Dissecting the roles of Escherichia coli hydrogenases in biohydrogen production
Redwood, Mark; Mikheenko, Iryna; Sargent, F; Macaskie, Lynne

DOI: 10.1111/j.1574-6968.2007.00966.x

Citation for published version (Harvard):

Link to publication on Research at Birmingham portal

General rights
Unless a licence is specified above, all rights (including copyright and moral rights) in this document are retained by the authors and/or the copyright holders. The express permission of the copyright holder must be obtained for any use of this material other than for purposes permitted by law.

• Users may freely distribute the URL that is used to identify this publication.
• Users may download and/or print one copy of the publication from the University of Birmingham research portal for the purpose of private study or non-commercial research.
• Users may use extracts from the document in line with the concept of 'fair dealing' under the Copyright, Designs and Patents Act 1988 (?)
• Users may not further distribute the material nor use it for the purposes of commercial gain.

Where a licence is displayed above, please note the terms and conditions of the licence govern your use of this document.

When citing, please reference the published version.

Take down policy
While the University of Birmingham exercises care and attention in making items available there are rare occasions when an item has been uploaded in error or has been deemed to be commercially or otherwise sensitive.

If you believe that this is the case for this document, please contact UBIRA@lists.bham.ac.uk providing details and we will remove access to the work immediately and investigate.

Download date: 02. Aug. 2019
Dissecting the roles of *E. coli* hydrogenases in biohydrogen production

Mark D. Redwood\(^1\), Iryna P. Mikheenko\(^1\), Frank Sargent\(^2\), Lynne E. Macaskie\(^1\)*

\(^1\) Unit of Functional Bionanomaterials, School of Biosciences, University of Birmingham, Edgbaston, Birmingham, B15 2TT UK.

\(^2\) Division of Molecular & Environmental Microbiology, College of Life Sciences, University of Dundee, Dundee DD1 5EH, Scotland.

* Corresponding author: l.e.macaskie@bham.ac.uk Tel: +44 1214145889 Fax: +44 1214145925

Abstract

*Escherichia coli* can perform at least two modes of anaerobic hydrogen metabolism and expresses at least two types of hydrogenase activity. Respiratory hydrogen oxidation is catalysed by two ‘uptake’ hydrogenase isoenzymes, hydrogenases -1 and -2, and fermentative hydrogen production is catalysed by hydrogenase-3. Harnessing and enhancing the metabolic capability of *Escherichia coli* to perform anaerobic mixed-acid fermentation is therefore an attractive approach for bio-hydrogen production from sugars. In this work, the effects of genetic modification of the genes encoding the uptake hydrogenases, as well as the importance of pre-culture conditions, on hydrogen production and fermentation balance were examined. In suspensions of resting cells pre-grown aerobically with formate, deletions in hydrogenase-3 abolished hydrogen production, whereas the deletion of both uptake hydrogenases improved hydrogen production by 37 % over the parent strain. Under fermentative conditions, respiratory H\(_2\) uptake activity was absent in strains lacking hydrogenase-2. The effect of a deletion in *hycA* on H\(_2\) production was found to be dependent upon environmental conditions, but H\(_2\) uptake was not significantly affected by this mutation.

1. Introduction

Biological approaches to energy production are growing in importance as fossil-fuel resources verge on the limits of economical extraction (Holmes & Jones, 2003) and the environmental cost of carbon emissions gain recognition in financial terms (Hopkin, 2004; Klepper & Peterson, 2006).

*Escherichia coli* is attractive for biotechnological applications such as biohydrogen production. In contrast to other H\(_2\)-producing micro-organisms, such as the clostridia, *E. coli* is fast-growing, non-sporulating, and well-characterised in physiological and biochemical terms. Furthermore, metabolic engineering using ‘crippled’ strains such as K12 (and its derivatives) provides information relevant to the future modification of a wild-type strain, while also mitigating against accidental release. When turnover rate is considered, the H\(_2\)-producing Hyd-3 of *E. coli* (a NiFe hydrogenase) is significantly slower than Fe hydrogenases (e.g. of clostridia) (Hallenbeck & Benemann, 2002), although the superiority of different fermentative bacteria is controversial and a detailed comparison is beyond the scope of this paper.

Formate is the sole precursor of H\(_2\) in *E. coli* (Ordal & Halvorson, 1939), being cleaved to H\(_2\) and CO\(_2\) by the formate hydrogenlyase complex (FHL) (Stephenson & Stickland, 1932; Sawers, 2005). Formate arises from the mixed acid fermentation of sugars (Fig. 1), with a maximum yield of 2 mol H\(_2\)/mol glucose (Clark, 1989). In practice, yields are typically ~1 mol H\(_2\)/mol glucose as several factors may affect the rate and yield of H\(_2\) production (Stephenson & Stickland, 1932; Bisaillon et al., 2006). In this study, the role of hydrogenases in the formation and uptake of H\(_2\) during fermentation of glucose was addressed, with the aim to maximise the rate and yield of H\(_2\) produced.

*E. coli* K-12 has the potential to express four hydrogenases (Hyd-l-4). With the exception of Hyd-4, which has never been biochemically characterised, the *E. coli* hydrogenases can operate reversibly in *vitro* but possess physiological directionality (Sawers, 1994). Hyd-3 is encoded by the *hyc* operon and forms, with a formate dehydrogenase (FDH\(_3\)) and numerous other electron transport proteins, the FHL complex, which is responsible for H\(_2\) production from formate (Rossman et al., 1991). The putative FHL-2 complex
(homologous to FHL) is hypothesised to carry out energy conservation by formate-dependent proton translocation and contains Hyd-4 (hyf operon) (Andrews et al., 1997; Skibinski et al., 2002). Hyd-2 (encoded by the hyb operon) functions in anaerobic respiration as an uptake hydrogenase (Ballantine & Boxer, 1985; Sawers et al., 1985). Hyd-1 (encoded by the hya operon) is also an uptake hydrogenase, and has been suggested to be expressed under fermentative conditions to recycle the H₂ produced from formate (Sawers et al., 1985; Sawers & Boxer, 1986). The physiological role of Hyd-1 is not yet clear and it has also been suggested to function in energy conservation under acid stress (King & Przybyla, 1999).

Attempts to negate residual hydrogen uptake activity under fermentative conditions, which detracts from the net H₂ production, have been successful in a range of H₂ producing organisms including anoxygenic photosynthetic bacteria (Willison et al., 1984; Toussaint et al., 1991; Jahn et al., 1994; Franchi et al., 2004; Kim et al., 2006), cyanobacteria (Happe et al., 2000; Masukawa et al., 2002; Yoshino et al., 2006), and recently in E. coli (Bisaillon et al., 2006; Penfold et al., 2006). This approach, which relies on physiological uni-directionality of the isoenzymes, would not be appropriate for other fermentative H₂-producers (e.g. clostridia and thermophilic archaea) in which H₂ uptake and production are performed by the same (reversible) hydrogenases (Hallenbeck, 2005).

Genetic techniques have been employed previously to improve H₂ production by E. coli. In particular, strain HD701 (devoid of HycA, the hyc operon repressor) was capable of upregulating H₂ production more rapidly than the parent strain (MC4100) upon transfer to H₂ producing conditions (Sauter et al., 1992; Sode et al., 2001; Penfold et al., 2003; Yoshida et al., 2005). Inactivation of the tat (twin arginine transport) export system effected a similar improvement in overall H₂ production, comparable to the HycA deficiency (Penfold et al., 2006). However, tat mutations are pleiotropic, causing defects in outer membrane biosynthesis and cell division, in addition to preventing the correct assembly of uptake hydrogenases and respiratory formate dehydrogenases (Sargent et al., 1998; Stanley et al., 2001). Therefore, the tat-deficient strains were assumed to exhibit the effects of reduced activity of the uptake hydrogenases (Hyd-1 and Hyd-2) although this was not proven. It was also assumed by Penfold et al. (2006) that H₂ uptake activity was not expressed by other isoenzymes. However, contrary to expectation, the superimposition of the tat deficiency phenotype onto the HycA deficiency phenotype did not result in any further increase in H₂ production, raising the possibility of a compensatory H₂ oxidation activity by Hyd-3 (Penfold et al., 2006).

In the current work, the fermentation balances of strains genetically deprived of specific hydrogenase activities were analysed. Evidence is provided that the respiratory hydrogenase-2 contributes to the vast majority of H₂ recycling activity during fermentative hydrogen production, which supports the suggestion that it is the loss of this activity, rather than other pleiotropic effects, that leads to an increased H₂ yield when the Tat system is inactivated.

2. Materials and Methods

2.1 Bacterial strains

Strain HD701 was provided by Professor A. Böck (Lehrstuhl für Mikrobiologie der Universität, Munich, Germany) and was derived from MC4100 (Sauter et al., 1992). All strains are listed in Table 1.

2.2 H₂ production experiments

E. coli stocks were maintained at −70 °C in 25 % glycerol (1 part overnight culture in nutrient broth, 1 part 50 % glycerol w/v) and revived on nutrient broth (Oxoid) at (37 °C, 8 h, 250 rpm) before plating on nutrient agar (Oxoid). Plates were stored at 4 °C for up to 1 week before use. For experiments, colonies were picked into 30 ml nutrient broth with added sodium formate (0.1 M) (6 hours, 37 °C, 250 rpm). Cells were harvested from late log phase cultures (4500 g, 10 min) consisting of 500 ml nutrient broth with added sodium formate (0.1 M) (0.001 % inoculum, 14-16 hours, 30 °C, 250 rpm). Cell pellets were washed twice in 100 ml phosphate buffered saline (PBS: 1.43 g Na₂HPO₄, 0.2 g KH₂PO₄, 0.8 g NaCl, 0.2g KCl per litre, pH 7.0) before resuspending in 10 ml PBS to produce a concentrate containing 30-40 mg dry weight/ml. Biomass concentration was estimated by reference to a previously determined conversion factor. An OD₆₀₀ of 1 corresponded to a concentration of 0.48-mg dry weight/ml.
The cell concentrate was made anaerobic by purging with argon (30 min) before 1-2 ml was transferred into ~120 ml anaerobic bottles containing 100 ml test medium (made anaerobic by 3 cycles of 30 min under vacuum and argon purging) to give an initial cell concentration of 0.5 mg dry weight/ml. OD600 was measured at the end of the experiment to estimate biomass growth. Test medium consisted of 0.1 M MES buffer (2-(N-Morpholino)ethanesulfonic acid), pH 6.80 supplemented with 6.96 g/l NaCl (final concentration), 0-100 µl 2 M NH4Cl and 0.3 ml trace elements solution given in (Hewitt et al., 2000). Unless otherwise stated the final concentration of NH4Cl was 1 mM.

Anaerobic bottles were connected to a gas collection apparatus (Macler et al., 1979) and allowed to equilibrate (30 °C, reciprocal shaking at 130 rpm, 5 min) before the fermentation was initiated by the addition of 1 ml degassed 2 M glucose (to 20 mM). The volume of H2 evolved was measured over a solution of 2 M NaOH containing universal indicator (Sigma, UK) for ~45 hours. A previous study confirmed that H2 and CO2 are the only gases evolved by E. coli (Penfold et al., 2003). The presence of H2 in the evolved gas was confirmed using a combustible gas meter (GMI, UK) and the removal of CO2 (to <0.5 % v/v) was confirmed using a ThermoQuest gas chromatograph (TraceGC2000) fitted with a Shincarbon ST column (100/120 mesh, length: 2 m, ID: 2 mm, Shimazu, Japan). The GC operating conditions were split 60:1, 40 °C + 15 °C/min for 10 min, and the injection volume was 1 ml.

2.3 Chemical analyses

Samples (2 ml) were filtered (0.2 µm supor membrane) and filtrates were stored at -20 °C before analysis. Organic acids were measured by anion HPLC using a Dionex 600-series system as described previously (Redwood & Macaskie, 2006). Glucose was assayed using the colorimetric dinitrosalicylic acid assay (Chaplin, 1986) and ethanol was determined colorimetrically by monitoring the enzymatic reduction of NAD (A340) using alcohol dehydrogenase (Sigma A-6338, assay concentration: 2.64 U/ml) after pre-removal of aldehyde by aldehyde dehydrogenase (Sigma A-7011, assay concentration: 16.18 U/l).

2.4 Analysis of fermentation balance

All products were measured as described above, with the exception of CO2 which was calculated (as described below). Unknown quantities of fermentation balance were estimated according to equations 1-4, substituting values for products formed (e.g. mol product/mol glucose) from Table 1. As described previously (Sode et al., 1999), equations 1-3 are derived from the metabolic pathway of mixed acid fermentation (Fig. 1).

\[
\text{H}_2 \text{uptake} = \text{acetate} + \text{ethanol} - \text{formate} - \text{H}_2 \text{formed} \quad (1)
\]

Succinate formation requires the incorporation of CO2 (Fig.1), which in a gas-scrubbed medium devoid of added carbonate would be derived from the decomposition of formate (HCOOH = CO2 + H2). Therefore, the net production of CO2 (CO2est) was estimated by subtracting the succinate formed from the theoretical formate decomposed (equation 2).

\[
\text{CO}_2 \text{est} = \text{acetate} + \text{ethanol} - \text{formate} - \text{succinate} \quad (2)
\]

The carbon balance (C. bal.) was obtained by summing the carbon fractions of the products of fermentation. The carbon allocation to biomass formation was determined from the observed increase in OD600 and conversion to dry weight using 53.1 % as the carbon fraction of E. coli biomass (Harris & Adams, 1979; Pramanik & Keasling, 1997). Therefore, a factor of 0.044 was applied for the conversion from g biomass/mol glucose to mol carbon/mol glucose (equation 3).

\[
\text{C. bal. ()} = \frac{3\text{lact.} + 2\text{acet.} + 2\text{ethanol} + 4\text{succ.} + \text{form.} + \text{CO}_2 + 0.044\text{biomass}}{6} \times 100 \quad (3)
\]
All experiments were replicated on at least 3 occasions (as stated) using independent cultures. Results are expressed as mean ± standard error of the mean.

3. Results

3.1 Effects of pre-growth conditions on \( \text{H}_2 \) production in *E. coli* MC4100 and HD701

For all tests on \( \text{H}_2 \) production, cultures were pre-grown before cells were harvested, washed and transferred to 100 ml reactors. The ability of resting cells to produce \( \text{H}_2 \) was independent of the availability of \( \text{NH}_4^+ \)-nitrogen (0-10 mM \( \text{NH}_4\text{Cl} \)) during the test reaction (1 mM was used subsequently), but it was dependent upon the presence or absence of oxygen and sodium formate during pre-growth. As expected, cells pre-grown anaerobically produced \( \text{H}_2 \), whereas aerobically pre-grown cells failed to produce \( \text{H}_2 \) even after prolonged incubation (24 h), attributable to the lack of expression of the genes encoding the FHL complex responsible for \( \text{H}_2 \) production (Gest, 1954; Sauter et al., 1992). Interestingly, the aerobic expression of the genes encoding FHL was induced by the addition of sodium formate (0.1 M) to the pre-growth medium. A significant difference was not observed (t-test, \( P > 0.05 \)) when the initial rate and total volume of \( \text{H}_2 \) production were compared, among cells pre-cultured with formate either anaerobically or aerobically. From a biotechnological point of view, therefore, this represents a significant advantage since the relative ease of biomass production and greater biomass yield/ml of aerobic pre-growth would certainly be more economically favourable for a scaled-up system. In previous studies \( \text{H}_2 \) was produced by aerobically grown formate-supplemented *Bact. coli* (Escherich) (Stephenson & Stickland, 1932) and significant *hyc* operon expression was measured during aerobic growth with sodium formate in *E. coli* MC4100 (Rossman et al., 1991). In the present study the addition of sodium formate during aerobic growth caused a 10 % reduction in biomass yield relative to growth in unsupplemented broth, but upon the establishment of fermentative conditions (after washing to remove formate), strain MC4100 produced \( \text{H}_2 \) immediately and with an equal initial rate, endpoint and yield to the anaerobically-grown controls (see above). Thus, the aerobic-formate condition represents the preferred method for the preparation of an *E. coli* culture having high \( \text{H}_2 \)-production activity.

3.2 Effects of Hyd-3 and HycA deletions on \( \text{H}_2 \) production and uptake

All strains expressing an active FHL complex ("Hyd-3") produced \( \text{H}_2 \) for approximately 45 h, during which at least 98 % of glucose (~2 mmol) was consumed and the pH decreased from 6.80 to 5.93 ± 0.06. The rates of \( \text{H}_2 \) production were identical in strains HD701 (HycA-), and MC4100 (parent) (Fig. 2A), confirming that pre-growth (of the parent strain) in the presence of formate overcame the requirement for use of an FHL up-regulated strain. This would also rule out a pleiotropic effect of the HycA deficiency in a possible co-upregulation of \( \text{H}_2 \) uptake, or, indeed any uptake hydrogenase activity of Hyd-3 (see below). Strains FTD147, FTD150 and HD705 (all devoid of Hyd-3), did not produce \( \text{H}_2 \) indicating that the remaining hydrogenases Hyd-1, Hyd-2 and Hyd-4 were not capable of \( \text{H}_2 \) production under these conditions. \( \text{H}_2 \) uptake by these strains was not investigated as it was shown previously that strain FTD89, which contains active Hyd-3 but no Hyd-1 or -2, and from which FTD147 and FTD150 were both derived, has no detectable in vivo fumarate-dependent \( \text{H}_2 \) uptake activity (Dubini et al., 2002). This activity would not be restored upon the addition of further genetic modifications to produce strains FTD147 and FTD150. Similarly, strain HD705 (having Hyd-1 and Hyd-2 but no Hyd-3) possesses in vivo fumarate-dependent \( \text{H}_2 \) uptake activity similar to the parent strain (Sargent et al., 1999).

3.3 Effects of Hyd-1 and Hyd-2 deletions on \( \text{H}_2 \) production and uptake

Strains FTD67 and FTD89 (which both lack Hyd-2) exhibited high rates of \( \text{H}_2 \) production, and were easily distinguishable from the parent strain from the outset, whereas a strain lacking Hyd-1 activity (FTD22) showed no significant change in \( \text{H}_2 \) production (Fig. 2B). The yields of \( \text{H}_2 \) from glucose (Table 1) mirrored this trend, both Hyd-2 deficient strains having significantly higher yields than the parent strain (\( P < 0.001 \)), whereas no significant difference was found between the Hyd-1 deficient strain and the parent strain (\( P = 0.15 \), or between the Hyd-2 deficient strain FTD67 and the -1 and -2 double deficient strain FTD89 (\( P = 0.35 \)).
The extent of H₂ recycling was calculated from the products formed (Table 1). For the parent strain (MC4100) hydrogen uptake activity resulted in a 31 % reduction in H₂ yield. Analysis of the activity of other, potentially competing, metabolic pathways shows very little variation in the proportions of lactate, succinate and (H₂formed + H₂ uptake), indicating that the increased H₂ yield resulted from the removal of H₂ uptake, rather than from secondary effects on the activity of competing pathways.

However, a secondary effect on the fermentation balance was observed. The ratio of acetate/ethanol was significantly higher in strains FTD67 and FTD89 (devoid of Hyd-2) than in the parent strain (t-test, P<5 %). This can be attributed to the involvement of H₂ uptake in redox balance, whereby the oxidation of H₂ would increase the required disposal of reductant by the normal mechanism: the reduction of acetyl-CoA to ethanol. The increased ratio of acetate/ethanol would hypothetically result in an increased yield of ATP and hence growth, although the observed increases in growth for strains FTD67 and FTD89 (compared to the parent strain) was not statistically significant (t-test, P>5 %).

4. Discussion

In this study, the HycA deficient strain (HD701) and the parent strain (MC4100) produced H₂ with equal rate and yield if formate was present in the pre-growth medium. This is interesting in light of previous observations that HycA deficient strains of *E. coli* showed increased FHL expression and increased rate of H₂ production in comparison to parent strains (Sauter et al., 1992; Sode et al., 2001; Penfold et al., 2003; Yoshida et al., 2005). The HycA repressor is thought to control the expression of the *hyc* operon (encoding FHL complex structural components) by competing with formate for binding sites on the FhlA activator (Skibinski et al., 2002). All data support the hypothesis that the absence of the HycA repressor results in a decreased threshold concentration of formate required to de-repress the expression of the FHL complex. The aerobic culture in a high sodium formate background (this study) is likely to have induced the expression to the maximum level, overcoming the effects of a deficiency in HycA, and permitting the rapid culture of cells possessing high H₂ production activity. Formate was shown previously to de-repress the *hyc* operon under aerobic conditions (Rossman et al., 1991). Although the use of sodium formate would represent an additional cost upon scale-up, the excess would contribute to H₂ production, and the quantity necessary to produce a pre-adapted culture (expressing FHL activity) may be significantly less than that used here (0.1 M), as a previous study used only 0.03 M (Rossman et al., 1991).

Increased H₂ production by *E. coli* in the absence of uptake hydrogenase activity has been observed by several authors (Sode et al., 1999; Bisaillon et al., 2006; Penfold et al., 2006) but a compensatory uptake function of the residual hydrogenases has not been previously excluded. In the light of the analysis of fermentation balance (Table 1), the improvement can be attributed predominantly to the inactivity of hydrogenase-2. The calculation of H₂ uptake was based on the imbalance between estimates of formate decomposed (ethanol + acetate - formate) and H₂formed (equation 1). As no oxidants were present, this imbalance cannot be attributed to the consumption of formate by respiratory formate dehydrogenases and the absence of H₂ uptake in the specific absence of Hyd-2 precludes any significant H₂ uptake activity by the remaining enzymes.

The H₂ yield reached only 52 % of the theoretical maximum (2 mol H₂/mol glucose). This was attributed to the formation of significant quantities of lactate and succinate, the quantities of which were not affected by deficiencies in Hyd-1 and Hyd-2. Therefore, the increased H₂ yield was due to decreased H₂ uptake and not to the decreased activity of lactate and succinate formation. The flow of carbon to these products, rather than through pyruvate formate-lyase (PFL) resulting in H₂ production, represented (on average) a loss of 37.9 % of potential H₂. Lactate and succinate formation can be controlled using strains defective in the fermentative lactate dehydrogenase and fumarate reductase, respectively (Mat-Jan et al., 1989; Sode et al., 1999; Sode et al., 2001), and lactate formation can also be decreased through the control of pH and substrate supply (M.D. Redwood and L.E. Macaskie, unpublished).

During anaerobic fermentation under conditions studied here, *E. coli* exhibits no significant hydrogenase uptake activity by any factors other than hydrogenase-2. The deletion of the genes encoding respiratory hydrogenase 1 had no significant effect on H₂ production, whereas the yield was improved by more than one third through the deletion of uptake hydrogenase-2. For the industrial application of this
work to bio-H₂ production the Hyd-1 and -2 deficient strain (FTD89) would be most advantageous. Further modifications to this strain to control lactate and succinate formation could result in yields close to 2 mol H₂/mol glucose.

6. Acknowledgements

This work was supported by the BBSRC (grant No. BB/C516128/1 and studentship 10703) and by a BBSRC/Royal Society Industry Fellowship to LEM in collaboration with C-Tech Innovation Ltd. FS is a Royal Society University Research Fellow.

7. References


### Table 1  Bacterial strains and fermentation balances

<table>
<thead>
<tr>
<th>Strain ID</th>
<th>Genotype</th>
<th>Strain source</th>
<th>Hyd-^a</th>
<th>H$_2$ formed</th>
<th>Formate</th>
<th>Acetate</th>
<th>Ethanol</th>
<th>Lactate</th>
<th>Succinate</th>
<th>CO$_2$ est$^b$</th>
<th>H$_2$ uptake$^c$</th>
<th>Growth$^d$ (g/mol glucose)</th>
<th>Carbon balance (%)$^e$</th>
</tr>
</thead>
<tbody>
<tr>
<td>MC4100</td>
<td>Parental strain</td>
<td>+ + +</td>
<td>0.764 (0.030)</td>
<td>0.149 (0.011)</td>
<td>0.499 (0.036)</td>
<td>0.649 (0.012)</td>
<td>0.318 (0.012)</td>
<td>0.494 (0.008)</td>
<td>0.504 (0.026)</td>
<td>0.236 (0.045)</td>
<td>2.61 (1.947)</td>
<td>100 (1.53)</td>
<td></td>
</tr>
<tr>
<td>HD701</td>
<td>ΔhycA</td>
<td>+ + +</td>
<td>0.737 (0.023)</td>
<td>0.132 (0.013)</td>
<td>0.363 (0.036)</td>
<td>0.667 (0.015)</td>
<td>0.359 (0.009)</td>
<td>0.470 (0.009)</td>
<td>0.422 (0.035)</td>
<td>0.162 (0.025)</td>
<td>2.57 (0.281)</td>
<td>95 (2.54)</td>
<td></td>
</tr>
<tr>
<td>FTD147</td>
<td>ΔhyaB, ΔhybC, ΔhycE</td>
<td>- - -</td>
<td>0 ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td></td>
</tr>
<tr>
<td>FTD150</td>
<td>ΔhyaB, ΔhybC, ΔhycE, ΔhyfB-R</td>
<td>- - -</td>
<td>0 ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td></td>
</tr>
<tr>
<td>HD705</td>
<td>ΔhycE</td>
<td>+ + -</td>
<td>0</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td></td>
</tr>
<tr>
<td>FTD22</td>
<td>ΔhyaB</td>
<td>- + +</td>
<td>0.800 (0.012)</td>
<td>0.181 (0.032)</td>
<td>0.528 (0.052)</td>
<td>0.695 (0.025)</td>
<td>0.312 (0.013)</td>
<td>0.452 (0.036)</td>
<td>0.590 (0.070)</td>
<td>0.242 (0.062)</td>
<td>3.01 (1.040)</td>
<td>102 (3.97)</td>
<td></td>
</tr>
<tr>
<td>FTD67</td>
<td>ΔhybC</td>
<td>+ - +</td>
<td>1.024 (0.040)</td>
<td>0.214 (0.026)</td>
<td>0.686 (0.016)</td>
<td>0.539 (0.005)</td>
<td>0.383 (0.030)</td>
<td>0.432 (0.024)</td>
<td>0.674 (0.061)</td>
<td>-0.001 (0.021)</td>
<td>2.52 (0.926)</td>
<td>104 (1.99)</td>
<td></td>
</tr>
<tr>
<td>FTD89</td>
<td>ΔhyaB, ΔhybC</td>
<td>- - +</td>
<td>1.043 (0.025)</td>
<td>0.176 (0.012)</td>
<td>0.640 (0.057)</td>
<td>0.583 (0.028)</td>
<td>0.372 (0.029)</td>
<td>0.436 (0.021)</td>
<td>0.611 (0.069)</td>
<td>0.004 (0.094)</td>
<td>3.62 (1.419)</td>
<td>104 (5.14)</td>
<td></td>
</tr>
</tbody>
</table>

^a present, - defective; ^b equation 2; ^c equation 1; ^d g bacterial dry weight; ^e equation 3; ^f (Sauter et al., 1992); ^g (Sargent, F - unpublished); ^h (Sargent et al., 1999); ^i (Dubini et al., 2002)

Values are the means of at least 4 replicates (± S.E.M.).

ND, Strains FTD147, FTD150 and HD705 produced no detectable H$_2$ and were not studied further.
Fig. 1. Metabolic scheme for mixed acid fermentation. The solid lines represent pathways contributing to H₂ production. The broken lines represent pathways competing with H₂ production. The ideal products are boxed. Ideally the values of lactate formation, succinate formation and H₂ uptake would be zero, and hence there would be no recycling of produced CO₂ in the carboxylation of PEP.

Fig. 2. H₂ production by *E. coli* strains deficient in HycA (A), and uptake hydrogenases (B). Bars represent standard errors.
Supplementary figure (not published)

Figure 3 was removed from the publication at the request of the editor and it is included here for clarity.

The figure illustrates that the sum of H₂ formed and H₂ uptake was reasonably constant, whereas Hyd-2 activity affected the distribution of potential H₂ between these two fates, whereas the effects on other aspects of fermentation balance were relatively minor.

![Figure 3](image)

**Figure 3.** Fates of potential H₂ in *Escherichia coli* strains deficient in HycA (A) and uptake hydrogenases (B).

In accordance with the scheme of mixed acid fermentation (Fig. 1), one mole of lactate, succinate, formate or ‘H₂ uptake’ represents one mole of potential H₂ production, whereas acetate and ethanol are produced concomitantly with H₂. Data are the normalised means of at least four replicate experiments. Means and standard errors (pre-normalisation) are given in Table 1. For each strain the sums of potential H₂ and measured H₂ were not significantly different from 2 mol H₂/mol glucose and did not vary significantly between strains.