The Microsomal Fraction from *Tetrahymena pyriformis* Strain ST: Characterization and Subfractionation

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SUMMARY

Post-mitochondrial supernatants isolated from *Tetrahymena pyriformis* contained high specific activities of antimycin A-insensitive NADH- and NADPH-cytochrome c oxidoreductases, acid and alkaline p-nitrophenylphosphatases, DNase and ATPase; many of the enzymes associated with mammalian microsomes were not present at detectable levels. The only haem detected was protohaem; cytochromes b5, P680 and P425 were present in microsomal fractions, and ethyl morphine and aniline HCl produced distinct changes in difference spectra. Post-mitochondrial supernatants were subfractionated by density gradient centrifugation. The distributions of NADH- and NADPH-cytochrome c oxidoreductases were different, and several distinct particles containing the latter enzyme system were distinguished. The distributions of acid p-nitrophenylphosphatase, acid DNase and ATPase were all different and indicative of several functionally distinct membrane systems. Alkaline p-nitrophenylphosphatase was non-sedimentable.

INTRODUCTION

The NADH- and NADPH-cytochrome c oxidoreductases of homogenates prepared from suspensions of *Tetrahymena pyriformis* show complex distributions after high speed zonal centrifugation on sucrose density gradients (Lloyd, Brightwell, Venables, Roach & Turner, 1971). While both these activities are in part associated with mitochondria (Turner, Lloyd & Chance, 1971), which equilibrate at \( \rho = 1.21 \), the regions of the gradient at \( \rho < 1.20 \) also contain both oxidoreductases. The distributions of these two enzyme systems are different, and they vary in homogenates of organisms harvested at different phases of the growth cycle of a batch culture (Lloyd et al. 1971).

In this paper we characterize the haemoproteins of the microsomal fraction of *Tetrahymena pyriformis*, strain ST and separate some of the component membrane systems by zonal centrifugation.

METHODS

*Maintenance, growth and harvesting of the organism. Tetrahymena pyriformis*, strain ST, was maintained, grown (in volumes of culture up to 15 l.), and harvested as previously described (Lloyd et al. 1971).

*Disruption of organisms and preparation of post-mitochondrial supernatants and microsomal fractions.* The organisms were washed once in preparation buffer consisting of 0.24 M-sucrose, 10 mM-tris HCl, and 0.5 mM-MgCl₂ (pH 7.4), and resuspended in 5 vol. of this buffer. The suspension was homogenized in a 50 ml. Kontes (Vineland, New Jersey, U.S.A.)
tight fitting (type B plunger) glass hand-homogenizer in ice, until almost 60% of the organisms were broken. Gentle strokes were used and care was taken to avoid cavitation. All centrifugation steps were carried out at 4° (in the 8 x 50 ml. rotor of an MSE 17 centrifuge except where stated). The whole homogenate was centrifuged for 5 min. at 300g ($r_w = 7.62$ cm.) to remove whole organisms, nuclei and pellicles. The supernatant was recentrifuged for 10 min. at 10,000g ($r_w = 7.62$ cm.) to remove mitochondria, peroxisomes and most of the lysosomes. The supernatant from this step is termed the ‘post-mitochondrial supernatant’ (PMS). The ‘microsomal fraction’ was prepared by centrifuging PMS for 1 h. at 106,000g ($r_w = 5.98$ cm.) in the 8 x 10 ml. rotor of an MSE 40 centrifuge. The sedimented material was resuspended in preparation buffer to a protein concentration of about 1 mg./ml.

Zonal centrifugation. Post-mitochondrial supernatants were fractionated using a B XIV rotor (Anderson et al. 1967). The rotor was loaded with the following volumes of sucrose solutions (all buffered to pH 7.4 at 4° with tris HCl and containing 0.5 mM-MgCl$_2$): 40 ml. each of 10, 12.5, 15, 17.5, 20, 22.5, 25, 27.5, 30, 32.5 and 37.5%; 140 ml. 60%; from 10 to 15 ml. PMS, 30 ml. each of 7 and 9% (all w/w). Loading was at 2500 rev./min.; the rotor was then accelerated to 35,000 rev./min. (36,500g at sample zone) and held at this speed. The rotor was unloaded at 2500 rev./min. through the flow cell of a Beckman recording spectrophotometer; extinction was monitored at 260 nm. Fractions (10 ml.) were collected at 5°. Sucrose concentrations were measured with a refractometer and density calculated from the data of de Duve, Berthet & Beaufay (1959). S-values were calculated by the method of Halsall & Schumaker (1969) as detailed by Poole et al. (1971).

Enzyme assays. Assays of acid p-nitrophenylphosphatase (EC 3.1.3.2), NADH- and NADPH-cytochrome c oxidoreductases (EC 1.6.99.3) were exactly as described by Lloyd et al. (1971). Methods for assay of ATPase (at pH 6.8, in the presence of 4 mM-MgCl$_2$), alkaline phosphatase and all the enzymes looked for but not detected have been previously published by Cartledge & Lloyd (1972). Precautions taken to ensure linearity of enzyme assays and proportionality of reaction rates to volumes used in assays of fractions from zonal centrifugation experiments have also been described previously in detail (Lloyd et al. 1971).

Analytical methods. Difference spectra were traced with a Cary model 14 split-beam spectrophotometer fitted with a 0 to 0.1 extinction slide wire. Sometimes an attachment for scanning at the temperature of liquid N$_2$ was also used.

Pyridine haemochrome derivatives were prepared according to the method of Falk (1964). Protein was measured by the method of Lowry, Rosebrough, Farr & Randall (1951) with bovine plasma albumin as a standard. P, was measured by the method of Leloir & Cardini (1957).

Materials. Antimycin A, ATP, NADH, NADPH, cytochrome c (horse-heart type III) and acid phosphatase substrate tablets were from Sigma Chemical Co., London, S.W. 6. Bovine Albumin Powder (fraction V from bovine plasma) was obtained from Armour Pharmaceutical Co. Ltd, Eastbourne, Sussex.

Presentation of results. Enzyme units are expressed as nmoles substrate transformed/min. or measured product formed/min. In Fig. 5 to 7 vertical lines divide the diagrams at density intervals of 0.05 g./ml.


**RESULTS**

*Enzymes present in post-mitochondrial supernatants.* Post-mitochondrial supernatants contained the following enzymes: NADH- and NADPH-cytochrome c oxidoreductases, acid and alkaline p-nitrophenylphosphatases, acid DNase and ATPase. Specific activities and percentage of the total units of the whole homogenate present in this fraction for cells harvested from 1-day (exponential phase) and 6-day-old (late-stationary phase) cultures are presented in Table I. Enzymes looked for but not present at detectable levels included PPase, TPPase, AMPase, UDPase, GDPase, ADPase, glucose-6-Pase, monoamine oxidase, aryl sulphatase, β-glucuronidase, N-ethyl morphine demethylase, UDP-glucosyl transferase, UDP-glucuronyl transferase, aniline hydroxylase, and aromatic nitroreductase.

*Difference spectra of microsomal fractions.* Extinction maxima at 555 to 558 nm. and 428 nm. in difference spectra (dithionite reduced minus oxidized) at room temperature (Fig. 1,B), or at 557, 526 to 530 and 425 nm. at low temperature (Fig. 1,C) were similar to

![Graph](image.png)

**Fig. 1.** Difference spectra of Tetrahymena microsomal fraction. The suspension of microsomes contained 0.66 mg. protein/ml. Curve A represents the baseline (oxidized minus oxidized). Curve B was obtained after the addition of excess sodium dithionite to the sample cuvette. Curve C is the difference spectrum (dithionite reduced minus oxidized) obtained at the temperature of liquid N₂. Path lengths were 1 cm. in A and B, and 2 mm. in C.
those observed for microsomes of mammalian origin (Estabrook & Cohen, 1969), and may be indicative of the presence of both cytochromes $b_5$ and $P_{450}$. The former component was specifically reduced by NADH or NADPH (Fig. 2, A), while the latter was best seen in dithionite reduced-CO minus dithionite reduced spectra (Fig. 2, B). Another CO-binding pigment is also present which gives a maximum at 422 nm.

Fig. 2. Difference spectra of Tetrahymena microsomal fraction. The suspensions contained 3·7 mg. protein/ml. Curve A was obtained after the addition of 1 mg. of NADH to the sample cuvette (NADH-reduced minus oxidized) and has been corrected for the baseline (oxidized minus oxidized). An identical spectrum was obtained when NADPH replaced NADH in this experiment. Further increases in extinction occurred at 555 and 424 nm. on adding excess Na-dithionite. Curve B represents the CO spectrum (dithionite reduced—CO minus dithionite reduced) corrected for the appropriate baseline (dithionite reduced minus dithionite reduced).

After treatment of the microsomal fraction by the method of Falk (1964), the presence of the pyridine haemochromogen derivative of protohaem (extinction maxima at 557 and 527 nm., Fig. 3, B) was demonstrated. This confirmed the presence of $b$-type cytochrome; no haems $a$ or $c$ were detected in this fraction.
**Microsomal fraction from Tetrahymena**

Fig. 3. Difference spectra for pyridine haemochrome derivatives from Tetrahymena microsomal fraction. The extract containing protohaem (and haem a if present; Falk, 1964) was resuspended in distilled water, as was the pellet obtained after extraction (containing haem c, if present). The difference spectrum was obtained after the addition of pyridine (1 ml.) and M-NaOH (0.5 ml.) to the preparations (4.5 ml.). To one cuvette 1 mg. of K-ferricyanide was added, and to the other 1 mg. of Na-dithionite. Curve A indicates that haem c was absent while curve B shows the presence of protohaem only.

Fig. 4. Difference spectra of the pigments of Tetrahymena microsomal fraction resulting from additions of aniline HCl and ethyl morphine. Curve A, oxidized minus oxidized (baseline). Curve B was obtained after adding 3 mM-aniline HCl to one cuvette (oxidized + aniline HCl minus oxidized) and curve C was traced after adding 3 mM-ethyl morphine (oxidized + ethyl morphine minus oxidized). Protein concentration was 0.68 mg./ml.
The addition of 3 mM-aniline hydrochloride to an oxidized microsomal preparation gave a spectrum with a trough at 390 nm and a peak at 410 nm. (Fig. 4.B). Ethyl morphine (3 mM) produced an extinction minimum at 415 nm and a maximum at 435 nm. (Fig. 4.C).

Fig. 5. Post-mitochondrial supernatant from organisms harvested after growth for 1 day (population 36,000 organisms/ml) fractionated in a BXIV zonal rotor. The post-mitochondrial supernatant (7:8 ml) contained 42 mg protein. This was diluted 1 in 40 and 0:2 ml was found to be a suitable volume for enzyme, phosphate and protein assays. Centrifugation was at 35,000 rev./min. for 165 min. (= 6 × 10⁶ g min. at the sample zone; \( \frac{4}{3} \omega^2 r t = 1.3 \times 10^{11} \text{ rad. s}^{-2} \)). (a) Sucrose density gradient (○), protein (■) and \( E_{280} \text{nm} \) (continuous line). (b) NADH- (■) and NADPH- (▲) cytochrome c oxidoreductases. (c) Acid p-nitrophenylphosphatase (●) and Pi (○).
Microsomal fraction from Tetrahymena

The supernatant obtained after sedimentation of the microsomal fraction contained no spectrally-detectable haemoproteins.

Subfractionation of post-mitochondrial supernatants by zonal centrifugation. In order to separate the component membrane systems of the PMS, they were centrifuged through sucrose gradients in the BXIV zonal rotor. The distributions of enzymes through the gradient after centrifugation of PMS (prepared from organisms from a 1-day-old culture) at 35,000 rev./min. for 165 min. is shown in Fig. 5. The profile of extinction at 260 nm. is complex

Fig. 6. Post-mitochondrial supernatant from organisms harvested after growth for 1 day (population 54,000 organisms/ml.) fractionated in a BXIV zonal rotor. The post-mitochondrial supernatant (17.5 ml.) contained 195 mg. protein. This was diluted 1 in 40 and 0.2 ml. was found to be a suitable volume for all the assays. Centrifugation was at 35,000 rev./min. for 6 h. (\( \equiv > 12 \times 10^6 \text{g} \cdot \text{min.} \) at the sample zone; \( \int_{0}^{t} \alpha^2 \, dt = 3.0 \times 10^{13} \text{rad.} \cdot \text{s}^{-1} \)). (a) Sucrose density gradient (○), protein (●), P\(_i\) (△) and \( E_{260}\text{nm.} \) (continuous line). (b) NADH- (●) and NADPH- (△) cytochrome c oxidoreductases. (c) Acid \( p\)-nitrophenylphosphatase (●), DNase (○) and ATPase (△).
(Fig. 5a); the major zone (4) contained (74S) ribosome monomers while the other zones contained (in order of increasing S-values) soluble nucleotides (1), 30S and 56S ribosome subunits (2, 3), 102S ribosome dimers (5) and 125S trimers (6). The gradient was not designed to demonstrate the presence of larger polyribosomes (Cameron et al. 1966; Hartman & Dowben, 1970a, b); an exponential gradient is best for this purpose (Marcus et al. 1967). Five distinct sedimentable populations of particles containing NADPH-cytochrome c oxidoreductase were revealed under these conditions (Fig. 5b). The distribution of this

![Graph](image_url)

Fig. 7. Post-mitochondrial supernatant from organisms harvested after growth for 6 days (population 2.5 × 10⁶ organisms/ml) fractionated in a BXIV zonal rotor. The post-mitochondrial supernatant (7.5 ml.) contained 120 mg. protein. This was diluted 1 in 40 and 0.2 ml. was found to be a suitable volume for all the assays. Centrifugation was at 35,000 rev./min. for 165 min. (≈ 6 × 10⁶g min. at the sample zone; ∫₀^t ω dt = 1.45 × 10¹⁴ rad. s⁻¹) (a) Sucrose density gradient (○), protein (●) and E₂₅₀nm (continuous line). (b) Acid (●) and alkaline (○) p-nitrophenylphosphatases. (c) NADH-(●) and NADPH- (▲) cytochrome c oxidoreductases.
Microsomal fraction from Tetrahymena

The preparation from Tetrahymena of post-mitochondrial supernatants and microsomal fractions which do not contain fragments of membrane of mitochondrial origin necessitates

discussion

There have been few studies on the components of post-mitochondrial supernatants of homogenates prepared from eukaryotic micro-organisms. Fatty-acid synthase and desaturase are present in yeast microsomal fractions (Klein, Volkmann & Chao, 1967), and anaerobically grown yeast contains five haemoproteins including cytochromes b₁ and P₄₅₀ (Ishidate, Kawaguchi, Tagawa & Hagihara, 1969). The subcellular distributions of NADH- and NADPH-cytochrome c oxidoreductases in aerobically grown yeast originally described by Schatz & Klima (1964) have been reappraised and examined in more detail by Cartledge & Lloyd (1972). Finally, polyribosome separations have been described for yeast (Marcus et al. 1967) and for Tetrahymena pyriformis (Cameron et al. 1966; Hartman & Dowben, 1970a, b).

The preparation from Tetrahymena of post-mitochondrial supernatants and microsomal fractions which do not contain fragments of membrane of mitochondrial origin necessitates
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Table 1. Specific activities of enzymes and their recoveries in whole homogenates and post-mitochondrial supernatants

Data calculated for the experiments shown in Fig. 5 to 7. Absence of a figure indicates enzyme not assayed (WH = whole homogenate, PMS = post-mitochondrial supernatant and P1 = pellet obtained on centrifuging WH at 10,000 g for 10 min.).

<table>
<thead>
<tr>
<th>Enzyme units</th>
<th>Specific activities of enzymes in WH</th>
<th>Recovery of enzymes in P1+PMS (%)</th>
<th>Recovery from PMS in WH (%)</th>
<th>Total units of WH in PMS (%)</th>
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<tr>
<td>Homogenates from 1-day organisms (Fig. 5)</td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Protein</td>
<td>—</td>
<td>—</td>
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<td>105</td>
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<td>NADH-cytochrome c oxidoreductase</td>
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<td>7.0</td>
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<td>53</td>
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<tr>
<td>ATPase</td>
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<tr>
<td>DNase</td>
<td>—</td>
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Homogenates from 1-day organisms (Fig. 6)

| Protein | — | — | 100 | 88 | — |
| NADH-cytochrome c oxidoreductase | 57.8 | 26.1 | 67 | 140 | 39 |
| NADPH-cytochrome c oxidoreductase | 13.5 | 9.7 | 99 | 113 | 61 |
| Acid p-nitrophenylphosphatase | 40.7 | 38.6 | 103 | 111 | 41 |
| Alkaline p-nitrophenylphosphatase | — | — | — | — | — |
| ATPase | 85.5 | 170.0 | 86 | 97 | 75 |
| DNase | 6.1 | 23.0 | 99 | 130 | 57 |

Homogenates from 6-day organisms (Fig. 7)

| Protein | — | — | 96 | 114 | — |
| NADH-cytochrome c oxidoreductase | 23.5 | 19.4 | 96 | 85 | 75 |
| NADPH-cytochrome c oxidoreductase | 8.5 | 9.5 | 83 | 87 | 76 |
| Acid p-nitrophenylphosphatase | 20.3 | 10.0 | 112 | — | — |
| Alkaline p-nitrophenylphosphatase | 18.6 | 31.3 | — | 102 | 77 |
| ATPase | — | — | — | — | — |
| DNase | — | — | — | — | — |

gentle disruption; if more than 60% of the organisms are broken, mitochondrial contamination does occur and is detected spectrophotometrically by the presence of the typically mitochondrial haemoproteins (Turner et al. 1971) and by partial antimycin-A sensitivity of the NADH-cytochrome c oxidoreductase. These criteria do not exclude the possibility of contamination by outer mitochondrial membranes and there are no unequivocal markers for these in Tetrahymena (G. Turner & D. Lloyd, unpublished work).

Inability to detect many of the enzymes present in microsomal fractions from mammalian tissues led us to study nicotinamide nucleotide linked oxidoreductases which are often associated with rough and smooth endoplasmic reticulum (see review by Reid, 1967); on isolation these membranes give rise to the ‘microsomal fraction’. The natural carriers in the mammalian microsomal electron-transport chains are cytochromes b5 and P450; similar respiratory pigments were detectable in Tetrahymena. All of the cytochrome b5 was reducible by either NADH or NADPH, while dithionite also reduced P450. In mammalian systems, P450 acts as the oxygen-activating enzyme and site of substrate interaction for oxidative transformations of various lipophilic foreign compounds and steroids, while cytochrome
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*b* is involved in oxidative desaturation of fatty acids (Sato, Nishibayashi & Ito, 1969). Mammalian cytochrome *c* acts as an artificial acceptor in these electron-transport chains, and its reduction provides a convenient marker for microsomal membranes.

The addition of drugs to microsomal fractions of mammalian cells gives distinctive spectral changes because they bind with cytochrome *P*$_{450}$ (Imai & Sato, 1966). With *Tetrahymena* microsomal fractions, aniline HCl gave the "type II" trough at 390 nm, but the maximum was at 410 nm, rather than at 430 nm. Ethyl morphine also gave a spectrum which was quite different from that with mammalian microsomes. Thus although enzymes involved in the metabolism of these drugs could not be detected in *Tetrahymena* (and could not be induced by growth in the presence, for example, of phenobarbital, L. Howells & D. Lloyd, unpublished results), these drugs can be bound to microsomal haemoprotein. Possibly the *P*$_{450}$ plays a role in this binding, as the spectral changes observed did not follow the classical pattern. This pigment (which may be similar to that formed on denaturation of mammalian *P*$_{450}$, Omura & Sato, 1964) must be a *b*-type cytochrome, as only protohaem was detectable in *Tetrahymena* microsomes.

Heterogeneity of microsomal membranes was evident after rate separation on a size basis in the zonal centrifuge. The most rapidly moving component had reached its isopycnic density (*p* = 1.23), contained both NADH- and NADPH-cytochrome *c* oxidoreductases, and had an extinction at 260 nm; this was followed by membrane fragments (sedimentation coefficients 125 S, 102 S and 74 S) rich in the NADPH-linked activity. Extended centrifugation sedimented all three zones to *p* = 1.20 to 1.23. As previously observed (Lloyd et al. 1971) the pattern of sedimentibility of these enzyme systems was altered in homogenates of stationary phase organisms.

The simplicity of distributions of acid *p*-nitrophenylphosphatase contrasted with the heterogeneity of organelles containing this enzyme seen when whole homogenates were centrifuged under similar conditions (Lloyd et al. 1971). Thus it seems that the smallest lysosomal vacuoles containing this enzyme were very homogeneous with respect to density, and that several of the populations of the whole homogenate (including that not sedimentable beyond *p* = 1.10) previously observed consisted of particles large and dense enough to have been sedimented with the mitochondria at 10$^6$g min. in 0.24 M-sucrose. Acid DNase was present in two major zones; the sedimentable zone was distinct from that containing the *p*-nitrophenylphosphatase. ATPase also shows a density distribution different from the other enzymes assayed.

These results suggest that there are many different populations of membranes in the microsomal fraction of *Tetrahymena* and may reflect a structural and functional diversity of the cytomembranes of intact organisms.

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**REFERENCES**


