some properties of the enzyme following purification by agarose-gel filtration, hydroxyapatite chromatography, and ion-exchange chromatography on diethyl-(2-hydroxypropyl)aminoethyl-Sephadex (QAE-Sephadex). The final product, recovered in about 30% yield, catalyzed the oxidation of 376 μ moles of NADH per min per mg protein.

MATERIALS AND METHODS

Standard assay

NADH dehydrogenase activity was determined as previously described³ except that bovine serum albumin was added to a final concentration of 40 μ g/ml to stabilize the enzyme during the assay. While the rate of dye reduction was proportional to the amount of added enzyme, these conditions did not measure the total amount of NADH dehydrogenase activity since the concentration of 2,6-dichlorophenolindophenol (DCIP) employed was only 2.3 times greater than its apparent $K_{\rm m}$. Higher concentrations of dye were inhibitory. A unit of activity is that amount of enzyme that reduces 1 μ mole of DCIP per min using standard assay conditions. Specific activity is defined as units/mg protein. The millimolar absorption for DCIP (20 mM⁻¹· cm⁻¹) was unaffected by the NaCl concentration.

Protein determinations

The protein concentration was determined either from the absorbance at 280 nm or by the Waddell procedure as described by Murphy and Kies¹². The presence of NADH in the QAE fraction interfered with the Waddell procedure. Therefore, NADH was removed by passing an appropriate aliquot of the enzyme through a

0.7 cm \times 20 cm volume of G-50 Sephadex equilibrated with 10 mM NaCl. The volume of effluent corresponding to the volume in which the blue dextran was eluted was employed for the protein determination. In control experiments using bovine serum albumin, from 98–103% of the added protein was recovered.

Reactivation

The enzyme, inactivated by incubating it in solutions of low ionic strength, was reactivated by the addition of solid NaCl to the enzyme to a final concentration of 3 M NaCl. Incubation at room temperature (approx. 22 °C) was the most effective temperature for reactivation, which was usually complete after 24–36 h.

Concentration of the enzyme

The volume of enzyme was reduced by ultrafiltration in an Amicon UF cell equipped with a PM-10 membrane. The cell was placed in an ice bath and operated at a pressure of 75 lb/inch² with nitrogen.

Chemicals and reagents

Hydroxyapatite (Bio-Gel HT), agarose gel (Bio-Gel A-0.5 m), and polyacrylamide gel (Bio-Gel P-10 and P-200) were products of Bio-Rad Laboratories. QAE-Sephadex (A-50), various Sephadex gels, and Blue Dextran were obtained from Pharmacia Fine Chemicals. All the gels and the QAE-Sephadex were swollen for 72 h at room temperature in appropriate buffers. Bio-Gel HT was suspended in 1.0 M NaCl-100 mM Tris-HCl-100 μ M NADH (pH 7.4), allowed to settle several times (decanting the fines each time), and equilibrated with at least three column volumes of the above buffer before use.

Bovine serum albumin (Fraction V), DCIP, and NADH were obtained from the Sigma Chemical Company. Deamino-NADH and the NAD analogs were products of P.L. Biochemicals, Inc. The oxidized analogs were reduced with horse liver alcohol dehydrogenase¹³ obtained from Boehringer. The products were recovered by passing the protein-free supernatant (prepared by placing reaction mixtures in a boiling water bath for 2 min and centrifuging for 10 min at 10 000 \times g) through a 1.5 cm \times 25 cm column of G-10 Sephadex which was equilibrated with 100 mM NaCl. The analogs, located spectrophotometrically, were well separated from the other components of the reaction mixture. The peak fractions were combined and concentrated by lyophilization. The absorbance of the cyanide complex of the oxidized analogs and the absorbance of the reduced analogs were used to determine their concentrations. The spectral data and constants required for these determinations were obtained from P.L. Biochemicals, Inc. ¹⁴. Reduction of the analogs was quantitative and the overall recoveries ranged from 50-94% of theory.

Molecular weight determinations were carried out according to the method of Andrews¹⁵ using a 1.5 cm × 24.5 cm column of P-200 polyacrylamide gel previously equilibrated with 2 M NaCl-100 mM Tris-HCl (pH 7.4). The column was calibrated with lactic dehydrogenase, fumarase, and lysozyme, obtained from Boehringer, and bovine serum albumin.

All other chemicals were obtained from the usual commercial sources.

RESULTS

Gel filtration

80 ml of crude extract (prepared as previously described¹) were diluted to a concentration of 22.9 mg protein per ml using 2 M NaCl-100 mM Tris-HCl (pH 7.4) as the diluent and passed through an agarose column equilibrated with 2 M NaCl-100 mM Tris-HCl (pH 7.4). As shown in Fig. 1, NADH dehydrogenase activity appeared at a V_e/V_0 of 1.5 and was separated from carotenoid-containing fractions which presumably were associated with membrane-rich materials. 1330 units of NADH dehydrogenase (spec. act. 0.72), were applied to the column. Following gel filtration, combination and concentration of Fractions 49–55 yielded a total of 1290 enzyme units at a specific activity of 6.4. Recoveries were usually 75% but ranged

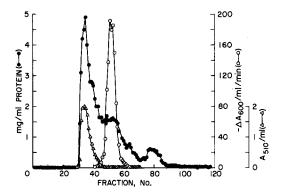


Fig. 1. Agarose gel filtration of crude extracts. 80 ml of crude extract (containing 22.9 mg of protein and 16.7 enzyme units/ml) were applied to a 2.5 cm \times 82 cm column of A-0.5 m agarose gel previously equilibrated with 2 M NaCl-100 mM Tris-HCl (pH 7.4). The column was washed at room temperature (approx. 22 °C) with the same buffer at a flow rate of 30 ml/h. 21-ml fractions were collected and assayed for NADH dehydrogenase activity (\bigcirc — \bigcirc), protein (\bigcirc — \bigcirc), and absorbance at 510 nm (\bigcirc — \bigcirc).

from 65-97%. The agarose fraction could be stored at -120 °C for at least 3 months with little loss of activity.

When gel filtration was carried out in the presence of 4 M NaCl-100 mM Tris-HCl (pH 7.4), 77% of the NADH dehydrogenase activity present in the crude extract appeared coincident with those fractions containing the carotenoid pigment. The remaining NADH dehydrogenase activity appeared in the included volume of the column.

Hydroxyapatite chromatography

22.5 ml of the agarose fraction were placed on a 2.5 cm \times 29.5 cm column of Bio-Gel HT previously equilibrated with 1 M NaCl-100 μ M NADH-100 mM Tris-HCl (pH 7.4).

Following adsorption of the agarose fraction, the gel was washed with 185 ml of 1.0 M NaCl-100 μ M NADH-100 mM Tris-HCl (pH 7.4). This resulted in the elution of some protein, but no NADH dehydrogenase (Fig. 2). The column was

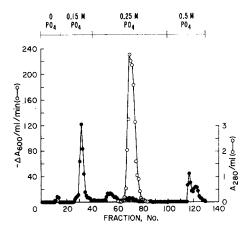


Fig. 2. Hydroxyapatite chromatography of the agarose fraction. 22.5 ml of the agarose fraction, containing 8.75 mg of protein per ml and a total of 1265 units, were placed on a 2.5 cm × 29.5 cm column of Bio-Gel HT equilibrated in 1.0 M NaCl-100 μM NADH-100 mM Tris-HCl (pH 7.4). The column was washed with 185 ml of the above buffer. Subsequently, the column was washed sequentially as indicated with ammonium phosphate-1.0 M NaCl-100 μM NADH buffers (pH 8.5) containing the following concentrations of ammonium phosphate: 150, 250, and finally 500 mM. 12-ml fractions were collected at a flow rate of 48 ml/h. The column was operated at room temperature (approx. 22 °C). NADH dehydrogenase ($\bigcirc-\bigcirc$); $A_{280~nm}$ ($\bigcirc-\bigcirc$).

washed sequentially with three column volumes of ammonium phosphate buffers (at pH 8.5) at the following concentrations: 150, 250, and 500 mM. Each of the buffers were 1.0 M with respect to NaCl and 100 μ M with respect to NADH. As shown in in Fig. 2, a large amount of protein but no enzyme activity was eluted with 150 mM ammonium phosphate. When the wash was changed to 250 mM ammonium phosphate, some protein was eluted followed by the enzyme. Additional protein but no NADH dehydrogenase activity was eluted with 500 mM ammonium phosphate. Fractions 68–79 were combined, concentrated, and designated as the HA fraction. About 60% of the units applied to the column were recovered with a 25-fold increase in spec. act.

QAE-Sephadex fractionation

Five HA fractions were combined, concentrated, and passed through a 1.5 cm \times 31 cm G-25 Sephadex column equilibrated, in 350 mM NaCl-100 μ M NADH-10 mM Na TES (pH 7.0). The NADH dehydrogenase was excluded from the column and was subsequently placed on a 2.5 cm \times 16 cm QAE-Sephadex column previously equilibrated with 350 mM NaCl-100 μ M NADH-10 mM Na TES (pH 7.0). After the addition of enzyme, the column was washed with 350 ml of the starting buffer. Thereafter, an NaCl gradient was established from 350 to 500 mM NaCl over a total volume of 400 ml. The enzyme was eluted from the column between 420 and 450 mM NaCl (Fig. 3). Those fractions of highest specific activity (Fractions 61–79) were combined and immediately reactivated. Following reactivation, the enzyme (QAE fraction) was concentrated, made 0.8% with respect to bovine serum albumin, and stored at -120 °C.

Table I summarizes the purification procedure. The QAE fraction oxidized 376 µmoles of NADH per min per mg protein which represented a 545-fold puri-

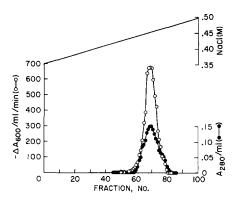


Fig. 3. QAE-Sephadex chromatography of fraction HA. 21 ml of fraction HT (containing 26.8 mg protein per ml and a total of 3420 units of enzyme) were passed through a 1.5 cm \times 31 cm G-25 Sephadex column equilibrated in 350 mM NaCl-100 μ M NADH-10 mM Na TES (pH 7.0). The enzyme was then placed on a 2.5 cm \times 16 cm column of QAE-Sephadex (A-50 previously equilibrated in 350 mM NaCl-100 μ M NADH-10 mM Na TES (pH 7.0). Following absorption of the enzyme to the column, the column was washed with 350 ml of the same buffer until the absorption at 280 nm reached a low and relatively constant value. Thereupon, a linear NaCl gradient was established in 10 mM Na TES-100 μ M NADH (pH 7.0) from 350 to 500 mM NaCl over a total volume of 400 ml. 5 ml fractions were collected at a flow rate of 36 ml/h. The column was operated at 4 °C. NADH dehydrogenase activity (\bigcirc — \bigcirc); $A_{280 \text{ nm}}$ (\bigcirc — \bigcirc).

fication of the activity present in the crude extract. The QAE fraction was colorless and could be stored at $-120\,^{\circ}\text{C}$ for at least 1 year without any loss of activity. When supplemented with bovine serum albumin to a final concentration of 0.8%, the enzyme could be frozen and thawed repeatedly with little loss of activity. Samples have been stored 4 °C for 1 month with less than a 10% loss of the initial activity.

Properties of the enzyme

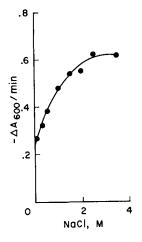
While NADH dehydrogenase activity was stimulated by the presence of NaCl (Fig. 4), considerable activity was observed in the absence of added salt. Extrapolation

TABLE I

PURIFICATION OF NADH DEHYDROGENASE ACTIVITY FROM STRAIN AR-I

68 g of cells (wet weight) were suspended in 100 mM Tris-HCl-4.0 M NaCl (pH 7.4) and disrupted by passage through a French press as previously described. The resulting suspension was centrifuged for 30 min at 10 000 \times g and the clear, red supernatant (crude extract) was diluted to a protein concentration of 22.9 mg/ml prior to passage through an agarose A-0.5 m gel column. The purification procedure was carried out with five aliquots of the diluted crude extract up to the QAE-Sephadex fractionation. At this stage, the 5 HA fractions were combined, concentrated, and the concentrated material purified by chromatography on a QAE-Sephadex column. A unit of activity is that amount of enzyme causing the reduction of 1 μ M of DCIP per minute. Specific activity in units/mg protein.

Fraction	Total volume (ml)	Total µnits	Recovery (%)	Total protein (mg)	Specific activity	Purified
Crude	400	6300	100	9130	0.69	1.0
Agarose	125	5940	94	1110	5.35	7.8
HĀ	2 I	3420	54	26.8	128	186
QAE	136	1880	30	5.0	376	545



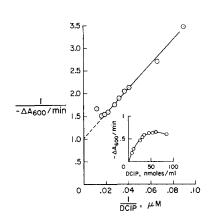


Fig. 4. Effect of NaCl on NADH dehydrogenase activity. Enzyme activity was determined in standard reaction mixtures in which only the NaCl concentration was varied as indicated. 0.03 unit of QAE fraction were assayed at each concentration of salt. When assayed in the absence of added NaCl, the concentration of NaCl was 15 mM, due to carry over of NaCl with the enzyme.

Fig. 5. Effect of DCIP on NADH dehydrogenase activity. NADH dehydrogenase activity was determined in standard reaction mixtures in which only the DCIP concentration was varied as indicated. 0.03 unit of QAE fraction were assayed at each concentration and the average of three determinations at each concentration are plotted.

to zero NaCl concentration gave a rate of NADH oxidation some 43% of the maximum rate observed at 2.5 M NaCl. The apparent K_m for DCIP, in the presence of 100 μ M NADH, was 30 μ M (Fig. 5). The enzyme was inhibited by DCIP at concentrations greater than 70 μ M. The apparent K_m for NADH, in the presence of 70 μ M DCIP, was 23 μ M. No inhibition of dye reduction was observed at concentrations of NADH as high as 400 μ M (Fig. 6). The maximal velocity when extrapolated to a saturating concentration of NADH (385 μ moles/min per mg protein) was about 70% of the extrapolated maximal velocity at a saturating concentration of DCIP.

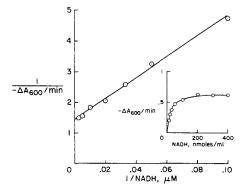


Fig. 6. Effect of NADH on NADH dehydrogenase activity. NADH dehydrogenase activity was determined in standard reaction mixtures in which only the NADH concentration was varied, as indicated. 0.03 unit of QAE fraction were assayed at each concentration and the average of three determinations is plotted.

No well defined pH optimum was observed when the enzyme was assayed in the presence of 2.5 M NaCl-50 mM imidazole-HCl buffer. The rate of dye reduction was constant from pH 6.6 to pH 7.0. At pH values greater than 7, the rate of dye reduction rapidly decreased. When assayed at pH values more acidic than 6.6 (using Tris-acetate buffers) the rate of dye reduction apparently increased. However, assays at these acidic pH values were complicated by the presence of an extremely high rate of non-enzymic dye reduction and made the acquisition of reliable data difficult.

Specificity of electron acceptors

A limited number of oxidants served as electron acceptors for the enzyme. Of those tested, only DCIP, menadione (2-methyl-1,4-naphthoquinone), and juglone (5-hydroxy-1,4-naphthoquinone) were reduced by the enzyme (Table II). The latter

TABLE II

ELECTRON ACCEPTOR SPECIFICITY OF THE NADH DEHYDROGENASE

The QAE fraction was assayed in the presence of variable concentrations of oxidant and substrate. When the oxidant concentration was varied, the NADH concentration was 150 μ M. When the NADH concentration was varied, the following oxidant concentrations were employed: DCIP, 70 μ M; menadione, 400 μ M; juglone, 200 μ M. The reported values for V and K_m were obtained from double-reciprocal plots. V is reported as μ moles of DCIP reduced per min per mg protein at saturating concentrations of oxidant or NADH.

Electron	Oxida	nt	NADI	I
acceptor	V	$K_m \ (\mu M)$	V	K_m (μM)
DCIP	568	30	385	22
Menadione	353	2 I	236	34
Juglone	326	133	221	17

two were only 60% as effective as DCIP when measured at saturating concentrations of oxidant. The maximal velocity, at a saturating concentration of NADH, was also affected by the nature of the oxidant with the greatest activity observed in the presence of DCIP. The apparent K_m for NADH was relatively unaffected by the nature of the electron acceptor.

The following electron acceptors were not reduced by the enzyme in the presence of NADH: potassium ferricyanide, lawsone (2-hydroxy-1,4-naphthoquinone) vitamin K_1 (2-methyl-3-phytyl-1,4-naphthoquinone), vitamin K_5 (4-amino-2-methyl-1-naphthol), coenzyme Q_6 , coenzyme Q_{10} , lipoic acid, lipoamide, and horse heart cytochrome c.

Specificity of electron donor

The substrate specificity of the enzyme was investigated at various concentrations of reduced NAD analogs and DCIP. The results of these experiments are summarized in Table III. Of the analogs tested, only 3-acetylpyridine-NADH, 3-acetylpyridine-deamino-NADH, and thionicotinamide-NADH were oxidized. The rates of dye reduction, extrapolated to infinite substrate concentration, varied from 35-47% of the rate observed at saturating concentrations of NADH. NADPH,

TABLE III

SUBSTRATE SPECIFICITY OF THE NADH DEHYDROGENASE

The QAE-fraction was assayed in the presence of variable concentrations of oxidant and sub strate. When the oxidant concentration was varied, the following substrate concentrations were employed: 3-acetylpyridine deamino-NADH, 800 μ M; thionicotinamide-NADH, 570 μ M; 3 acetylpyridine NADH, 630 μ M. The DCIP concentration was 70 μ M when the substrate concentration was varied. The reported values for V and K_m were obtained from double reciprocal plots V is reported as μ moles of DCIP reduced per min per mg protein at saturating concentrations o oxidant or NADH.

Substrate	Substrate		DCIP	
	\overline{V}	μM	\overline{V}	μM
NADH	385	23	568	30
3-Acetylpyridine deamino-NADH	180	100	146	25
Thionicotinamide-NADH	173	13	241	30
3-Acetylpyridine-NADH	135	100	227	53

deamino-NADH, 3-pyridine aldehyde NADH, and 3-pyridine aldehyde deamino-NADH did not serve as substrates.

When NADH oxidation was carried out in the presence of the various inactive analogs, only 3-pyridine aldehyde NADH inhibited substrate oxidation. As shown in Fig. 7a, the inhibition was competitive with respect to NADH; the K_i was 400 μ M about 20 times greater than K_m for NADH. The patterns of substrate specificity and inhibition suggested that the presence of the 6-amino nitrogen in the purine ring was

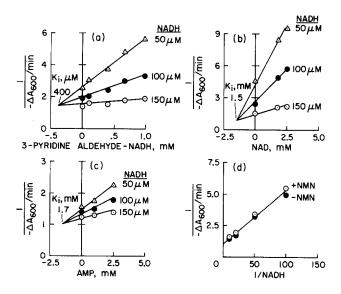


Fig. 7. Inhibition of NADH dehydrogenase activity. 0.03 unit of QAE fraction were assayed ir standard reaction mixtures containing the indicated concentration of NADH and inhibitor. The results are presented as the average of two determinations. (a) Inhibition by 3-pyridine aldehyde NADH; (b) inhibition by NAD; (c) inhibition by AMP; (d) effect of NMN on NADH dehydrogenase activity. Figures 7 (a-c) are Dixon plots¹⁶ whereas Fig. 7d is a double-reciprocal plot (\bigcirc , 0.1 mM NMN; \bigcirc , no added NMN).

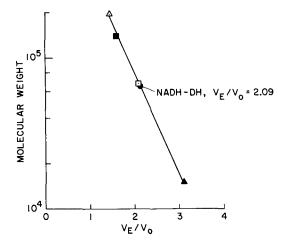


Fig. 8. Molecular weight of NADH dehydrogenase by gel filtration. 0.5 ml QAE fraction, containing 35 μ g protein per ml, were placed on a 1.5 cm \times 24.5 cm column of P-200 polyacrylamide gel previously equilibrated in 2 M NaCl-100 mM Tris-HCl (pH 7.4). The column was operated at room temperature (approx. 22 °C) and 1.0-ml fractions were collected. Fumarase (\triangle), lactate dehydrogenase (\blacksquare), bovine serum albumin (\square), QAE fraction (\blacksquare) and lysozyme (\blacktriangle).

essential for binding. This was consistent with the observations of Rossman $et\ al.^{17}$ that NAD was hydrogen-bonded to lactic dehydrogenase via the 6-amino and nitrogen of the adenosine ring. In further confirmation of this hypothesis, NADH oxidation was observed to be competitively inhibited by AMP (Fig. 7b) and NAD (Fig. 7c), the K_i values being 1.5 and 1.7 mM, respectively, while NMN failed to inhibit the enzyme (Fig. 7d). At the present time, we are unable to explain the oxidation of 3-acetyl pyridine deamino-NADH.

Molecular weight determination

Two molecular weight determinations were made using P-200 gel (Fig. 8). The enzyme was eluted after bovine serum albumin monomer. The two values obtained for the molecular weight were 60 000 and 68 000. When a crude extract was diluted in 2 M NaCl-100 μ M NADH-10 mM Na TES (pH 7.0) and passed through the P-200 column, NADH dehydrogenase activity was located at V_e/V_0 of 2.09 corresponding

TABLE IV

FLAVIN CONTENT OF THE QAE-FRACTION

o.5 ml of the QAE-fraction was analyzed for protein⁸ and (following trichloroacetic acid extraction and hydrolysis) flavin¹⁴. FAD was calculated as the difference between the total flavin as determined by acid hydrolysis and the flavin present prior to hydrolysis. The latter was assumed to represent FMN.

Component	Total content		
	μg	μmole	
Protein	19.1		
FMN	0.029	0.064	
FAD	0.296	0.377	

to a molecular weight of 60 000. This suggested that following gel filtration subsequent purification did not produce an enzyme species of lower molecular weight.

Flavin analysis

Flavin analysis of the QAE fraction according to the method of Burch¹⁸ (Table IV) indicated that FAD represented 85% of the total flavin. The remaining flavin was presumably FMN. Although the presence of both flavins made identification of the flavin associated with the enzyme equivocal, the flavin to protein ratio was consistent with the assumption that FAD was associated with the enzyme. Assuming a flavin to protein ratio of I, the minimum molecular weight for the enzyme was calculated to be 50 700 if FAD were the coenzyme (and 299 000 if FMN were the flavin). The former value was consistent with the molecular weight determined from polyacrylamide gel filtration (Fig. 8).

Stability

As shown in Fig. 9a, the enzyme was unstable in 100 mM and 250 mM NaCl when the salt concentration was adjusted by diluting the enzyme with buffer. In 100 mM NaCl, the loss of enzyme activity was immediate and exponential, whereas in 250 mM NaCl, the enzyme appeared stable for about 30 min before the loss of

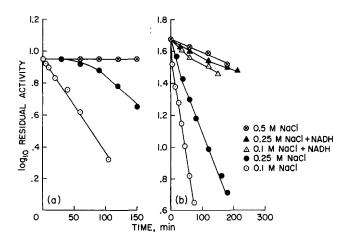


Fig. 9. Stability of NADH dehydrogenase as a function of salt concentration. (a) 0.1 ml of QAE fraction, containing 675 units of activity per ml, was diluted to the desired salt concentration with buffer containing 100 mM Tris–HCl (pH 7.4). When necessary, a further dilution was made using buffer at the desired final NaCl concentration so that the final protein concentration was the same in all cases. The diluted enzyme was incubated at 4 °C; samples were removed periodically, and immediately assayed in standard reaction mixtures. The observed initial rate of DCIP reduction was taken as the residual enzyme activity. (b) 0.2 ml of QAE-fraction, containing 12 units of enzyme activity per ml were passed through a 0.7 cm \times 19 cm P-10 polyacrylamide-gel column equilibrated with buffer containing the desired salt concentration and where indicated was 100 μ M with respect to NADH. The void volume, as determined with blue dextran, was collected and incubated at 4 °C. It was assayed periodically for residual NADH dehydrogenase activity in the standard reaction mixture. Zero time was taken as the time when the added QAE fraction had entered the gel bed. In control experiments, from 90 to 95% of the total units in a QAE fraction were recovered following passage through a P-10 column equilibrated in 3 M NaCl-100 mM Tris–HCl (pH 7.4).

activity became exponential. When incubated in 500 mM NaCl, the enzyme was stable during the time course of the experiment (150 min).

An entirely different response was observed when the salt concentration was adjusted by passing the enzyme through a P-10 polyacrylamide-gel column. The enzyme lost activity in a biphasic manner (Fig. 9b) in which a rapid initial phase was followed by a slower second one. In addition, there was no evidence of a "lag" prior to the loss of enzyme activity. When the enzyme was adjusted to a particular salt concentration by gel filtration using a buffer containing NADH, the loss of activity was considerably retarded (Fig. 9b). The first order decay constants for the second phase, in the absence of NADH, were calculated to be 0.035 min⁻¹ and 0.011 min⁻¹ in 100 and 250 mM NaCl, respectively. In the presence of NADH, they were 0.0026 min⁻¹ and 0.0013 min⁻¹.

DISCUSSION

The NADH dehydrogenase obtained from the halophilic bacterium AR-I exhibited two properties usually associated with enzymes obtained from extremely halophilic bacteria: instability in solutions of low ionic strength; stimulation of activity by high concentrations of NaCl. The stability of the NADH dehydrogenase from AR-I was markedly affected by the presence of its substrate (NADH). Similar substrate stabilization has been noted with other enzymes obtained from extremely halophilic bacteria^{19–22}. When the salt concentration was adjusted by dilution, the enzyme was more stable than when the salt concentration was adjusted by gel filtration. Furthermore, dilution also resulted in a lag prior to the loss of activity. These results are consistent with the hypothesis that dilution did not adequately reduce the concentration of an enzyme-bound factor (possibly NADH) and that the lag prior to decay represented the time required for the enzyme-bound component to dissociate.

NADH dehydrogenase activity was stimulated by NaCl, although considerable activity was present in the absence of added salt. This type of salt response has been observed with other enzymes obtained from halophilic bacteria^{23,24} and may suggest that extraordinarily high concentrations of salt may not be necessary to activate all of the enzymes obtained from extremely halophilic bacteria. However, this response was much different from that reported for the NADH dehydrogenase obtained from Halobacterium salinarium⁸ and the menadione reductase obtained from H. cutirubrum²⁵. The enzyme from H. salinarium was completely inactive at salt concentrations less than 1.0 M NaCl. At salt concentrations greater than 1 M, the response to increasing salt concentrations appeared sigmoidal. This kind of sigmoidal response has been reported to be due to preincubating halophilic enzymes at suboptimal concentrations of salt²⁰, thus measuring the residual activity following inactivation of the enzyme. Since no experimental details were described², it cannot be determined whether this explanation could account for the differences in the salt response exhibited by the enzymes from AR-I and H. salinarium.

The menadione reductase from *H. cutirubrum* also responded differently than the NADH dehydrogenase from AR-I. Both enzymes were maximally active at about the same salt concentration. However, the *H. cutirubrum* menadione reductase was inactive in the absence of added salt. Since the activity reported for *H. cutirubrum*

menadione reductase was obtained from initial rate determinations, this disparity represented a difference in the activity of the enzymes to salt. In addition, the menadione reductase from H. cutirubrum was maximally active in 1.5 M NaCl while the NADH dehydrogenase from AR-I, using menadione as an acceptor, was maximally active in 0.5 M NaCl and considerable activity was observed in the absence of added salt (Hochstein, L. I. and Dalton, B. P., unpublished). These differences, as well as differences in molecular weight, pH optima, pH stability, and light sensitivity (Lanyi, J. K., personal communication) suggest that these NADH dehydrogenases (even though membrane-bound and analogous in function) may be constructed along sufficiently different lines so that the molecular forces responsible for structural integrity, as well as enzyme activity, may be radically different. A survey of the NADH dehydrogenases from a wide range of halophilic bacteria, and a comparison of their kinetic properties may shed light on the significance of this apparent discrepancy.

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