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The electron-bifurcating FeFe-hydrogenase Hnd is involved in ethanol metabolism in *Desulfovibrio fructosovorans* grown on pyruvate

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Abstract

Desulfovibrio fructosovorans, a sulfate-reducing bacterium, possesses six gene clusters encoding six hydrogenases catalyzing the reversible oxidation of H_2 into protons and electrons. Among them, Hnd is an electron-bifurcating hydrogenase, coupling the exergonic reduction of NAD^+ to the endergonic reduction of a ferredoxin with electrons derived from H_2. It was previously hypothesized that its biological function involves the production of NADPH necessary for biosynthetic purposes. However, it was subsequently demonstrated that Hnd is instead a NAD^+-reducing enzyme, thus its specific function has yet to be established. To understand the physiological role of Hnd in *D. fructosovorans*, we compared the *hnd* deletion mutant with the wild-type strain grown on pyruvate. Growth, metabolites production and comsumption, and gene expression were compared under three different growth conditions. Our results indicate that *hnd* is strongly regulated at the transcriptional level and that its deletion has a drastic effect on the expression of genes for two enzymes, an aldehyde ferredoxin oxidoreductase and an alcohol dehydrogenase. We demonstrated here that Hnd is involved in ethanol metabolism when bacteria grow fermentatively and proposed that Hnd might oxidize part of the H_2 produced during fermentation generating both NADH and reduced ferredoxin for ethanol production via its electron bifurcation mechanism.

43 **Introduction**

44 Sulfate reducers belonging to the δ-Proteobacterial genus *Desulfovibrio* are ubiquitous in anoxic
45 habitats and employ a respiratory metabolism with sulfate as the terminal electron acceptor. Molecular
46 hydrogen plays an important role in the energy metabolism of these bacteria which can switch from
47 respiration to fermentation. Depending on the growth conditions, H_2 can be used as the sole energy source
48 during respiration or produced in order to oxidize reduced electron carriers to maintain the continuous
49 conversion of the substrates during fermentation (Thauer *et al.*, 2007, Fauque *et al.*, 1988, Rabus *et al.*, 2013).
50 This ability of *Desulfovibrio* to consume and produce hydrogen is exploited during syntrophic associations
51 anaerobic environments (Bryant *et al.*, 1977, Stolyar *et al.*, 2007, Meyer *et al.*, 2013a, Meyer *et al.*, 2013b).

52 Hydrogenases, the key enzymes involved in the metabolism of molecular hydrogen, catalyze the
53 reversible oxidation of H_2 into protons and electrons. Most of the known hydrogenases are iron-sulfur proteins
54 and are classified into two main distinct families according to the two metal atoms at their active site, the
55 [NiFe]-hydrogenases (Volbeda *et al.*, 1995, Higuchi *et al.*, 1997) and the [FeFe]-hydrogenases (Peters *et al.*,
56 1998, Nicolet *et al.*, 1999). These enzymes are widely distributed in *Bacteria* and *Archaea* as well as in
57 unicellular eukaryotes (Vignais *et al.*, 2001, Vignais & Billoud, 2007, Benoit *et al.*, 2020).

58 The versatility of the *Desulfovibrio* H_2 metabolism is due to a complex hydrogenase system composed
59 of several different enzymes located in different cellular compartments (Thauer *et al.*, 2007, Pereira *et al.*,
60 2011, Baffert *et al.*, 2019). The number, the type and the cellular location of these enzymes vary considerably
61 from one *Desulfovibrio* species to another (Pereira *et al.*, 2011, Baffert *et al.*, 2019) and this diversity makes the
62 role of these various hydrogenases difficult to determine. Forty years ago, a model for the growth of
63 *Desulfovibrio* in lactate medium in the presence of sulfate, the "hydrogen cycling model", was proposed (Odom
64 & Peck, 1981). In this model, electrons and protons produced by lactate oxidation are used by a cytoplasmic
65 hydrogenase to produce H_2. After the diffusion through the cytoplasmic membrane, H_2 is re-oxidized by a
66 periplasmic hydrogenase contributing to the proton gradient across the membrane used for ATP synthesis. The
67 electrons generated by this oxidation are then returned to the cytoplasm through several integral membrane
68 complexes where they are used for sulfate reduction. Since then, several models for energy conservation in

69 *Desulfovibrio* have been proposed in which, in addition to the H_2 recycling pathway, there is another H_2-
70 independent pathway involving a direct electron transfer from the donor to the acceptor (Keller & Wall, 2011,
71 Noguera *et al.*, 1998, Sim *et al.*, 2013).

72 In *Desulfovibrio fructosovorans*, our biological model, three hydrogenases have been already
73 characterized: Hyn, a periplasmic [NiFe]-hydrogenase (Hatchikian *et al.*, 1990, Rousset *et al.*, 1990); Hyd, a
74 periplasmic [FeFe]-hydrogenase (Casalot *et al.*, 1998) and Hnd, a cytoplasmic [FeFe]-hydrogenase (Malki *et al.*,
75 1995, de Luca *et al.*, 1998, Kpebe *et al.*, 2018). *D. fructosovorans* genome analysis revealed the presence of
76 three genes clusters encoding three additional putative hydrogenases (Baffert *et al.*, 2019): a membrane-
77 bound Ech-type hydrogenase, a cytoplasmic trimeric [FeFe]-hydrogenase Hnt similar to the electron-bifurcating
78 hydrogenase from *Thermotoga maritima* (Schut & Adams, 2009), and a [FeFe] cytoplasmic hydrogenase
79 showing similarity with the putative sensory [FeFe]-hydrogenase HydS from *T. maritima* (Chongdar *et al.*, 2018)
80 or the Hfs hydrogenase from *Thermoanaerobacterium saccharolyticum* (Shaw *et al.*, 2009). The specific
81 function of these six enzymes is not yet clearly established in *D. fructosovorans*. Marker-exchange mutagenesis
82 was performed to determine the role of hydrogenases in the energy metabolism of the bacterium (Malki *et al.*,
83 1997, Casalot *et al.*, 2002a, Casalot *et al.*, 2002b). Results clearly indicated an effect of the depletion of
84 hydrogenases on the growth behavior of *D. fructosovorans*. However, it was difficult to hypothesize on the
85 physiological implications of each hydrogenase due to enzymatic compensation processes as the result of the
86 deletion of the genes encoding one, two or three hydrogenases (Malki *et al.*, 1997, Casalot *et al.*, 2002a,
87 Casalot *et al.*, 2002b, Rousset *et al.*, 1991).

88 We recently produced and purified a recombinant form of Hnd and showed that it is an electron-
89 bifurcating hydrogenase that simultaneously reduces two different electron acceptors, NAD^+ and a
90 ferredoxin in the presence of H_2 (Kpebe *et al.*, 2018), despite it being previously described as an $NADP^+$-
91 reducing enzyme (Malki *et al.*, 1995, de Luca *et al.*, 1998). Flavin-based electron bifurcation is an important
92 mechanism of energy conservation, mainly found in anaerobic microorganisms, coupling an endergonic
93 redox reaction to an exergonic redox reaction (Buckel & Thauer, 2018a, Buckel & Thauer, 2018b). This
94 tetrameric enzyme is encoded by the *hnd* operon, in which *hndA* and *hndC* encode the NAD-dependent unit

95 and *hndD* encodes the [FeFe]-hydrogenase subunit, which is closely related to the hydrogenase CpI from
96 *Clostridium pasteurianum* (Malki *et al.*, 1995). The function of the product of the *hndB* gene is unknown.
97 This cytoplasmic Hnd complex catalyzes, *in vitro*, the coupled endergonic reduction of ferredoxin and the
98 exergonic reduction of NAD^+ by the oxidation of H_2 (Kpebe *et al.*, 2018).

99 Initially, it was hypothesized that the biological function of Hnd involves the production of NADPH
100 necessary for biosynthetic purposes (de Luca *et al.*, 1998) but because it was subsequently determined that
101 Hnd is in fact a NAD^+-reducing enzyme (Kpebe *et al.*, 2018), its specific function has yet to be established. In
102 order to understand the involvement of the electron-bifurcating Hnd hydrogenase in the energy-generating
103 metabolism in *D. fructosovorans*, we compared the *hndD* deletion mutant strain (SM4) (Malki *et al.*, 1997)
104 with the wild-type strain grown on different pyruvate-containing media. Our results indicate that Hnd is not
105 essential for the bacterial growth when pyruvate is used as the carbon source, and that this hydrogenase is
106 involved in ethanol metabolism when bacteria grow fermentatively.

107

108 **Results**

109 *Growth of D. fructosovorans on pyruvate-containing media*

110 The growth of the wild-type strain and the SM4 strain, in which the *hndD* gene encoding the
111 hydrogenase catalytic subunit of Hnd is deleted (Malki *et al.*, 1997) was measured in batch cultures (Figure
112 1). Two different growth conditions were compared, both containing 25 mM pyruvate as the only source of
113 energy: a medium containing 20 mM sulfate as electron acceptor (PS20 medium, respiratory condition) and
114 a medium without any electron acceptor (PS0 medium, fermentative condition). Since growth during
115 fermentation is very slow compared to sulfate respiration, the cells were also grown under a third condition
116 in which they grow faster on a medium that contains a limiting concentration of sulfate (PS2 medium
117 containing 2mM sulfate, mixed culture condition). In each condition, there were no striking differences
118 among the growth curves of the two strains (Figure 1). However, growth yields as well as doubling times of
119 both strains are significantly different under the three conditions (Table 1). In the fermentative condition,

120 the growth is slow for both strains but even slower for the mutant strain, with a doubling time of 369 h for
121 the WT compared to 519,5 h for the mutant. However, the overall growth yield of the mutant is unaffected,
122 because a similar maximum absorbance around 0.70 at 600 nm is reached for the two strains that
123 correspond to 6.7/6.9. 10^9 cells/mL. In the respiratory condition (PS20), the growth is faster and both
124 strains behave similarly: the growth reaches a maximum absorbance of 1.3-1.4 at 600 nm (1.33-1.41. 10^9
125 cells/mL) and the generation time is around 20 h for the WT strain and 15h for SM4. Under sulfate-limited
126 conditions, the growth exhibits two different phases, a rapid one (phase 1, until around 40 h) before the
127 sulfate is exhausted (see Figure S1 for the quantification of sulfate) and a slow one (phase 2, from around
128 40 h to 110 h) in which there is no more sulfate in the medium. While the generation times of phase 1
129 measured for both strains are similar to those of the respiratory condition, those of phase 2 are much
130 faster than that of the fermentation condition and in this phase, the growth of the mutant strain is slightly
131 slower than that of the WT strain. Taken together, these results indicate that Hnd is not essential for
132 bacterial growth under either fermentative or respiratory conditions when pyruvate is used as the carbon
133 source and that in the SM4 mutant, the generation time is affected only when there is no sulfate in the
134 medium (fermentative condition or phase 2 of the mixed condition). On the other hand, biomass yields
135 (maximum cell counts/mL) are not affected at all in the mutant regardless of the growth conditions.

136

137 *Impact of hnd deletion on metabolite production and consumption*

138 To evaluate the impact of *hndD* deletion on *D. fructosovorans* physiology, we compared pyruvate
139 consumption as well as acetate, ethanol and H_2 production (Figure 2). The pyruvate is completely
140 consumed, with the rate depending on the initial sulfate concentration in the medium: the more sulfate
141 there is, the faster the consumption. Pyruvate consumption and acetate production are not significantly
142 different between the two strains on PS20 and PS2 media whereas, in the absence of sulfate, both pyruvate
143 and acetate are respectively consumed or produced slowly by the mutant than by the WT strain. However,
144 there is a striking difference between the two strains in terms of the production of ethanol (Figure 2). Both
145 strains produce ethanol only during mixed and fermentation conditions. In both conditions, the mutation

146 significantly affects the ethanol formation, since the SM4 mutant produces less ethanol than the WT strain
147 (4 times less in fermentation condition and 10 times less in mixed growth condition). The highest level of
148 produced ethanol is reached under fermentation conditions for both strains.

149 There is also a notable difference in H_2 production between the two strains (Figure 2). There is no
150 H_2 production in respiratory conditions for either strain. Under fermentation conditions, however, H_2
151 production is more than twice as high in the mutant as in the WT strain. Under mixed conditions, the
152 amount of H_2 in the headspace at the end of the exponential phase is 1.5 times higher for SM4 than for the
153 WT strain. However, the H_2 amount at the end of the growth is identical for both strains due to differences
154 of production kinetics. Collectively, these results show that the SM4 mutant strain is affected under mixed
155 and fermentation conditions but not under respiratory conditions, suggesting that Hnd has a role in
156 fermentative metabolism. Under fermentative conditions, the mutant produces more H_2 and less ethanol
157 than the WT strain, indicating that H_2 and ethanol production pathways are therefore affected in the
158 mutant. In this study, all subsequent analyses were performed on strains grown under respiration and
159 mixed conditions because under fermentation conditions, growth is very slow and very little cellular
160 material is obtained.

161

162 *Impact of hnd deletion at the protein level*

163 Coomassie-blue-stained SDS-PAGE was used to compare the soluble protein pattern of the WT and
164 SM4 strains grown under mixed or respiratory conditions. At the end of the exponential phase of growth,
165 total soluble proteins were prepared and migrated on SDS-PAGE (Figure 3A). The bands indicating
166 significant differences in protein levels between the two strains were cut out from the gel and the proteins
167 were identified by mass spectrometry (Figure 3B and Table S1 for complete list of identified proteins). As
168 shown in Figure 3, the protein profiles are different for the two strains. Three bands (1, 2 and 3) that were
169 significantly more intense in the WT strain than in the mutant strain were analyzed. Results are reported in
170 Figure 3B in which only proteins identified with the highest score in each gel band are reported (for a

171 complete list of identified proteins, see Table S1). The most striking difference concerns band 1
172 corresponding to a protein whose gene has been annotated as iron-containing alcohol dehydrogenase
173 (Adh) (locus tag: DesfrDRAFT_3929). The intensity of this band suggests that this protein is very strongly
174 produced in the WT strain whereas it is almost absent in the mutant strain under both growth conditions.
175 Similarly, the analysis of band 3 (Figure 3) reveals the presence of a protein whose gene is annotated as
176 aldehyde ferredoxin oxidase (Aor) (locus tag: DesfrDRAFT_2487). Band 2 (Figure 3) corresponds to the
177 HndC subunit of Hnd. The intensities of the Adh and Aor bands in Figure 3 suggest that the amount of these
178 two enzymes is greater in the WT strain grown in PS2 medium than in PS20.

179

180 *Expression of hnd on pyruvate medium*

181 Metabolite production analysis suggests that Hnd has a role in fermentative metabolism.
182 Expression of *hndD* was determined in the WT strain using RT-qPCR under both mixed and respiratory
183 conditions. Figure 4 shows that *hndD* expression is much higher (by a factor of 80) in cells grown in PS2
184 than in PS20. Hnd production was followed by western blot (Figure 5A). While the enzyme is detected in
185 bacteria that grew under mixed conditions (PS2), it is not detected in those that grew in respiration
186 condition (PS20). The same profile of Hnd production is obtained when *D. fructosovorans* used a limiting
187 concentration of fumarate or sodium thiosulfate as electron acceptor instead of sulfate (Figure S2).

188 Cytoplasmic extracts of the WT strain at the early stationary phase grown in PS2 or PS20 medium were
189 migrated on a Blue-Native gel electrophoresis followed by in-gel detection of hydrogenase activity (Figure
190 5B). An activity band, corresponding to Hnd (Kpebe *et al.*, 2018), is visible when the strain grew under
191 mixed condition but not under respiratory condition, which is consistent with the higher *hndD* gene
192 expression and the higher protein production under mixed condition than under respiration. Taken
193 together, these results demonstrate that the expression of *hnd* operon is not constitutive and is strongly
194 regulated at the transcriptional level, and that *hnd* expression is much higher under mixed condition than
195 respiratory condition suggesting that the enzyme has a role in fermentative metabolism.

196

197 *aor and adh gene expression*

198 The expression of *adh* and *aor* genes was analyzed by RT-qPCR to determine if the difference in the
199 amount of the two enzymes in both strains was due to a difference in their gene expression (Figure 4). In
200 the WT strain, as for the *hnd* gene, *adh* and *aor* expressions are much higher when bacteria grow in mixed
201 condition than in respiration (increased by a factor of 13 for *adh* and 10 for *aor*) indicating a transcriptional
202 regulation. However, the expression of both genes is strongly decreased in the mutant strain, with almost
203 no expression of either gene being detected. Gene expression analysis shows that the deletion of the *hndD*
204 gene drastically impacts the expression of both *adh* and *aor* genes, which is consistent with the findings of
205 the proteomics analysis.

206

207 *Adh level in the periplasmic FeFe-hydrogenase deletion strain*

208 Haveman *et al.* pointed out that, in DvH, in the mutant strain deleted of the periplasmic FeFe-
209 hydrogenase, the *adh* gene is strongly downregulated (Haveman *et al.*, 2003). We compared, using SDS-
210 PAGE, the production of Adh by the *D. fructosovorans* WT strain with the mutant strain that is deleted of its
211 periplasmic FeFe-hydrogenase (SF mutant) (Casalot *et al.*, 2002b) to verify whether, as in DvH, the deletion
212 of this hydrogenase in *D. fructosovorans* has an impact on the level of Adh (Figure S3). In contrast to what
213 was observed in the DvH hydrogenase mutant (Haveman *et al.*, 2003), the amount of Adh in the SF strain is
214 comparable to that present in the WT strain. Furthermore, the SF strain grows as well as the WT strain on
215 PS2 medium (Figure S4). These results suggest that the regulatory mechanisms involved are different in the
216 two *Desulfovibrio* species.

217

218 *Complementation of the hnd deletion*

219 In order to confirm that the phenotype of the SM4 deletion strain resulted from the absence of the
220 Hnd hydrogenase, complementation analyses were performed. The growth of the complementation strain
221 SM4/pBGhnd6 on PS2 medium is similar to that of WT and SM4 strains (Figure S3). The *hnd* operon is
222 expressed from the pBGhnd6 plasmid in the SM4 strain, as can be observed in Figure 6A showing the
223 relative quantification of *hndD* mRNA levels measured by RT-qPCR. However, in the SM4/pBGhnd6 strain,
224 the expression level does not reach that of the WT strain. Western blot analysis indicates that whereas the
225 level of HndD is very high in the WT strain grown under mixed culture conditions, it is lower in the
226 complementation strain (Figure 5A). Quantification of the intensity of the band corresponding to HndD for
227 the complementation strain on PS2 is almost 2.5 times less intense than for the WT strain. Similarly, the
228 complementation strain produces an intermediate amount of ethanol between that produced by the WT
229 and SM4 strains (Figure 6B). Taken together, these results indicate first that the expression of *hnd* from the
230 pBGhnd6 plasmid does not fully complement the SM4 strain but also that the low expression of *hnd*
231 partially restores ethanol production in this strain.

232

233 **Discussion**

234 In this study, *D. fructosovorans* WT strain was compared to the SM4 mutant strain lacking Hnd (Δ*hndD*)
235 (Malki *et al.*, 1997) in order to get new insights into the physiological role of this electron-bifurcating
236 hydrogenase when the bacteria grow on pyruvate as a carbon and energy source, under respiratory (PS20
237 medium) and fermentative (PS0 medium) conditions. We have also tested a mixed culture condition (PS2
238 medium) using a limiting sulfate concentration, making it possible to reach a higher growth rate as compared
239 to the fermentative condition. After sulfate depletion, the metabolism switches from respiration to
240 fermentation. Under this condition, the *hnd* operon is much more expressed than in the respiratory condition
241 (PS20 medium) (Figure 4). The increase in expression level is followed by an increase in enzyme production as
242 revealed by western blot and in-gel hydrogenase activity detection (Figure 5). This suggests that Hnd
243 hydrogenase plays a role under fermentative conditions.

244 Deletion of the *hndD* gene leads to a drastic decrease in the expression of the two genes *adh*
245 (DesfrDRAFT_3929) and *aor* (DesfrDRAFT_2487) on PS2 medium, coding respectively for proteins annotated as
246 iron-containing alcohol dehydrogenase (Adh) and aldehyde ferredoxin oxidoreductase (Aor) (Figures 3 and 4).
247 Alcohol dehydrogenases are a group of oxidoreductases that catalyze the interconversion of alcohols to
248 aldehydes or ketones. They are ubiquitous and most of them are NAD- or NADP-dependent enzymes. The size
249 and metal content of Adh vary (for reviews, see (Gaona-Lopez *et al.*, 2016, Radianingtyas & Wright, 2003, Reid
250 & Fewson, 1994)). Adh3929 from *D. fructosovorans* shows high sequence identity with iron-containing alcohol
251 dehydrogenases from various bacteria (52 % with the iron-containing Adh (GI 56552492) from *Zymomonas*
252 *mobilis* for example) and contains a conserved iron-binding motif ($GX_2HX_2AHX_2GX_5PHG$ where X denotes any
253 amino acid). Adh3929 is highly expressed in *D. fructosovorans* (Figures 3 and 4) and it has been shown
254 previously that it is one of the most abundant enzyme in *Desulfovibrio* (Haveman *et al.*, 2003, Ramos *et al.*,
255 2015). Ramos *et al*. purified Adh1 (DVU2405) from *D. vulgaris* Hildenborough (DvH), which has 81 % sequence
256 identity to Adh3929, and showed that this enzyme is NAD-dependent and uses ethanol as substrate (Ramos *et*
257 *al.*, 2015). Aor are tungsten-containing enzymes sensitive to O_2. They catalyze the reversible oxidation of an
258 aldehyde to the corresponding acid using a ferredoxin. Aor2487 from *D. fructosovorans* shows 37% sequence
259 identity with Aor from *Pyrococcus furiosus* whose crystallographic structure has been solved (Chan *et al.*,
260 1995). These two enzymes Adh and Aor can therefore be involved in the same metabolic pathway since the
261 product of one can be the substrate of the other. Taken together, our data reveal that Hnd is involved in
262 ethanol metabolism when *D. fructosovorans* grows in pyruvate under mixed conditions, which led us to
263 propose a model in which the hydrogenase Hnd would oxidize part of the H_2 produced during fermentation
264 generating both NADH and reduced ferredoxin as a result of its electron bifurcation mechanism (Figure 7). H_2
265 production results from the release of reducing power in the absence of terminal electron acceptors, enabling
266 the oxidation of pyruvate. In this model, pyruvate would be converted into acetate by the two enzymes
267 pyruvate:ferredoxin oxidoreductase and acetyl-CoA synthase. H_2 could be produced by the membrane
268 hydrogenase Ech from reduced ferredoxin, which would contribute to the electrochemical proton gradient for
269 ATP synthesis. This model proposes that the role of the Hnd hydrogenase would be to produce reducing
270 equivalents (NADH and reduced ferredoxin) from H_2, allowing the production of ethanol by Adh3929 and

271 Aor2487. The lower H_2 production of the WT compared to the SM4 mutant strains is also in agreement with
272 the hypothesis that the physiological role of Hnd when pyruvate is present is thus to consume H_2.

273 The determination of the hydrogenase activity, both H_2-production and H_2-oxidation, on total soluble extracts
274 of WT and SM4 mutant strains grown under mixed condition (PS2) shows that both activities are strongly
275 decreased in the mutant strain (Table S2). It is our assumption that the increased H_2 release in strain SM4
276 (Figure 2) is due to a lack of consumption by Hnd, not an overproduction by Ech. Preliminary proteomic results
277 demonstrate that Ech expression does not vary based on strain or growth condition (data not shown), and
278 there is no indication that its activity would differ between the two strains. In strain SM4, when Hnd is not
279 present, the H_2-production activity measured in the soluble fraction is 44 times less than when is it present in
280 the WT strain (Table S2). Moreover, H_2-oxidation activity shows that strain SM4 consumes 18 times less H_2 than
281 the WT (Table S2) most likely due to the lack of Hnd in this strain.

282 The recently characterized electron-bifurcating hydrogenases were isolated from the anaerobic bacteria
283 *Thermotoga maritima* (Schut & Adams, 2009), *Acetobacterium woodii* (Schuchmann & Müller, 2012), *Moorella*
284 *thermoacetica* (Wang et al., 2013), and *Ruminococcus albus* (Zheng et al., 2014). In the acetogenic bacteria *A.*
285 *woodii* and *M. thermoacetica* which can produce acetate from CO_2 with H_2 as the reductant, these enzymes
286 were found to catalyze the reduction of ferredoxin and NAD^+ with H_2. NADH and reduced ferredoxin are used
287 for CO_2 reduction and to contribute to the ion gradient across the membrane (Schuchmann & Müller, 2012,
288 Wang *et al.*, 2013). In *R. albus* and *T. maritima*, which are glucose fermenting bacteria, trimeric HydABC
289 hydrogenase mediates H_2-production by coupling the endergonic reduction of protons with NADH to the
290 exergonic reduction of protons with reduced ferredoxin (Schut & Adams, 2009, Zheng *et al.*, 2014). *R. albus*, a
291 rumen bacterium, fermentatively produces acetate, ethanol, CO_2 and H_2 in pure culture and in this high H_2-
292 condition, H_2 is mainly generated *via* a ferredoxin-dependent hydrogenase (HydA2). However, *R. albus*
293 redirects carbon flux from ethanol production to the more energetically efficient pathway of acetate
294 production when it grows in co-culture with a hydrogenotrophic bacterium that keeps the H_2 partial pressure
295 sufficiently low through interspecies hydrogen transfer. Under this low H_2-condition, only acetate, CO_2 and H_2
296 are produced. The acetate-only pathway generates more ATP per mole of glucose and equimolar amounts of

297 NADH and reduced ferredoxin, which are then re-oxidized *via* the electron-confurcating HydABC hydrogenase
298 to produce H_2 (Zheng *et al.*, 2014, Greening *et al.*, 2019). *D. fructosovorans,* like *R. albus,* also produces acetate,
299 H_2, ethanol and CO_2 (not measured in this study) when growing on pyruvate in the absence of an electron
300 acceptor. In DvH, ethanol is also a minor product of pyruvate fermentation (Ramos *et al.*, 2015, Traore *et al.*,
301 1981) and the electron flow is redirected towards ethanol when H_2 accumulates at the expense of the
302 energetically more favourable production of acetate (Ramos *et al.*, 2015). However, in *R. albus*, HydABC is
303 responsible for the production of H_2 when the pH_2 is kept very low whereas in *D. fructosovorans*, under
304 fermentative conditions, Hnd is involved in the consumption of H_2 when H_2 accumulates allowing the reduction
305 of NAD^+ for ethanol production.

306 In the WT strain, the expression profile of the three genes *hndD*, *adh* and *aor* is conserved in both PS2 and
307 PS20 media (although *adh* has an expression level that is about twice that of the two genes in PS2) (Figure
308 4) and shows that their expression is much higher in the mixed condition than in the respiration condition.
309 Adh and Aor are thus overproduced when Hnd is overproduced. Their expression is thus strongly regulated
310 at the transcriptional level, but the mechanism of regulation involved remains to be elucidated. Likewise,
311 the molecular basis of the strong drop in *adh* and *aor* expression in the mutant has not yet been
312 deciphered. The drop of Adh level in the SM4 mutant is specific for the deletion of *hnd* in *D. fructosovorans*
313 and is not observed when another FeFe-hydrogenase gene is deleted (in the SF mutant, Figure S3) whereas
314 in DvH, in the periplasmic FeFe-hydrogenase deleted strain, *adh* expression decreases drastically. It should
315 be noted that DvH does not contain any electron-bifurcating hydrogenases.

316 We propose that the regulation of *hnd* expression might be under the control of Rex, which has been
317 described as a global redox-sensing transcriptional repressor that is controlled by the intracellular NAD^+/NADH
318 ratio, a critical indicator for the redox state of the cell. NADH disrupts the interaction of Rex with its respective
319 binding sites, proposed to be induced by a conformational change in the N-terminal domains of the Rex
320 homodimer depending on NAD^+ or NADH binding (Park *et al.*, 2018, Christensen *et al.*, 2015, Brekasis & Paget,
321 2003).Rex has been shown in several bacteria to regulate genes for central metabolism, for proteins involved in
322 energy conversion and in a variety of metabolic processes (Ravcheev *et al.*, 2012). The presence of a predicted

323 Rex-binding site in the upstream untranslated region of the *hnd* operon (Figure S5) suggests that its expression
324 might be controlled by the intracellular NAD^+/NADH redox state. In DvH, Rex was demonstrated to be a
325 transcriptional repressor of *sat*, a gene encoding for a sulfate adenyl transferase which is involved in sulfate
326 respiration. Surprisingly, *sat* transcript levels were highest when the cells were grown with pyruvate in the
327 absence of sulfate, with the highest levels being found in the Δ*rex* strain, suggesting that Rex induces the
328 expression of genes encoding for proteins that are involved in scavenging sulfate and those that are implicated
329 when the preferred electron acceptor is limiting (Christensen *et al.*, 2015). In *D. fructosovorans*, a putative *rex*
330 gene (DesfrDRAFT_2623) encodes a 24.8 kDa protein that shows 47 % sequence identity with the Rex repressor
331 from *Thermotoga maritima* whose crystallographic structure has been solved (Park *et al.*, 2018). In the
332 anaerobic hyperthermophile bacterium C*aldicellulosiruptor bescii*, structural genes for the NiFe Ech-type
333 hydrogenase and the FeFe Hnd-type hydrogenase are members of the Rex regulon (Sander *et al.*, 2019,
334 Ravcheev *et al.*, 2012). This suggests that Rex may play an important role in H_2 metabolism in this bacterium. In
335 *D. fructosovorans*, the involvement of the putative Rex regulator remains to be determined experimentally. In
336 contrast, a Rex binding site was not found in the promoter of *aor*2487 and *adh3*929, suggesting that although
337 the expression profile of these three genes is similar, their expression is not under the control of the same
338 regulators.

339 As already mentioned, *D. fructosovorans* harbors a gene cluster for a putative H_2-sensing [FeFe]-
340 hydrogenase, called Hfs or HydS (DesfrDRAFT_3590) whose mechanism has yet to be elucidated. This type
341 of hydrogenase appears to have a regulatory role and the hydrogenase domain containing a non-canonical
342 active site (Chongdar *et al.*, 2018) is fused to a C-terminal PAS domain. The sensory function of HydS has
343 been predicted based on the presence of this PAS domain (Greening *et al.*, 2016). PAS domains are widely
344 utilized for various signal transduction and sensory functions (Henry & Crosson, 2011) and are frequently
345 found in signal transduction cascades involving serine/threonine protein kinases and phosphatases.
346 Transcriptional studies of *R. albus* have provided some insights into the regulatory function of HydS (Zheng
347 *et al.*, 2014). In this bacterium, the genes encoding for HydS are co-transcribed with the transcriptional
348 repressor Rex and the ferredoxin-dependent [FeFe]-hydrogenase HydA2, whereas ~~there is an~~ genes
349 encoding the electron-bifurcating hydrogenase HydABC are located on a separate operon (Zheng *et al.*,

350 2014). It is likely that HydS, in tandem with Rex, is sensing the NADH/NAD^+ ratio of the cell *via* the H_2 partial
351 pressure, with the ratio being higher at high H_2 concentrations, and modulating the transcription of genes
352 so that the NADH/NAD^+ ratio is balanced (Zheng *et al.*, 2014). Greening *et al*. also proposed that in *R. albus*,
353 FeFe-hydrogenases are regulated by HydS as a result of direct H_2-sensing (Greening *et al.*, 2019). It is of
354 note that the presence of a *hydS* gene in the genome of *Desulfovibrio* species is always correlated with the
355 presence of *hnd* genes (Baffert *et al.*, 2019). The coexistence of multimeric [FeFe]-hydrogenases and HydS
356 is also found in other H_2-forming bacteria such as in *Thermoanaerobacterium saccharolyticum*,
357 *Thermoanaerobacter tengcongensis* and *Thermotoga maritima* (Chongdar *et al.*, 2018, Pan *et al.*, 2003,
358 Shaw *et al.*, 2009, Soboh *et al.*, 2004) however the extent of the role of HydS in the regulatory cascade still
359 needs to be clarified.

360 In DvH, an hexameric NADH dehydrogenase/heterodisulfide reductase complex Hdr-Flx is involved
361 in ethanol metabolism. Strains mutated in genes that encode the proteins of this complex also produce a
362 reduced amount of ethanol compared to the WT strain during pyruvate fermentation (Ramos *et al.*, 2015).
363 The Hdr-Flx complex is proposed to be essential for NADH oxidation during growth on ethanol, probably
364 using an electron bifurcation mechanism that leads to the reduction of a ferredoxin and a small protein,
365 DsrC, involved in sulfate reduction, whereas during fermentation, the complex would function in the
366 opposite direction reducing NAD^+ for ethanol production (Ramos *et al.*, 2015). In *D. fructosovorans*, the 7
367 genes encoding this complex are present in the genome immediately downstream of the *adh* gene
368 (desfrDRAFT_3930 to 3936), suggesting that it may also be involved in ethanol metabolism but its role in *D.*
369 *fructosovorans* remains to be determined.

370 In conclusion, we demonstrated that the electron-bifurcating hydrogenase Hnd is involved in
371 ethanol metabolism in *D. fructosovorans* in pyruvate medium under fermentative conditions. The deletion
372 of the *hnd* gene has a drastic effect on the expression of both *adh* and *aor* genes. Although the link
373 between the deletion of *hnd* and the decrease in the expression of both *adh* and *aor* as well as the
374 regulatory mechanisms at play remain to be understood, this study nevertheless provides a significant
375 advance in the function of Hnd in *D. fructosovorans*.

376

377 **Experimental procedures**

378 *Bacterial strains and growth conditions.*

379 The WT strain of *Desulfovibrio fructosovorans* DSM 3604 (Ollivier *et al.*, 1988) and the two mutants, SM4
380 and SF strains, which are deleted of *hndD* encoding the hydrogenase catalytic subunit of Hnd (Δ*hndD*, Cm^R)
381 (Malki *et al.*, 1997) or of *hydAB* encoding the small and large subunits of the periplasmic [FeFe]-
382 hydrogenase (Δ*hydAB*, Gm^R) (Casalot *et al.*, 2002b), respectively, were used in this study. To complement
383 the deletion strain SM4, the pBGhnd6 plasmid containing the entire *hnd* operon including the promoter
384 region (600 bp) was constructed and used to transform the SM4 strain as previously described (Kpebe *et*
385 *al.*, 2018) to produce the SM4/pBGhnd6 strain.

386 Strains were grown anaerobically at 37°C in different media. The basal medium (pH 6.8) contains 25 mM
387 sodium pyruvate, 8 mM NH_4Cl, 1.3 mM $CaCl_2$, 17.1 mM NaCl, 6.7 mM KCl, 2.1 mM $MgCl_2$ and trace
388 elements (Rousset *et al.*, 1998) and corresponds to the PS0 medium. Na_2SO_4 was added to the basal
389 medium to obtain the PS20 medium containing 20 mM sulfate. $MgCl_2$ and $CaCl_2$ in the basal medium were
390 replaced by 1 mM $CaSO_4$ and 1 mM $MgSO_4$ to obtain the PS2 medium containing 2 mM sulfate. Prior to
391 inoculation, 20 mM KH_2PO_4 pH 6.8, 2.5 mM Na_2S and 10 mM $NaHCO_3$ were added. Thiamphenicol (35
392 µg/mL) or gentamicin (20 µg/mL) were added to the SM4 or SF mutant culture media. The media were
393 inoculated with 5% (v/v) of fresh cultures.

394 *Hydrogen production measurement*

395 Cells were grown in 100 mL bottles containing 90 mL of PS0, PS2 or PS20 medium. The media were
396 inoculated with fresh cultures of WT or SM4 strains grown on PS2 medium. Each culture was done in
397 triplicate. For H_2 quantification, 100 µL of headspace gas was removed periodically using a gastight syringe
398 and injected into a gas chromatography system (Agilent 7820A) equipped with a thermal conductivity
399 detector and a GS-Carbonplot 115-3133 column (30 m, 530 µm, 3 µm), using nitrogen as the carrier gas, at

400 a flow rate of 8.2 ml/min, an oven temperature of 30 °C and a detector temperature of 200 °C. The H_2
401 production is expressed as micromols of H_2 accumulated in the headspace.

402 *HPLC analysis*

403 Acetate production, pyruvate and ethanol consumption were followed by HPLC. The analysis was
404 performed on the same *D. fructosovorans* cultures as those used to measure H_2 production and as those
405 used for the growth curves. 1 mL of culture samples were collected at different growth phase, centrifuged
406 at 14 100 g for 6 min to remove the cells, filtered through a 0.22 µm filter and stored at -20°C until use.
407 Immediately before the analysis, 10 µL of H_2SO_4 0,5 M were added to 490 µL of sample to obtain a final
408 concentration of 10 mM of H_2SO_4 and the samples were centrifugated for 5 min. The analysis was carried
409 out on an Agilent 1200 HPLC system equipped with a refractometer (Agilent Technologies). Acetate,
410 ethanol and pyruvate separation was achieved with an Agilent Hi-Plex H column (300 x 7.7mm) set at 50 °C.
411 25 µL of samples were injected. The compounds were eluted with 10mM sulfuric acid mobile phase at a
412 flow rate of 0.6 $mL.min^{-1}$.

413 *Ethanol quantification with an enzymatic kit*

414 When indicated, ethanol production in the growth medium was determined with an enzymatic kit
415 from Boehringer Mannheim/R-Biopharm according to the manufacturer instructions. This method is based
416 on quantifying NADH formed from ethanol through the combined action of Adh and aldehyde
417 dehydrogenase.

418 *Sulfate determination*

419 The concentration of sulfate was measured using a turbidimetric method previously described
420 (Marietou *et al.*, 2009), based on the reaction of sulfate with barium chloride, resulting in the precipitation
421 of barium sulfate. At different growth times, 5 mL culture samples were harvested, 0.22 µm filter-sterilized
422 and stored at 4°C. 100 µL of these samples were added to 900 µL of conditioning agent (10.2 mM glycerol,
423 6 mM concentrated HCl, 22.3 mM NaCl, 1.7 % ethanol) and 100 µL of 1 M barium chloride. The solution was
424 then vortexed for 30 s and incubated at room temperature for 45 min to allow the precipitation of barium

425 sulfate. The absorbance of the solution at 420 nm was determined and the concentration of sulfate in the
426 samples was calculated from the calibration curve prepared using standard solutions of sodium sulfate.

427 *Separation of proteins by SDS-PAGE*

428 *D. fructosovorans* cells were grown in 1L bottles containing 900 mL medium, harvested at the end
429 of exponential phase of growth by centrifugation. The cell pellet was resuspended in buffer Tris-HCl 20 mM
430 pH 7.6 supplemented with protease inhibitors (SIGMAFAST™ Protease Inhibitor Cocktail Tablet, Sigma-
431 Aldrich), DNase I (Roche) and Lysozyme (Sigma-Aldrich). Cells were disrupted by two passages through a
432 chilled French press cell at a pressure of 100 MPa. After an ultracentrifugation at 200 000 g for 45 min at
433 4°C, proteins were separated on 10% polyacrylamide denaturing gels (SDS-PAGE) using a mini VE
434 electrophoresis apparatus (Amersham Pharmacia). After migration, gel was stained with Coomassie blue
435 staining solution (20% ethanol, 10% acetic acid and 0.15% Coomassie blue R250) and destained by soaking
436 for at least two hours in a solution of ethanol/acetic acid/water (20:10:70 vol/vol/vol).

437 *Blue-Native gel (BN-gel) electrophoresis and in-gel hydrogenase activity detection*

438 *D. fructosovorans* cells were grown in 1L bottles containing 900 mL medium, harvested at the end
439 of exponential phase of growth by centrifugation. Periplasmic extract was removed from the soluble
440 sample to avoid periplasmic hydrogenase activity bands on the BN gel. The cell pellet was resuspended in 5
441 mL TRIS-HCL 50 mM pH 9, sodium carbonate 170 mM, EDTA 50 mM and incubate 30 min at 30°C under
442 gentle agitation (100 RPM). After centrifugation for 20 min at 20000 g, the incubation step was repeated
443 another time in the same condition. The cell pellet was then used to prepare the soluble extract as
444 described for the SDS-PAGE. BN gels were performed on 5-13% acrylamide gradient gel, according to the
445 method of Schägger (Schägger *et al.*, 1994, Schägger & von Jagow, 1991), as described by Le Laz et al.
446 (2014) (Le Laz *et al.*, 2014). In-gel hydrogenase activity was detected as described previously by Kpebe et al.
447 (2018) (Kpebe *et al.*, 2018) using methyl viologen as electron acceptor.

448 *Western immunoblots*

449 *D. fructosovorans* cells were grown in 100 mL bottles containing 90 mL of PS2 or PS20 medium.
450 When indicated, sulfate was replaced by 2 or 20 mM sodium thiosulfate, or 4 or 40 mM sodium fumarate.
451 Cells were harvested at late exponential phase or stationary phase of growth. Cells were disrupted at 100°C
452 for 10 min in a loading buffer in the presence of 215 mM β-mercaptoethanol, 15 mM DTT and 2 % SDS and
453 the extracts were centrifuged at 14 000g for 10 min. Soluble proteins in the supernatant were quantified
454 with the Bio-Rad protein assay based on Bradford dye binding method, using bovine serum albumin (BSA)
455 as a standard. Proteins were separated by 10% SDS-PAGE and electrotransferred to a nitrocellulose
456 membrane (Fastblot, Biometra). The membrane was blocked for 1 h in TBST (500 mM Tris-HCl pH 7.5, 1.5 M
457 NaCl, 0.2% Tween 20) containing 5% skim milk and incubated overnight at 4°C with a 5000-fold dilution of
458 the primary rabbit anti-HndD antibody in the same buffer. After three 10 min washes in TBST, the
459 membrane was developed using a 1/20 000 dilution of horseradish peroxidase-conjugated goat anti-rabbit
460 secondary antibody for 1 h and the ECL western blotting detection reagents (Amersham). The primary anti-
461 HndD antibody was generated by Eurogentec from a rabbit immunized with gel purified his-tagged HndD
462 protein. IgG from serum were purified by affinity chromatography (protein G Sepharose, GE Healthcare).
463 Protein loading was controlled by performing two identical SDS-PAGE in parallel. The first one was used for
464 western immunoblotting experiment while the second one was stained with Coomassie blue staining
465 solution. Protein quantification was done with Image J free software (NIH, LOCI, University of Wisconsin)
466 (Schneider *et al.*, 2012).

467 *Protein Identification by In-gel Digestion and Mass Spectrometry*

468 Gel electrophoresis bands of proteins from SDS-PAGE were put into a 96-well microplate (Greiner)
469 and in-gel trypsin digestion of proteins was performed according to Guiral et al. (2009) (Guiral *et al.*, 2009).
470 Proteins were identified by LC-MSMS as described previously by Guiral et al (2009) (Guiral *et al.*, 2009)
471 except that the peptides were separated by one dimension liquid chromatography on the reversed-phase
472 column C18 only, and that the proteins analysed here are soluble proteins instead of membrane proteins.
473 The database *Desulfovibrio fructosovorans* (TxID 878, 4701 entries) used was extracted from NCBI.

474 *Hydrogenase activity in total soluble extracts*

475 *Preparation of soluble extracts*

476 *D. fructosovorans* cells, grown in 1 L bottles containing 900 mL of PS2 medium were harvested at
477 the end of the exponential phase and resuspended in 10 mL of 100 mM Tris-HCl pH 8 supplemented with
478 protease inhibitors (SIGMAFAST™ Protease Inhibitor Cocktail Tablet, Sigma-Aldrich), DNase I (Roche) and
479 Lysozyme (Sigma-Aldrich). The cells were broken in an anaerobic glovebox (Jacomex) using a sonicator
480 (Hielscher) in 10 cycles of 1 minute of sonication then 1 minute of rest in a water bath chilled at 4°C. The
481 cell extract was ultracentrifuged at 200 000 g for 45 min at 4°C, then the soluble fraction was recovered,
482 and the total protein was quantified using the Bio-Rad protein assay based on Bradford dye binding
483 method, using bovine serum albumin (BSA) as a standard.

484 *H_2 evolution assays*

485 H_2 evolution assays were carried out using dithionite-reduced methyl viologen (50 mM reduced
486 with 23 mM sodium dithionite) as electron donor, in anaerobic 6.5 mL-serum bottles containing 1 mL
487 reaction mixture composed of Tris-HCl 0.1 M pH8, at 30°C. The gas phase was 100% N_2. The reaction was
488 started by the addition of 26.3 µg proteins of WT *D. fructosovorans* soluble extract or 226.5 to 377.5 µg
489 proteins of SM4 strain soluble extract. H_2 production was measured using gas chromatography (GC). Fifty
490 microliters of headspace gas was removed periodically from the vials using a gastight syringe and injected
491 into a GC system (Agilent 7820) equipped with a thermal conductivity detector and a Carbon-plot capillary
492 column (30 m, 0.53 mm, 3 µm), using nitrogen as the carrier gas, at a flow rate of 8.15 mL/min, an oven
493 temperature of 30 °C and a detector temperature of 200 °C. One unit of hydrogenase activity corresponds
494 to the production of 1 µmol of H_2/min.

495 *H_2 oxidation assays*

496 H_2-oxidizing activity measurements were performed in anaerobic quartz cuvettes, under 1 bar-
497 pressure of $_{H2,}$ in 800 µL of reaction mixture containing 100mM Tris-HCl pH 8.0, 2mM dithiothreitol (DTT),
498 and 50mM methyl viologen (Sigma Aldrich) as artificial electron acceptor. The reaction was started by the
499 addition of 0.5 to 7.5 µg proteins of WT *D. fructosovorans* soluble extract or SM4 strain soluble extract to

500 the mixture to start the reaction and methyl viologen reduction was monitored at 604 nm
501 (ε=13,600$M^{-1}.cm^{-1}$) using a UV-Vis spectrophotometer Lambda 25 (Perkin Elmer). One unit of hydrogenase
502 activity corresponds to the uptake of 1 µmol of H_2/min.

503 *RNA preparation*

504 *D. fructosovorans* cells, grown in 2 L bottles containing 1.8 L of PS2 or PS20 medium, were
505 harvested at the end of the exponential phase of growth. 10^{10} cells were pelleted, washed three times, and
506 resuspended in 200 µL of 10 mM Tris-HCl, pH 8. Total RNA was prepared using the High Pure RNA kit from
507 Roche Diagnostics according to the manufacturer's instructions. To remove genomic DNA contamination,
508 total RNA was then treated with the TURBO DNA-free™ kit (Life Technologies). RNA concentration and
509 purity were determined with a NanoDrop 2000 spectrophotometer (Thermo Scientific) and electrophoretic
510 migration on an agarose gel was performed to verify the absence of RNA degradation. The absence of
511 contaminant DNA was verified by PCR with the *Taq* DNA-dependent DNA polymerase (Fermentas) using
512 *16S* specific primers (16S-F and 16S-R, Table S3).

513 *Real-time quantitative PCR (RT-qPCR).*

514 Reverse transcription was performed on 500 ng of total RNA by using the SuperScriptIII reverse
515 transcriptase and random primers (Invitrogen). Real-time PCR runs were carried out on a CFX96 Real time
516 System (Bio-Rad). Cycling parameters of the real time PCR were 98°C for 2 min, followed by 45 cycles of
517 98°C for 5 s and 60°C for 10 s, ending with a melting curve analysis from 65°C to 95°C to determine the
518 specificity of the amplification. To determine the amplification kinetics of each product, the fluorescence
519 derived from the incorporation of EvaGreen into the double-stranded PCR products was measured at the
520 end of each cycle using the SsoFast™ EvaGreen® Supermix 2X Kit (Bio-Rad). The results were analyzed using
521 the Bio-Rad CFX Manager Software 3.0. The 16S rRNA gene was used as a reference for normalization. The
522 real-time quantitative PCR experiments were performed in duplicate assays with total RNA from at least
523 three independent growth experiments. Primers used for the real time PCR are listed in Table S3.

524

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533 The authors have no conflict of interest to declare.

534 **Author Contributions**

535 Conception and design of the study: MB and LS; acquisition, analysis, or interpretation of the data, NP, AK,
536 CG, CB, JR, RL and YD, LS and MB; writing of the manuscript: MB, NP and AK. All authors reviewed the
537 manuscript.

538

539 **Figure legends**

540 Figure 1: Growth curves of *Desulfovibrio fructosovorans* WT and SM4 strains. Bacteria were grown in PS0
541 (A, fermentation), PS2 (B, mixed culture condition) and PS20 (C, respiration) media containing no, 2 mM
542 and 20 mM sulfate respectively and 25 mM pyruvate as electron donor. WT strain, black curves; SM4 strain,
543 red curves. OD600 was followed as a function of time. OD units were converted into number of cells (1 mL
544 of cells at OD600 of 1 represents 10^9 cells). Data represent the averages of the results of three replicate
545 growths. Error bars correspond to standard deviations.

546 Figure 2: Pyruvate, acetate, ethanol and H_2 quantification. Pyruvate (open squares), acetate (closed
547 triangles) and ethanol (closed circles) in the growth medium and H_2 (open diamonds) in the headspace
548 were quantified by HPLC or GC during the growth of the *D. fructosovorans* WT strain (black curves) or SM4

549 mutant strain (red curves) under fermentation (PS0, A and D), mixed culture condition (PS2, B and E) or
550 respiration (PS20, C and F). Analysis were performed on the same *D. fructosovorans* cultures as those used
551 for the growth curves. Times indicated on the x-axis correspond to those in Figure 1. Data represent the
552 averages of the results of three replicate growths. Error bars correspond to standard deviations.

553 Figure 3: Proteomic analysis. (A) Separation by Coomassie-blue-stained SDS-PAGE of soluble proteins from
554 WT (lanes 1 and 3) and SM4 mutant (lanes 2 and 4) strains of *Desulfovibrio fructosovoran*s grown under
555 mixed (lanes 1 and 2) or respiratory (lanes 3 and 4) conditions. Cells were harvested at the end of the
556 exponential phase. 45 µg of soluble proteins were loaded in each lane of a 10 % SDS-PAGE. Molecular mass
557 markers (lane 5) are indicated in kDa. (B) Proteins identified by mass spectrometry (ion trap MS/MS) in
558 bands showing a different intensity in the two strains. Data correspond to identified proteins in bands 1, 2
559 and 3 from WT cells grown under mixed condition (panel A, lane 1). Only proteins identified with the
560 highest score in each gel band are reported (for the complete list of identified proteins, see Table S1). Table
561 heading: Protein name, protein name in NCBI database. NCBI entry, accession number. Unique peptides:
562 number of distinct peptides matching to protein sequence and unique to this protein. Sequence coverage,
563 protein sequence coverage by the matching peptides (in %). Theor. M_r, theoretical molecular mass in kDa of
564 the identified protein. These results are representative of several similar experiments.

565 Figure 4: Relative expression of the *adh*, *aor* and *hndD* genes quantified by RT-qPCR. *D. fructosovorans* WT
566 and SM4 strains were grown under mixed culture condition (PS2 medium) or under respiratory condition
567 (PS20 medium) and samples were collected at the end of the exponential phase of growth. Expression of
568 the genes was normalized to that of the 16S rRNA gene. These results are representative of several similar
569 experiments.

570 Figure 5: Hnd hydrogenase production and detection of its activity on BN-gel. (A) Western blot analysis of
571 HndD production by WT (lanes 1 and 2), SM4 (lane 3) and SM4/pBGhnd6 (lane 4) cells of *D. fructosovorans*
572 grown in medium containing 2 mM (PS2) (lanes 1, 3 and 4) or 20 mM (PS20) (lane 2) sulfate. Cells were
573 harvested at stationary phase of growth and 25 µg of total proteins from whole-cell protein extracts were
574 separated by 10% SDS-PAGE and subjected to Western blotting using an antibody raised against HndD. The

575 SDS-PAGE gel below the western blot is a loading control. (B) In-gel detection of hydrogenase activity in on
576 BN-gel of cytoplasmic proteins prepared from *D. fructosovorans* WT strain grown on PS20 (lane 1) or PS2
577 (lane 2) medium. 35 µg of cytoplasmic proteins were loaded on a 5–13% polyacrylamide gel. Molecular
578 weight markers are indicated in kDa (lane 3).

579 Figure 6: Relative *hndD* gene expression and production of ethanol by *D. fructosovorans* WT strain and the
580 complementation strain SM4/pBGhnd6 grown under mixed culture condition (PS2 medium). Samples were
581 collected at the end of the exponential phase of growth. (A) Relative expression of the *hndD* gene
582 quantified by RT-qPCR. Expression of the gene was normalized to that of the 16S rRNA gene. Error bars
583 correspond to standard deviations. (B) Ethanol concentration in the growth medium quantified with an
584 enzymatic kit. These results are representative of several similar experiments.

585 Figure 7: Model of the pyruvate oxidation pathway by *D. fructosovorans* under pyruvate fermentation
586 conditions. Pyruvate is converted into acetate by the 2 enzymes Pfo and Acs. Part of the acetate is
587 converted into ethanol by Aor and Adh. H_2 could be produced by the membrane NiFe-hydrogenase Ech
588 from reduced ferredoxin, which would contribute to the electrochemical proton gradient for ATP synthesis.
589 This model proposes that the role of the Hnd hydrogenase would be to produce reducing equivalents
590 (NADH and reduced ferredoxin) from H_2, allowing the production of ethanol. Pfo, pyruvate ferredoxin
591 oxidoreductase; Acs, Acetyl-CoA synthase; Aor, Aldehyde ferredoxin oxidoreductase; Adh, Alcohol
592 dehydrogenase; Ech and Hnd, Hydrogenases. Fd_{ox}, oxidized ferredoxin; Fd^{2-}, reduced ferredoxin. This figure
593 was created with BioRender.com.

594 Figure S1: Growth curve, sulfate consumption and H_2 production by *D. fructosovorans* WT cells. Bacteria
595 were grown in PS2 medium (mixed culture condition). Sulfate concentration in the growth medium was
596 determined using a turbidimetric method with barium chloride. H_2 in the headspace was quantified using
597 GC. H_2 starts to accumulate when sulfate is completely reduced.

598 Figure S2: Western blot analysis of HndD production by *D. fructosovorans* WT cells grown in medium
599 containing 25 mM pyruvate and 20 mM thiosulfate (lane 1), 2 mM thiosulfate (lane 2), 40 mM fumarate

600 (lane 3) or 4 mM fumarate (lane 4) as electron acceptor. Cells were harvested at late exponential phase of
601 growth and 2 µg of total proteins from whole-cell protein extracts were separated by 10% SDS-PAGE and
602 subjected to western blotting using an antibody raised against HndD. The SDS-PAGE gel below the western
603 blot is a loading control.

604 Figure S3: Separation by Coomassie-blue-stained SDS-PAGE of soluble proteins from WT (lane 2), SM4
605 mutant (lane 3) and SF mutant (lane 4) strains of *Desulfovibrio fructosovoran*s grown under mixed
606 conditions (PS2). Cells were harvested at the end of the exponential phase. 45 µg of soluble proteins were
607 loaded in each lane of a 10 % SDS-PAGE. Molecular mass markers (lane 1) are indicated in kDa.

608 Figure S4: Growth curves of *Desulfovibrio fructosovorans* WT, SM4 (Δ*hndD*), SM4/pBGhnd6 and SF
609 (Δ*hydAB*) strains. Bacteria were grown in PS2 medium containing 25 mM pyruvate as electron donor and 2
610 mM sulfate as electron acceptor (mixed culture condition).

611 Figure S5: Predicted Rex binding-site in the promoter region of *hnd*. (A) Sequence logo of the DNA
612 recognition motif for all Rex sites in the order Desulfovibrionales. The sequence logo was constructed
613 based on the alignment of 117 sites identified as Rex recognition sequences (available in the RegPrecise
614 database). (B) Consensus sequence of the Rex binding sites in the promoter region of the tetrameric,
615 cytoplasmic [FeFe] hydrogenases found in *Desulfovibrio.* The consensus sequence was constructed by
616 aligning the known sites with ClustalW multiple alignment. (C) The Rex binding sites and their locations in
617 the promoter region of the tetrameric, cytoplasmic [FeFe] hydrogenases in *Desulfovibrio* species. The
618 promoter region sequences were taken from NCBI and the Rex-binding site was mapped. Identical residues
619 between the species are highlighted in red.

620

621 **Table**

622 Table 1: Growth parameters of WT and SM4 *D. fructosovorans* strains.

Medium		Doubling time (h)		Maximum cell count/mL†	
		WT	SM4	WT	SM4
PS0		369.0±73.5	519.5±100.7	$6.90\times10^{8} \pm 4.0\times10^{7}$	$6.70\times10^{8} \pm 3.0\times10^{7}$
PS2	**Phase 1** 0-40 hrs	17.2±0.9	17.4±5.7	$1.12\times10^{9} \pm 1.0\times10^{7}$	$1.16\times10^{9} \pm 2.0\times10^{7}$
	Phase 2 40-110 hrs	89.3±3.5	114.2±1.1		
PS20		20.5±0.3	15.3±1.2	$1.33\times10^{9} \pm 1.0\times10^{7}$	$1.41\times10^{9} \pm 4.0\times10^{7}$

623 † The highest optical density at 600 nm was converted into number of cells (1 mL of cells at OD600 of 1
624 represents 10^{9} cells). Data are mean values +/- standard deviation and were obtained from triplicate
625 separated experiments.

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