Anaerobic pathways of glycerol dissimilation by Enterobacter agglomerans CNCM 1210: limitations and regulations

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Continuous cultures of Enterobacter agglomerans CNCM 1210 were performed under regulated pH conditions (pH 7.0) with glycerol or glucose (20 g l^-1^) as carbon source. Cultures grown on glucose produced mainly acetate, ethanol and formate. In contrast, 1,3-propanediol (PPD) was the main product with glycerol. The carbon flow distribution at branching metabolic points was investigated. Higher PPD yields with increased dilution rate were correlated with an important increase in the relative ratio of glycerol dehydratase to glycerol dehydrogenase. Determination of intracellular triose-phosphate and fructose 1,6-biphosphate concentrations demonstrated that glyceraldehyde-3-phosphate dehydrogenase is the limiting step in glycerol dissimilation. At the pyruvate branching point, pyruvate dehydrogenase (PDH) activity was systematically detected. The pyruvate flow shifted to PDH is suspected to represent up to 22% of the acetyl-CoA formed. In addition, this enzyme pattern combined with the enhanced in vitro lactate dehydrogenase activity at high growth rates, was correlated with a decrease in the pyruvate formate-lyase activity. A regulation of this latter enzyme by the accumulation of triose-phosphate is suspected.

Keywords: Enterobacter agglomerans, glycerol, carbon flow distribution and regulation, reducing equivalent flow, 1,3-propanediol

INTRODUCTION

Due to the scheduled expansion of vegetable oil processing activities (biodiesel), abundant glycerol sources are expected to be generated (Eggersdorfer et al., 1992; Chowdhury & Fouhy, 1993). For this reason, microbial conversion of glycerol to various compounds has been investigated recently and particularly focused upon 1,3-propanediol (PPD) production (Günzel et al., 1991; Biebl et al., 1992; Petitdemange et al., 1995). This hallmark product is of interest in the synthesis of polyesters because of the outstanding properties it confers to the material in terms of mechanical resistance (Elm et al., 1980) and biodegradability (Witt et al., 1994).

The fermentation of glycerol to PPD has been mainly studied with micro-organisms such as Klebsiella pneumoniae (Ogbe Solomon et al., 1994; Zeng et al., 1993; Streekstra et al., 1987), Citrobacter freundii (Homann et al., 1990; Boenigk et al., 1993) and Clostridium butyricum (Abbad-Andaloussi et al., 1996; Saint Amans, 1994; Forsberg, 1987). Enterobacter agglomerans is able to convert glycerol to PPD as the major product and to acetic, formic, lactic and succinic acids and ethanol as by-products (Barbirato et al., 1995). The metabolic flexibility of this strain was demonstrated by varying the initial glycerol content during batch fermentation regulated at pH 7.5: the higher the initial substrate concentration, the higher the PPD conversion yield. However, increasing glycerol content, and thus glycerol uptake rate, resulted in the accumulation of an intermediate metabolite. Identified as 3-hydroxypropionaldehyde (3-HPA), it caused cessation of both growth and product formation (Barbirato et al., 1996a, b).

In the present study, we investigated the metabolic
behaviour of *E. agglomerans* growing anaerobically in a continuous culture with glycerol or glucose as sole carbon source. On the one hand, this was accomplished by altering the metabolic pathway used for conversion of glycerol into pyruvate and lactate, as well as the regeneration of reducing equivalents. On the other hand, the activities of key enzymes involved in the dissimilation of glycerol and nucleotide pools were measured. Effects of a high specific rate of glycerol dissimilation on the metabolic pathways used are discussed.

**METHODS**

**Bacterial strain and growth conditions.** The bacterial strain *Enterobacter agglomerans* CNCM 1210 (Collection Nationale de Cultures de Microorganismmes, Institut Pasteur, Paris, France) was grown in carbon-source-limited, anaerobic continuous cultures. Feed medium contained (per litre deionized water): 20 g glycerol or glucose as carbon source, 1 g K_{2}HPO_{4}, 0.5 g KH_{2}PO_{4}, 2 g (NH_{4})_{2}SO_{4}, 0.4 g MgSO_{4}, 7H_{2}O, 0.1 g CaCl_{2}, 2H_{2}O, 4 mg CoCl_{2}, 2 g yeast extract (Biokar diagnostic), 0.5 g bactopeptone (Difco), 0.3 g bacteriological meat extract (Biokar) and 1 ml of a mineral solution containing (per litre deionized water): 5 g EDTA, 2 g FeSO_{4}, 7H_{2}O, 1 g MnCl_{2}, 4H_{2}O, 0.2 g CuCl_{2}, 2H_{2}O, 0.2 g H_{3}BO_{3}, 30 mg Na_{2}MoO_{4}, 2H_{2}O, 30 mg NiCl_{2}, 2H_{2}O and 0.1 g ZnSO_{4}, 7H_{2}O. Bottles (10 or 20 litres) containing the feed medium were degassed for 20–24 h after a sterile nitrogen flux after being autoclaved (30 min at 120 °C). Experiments were carried out in 1 litre glass reactors with a constant liquid volume of 0.8 l, that were sparged daily with sterile nitrogen and constantly maintained under a low pressure. The reactors were equipped with pH regulation (2300 Ingold transmitter controlling 5 M NaOH addition) and magnetic stirring. Temperature was maintained at 30 °C by a thermostatted water circulation system.

**Analysis.** Biomass concentration was determined by measurements of cell dry weight using a predetermined correlation between OD_{590} (Uvikon 930 spectrophotometer) and cell dry weight. Fermentation products were quantified by HPLC. Fermenter gas effluents were analysed by gas chromatography. All the operating conditions have been described previously (Barbirato et al., 1995).

**Preparation of cells and cell-free extracts.** Cells (25–30 mg dry wt) were harvested from steady-state chemostat cultures, transferred to a nitrogen-purged tube and centrifuged immediately for 8 min at 8000 g and 4 °C (J2-MC, Beckmann). The supernatant was discarded, and the cell pellet was stored under a nitrogen atmosphere at −80 °C until the preparation of cell-free extracts.

Cell-free extract preparation conditions depended on the enzyme activities. For alcohol dehydrogenase, aldehyde dehydrogenase, phosphotransacetylase, formate dehydrogenase and pyruvate formate-lyase, all manipulations were performed under anaerobic conditions. The harvested cells were washed with 5 ml 100 mM KPB (pH 7.5). After centrifugation for 12 min at 12000 g and 4 °C, the washed pellet was resuspended in 3 ml of the same buffer. Cells were then disrupted at 4 °C with a mechanical cell breaker with 3 g glass beads (0·1 μm) for 8 cycles of 1 min with 4 min cooling intervals. Using these conditions, protein extraction was as efficient as using the ultrasonic disintegrator without affecting enzyme activities. Cell debris and glass beads were removed by centrifugation at 15000 g for 15 min.

For the activities of 1,3-propanediol dehydrogenase, pyruvate dehydrogenase, ferricyanide-NADH oxidoreductase and pyruvate kinase, the same operating conditions were used with 100 mM MOPS (pH 7.5) instead of KPB buffer.

Finally, for glycerol dehydratase, an oxygen-free 100 mM glycine/KOH buffer (pH 8.1) containing 250 mM KCl and 1% (w/v) glycerol was used for washing and disrupting steps. Cells were disrupted with the mechanical cell breaker because this method allowed a higher recovery of this enzyme activity in comparison with the ultrasonic disintegrator treatment. Anaerobic conditions were maintained using a nitrogen flux at each step of the cell-free extract preparation.

Cell-free extracts were stored at 4 °C until the assay procedure.

**Enzyme assays.** Enzyme activities were systematically determined in their physiological direction at 30 °C. All reagent solutions were prepared in deionized water and degassed if necessary. A Uvikon 930 spectrophotometer (Kontron) was used for the enzyme assays performed under aerobic conditions. A Lambda 3 spectrophotometer (Perkin Elmer) was employed for the assays carried out in the anaerobic workstation. One unit of enzyme activity is defined as the amount of enzyme that catalyses the conversion of 1 μmol substrate min⁻¹.

Glycerol dehydrogenase (EC 1.1.1.6) activity (Glyc DH) was measured by following the glycerol-dependent formation of FADH at 340 nm (Ruch et al., 1974). The assay mixture contained 100 mM potassium bicarbonate (pH 9.0), 2 mM FAD, 30 mM (NH_{4})_{2}SO_{4} and 200 mM glycerol (ε_{340} = 6.22 mM⁻¹ cm⁻¹).

Glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) (G3PDH) was measured by following the G3P-dependent formation of NADH. The assay system contained 50 mM potassium bicarbonate (pH 9.0), 0.5 mM NAD and 5 mM G3P.

Dihydroxyacetone (DHA) kinase (EC 2.7.1.29) activity was followed in a coupled system in which NADH-dependent reduction of the reaction product, dihydroxyacetone phosphate (DHAP), to G3P was measured in a modified assay based on that described by Johnson et al. (1984). The assay mixture contained 50 mM potassium bicarbonate (pH 9.0), 2.5 mM ATP, 0.4 mM NADH, 15 mM MgCl₂, 2 mM DTT, 18 U glycerophosphate dehydrogenase from rabbit muscle.
Glycerol catabolism by \textit{E. agglomerans}

and 10 mM DHA. To prevent any secondary reaction (with Glyc DH), 15 mM \(\alpha,\alpha'\)-dipyridyl was systematically added to the assay mixture (Lin & Magasanik, 1960).

Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) activity (GAP DH) was estimated by a procedure adopted from Lovitt et al. (1988). The assay system contained 100 mM Tricine/NaOH buffer (pH 8.1), 10 mM KH\(_2\)AsO\(_4\), 1 mM NAD, 7.5 mM K\(_2\)HPO\(_4\), 2 mM DTT, 4 U aldolase from baker’s yeast and 4 mM fructose-1,6-biphosphate (FBP).

Pyruvate kinase (EC 2.7.1.40) activity was determined by following the NADH-dependent reduction of the reaction product (pyruvate) to lactate at 340 nm (Hess & Wicker, 1974). The reaction mixture consisted of 100 mM Tricine/NaOH buffer (pH 7.6), 2 mM ADP, 1 mM NAD, 7.5 mM K\(_2\)HPO\(_4\), 2 mM DTT and 4 U aldolase from rabbit muscle and 0.5 mM fructose-1,6-biphosphate (FBP).

Pyruvate dehydrogenase complex (EC 1.2.2.2) activity (PDH) was measured by following, at 430 nm, the NADH-dependent reduction of pyruvate to acetyl-CoA by the reaction product, acetyl-CoA, in the presence of 20 mM pyruvate and 0.5 mM NADH. Activity was calculated by measuring the reduction of NADH to its half-life in the presence of 0.5 mM ATP and 0.4 mM NADH. For the ADP determination, 0.4 mM ADP was added to the assay mixture.

NAD, 2 mM DTT, 0.1 mM CoASH, 14 U malic dehydrogenase from bovine heart, 10 U citrate synthase from porcine heart, 20 mM pyruvate and 6 mM malate.

Formate dehydrogenase activity (EC 1.2.1.2) was assayed in a reaction mixture, adopted from Snoep et al. (1990), containing 100 mM KPB, 1 mM NAD and 100 mM formate.

Lactate dehydrogenase activity (LDH) was measured by following the NADH-dependent reduction of pyruvate into lactate at 340 nm (Abbe et al., 1982). The assay mixture contained 20 mM KPB (pH 7.4), 0.4 mM NADH, 1 mM FBP and 20 mM pyruvate.

Phosphotransacetylase activity (EC 2.3.1.8) was determined by following, at 405 nm, the reaction between the coenzyme A liberated and 5,5’-dithiobis(2-nitrobenzoic acid) (DTNB) (Andersch et al., 1983). The reaction system contained 100 mM KPB (pH 7.4), 0.2 mM DTNB and 0.3 mM acetyl-CoA (\( \epsilon_{380} = 13.6 \text{mM}^{-1} \text{cm}^{-1} \)).

Acetate kinase (EC 2.7.2.1) activity was measured according to the assay adopted from Lamed & Zeikus (1980). The reaction mixture contained 80 mM Tris/HCl buffer (pH 7.2), 2 mM ATP, 1 mM NADP, 1 mM DTT, 15 mM MgCl\(_2\), 20 mM glucose, 2 U hexokinase from baker’s yeast, 2 U glucose-6-phosphate dehydrogenase from baker’s yeast and 10 mM acetylphosphate.

Aldehyde dehydrogenase (EC 1.2.1.10) was assayed by following the NADH-dependent reduction of acetyl-CoA (Dürre et al., 1987). The assay system consisted of 100 mM potassium bicarbonate (pH 9.0), 0.2 mM NADH, 2 mM DTT, 40 mM semicarbazide and 0.6 mM acetyl-CoA.

Alcohol dehydrogenase (EC 1.1.1.1) activity (ADH) was determined by following the NADH-dependent reduction of acetaldehyde at 340 nm. The assay mixture contained 100 mM KPB (pH 7.4), 0.2 mM NADH, 2 mM DTT and 40 mM acetaldehyde (Lamed & Zeikus, 1980).

Protein concentration was determined by use of the Coomassie Brilliant Blue G250 protein assay reagent supplied commercially by Bio-Rad with bovine serum albumin as standard.

Nucleotide extraction. NADH, NAD, ATP and ADP levels were measured after extraction of a culture broth sample as described by Vasconcelos et al. (1994). Samples collected were immediately transferred (in less than 5 s) into the extraction solution (NaOH or HCl). NADH was extracted at pH 12.3 with 10 M KOH. After a 10 min incubation at 30 °C, the alkaline solution was centrifuged for 8 min at 5000 g and 4 °C and the supernatant was collected. NAD, ATP and ADP were extracted at pH 1 with 6 M HCl by incubation for 10 min at 50 °C. After centrifugation for 8 min at 5000 g and 4 °C, a third of the supernatant was collected and stored for ATP determination. The second third was progressively neutralized with 2 M NaOH for NAD assay. For the ADP determination, ADP was converted to ATP by ATP by creatine phosphokinase in a reaction mixture containing the last third of the supernatant, 50 mM glycine buffer (pH 9.0), 0.4 mM MgSO\(_4\) and 7 U creatine phosphokinase from rabbit muscle maintained for 20 min at 30 °C. The reaction was stopped by addition of HCl (pH 2.0) and the mixture centrifuged. Samples were stored at −80 °C until the assay.

Nucleotide pool assays. Nucleotide pools were measured by use of a Hitachi fluorometer (model F-2000) according to procedures adopted from Le Bloas (1992). The wavelength of the fluorescence excitation and emission were, respectively,
340 and 460 nm. Nucleotide concentrations were deduced from a calibration curve of pure commercial NADH in a concentration range 0.1–7 μM. Dilutions were performed in 80 mM triethanolamine buffer (pH 7.6), 0.8 mM EDTA and 3 mM MgSO₄.

NADH concentration was determined by measuring the fluorescence decrease linked to the NADH-dependent conversion of pyruvate into lactate. The reaction mixture contained 100 mM triethanolamine (pH 7.6), 5 mM NADH, 0.8 mM EDTA, 4 mM pyruvate and 25 U LDH from rabbit muscle.

NAD pools were estimated by quantifying the increase in fluorescence following the oxidation of ethanol. The assay system contained 150 mM pyrophosphate buffer (pH 8.8), 0.8 g semicarbazide l⁻¹, 10 mM ethanol and 27 U ADH from baker's yeast.

ATP concentration was determined by a coupled system in which decrease in NADH was followed. The assay mixture contained 100 mM triethanolamine (pH 7.6), 5 μM NADH, 3 mM MgSO₄, 0.8 mM EDTA, 2 mM 3-phosphoglycerate, 9 U G3P DH from rabbit muscle and 25 U 3-phosphoglyceric phosphokinase from baker's yeast.

Intermediate metabolite assays. Triose phosphates, GAP and dihydroxyacetone phosphate (DHAP), and FBP were extracted at acid pH as described for NAD and stored at -80 °C until assay. Assays were performed with an SLM-Amino photon counting spectrofluorimeter (model 8000 C). Excitation and emission wavelengths were as described for the nucleotide assays. A calibration curve was created with pure commercial NADH.

The reaction mixture contained 50 mM MES (pH 6.5), 50 mM KCl, 5 mM MgCl₂, 0.05 mM Na₂CO₃ and 12.5 μM NADH and extract. DHAP concentration was deduced from the variation of NADH emission after addition of 4.2 U G3P DH to the assay mixture; the concentration of GAP was determined after addition of 100 U triose phosphate isomerase and FBP content was deduced from the variation of the NADH emission after addition of 2.5 U aldolase.

Transmembrane pH determination. The ApH was assayed by measuring the accumulation of [¹⁴C]benzoate by the oil centrifugation technique (Loubiere et al., 1992). After concentration of the fermentation sample by centrifugation (8000 g for 8 min) and suspension of the pellet in 0.5 ml supernatant, the cell suspension was incubated for 10 min at 30 °C with 3.3 μM [¹⁴C]benzoate (14.1 x 10⁶ Bq mmol⁻¹) and 12.5 μM NaOH. Supernatant fractions were collected and transferred into vials containing 10 ml of Ready Protein scintillation cocktail (Beckman). Radioactivity content was measured using a Packard liquid scintillation analyser. The remaining supernatant and the oil fraction were removed, and the wall of the centrifuge tube was carefully wiped clean. Five-hundred micro litres of 0.5 M NaOH was added to the cell pellet. After homogenization, the suspension was incubated for lysis at room temperature for 30 min and transferred into counting vials containing 10 ml scintillation cocktail. The intracellular benzoate concentration was calculated together with the internal volume.

For the measurement of intracellular volume, the same amount of cell suspension was used. Incubation of the cell suspension was performed with 0.74 x 10⁶ Bq ³H₂O (0.37 x 10⁶ Bq ml⁻¹) and 13.7 x 10⁶ Bq ¹⁴C-PEG 4000 (5.92 x 10⁸ Bq g⁻¹). Conditions were the same as described above. Intracellular volume, deduced from the differential partitioning of ³H₂O and ¹⁴C-PEG, allowed the calculation of the intracellular benzoate concentration. Intracellular pH was deduced from the internal and external benzoate concentrations as described by Padan et al. (1981).

Calculations. For the glucose and glycerol-fed cultures, the ATP yield is defined as \( Y_{ATP} = D \times 1000/[2 \times (q_{ATP} + q_{Lact} + q_{Acet} + q_{Form} + q_{Succ} + q_{But})] \), where \( q_{ATP} \), \( q_{Lact} \), \( q_{Acet} \), and \( q_{Succ} \) are the specific rates (expressed in mmol g⁻¹ h⁻¹) of production of acetate, ethanol, lactate and succinate, respectively. \( D \) is the dilution rate (h⁻¹). \( Y_{ATP} \) is expressed as g cell per mol ATP produced.

For the glycerol-fed culture, the specific rate of production of NAD is \( q_{NAD} = q_{PPD} + q_{Lact} + 2q_{Acet} + 2q_{Form} \), where \( q_{PPD} \) is the specific rate of production of PPD.

For PDH activity, the specific rate of formation of NADH is \( q_{NADH} = 3q_{Acet} + 3q_{But} - q_{Form} + 2q_{Lact} + 2q_{Succ} + 8.035 \mu \) where \( q_{Form} \) is the specific rate of formation of formate, 8.035 is the amount, expressed in mmol (g cell⁻¹), of the NADH requirement for the biomass formation with glycerol as substrate (Ingraham et al., 1983).

For the glucose-fed culture, the specific rate of formation of NAD is the same as described above. The specific rate of formation of NADH is \( q_{NADH} = 2q_{Acet} + q_{But} - q_{Form} + q_{Lact} + q_{Succ} + 14.678 \mu \) where 14.678 is the amount, expressed in mmol (g cell⁻¹), of the NADH requirement for the biomass formation with glucose as substrate (Ingraham et al., 1983).

The redox recovery is defined as 100(\( q_{NAD} / q_{NADH} \)).

Chemicals. All chemicals, enzymes and co-enzymes were purchased from Sigma. The radiochemical compounds, ³H₂O and ¹⁴C-PEG were purchased from Amersham, and ¹⁴C-benzoate from ICN Pharmaceuticals. 3-HPA was synthesized from acrolein by the method of Hall & Stern (1950).

RESULTS

Comparison of the glycerol- and glucose-fed continuous cultures

(1) Fermentation profile. \( E. \) agglomerans was grown anaerobically at pH 7 in chemostat culture at a dilution rate of 0.05 h⁻¹ under glycerol or glucose limitation. Fermentation profiles, shown in Table 1, showed that acetic acid, ethanol and formic acid were the main products of the glucose fermentation. Lactic and succinic acids were only produced as by-products of the fermentation. Very low amounts of PPD and 2,3-butanediol were measured. In contrast, with glycerol as carbon source, PPD was the major fermentation product. Acetic acid, ethanol and formic acid were the main by-products, while lactic and succinic acids were produced in small quantities. No significant microbial energetic changes were observed when using these two different substrates, the ATP yields being almost similar. Biomass concentration was higher with glucose than
Table 1. Fermentation product profiles of E. agglomerans grown anaerobically under glucose- and glycerol-limited continuous cultures

Data are given with a 3% precision. Carbon recovery is defined as the amount of carbon that is retrieved in biomass and analysed products. Redox recovery is defined in Methods.

<table>
<thead>
<tr>
<th>Substrate</th>
<th>D (h⁻¹):</th>
<th>0.05</th>
<th>0.15</th>
<th>0.25</th>
<th>0.31</th>
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<tbody>
<tr>
<td></td>
<td>Glucose</td>
<td>Glycerol</td>
<td>Glycerol</td>
<td>Glycerol</td>
<td></td>
</tr>
<tr>
<td>Residual conc (g l⁻¹)</td>
<td>&lt; 0.1</td>
<td>&lt; 0.1</td>
<td>0.2</td>
<td>1.0</td>
<td>1.2</td>
</tr>
<tr>
<td>Biomass (g l⁻¹)</td>
<td>1.6</td>
<td>1.05</td>
<td>1.06</td>
<td>0.97</td>
<td>0.82</td>
</tr>
<tr>
<td>Yₐₕₚ (g mol⁻¹)</td>
<td>6.44</td>
<td>6.89</td>
<td>7.83</td>
<td>7.92</td>
<td>7.02</td>
</tr>
<tr>
<td>Eff (mol mol⁻¹)</td>
<td>2.3</td>
<td>0.71</td>
<td>0.63</td>
<td>0.59</td>
<td>0.57</td>
</tr>
<tr>
<td>Product yields (mol mol⁻¹)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1,3-Propanediol</td>
<td>&lt; 0.013</td>
<td>0.44</td>
<td>0.52</td>
<td>0.55</td>
<td>0.57</td>
</tr>
<tr>
<td>Acetate</td>
<td>0.70</td>
<td>0.21</td>
<td>0.20</td>
<td>0.20</td>
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</tr>
<tr>
<td>Ethanol</td>
<td>0.73</td>
<td>0.23</td>
<td>0.16</td>
<td>0.10</td>
<td>0.07</td>
</tr>
<tr>
<td>Formate</td>
<td>1.365</td>
<td>0.40</td>
<td>0.31</td>
<td>0.24</td>
<td>0.21</td>
</tr>
<tr>
<td>Lactate</td>
<td>0.066</td>
<td>0.020</td>
<td>0.055</td>
<td>0.080</td>
<td>0.090</td>
</tr>
<tr>
<td>Succinate</td>
<td>0.050</td>
<td>0.035</td>
<td>0.014</td>
<td>0.013</td>
<td>0.012</td>
</tr>
<tr>
<td>2,3-Butanediol</td>
<td>&lt; 0.013</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Carbon recovery (%)</td>
<td>89</td>
<td>100</td>
<td>100</td>
<td>99</td>
<td>98</td>
</tr>
<tr>
<td>Redox recovery (%)</td>
<td>95</td>
<td>94</td>
<td>98</td>
<td>97</td>
<td>98</td>
</tr>
</tbody>
</table>

with glycerol because of a greater efficiency of ATP generation per mol substrate. A good redox balance was obtained, with a reducing equivalent recovery of 94% on glycerol and 95% on glucose.

(ii) Enzymic study. Table 2 shows the enzyme profile of E. agglomerans grown in chemostat cultures. In contrast to the glucose-limited culture, glycerol leads to a 30–120-fold increase in the levels of Glyc DH, DHA kinase, Glyc DA and PPD DH. The expression of the structural genes of these enzymes, encoded by the dha regulon, is subject to catabolite repression or is induced by glycerol in Klebsiella pneumoniae (Lin, 1976). A similar regulation seemingly occurs in E. agglomerans. Moreover, activities of glycerol kinase and G3P DH were not detected indicating that this metabolic route is not present under anaerobic conditions. Glycolytic enzymes exhibited higher levels of activity on glucose in comparison with the glycerol-limited culture. This is particularly pronounced for GAP DH. PFL activity was lower in the glycerol-limited culture. This is particularly pronounced for GAP DH. PFL activity was lower in the glycerol-limited culture while PDH activity was detected in both cultures, which suggested that PFL is not the only enzyme generating acetyl-CoA from pyruvate. Formate dehydrogenase activity, belonging to the formate hydrogen-lyase complex, was not detected, which is in accordance with the findings of De Vos et al. (1983) who reported the inability of E. agglomerans to decompose formate into CO₂ and H₂, and those of Ewing & Fife (1972) who described an extremely low gas production by this strain. Acetic-acid-producing enzymes were threefold higher on glucose than on glycerol. The ethanol production pathway exhibited a high level of aldehyde dehydrogenase activity on glucose while a lower ADH activity was observed on glucose, which shows that the most reduced substrate gave highest ADH activity as described by McPhedran et al. (1961).

(iii) Intracellular nucleotide and metabolite concentrations and pH. The NAD:NADH ratio was slightly lower on glycerol (2.8) than on glucose (3.1) (Table 2). The ATP level was similar for the two cultures, while the ADP level was higher on glucose. DHAP and FBP concentrations were higher on the glycerol- than on the glucose-fed culture although the carbon flow at that level was lower. GAP concentration, in equilibrium with DHAP, remained low in both cultures. Transmembrane pH of Clostridium acetobutylicum was shown to be inverted when glycerol was co-added to a glucose-limited chemostat culture (Gibral et al., 1994). To investigate whether the same occurred in E. agglomerans, the ΔpH was measured on glucose- and glycerol-fed cultures. An almost similar positive transmembrane pH was found in both conditions despite the different redox states of the substrates.

Effect of the dilution rate on the glycerol-fed culture

(i) Carbon flow distribution. As depicted in Table 1, increasing dilution rate resulted first in an incomplete substrate exhaustion particularly at D = 0.25 h⁻¹ and 0.31 h⁻¹. For such growth rates, biomass concentration decreased concomitantly with the ATP yield and the energetic efficiency. In terms of carbon flow distribution, we paid attention to three branching points. When growth rate was increased, the glycerol entering the cell was preferentially directed towards the PPD formation.
Table 2. In vitro enzyme levels of *E. agglomerans* grown in continuous cultures fed with 20 g l⁻¹ glucose or glycerol

Activities are expressed in μmol mg⁻¹ min⁻¹. Nucleotide and intermediate metabolite concentrations are expressed in μmol (g dry cell wt)⁻¹. Data in parentheses are SD deduced from eight determinations. ND, Not determined.

<table>
<thead>
<tr>
<th>D (h⁻¹):</th>
<th>0.05</th>
<th>0.31</th>
</tr>
</thead>
<tbody>
<tr>
<td>Substrate:</td>
<td>Glucose</td>
<td>Glycerol</td>
</tr>
<tr>
<td><strong>Glycerol catabolism enzymes</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Glycerol dehydrogenase</td>
<td>0.16 (0.028)</td>
<td>13.03 (2.88)</td>
</tr>
<tr>
<td>Dihydroxyacetone kinase</td>
<td>0.305 (0.021)</td>
<td>9.34 (1.23)</td>
</tr>
<tr>
<td>Glycerol dehydratase</td>
<td>0.0045 (0.0018)</td>
<td>0.18 (0.04)</td>
</tr>
<tr>
<td>1,3-Propanediol dehydrogenase</td>
<td>0.078 (0.021)</td>
<td>9.16 (2.2)</td>
</tr>
<tr>
<td><strong>Central axis enzymes</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Glyceraldheyde-3-phosphate dehydrogenase</td>
<td>5.51 (0.37)</td>
<td>2.31 (0.1)</td>
</tr>
<tr>
<td>Pyruvate kinase</td>
<td>1.35 (0.09)</td>
<td>0.80 (0.08)</td>
</tr>
<tr>
<td>Pyruvate formate lyase</td>
<td>9.35 (1.50)</td>
<td>3.42 (0.31)</td>
</tr>
<tr>
<td>Pyruvate dehydrogenase</td>
<td>0.074 (0.005)</td>
<td>0.16 (0.03)</td>
</tr>
<tr>
<td><strong>Acid producing enzymes</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Phosphotransacetylase</td>
<td>19.11 (2.67)</td>
<td>5.31 (0.8)</td>
</tr>
<tr>
<td>Acetate kinase</td>
<td>51.3 (4.7)</td>
<td>17.06 (3.01)</td>
</tr>
<tr>
<td>Lactate dehydrogenase</td>
<td>1.26 (0.09)</td>
<td>1.33 (0.20)</td>
</tr>
<tr>
<td><strong>Ethanol producing enzymes</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Aldehyde dehydrogenase</td>
<td>0.030 (0.008)</td>
<td>0.0035 (0.0012)</td>
</tr>
<tr>
<td>Alcohol dehydrogenase</td>
<td>0.205 (0.014)</td>
<td>0.94 (0.17)</td>
</tr>
<tr>
<td><strong>Nucleotide levels</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NADH</td>
<td>1.39 (0.28)</td>
<td>2.38 (0.40)</td>
</tr>
<tr>
<td>NAD⁺</td>
<td>4.28 (0.39)</td>
<td>6.78 (0.53)</td>
</tr>
<tr>
<td>ATP</td>
<td>4.43 (0.59)</td>
<td>4.49 (0.39)</td>
</tr>
<tr>
<td>ADP</td>
<td>2.03 (0.42)</td>
<td>0.70 (0.28)</td>
</tr>
<tr>
<td><strong>Intermediate metabolites</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Dihydroxyacetone phosphate</td>
<td>6.93 (0.83)</td>
<td>9.64 (0.81)</td>
</tr>
<tr>
<td>Glyceraldehyde 3-phosphate</td>
<td>0.55 (0.34)</td>
<td>0.95 (0.39)</td>
</tr>
<tr>
<td>Fructose 1,6-bisphosphate</td>
<td>1.13 (0.49)</td>
<td>6.91 (0.62)</td>
</tr>
<tr>
<td><strong>Transmembrane pH</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ΔpH</td>
<td>0.46 (0.08)</td>
<td>0.37 (0.07)</td>
</tr>
</tbody>
</table>

(ii) Enzyme activities. Evolution of glycerol catabolizing enzyme activities were different in the reductive or the oxidative branch (Table 2). Activities of Glyc DH and DHA kinase decreased 2.5-fold when *D* increased from 0.05 h⁻¹ to 0.31 h⁻¹. By contrast, activity of Glyc DA showed a 34-fold increase while the level of PPD DH remained stable. Such an increase of Glyc DA activity as a result of increasing the growth rate has been reported previously in *C. freundii* grown in glycerol-limited continuous culture: it increased from 0.05 U mg⁻¹ at *D* = 0.08 h⁻¹ to 13 U mg⁻¹ at *D* = 0.36 h⁻¹ (Boenigk et al., 1993). The preferential distribution of glycerol towards the PPD pathway at high dilution rates, reported above, was thus correlated with the increase of the relative ratio of Glyc DA to Glyc DH. Central axis enzymes presented a uniform 1.4-fold increase except for PDH activity which decreased slightly. Enzymes associated with acetic acid formation showed a two-fold increase at high dilution rate. In contrast, LDH presented a twofold decrease of activity between...
**Glycerol catabolism by E. agglomerans**

\[ \text{Glycerol} \rightarrow \text{PPD} \rightarrow \text{DHAP} \rightarrow \text{FBP} \rightarrow \text{GAP} \rightarrow \text{PEP} \rightarrow \text{Succinate} \rightarrow \text{Lactate} \rightarrow \text{Formate} \rightarrow \text{Acetate} \rightarrow \text{Acetyl-CoA} \rightarrow \text{Ethanol} \]

**Fig. 1.** Quantitative flow schemes at \( D = 0.05 \text{ h}^{-1} \) (a), \( 0.15 \text{ h}^{-1} \) (b) and \( 0.31 \text{ h}^{-1} \) (c). Values are expressed in mmol g\(^{-1}\) h\(^{-1}\).

Abbreviation: PEP, phosphoenolpyruvate.

\( D = 0.05 \text{ h}^{-1} \) and \( 0.31 \text{ h}^{-1} \), although *in vivo* activity was significantly enhanced. Levels of aldehyde dehydrogenase and ADH showed a 1.6- and 1.8-fold drop in activity, respectively, at high growth rate.

**(iii) Intracellular nucleotide and metabolite concentrations.** A slight increase in the NAD pool was observed, while the NADH pool was not affected (Table 2). Consequently, the relative ratio NAD: NADH increased from 2.85 at \( D = 0.05 \text{ h}^{-1} \) to 3.45 at \( D = 0.31 \text{ h}^{-1} \). ATP and ADP pools presented respectively a 1.4- and 3.1-fold increase resulting in a 2.2-fold decrease of the ATP: ADP ratio. Triose-phosphates and FBP concentrations increased significantly at the higher dilution rate, while the GAP concentration remained low.

**DISCUSSION**

In *K. pneumoniae* anaerobic pathways of glycerol dissimilation involve the utilization of PFL to catalyse the oxidation of pyruvate to acetyl-CoA (Streekstra *et al.*, 1987). When grown in batch culture under low initial glycerol content, and hence low glycerol uptake rate, *E. agglomerans* was thought to exclusively use PFL to funnel pyruvate to acetyl-CoA: a perfect relationship between the molar amount of formate and acetate plus ethanol was established (Barbirato *et al.*, 1995). Nevertheless, this correlation was not verified when batch cultures were performed with higher glycerol concentrations. In the chemostat culture, an unbalanced relationship was noticed between the molar amount of formate and acetate plus ethanol produced in addition to the lack of formate dehydrogenase activity, suggesting the utilization of a parallel pathway for the conversion of pyruvate to acetyl-CoA. PDH activity is commonly observed under aerobic conditions whereas PFL, which shows extremely high sensitivity to molecular oxygen (Abbe *et al.*, 1982), is expressed and is only active under strict anaerobiosis (Sawers & Böck, 1988). However, PDH was shown to be active under anaerobiosis in *Streptococcus mutants* (Carlsson *et al.*, 1985) and it was revealed that an important part of the pyruvate flow was shifted to PDH at high NAD: NADH ratios in *Enterococcus faecalis* (Snoep *et al.*, 1990). *In vitro* PDH activity was detected in *E. agglomerans* in both glucose- and glycerol-fed cultures. Moreover, the redox balance was better equilibrated by suppressing PDH activity, and the intracellular NAD: NADH ratio was also favourable to the *in vivo* activity of the enzyme. These results argue for the presence of PDH activity in *E. agglomerans*: between 9% and 22% of the pyruvate flow to acetyl-CoA is shifted to PDH. CO\(_2\) production from the decarboxylation of pyruvate by PDH was less than expected and its utilization by carboxylating steps in the metabolism is suspected, as well as its absorption by the feed medium with the formation of carbonate (Zeng, 1995). PDH activity thus occurred in *E. agglomerans*, as depicted in Fig. 2.

At the pyruvate branching point, distribution of the carbon flow through LDH, PFL and PDH activities occurred. The proportion of the pyruvate flow shifted to PFL represented 87% at \( D = 0.05 \text{ h}^{-1} \) and only 58% at \( D = 0.31 \text{ h}^{-1} \). Such behaviour probably results from a
carbon flow conversion limitation at the level of PFL. This phenomenon is particularly pronounced at high dilution rate when glycerol is provided in excess. PFL activity is known to be activated by pyruvate (Knappe et al., 1982). In comparison to levels reached in the glucose-fed culture, intracellular concentrations of triose-phosphates and FBP were higher in the culture supplied with glycerol. This is surely linked to the lower GAP DH activity measured in the latter culture, suggesting that this metabolic step is partially inhibition of PFL by intracellular triose phosphates, particularly DHAP. The enhanced in vitro PDH activity thus may allow the decarboxylation of the excess pyruvate (Hansen & Henning, 1966) and hence the prevention of any deleterious effect by that compound (Collins, 1972), and also the increase in the global rate of NADH generation, limited at the level of the GAP DH, thus contributing to the redox balance. The increase of in vivo LDH activity may result from an intracellular accumulation of pyruvate (Tarmy & Kaplan, 1968).

High rates of glycerol dissimilation thus involve both a preferential distribution towards the PPD metabolic pathway and a limitation by GAP DH. As glycerol is the branching point of the reductive and oxidative pathways, the carbon flux through the reductive branch is not exclusively controlled by the glycolytic flux. The PPD pathway acts as a pacemaker of the oxidative metabolism by increasing the regeneration, and hence the availability, of the NAD necessary at the glycolytic level to minimize the limiting step. This explains why a high NAD:NADH ratio is observed despite the fact that the organism is grown on a reduced substrate. Despite this ‘overflow metabolism’ (Streekstra et al., 1987), an accumulation of triose phosphates occurred, indirectly causing an enhanced pyruvate flow distribution toward PDH and LDH. Parameters such as pyruvate and triose phosphate intracellular concentrations and the NAD:NADH ratio could play a key role in this proposed regulation. Obviously, this hypothetical regulation scheme at the level of the pyruvate branching point needs to be confirmed.

ACKNOWLEDGEMENTS

This research was supported by the Agence de l'Environnement et de la Maîtrise de l'Energie (ADEME), the Organisation Nationale Interprofessionnelle des Oléagineux (ONIDOL) and INRA. The authors thank Christel Garrigues and Muriel Coaig (INSA, Toulouse, France) for their help in nucleotide concentration determinations and John Davison (INRA Narbonne, France) for correcting the English version of the manuscript.

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Received 9 September 1996; revised 26 February 1997; accepted 1 March 1997.