Title

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Journal

Applied and Environmental Microbiology, 86(11)

ISSN

0099-2240

Authors

Nies, Salome C
Dinger, Robert
Chen, Yan
et al.

Publication Date

2020-05-19

DOI

10.1128/aem.03038-19

Peer reviewed

A systems analysis of NADH dehydrogenase mutants reveals flexibility and limits of *Pseudomonas taiwanensis* VLB120's metabolism

Salome C. Nies[1], Robert Dinger[2], Yan Chen[3], Gossa G. Wordofa[4], Mette Kristensen[4], Konstantin Schneider[4], Jochen Büchs[2], Christopher J. Petzold[3,5], Jay D. Keasling[3,4,5,6,7,8,9,10], Lars M. Blank[1*], Birgitta E. Ebert[1,11,12]

[1]iAMB-Institute of Applied Microbiology, ABBt-Aachen Biology and Biotechnology, RWTH Aachen University, Aachen, DE
[2]AVT – Biochemical Engineering, RWTH Aachen University, Aachen, DE
[3]Joint BioEnergy Institute, Emeryville, CA 94608, USA.
[4]Novo Nordisk Foundation Center for Biosustainability, Technical University of Denmark, DK-2800 Lyngby, DK
[5]Lawrence Berkeley National Laboratory, Biological Systems and Engineering Division, Berkeley, CA 94720, USA.
[6]Virtual Institute of Microbial Stress and Survival, Lawrence Berkeley National Laboratory, Berkeley, CA 94720, USA
[7]Physical Biosciences Division, Lawrence Berkeley National Laboratory, Berkeley, CA 94720, USA
[8]Dept. of Bioengineering, University of California, Berkeley, CA 94720, USA
[9]Dept. of Chemical Engineering, University of California, Berkeley, CA 94720, USA
[10]Synthetic Biochemistry Center, Institute for Synthetic Biology, Shenzhen Institutes for Advanced Technologies, Shenzhen, China
[11]Australian Institute for Bioengineering and Nanotechnology (AIBN), the University of Queensland, Brisbane, QLD 4072, Australia
[12]CSIRO Future Science Platform in Synthetic Biology, Commonwealth Scientific and Industrial Research Organisation (CSIRO), Black Mountain, ACT 2601, Australia

* Corresponding author

Running title: NADH dehydrogenase deficiency in *P. taiwanensis*

Keywords *Pseudomonas*; NADH dehydrogenase; respiratory activity; oxidative stress; electron transport chain

Abstract

Obligate aerobic organisms rely on a functional electron transport chain for energy conservation and NADH oxidation. Because of this essential requirement, the genes of this pathway are likely constitutively and highly expressed to avoid a cofactor imbalance and energy shortage under fluctuating environmental conditions. We here investigated the essentiality of the three NADH dehydrogenases of the respiratory chain of the obligate aerobe *Pseudomonas taiwanensis* VLB120 and the impact of the knockouts of corresponding genes on its physiology and metabolism. While a mutant lacking all three NADH dehydrogenases seemed to be nonviable, the generated single or double knockout strains displayed no, or only a weak, phenotype. Only the mutant deficient in both type-2 dehydrogenases showed a clear phenotype with biphasic growth behavior and a strongly reduced growth rate in the second phase. In-depth analyses of the metabolism of the generated mutants including quantitative physiological experiments, transcript analysis, proteomics, and enzyme activity assays revealed distinct responses to type-2 and type-1 dehydrogenase deletions. An overall high metabolic flexibility enables *P. taiwanensis* to cope with the introduced genetic perturbations and maintain stable phenotypes, likely by re-routing of metabolic fluxes. This metabolic adaptability has implications for biotechnological applications. While the phenotypic robustness is favorable in large-scale applications with inhomogeneous conditions, the possible versatile redirecting of carbon fluxes upon genetic interventions can thwart metabolic engineering efforts.

Importance

While *Pseudomonas* has the capability for high metabolic activity and the provision of reduced redox cofactors important for biocatalytic applications, exploitation of this characteristic might be hindered by high, constitutive activity of and, consequently,

competition with the NADH dehydrogenases of the respiratory chain. The in-depth analysis of NADH dehydrogenase mutants of *Pseudomonas taiwanensis* VLB120 presented here, provides insight into the phenotypic and metabolic response of this strain to these redox metabolism perturbations. The observed great metabolic flexibility needs to be taken into account for rational engineering of this promising biotechnological workhorse towards a host with controlled and efficient supply of redox cofactors for product synthesis.

Introduction

Many industrially relevant molecules, e.g., ethanol, butanediol or isoprene, are more reduced than the industrially-used sugars glucose and sucrose or alternative, upcoming carbon sources such as xylose or glycerol (1-3). The microbial production of those favored compounds hence is inherently redox limited, i.e., by the supply of reduced redox cofactors, generally NADH or NADPH. This bottleneck has been overcome in some cases, e.g., 1,4 butanediol and 1,3-propanediol production in *Escherichia coli* (4, 5) or L-lysine synthesis in *Corynebacterium glutamicum* (6). The strategies applied optimized the host metabolism by metabolic engineering (4, 7, 8) or adapted the process conditions by (co-)feeding reduced substrates (9), applying microaerobic conditions or using nongrowing cells with reduced competition and cellular demand for the redox cofactor (10-13). Alternatively, microorganisms can be applied that naturally outperform the classic, industrial workhorses with respect to redox cofactor supply. Pseudomonads are outstanding in this regard as they exhibit a driven-by-demand phenotype, which allows them to strongly enforce the metabolic activity under stress conditions with increased energy demand, reported to result in a more than 2-fold carbon uptake rate and an even 8-fold increase of the NAD(P)H regeneration rate relative to standard growth conditions (12, 14, 15). This behavior holds great promise for using this species for the bioproduction of highly reduced chemicals such as phenol, (*S*)-styrene oxide, rhamnolipids, and methyl ketones (16-20). Yet, competition is high as the NAD^+/NADH couple functions as a coenzyme in over 300 oxidation/reduction reactions (21). *Pseudomonas* strains without apparent fermentative metabolism are obligate aerobes that rely on constitutive activity of the NADH dehydrogenases to ensure adequate oxidation of NADH to NAD^+. Hence, we argue here that a naturally high NADH oxidation activity might impair the effective fueling of production pathways with reducing equivalents. We here set out to provide an in-depth analysis of the redox metabolism of *Pseudomonas taiwanensis* VLB120, a

strictly aerobic bacterium, focusing on the role and essentiality of the individual NADH dehydrogenases for NADH oxidation and energy conservation.

While the mammalian mitochondrial electron transport chain constitutes only NADH dehydrogenase type-1, a multi-subunit enzyme referred to as Nuo or complex 1 (22), which couples the electron transfer to proton translocation and hence contributes to ATP generation (23), aerobic bacteria have developed diverse NADH oxidation capabilities linked to the respiratory chain. Besides, the Nuo complex, most species possess one to two isozymes of the non-proton translocating type-2 dehydrogenase (Ndh), also termed alternative NADH dehydrogenase, which transfers electrons from NADH to ubiquinone but does not contribute to the membrane potential (23, 24). In some species a third sodium pumping type-3 dehydrogenase (Nqr) can be found. As with the facultative aerobic yeast *Saccharomyces cerevisiae*, several bacteria lack the Nuo complex and only possess a type-2 dehydrogenases or are reported to mainly rely on the activity of this enzyme for NADH re-oxidation (25, 26). Likewise, the genome of *P. taiwanensis* VLB120 encodes two types of NADH dehydrogenases, type-1 (EC 7.1.1.2) and two isoforms of type-2 (EC 1.6.99.3). Type-1 is encoded by the genes PVLB_15600-15660 designated as the *nuo* operon. The two type-2 NADH dehydrogenases are encoded by PVLB_13270 and PVLB_21880, designated as *ndh1* and *ndh2*, respectively. Ndh1 and Ndh2, both consist of a single polypeptide chain.

In the present study, NADH dehydrogenase mutants of *P. taiwanensis* VLB120 were generated and characterized regarding growth, respiratory activity, and transcriptional and proteomic changes to elucidate the impact of redox metabolism perturbation on the cellular physiology.

Results

NADH dehydrogenase activity is vital for *P. taiwanensis* but single enzymes of the redundant oxidation system are dispensable.

The NADH dehydrogenase type-1 operon encoded by *nuoA-N* (PVLB_15600-15660) and the two type-2 NADH dehydrogenases encoded by *ndh1* (PVLB_13270) and *ndh2* (PVLB_21880) were successfully deleted from the *P. taiwanensis* VLB120 genome using the I-SceI-based pEMG plasmid (27). The double knockout mutants ΔΔ*ndh* and Δ*nuo*Δ*ndh1* were successfully obtained, however, several attempts failed to generate the double knockout of *Δnuo* and *Δndh2*. All gene deletions were confirmed by Sanger sequencing. The five NADH-dehydrogenase mutants demonstrated that the NADH dehydrogenases, Nuo, Ndh1, and Ndh2 are not essential individually. While the presence of either Nuo or Ndh2 is sufficient to sustain the viability of *P. taiwanensis* VLB120, Ndh1 seems to be unable to compensate for the loss of Nuo and Ndh2. Similarly, it has been reported that single deletions of NADH dehydrogenases in *P. aeruginosa* PAO1 did not result in a growth defect or decrease in NADH oxidation activity, whereas in the double (Δ*nuoIJ*Δ*ndh*) and triple knockout (Δ*nuoIJ*Δ*ndh*Δ*nqrA-F*) the NADH oxidation activity was abolished (28). Concludingly, Nuo and Ndh account for the total NADH dehydrogenase activity in this *Pseudomonas* strain. Note that *P. aeruginosa* is a facultative anaerobe able to respire on nitrate and ferment pyruvate while *P. taiwanensis* VLB120 does not possess the necessary enzymatic makeup.

A likewise total loss of NADH dehydrogenase activity in the obligate aerobic *P. taiwanensis* VLB120 strain seems to be lethal indicating that the strain relies on the presence of these dehydrogenases for NADH oxidation and that alternative, native NADH consuming reactions do not suffice to efficiently re-oxidize this vital cofactor under the tested conditions.

The ΔΔ*ndh* mutant exhibits a growth-phase dependent growth defect

P. taiwanensis VLB120 and the five NADH dehydrogenase deletion strains Δ*ndh1*, Δ*ndh2*, ΔΔ*ndh*, Δ*nuo*, and Δ*nuo*Δ*ndh1* were characterized for growth, glucose utilization, CO_2 formation, and oxygen consumption in batch shake-flask experiments. The single NADH-dehydrogenase type-2 mutants, Δ*ndh1* and Δ*ndh2*, showed the same growth and

147 sugar co-utilization profile as the wild type *P. taiwanensis* VLB120 (Figure 1A, B, and C).
148 The loss of the megaplasmid pSTY during NADH dehydrogenase deletions resulted in a
149 growth advantage for the generated mutants, which was determined to result in a 14 %
150 higher growth rate for *P. taiwanensis* VLB120 pSTY$^-$ compared to the pSTY$^+$ wild type
151 (29). For a comparison of mutants and wild type, the growth rate of the wild type was
152 corrected accordingly and is referred to as μ_{recalc}.
153 While the single gene deletion mutants Δ*ndh1* and Δ*ndh2* showed a wild-type physiology
154 (Figure 1, Table 1), the type-2 double mutant ΔΔ*ndh* reproducibly showed two growth
155 phases (Figure 1D). After wild type-like growth in the first phase, the growth rate dropped
156 drastically in the second growth phase. Interestingly, the strong decrease in the growth
157 rate (~86 %) was not correlated with an equal reduction of the carbon uptake, which
158 showed a decrease of only ~38 %.
159 *Pseudomonas* can catabolize glucose either via the phosphorylative or the oxidative
160 pathway. In the latter, a membrane-bound glucose dehydrogenase (*gcd*) oxidizes
161 periplasmic glucose to gluconate coupled with the reduction of pyrroloquinoline quinone
162 (PQQ). The phosphorylative pathway starts in the cytoplasm with the phosphorylation of
163 glucose to glucose-6-phosphate catalyzed by the glucokinase (Glk) (30, 31).
164 The mutant ΔΔ*ndh* showed a significant increase in the specific gluconate yield in the
165 early exponential growth phase. The same behavior was observed in the Δ*nuo* and
166 Δ*nuo*Δ*ndh1* mutants (Table 1).
167 Besides the characterization for growth and glucose consumption, the respiratory
168 behavior of the wild type and NADH dehydrogenase mutants was studied (Figure 2,
169 Supplementary Figure S1). Again, only the ΔΔ*ndh* mutant showed a different phenotype
170 characterized by a stagnating oxygen transfer rate (OTR) after 6 hours (Figure 2B). This
171 change in the OTR development is an indication for substrate inhibition, here, potentially
172 by NADH, which cannot be oxidized at the rate required for fast growth. The onset of the

reduced specific oxygen uptake rate also correlated well with the change of the growth rate (Figure 1D).

During growth on glucose, the respiratory quotient (RQ), defined as the ratio of OTR and CTR, is generally close to one (32, 33). Due to the oxidation of glucose to gluconate in the periplasm of *Pseudomonas* strains, the measured OTR for all tested mutants during the first 6 hours of cultivation was higher than the CTR resulting in an RQ below 1 (Figure 2A, Supplementary Figure S1). Indeed, the surplus of consumed oxygen, calculated from the sectional integrals between the OTR and CTR ($\int OTR\, dt - \int CTR\, dt$), correlated with the produced gluconate (Table 1, Figure 2A). During glucose conversion, roughly half of the overall consumed oxygen was used for the oxidation of glucose to gluconate and the re-oxidation of the reduced PQQ formed by the glucose dehydrogenase activity. Consequently, in the glucose phase, the cells can partially uncouple glucose oxidation and energy provision from NADH formation, relieving the dependence on NADH dehydrogenase activity. The O_2 and CO_2 transfer rate (CTR) of Δ*ndh2* and ΔΔ*ndh* (Supplementary Figure S1) showed a double peak, which occurred in the same time frame as glucose depletion, and, hence, might be due to the diauxic shift from glucose to gluconate. We assume that the diauxic shift also occurred in the other strains but was not recorded by the measurement frequency of three measurements per hour. The respiratory coefficient on gluconate was close to one for all *Pseudomonas* strains, indicating that no products other than biomass and CO_2 were formed during catabolism of this substrate.

NADH dehydrogenase gene deletions affect expression levels but do not result in altered *in vitro* NADH oxidation activities

To further elucidate the NADH oxidation activity in the different mutants, and hence, the importance of the three NADH dehydrogenases for oxidizing NADH and fueling the electron transport chain, we performed *in vitro* NADH oxidation assays. Inverted

membrane vesicles were prepared at early-, mid-, and late-exponential growth phase, and the NADH oxidation rate was determined from the decrease in absorbance at 340 nm over time. Note that the SDS PAGE of the membrane fraction showed up to 21 prominent protein bands (data not shown). Therefore, we cannot exclude the presence of further membrane-bound NADH-dependent enzymes, e.g., the transhydrogenase PntAB, which might have contributed to the measured NADH oxidation rate. However, there is a high probability that the NADH oxidation is very specific for NADH dehydrogenases as most NADH-dependent enzymes, e.g., alcohol or aldehyde dehydrogenase, require electron acceptors other than O_2. Additional experiments with alternative electron acceptors have not been performed. In the early-exponential growth phase, in which none of the strains showed a growth defect, all single mutants possessed NADH oxidation activities at levels similar to the wild type of around 1.2 U mg protein^{-1} (Table 4), which is in the range of *in vitro* rates reported for other organisms (34). Overall, the NADH oxidation rate was rather stable in all mutants, indicating high metabolic flexibility of *P. taiwanensis* VLB120 to maintain redox homeostasis.

To further substantiate this hypothesis, we examined potential changes at the transcriptional level by qPCR on samples taken in the early, mid-, and late-exponential growth phase. HPLC analysis showed that glucose and/or gluconate were still left when sampling the late-exponential growth phase, i.e., the cells were still metabolically active (data not shown). The fold changes were normalized against the wild type in the corresponding growth phase. The single and double deletions of the type-2 NADH dehydrogenase encoding genes (Figure 3A-C) had only minor effects (fold change < 2) on the remaining NADH dehydrogenase gene expression. While the type-1 deletions strains, Δ*nuo* and Δ*nuo*Δ*ndh1*, showed a substantial upregulation of the *ndh2* gene expression (Figure 3D-E). The expression of the *ndh1* gene in both the Δ*nuo* and Δ*nuo*Δ*ndh1* was unaffected; we only observed a small increase for mutant Δ*nuo* in the

early growth phase. This finding suggests that *ndh2* is probably the only NADH dehydrogenase gene that is regulated in response to the cellular NADH/NAD^+ ratio. The consequent essentiality would further explain why the double deletion of *nuo* and *ndh2* was lethal. The observation that Δ*ndh* is only growth impaired during mid- to late-exponential growth indicates that either the Nuo complex is less active in these phases or that the PQQ-dependent glucose dehydrogenase activity during the early growth phase enables sufficient ATP synthesis independent of NADH dehydrogenase activity.

Double deletion of the type-2 NADH dehydrogenases affect intracellular redox cofactor levels

We found that the NADH oxidation rate was not or only slightly compromised by the introduced gene deletions but that the *ndh2* level was significantly upregulated, suggesting that its expression is controlled by the redox state of the cell. Moreover, even though we performed the *in vitro* enzyme assay with a physiological meaningful NADH concentration of 125 µM (35) to mimic *in vivo* conditions, we cannot exclude differences between the actual *in vivo* NADH dehydrogenase activities of the mutants as the redox cofactor levels might have been altered.

For that reason, we determined the intracellular abundance of NADH and NAD^+ in the early-, mid-, and late-exponential growth phase. Since the two single mutants of type-2 had no growth phenotype and showed no apparent changes on the transcriptional level, we restricted the analysis to the two double mutants and single *nuo* deletion mutant Δ*nuo*, Δ*ndh,* and Δ*nuo*Δ*ndh1*.

The Δ*nuo*Δ*ndh1* showed a higher NADH/NAD^+ ratio in the late-exponential growth phase but also a high variability in the triplicate experiments curtailing the statistical significance. The double mutant Δ*ndh* had a significantly increased NADH/NAD^+ ratio in the mid- and late-exponential growth phase compared to the wild type (Figure 4). This significantly increased NADH/NAD^+ ratio in Δ*ndh* probably triggered the observed drop in the growth rate in the mid-exponential phase, e.g., because of a potential inhibition of the Nuo

complex. To prove this hypothesis, we overexpressed the water-forming NADH oxidase (Nox) from *Streptococcus pneumoniae* (36). Nox is known to be very specific for NADH, unable to oxidize NADPH and has been described to produce no toxic hydrogen peroxide (37). The enzyme activity hence solely results in NADH oxidation and is suitable to elucidate the effect of relief from NADH accumulation. The overexpression of *nox* did not restore the wild type phenotype but we observed a higher respiratory activity in mutant Δ*ndh* Nox$^+$ in comparison to mutant Δ*ndh* (Supplementary Figure S3). In contrast to the response of *P. putida* KT2440, Nox activity in Δ*ndh* did not lead to a decrease in growth rate or biomass yield (14, 38).

Proteomics analysis reveals re-routing of the carbon flux in the Δ*ndh* mutant

We further performed shotgun proteomics analysis to explain possible metabolic changes in early-, mid-, and late-exponential growth phase in *P. taiwanensis* VLB120 due to NADH dehydrogenase deletions. The relative quantitative data were used to categorize the detected proteins into three groups: (1) significantly upregulated or (2) downregulated proteins (fold change > 2, adjusted p-value < 0.05), and (3) weak/no effect proteins (fold change < 2). The proteins were further grouped into functional categories according to the KEGG database classification (39), e.g., transport, carbohydrate metabolism, amino acid metabolism (Supplementary Table S 2). The most strongly represented categories are summarized in Figure 5.

Per the physiological and transcript data, we did not observe significant changes in the proteome for either NADH dehydrogenase type-2 single mutants (Δ*ndh1*: 9 of 24 proteins significantly up/downregulated, Δ*ndh2*: 8 of 36 proteins significantly up-/downregulated; Figure 5, Supplementary Table S2, Supplementary File S3). Proteomic changes in both type-1 mutants (Δ*nuo*: 50 of 139 proteins significantly up-/downregulated, Δ*nuo*Δ*ndh1*: 60 of 165 proteins significantly up-/downregulated) were more significant compared to the type-2 single-gene knockout mutants and very similar to each other (Figure 5). The double deletion mutant Δ*ndh* showed more alterations in the proteome in the early- and

279 late-exponential phase (17 and 37 of 107 proteins significantly up-/downregulated) than
280 in the mid-exponential phase (2 significantly up-/downregulated proteins) (Figure 5 and
281 Supplementary Table S2).
282 In the following paragraphs, we are focusing on changes observed in the ΔΔ*ndh* mutant
283 for proteins related to carbon uptake, energy generation, and oxidative stress response
284 and are highlighting distinct differences to the type-1 NADH dehydrogenase mutants.
285 The OprB-I porin (PVLB_20075), a carbohydrate selective porin, and the D-gluconate
286 transporter GntT (PVLB_13665) located in the outer and inner membrane, respectively,
287 were higher increased in the ΔΔ*ndh* mutant during the early- and late-exponential growth
288 phase, while the glucokinase quantity was strongly reduced in all growth phases. These
289 data suggest that ΔΔ*ndh* oxidized glucose via glucose dehydrogenase (Gcd) to gluconate
290 to a greater extent than the wild type. In contrast, the quantity of OprB-I in the type-1
291 NADH dehydrogenase mutants during the later growth phase was decreased. This
292 change might, however, be explained by the faster glucose depletion in these mutants
293 (Figure 1).
294 During the late-exponential growth of the ΔΔ*ndh* mutant, all enzymes of the arginine
295 deiminase (ADI) pathway were more strongly expressed while they were significantly
296 downregulated in the NADH dehydrogenase type-1 mutants (Table 6). This pathway
297 catalyzes a three-step conversion of arginine to ornithine, ammonium, and carbon dioxide
298 coupled to ATP generation (40). Likewise, the isocitrate lyase (AceA), the first enzyme of
299 the glyoxylate shunt, was upregulated in the ΔΔ*ndh* mutant but downregulated in the Δ*nuo*
300 mutant, which instead showed a slight upregulation of the 2-oxoglutarate dehydrogenase
301 complex of the TCA cycle during mid- and late-exponential growth. These changes
302 indicate that the mutant ΔΔ*ndh* used the glyoxylate shunt and not exclusively the TCA
303 cycle in the late-exponential growth phase.

We further observed remarkable changes in proteins combating oxidative stress. While deletion of the *nuo* operon (Δ*nuo* and Δ*nuo*Δ*ndh1)* resulted in a generally reduced abundance of proteins involved in the oxidative stress response, those mutants deficient in one of the two type-2 dehydrogenases displayed increased levels of peroxidases and peroxiredoxin proteins. The abundance of the catalase-peroxidase KatG was strongly decreased in both type-1 mutants, whereas it was weakly increased in the ΔΔ*ndh* mutant. Additionally, only the peroxidase encoded by PP_0235 and the quinone reductase ChrR were more highly expressed in the ΔΔ*ndh* mutant with the latter being reported to be induced by superoxide (41) while peroxiredoxin AhpC was weakly upregulated in the single-gene deletion mutants, Δ*ndh1* and Δ*ndh2* (Supplementary File S3). These findings indicate that the deletion of both type-2 dehydrogenases increases oxidative stress. We determined ROS formation in *P. taiwanensis* VLB120 and mutant ΔΔ*ndh* using the ROS–sensitive dye H_2-DCFA (2',7'-dichlorodihydrofluorescein diacetate), which is oxidized by ROS to fluorescent DCF. Indeed, we observed an increase in ROS formation in ΔΔ*ndh* concomitant with the reduction in growth (Supplementary Figure S2) underlining the proteomics results and strengthening our hypothesis.

Discussion

The presented in-depth analysis of NADH dehydrogenase mutants revealed high metabolic robustness of *P. taiwanensis* VLB120 to a partial loss of the three NADH dehydrogenases, but also the essentiality of residual NADH dehydrogenase activity, as the simultaneous deficiency of Nuo and Ndh2 was lethal likely due to inefficient NADH oxidation or ATP provision.

In accordance with the observed phenotypic robustness of most mutants, *in vitro* NADH oxidation activities in the mutant strains were not reduced. While this can be explained for those mutants deficient in the *nuo* operon with a significant upregulation of *ndh2*, no transcriptional changes of NADH dehydrogenase related genes were observed for the

other mutants. In contrast, the mutant with Nuo as the sole NADH dehydrogenase (ΔΔ*ndh*) showed a growth phenotype in the mid-exponential growth phase. While the *in vitro* NADH oxidation capacity was not altered, several changes in protein and metabolite levels were observed. We have summarized our current model of the potential underlying metabolic changes in Figure 6. The wild type-like growth of the ΔΔ*ndh* mutant on glucose is likely sustained by periplasmic glucose oxidation to gluconate instead of phosphorylation, which partially uncouples the oxidation of the carbon source from NADH formation. The increased gluconate yield of the ΔΔ*ndh* mutant underlines this hypothesis. The monitored respiratory activity and the match of gluconate accumulation and surplus oxygen consumption emphasize that no side products other than gluconate were produced to sustain the wild type-like growth. *In vitro* studies have shown the formation of reactive oxygen species (ROS) such as superoxide ($O_2^{\bullet -}$) and hydrogen peroxide (H_2O_2) by enzymes of the electron transport chain due to electron leakage to oxygen. Cells activate antioxidant defense system to combat ROS, which can result in severe cell damage or even death. Nuo (complex I) and cytochrome bc1 (complex III) are considered the main sites for ROS in mitochondria and *P. fluorescens* (42, 43) but rather the type-2 dehydrogenase in *E. coli*, which does not possess complex III (44). It has further been reported that an oversupply of NADH can enhance ROS production (45, 46).

The observed ROS accumulation in ΔΔ*ndh* during mid-exponential growth phase might, hence, be either due to an increased Nuo activity relative to the wild type or the elevated $NADH/NAD^+$ ratio. In line with this hypothesis, it has been shown that *M. tuberculosis* NADH dehydrogenase mutants with a similarly elevated $NADH/NAD^+$ ratio were more susceptible to (additional) oxidative stress than those with a lower $NADH/NAD^+$ ratio (47). ROS induced stress but also a potential NADH inhibition of metabolic enzymes might further explain the reduced growth and respiratory activity. However, while the latter

355 increased upon *nox* expression, Nox mediated NADH oxidation did not restore growth,
356 indicating that further limitations remained.
357 The activation of the glyoxylate shunt in ΔΔ*ndh*, as indicated by the proteome data, might
358 contribute to stress reduction in two ways. Firstly, this shortcut of the TCA cycle bypasses
359 NAD(P)H-producing steps (48-50). For *Pseudomonas putida* KT2440, the production of
360 a surplus of NADPH during growth on glucose has been reported (51) and it was
361 speculated that the excess NADPH is converted to NADH by the transhydrogenase
362 PntAB, which has been shown to be expressed in this strain under similar growth
363 conditions (38). Assuming PntAB transhydrogenase activity in *P. taiwanensis*, which is
364 equipped with the respective genes, attenuated $NADP^+$ reduction would, hence, result in
365 an overall reduced NADH formation. Secondly, the glyoxylate formed by the isocitrate
366 lyase AceA activity, which was upregulated in ΔΔ*ndh*, can react with hydrogen peroxide
367 to produce formate and CO_2 (48, 52). This ROS combating strategy has been reported
368 for *Pseudomonas aeruginosa*, *Burkholderia cenocepacia*, and *Staphylococcus aureus*,
369 even though *S. aureus* has no functional glyoxylate shunt (48, 53-55). Note, however,
370 that neither higher formate dehydrogenase abundance nor formate accumulation was
371 observed in the ΔΔ*ndh* mutant.
372 The deletion of *nuo* and the accompanied higher Ndh2 activity did not result in a similar
373 stress response, which is in accordance with corresponding *M. tuberculosis* mutants (47).
374 A probable energy shortage due to reduced respiratory activity might have been
375 counteracted by ATP generation via the ADI pathway, which seems to be activated in
376 ΔΔ*ndh* according to the proteome data. This pathway generates 1 mol ATP per mol
377 arginine (40, 56) and was described to be activated upon energy depletion in lactic
378 bacteria (57) and Pseudomonads, e.g., in *P. putida* DOT-T1E under energy-demanding
379 solvent stress conditions (58, 59) and in *P. aeruginosa* under oxygen limiting conditions
380 (40).

In this study, we showed high metabolic flexibility of *P. taiwanensis* VLB120 to interventions in the redox metabolism, which confers robust phenotypic behavior by a possible re-routing of metabolic fluxes. This metabolic adaptability and phenotypic robustness can be advantageous for biocatalysis but simultaneously be challenging because it impedes the prediction of mutant behavior and can lever out metabolic engineering efforts. Hence, to effectively turn this promising microbe into a controllable, biotechnological workhorse, further systems biological and physiological analyses, such as ^{13}C-metabolic flux analysis, are needed.

Materials and Methods

Strains, media and culture conditions

Bacterial strains used in this study are listed in Table 4. Strains were propagated in Lysogeny Broth (LB) containing 10 g L^{-1} peptone, 5 g L^{-1} sodium chloride, and 5 g L^{-1} yeast extract (60). Cetrimide agar (Sigma-Aldrich, St. Louis, MO, USA) was used after mating procedures to select for *Pseudomonas*. Growth and characterization experiments were performed using mineral salt medium (MSM) (61) containing 3.88 g L^{-1} K_2HPO_4, 1.63 g L^{-1} NaH_2PO_4, 2 g L^{-1} $(NH_4)_2SO_4$, 0.1 g L^{-1} $MgCl_2{\cdot}6H_2O$, 10 mg L^{-1} EDTA, 2 mg L^{-1} $ZnSO_4{\cdot}7\ H_2O$, 1 mg L^{-1} $CaCl_2{\cdot}2H_2O$, 5 mg L^{-1} $FeSO_4{\cdot}7\ H_2O$, 0.2 mg L^{-1} $Na_2MoO_4{\cdot}2H_2O$, 0.2 mg L^{-1} $CuSO_4{\cdot}5\ H_2O$, 0.4 mg L^{-1} $CoCl_2{\cdot}6\ H_2O$, 1 mg L^{-1} $MnCl_2{\cdot}2\ H_2O$ supplemented with 25 mM glucose. For the preparation of solid LB, 1.5 % agar was added to the medium. For plasmid maintenance and in the gene deletion procedure, antibiotics were added to the medium as required. Gentamycin and kanamycin were used at concentrations of 25 mg L^{-1} and 50 mg L^{-1}, respectively. Because of the leaky expression of *nox* from plasmid pS2311, *P. taiwanensis* VLB120 strains bearing plasmid pS2311·were grown without the addition of the inducer cyclohexanone.

Batch flask experiments were performed in 50 mL medium in 500-mL flasks under oxic conditions on a horizontal rotary shaker with a throw of 50 mm and frequency of 300 rpm.

E. coli was grown at 37 °C, *Pseudomonas* at 30 °C. The chemicals used in this work were obtained from Carl Roth (Karlsruhe, Germany), Sigma-Aldrich (St. Louis, MO, USA), or Merck (Darmstadt, Germany) unless stated otherwise. The main cultures were inoculated from liquid pre-cultures to an approximate OD_{600nm} of 0.05. All experiments were performed in biological triplicates unless stated otherwise.

Plasmid cloning and generation of deletion strains

Genomic DNA of *P. taiwanensis* VLB120 was isolated using the High Pure PCR Template Preparation Kit (Hoffmann-La-Roche, Basel, Switzerland). Upstream (TS1) and downstream (TS2) regions with a length of 400-800 bp flanking the specific target gene were amplified using Q5 High-Fidelity Polymerase (New England Biolabs, Ipswich, MA, USA). Primers were ordered as unmodified DNA Oligonucleotides from Eurofins Genomics (Ebersberg, Germany) and are listed in Table S5. The suicide delivery vector pEMG was isolated using the NEB Monarch Plasmid Miniprep Kit (New England Biolabs, Ipswich, MA, USA). The isolated plasmid was digested with restriction enzymes purchased from New England Biolabs (Ipswich, MA, USA). For plasmid construction, Gibson Assembly using NEB Builder Hifi DNA Assembly (New England Biolabs, Ipswich, MA, USA) was used. Plasmids were transformed into electrocompetent *E. coli* DH5α λpir1 via electroporation (62). Transformants and chromosomally engineered *Pseudomonas* were screened by colony PCR using OneTaq 2x Master Mix (New England Biolabs, Ipswich, MA, USA). The cell material was lysed in alkaline polyethylene glycol for enhanced colony PCR efficiency as described previously (63).

Targeted gene deletions were performed using the I-SceI-based system developed by Martinez-Garcia and de Lorenzo (27). The conjugational transfer of the mobilizable knock-out plasmids from *E. coli* DH5α λpir1 to *Pseudomonas* was performed via triparental patch mating (16). After conjugation, the pSW-2 plasmid encoding the I-SceI-endonuclease was conjugated into *Pseudomonas* co-integrates. The addition of 3-methylbenzoate for the induction of I-SceI expression was omitted as the basal

expression level was sufficient. Kanamycin-selective clones were directly isolated, positive clones were cured of pSW-2 and restreaked several times. The gene deletion was confirmed by colony PCR and Sanger sequencing. No complementation studies were performed becauseforit has been shown the I-SceI scarless gene deletion method we used that the double strand breaks do not result in random mutations. Moreover the method does not introduce foreign DNA material making side effects very unlikely.

Analytical methods

The optical density of cell suspensions was measured at a wavelength of 600 nm using an Ultrospec 10 spectrophotometer (GE Healthcare, Chicago, IL, USA). The cell dry weight (CDW) was calculated by multiplying OD_{600nm} with a gravimetrically determined correlation factor of 0.39. For HPLC analysis the samples were centrifuged at 17,000 x g for 5 min and the supernatant was stored at -20°C until further analysis.

Glucose and gluconate concentrations were measured by high-performance liquid chromatography using a Beckman System Gold 126 Solvent Module equipped with a System Gold 166 UV-detector (Beckman Coulter) and a Smartline RI detector 2300 (KNAUER Wissenschaftliche Geräte, Berlin, Germany). Analytes were separated on the organic resin column Metab AAC (ISERA, Düren, Germany) eluted with 5 mM H_2SO_4 at an isocratic flow of 0.6 mL min^{-1} at 40 °C for 20 min. Glucose and gluconate were analyzed using the RI detector whereas gluconate was determined with the UV detector at a wavelength of 210 nm.

Proteomic profiling of NADH dehydrogenase mutants

Samples for proteome profiling were taken during early-, mid-, and late-exponential growth at an OD_{600nm} of 0.5, 2.5, and after depletion of glucose, checked with test strips for rapid detection of glucose (Medi-Test, Macherey-Nagel, Düren, Germany), respectively. Proteins were extracted from cell biomass and subsequently prepared for shotgun proteomic experiments as described previously (64). All samples were analyzed on an Agilent 6550 iFunnel Q-TOF mass spectrometer (Agilent Technologies, Santa

Clara, CA) coupled to an Agilent 1290 UHPLC system. Twenty (20) µg of peptides were separated on a Sigma–Aldrich Ascentis Peptides ES-C18 column (2.1 mm × 100 mm, 2.7 µm particle size, operated at 60°C) at a 0.400 mL min^{-1} flow rate and eluted with the following gradient: initial condition was 95 % solvent A (0.1 % formic acid) and 5 % solvent B (99.9 % acetonitrile, 0.1 % formic acid). Solvent B was increased to 35 % over 120 min, and then increased to 50 % over 5 min, then up to 90 % over 1 min, and held for 7 min at a flow rate of 0.6 mL min^{-1}, followed by a ramp back down to 5 % B over 1 min where it was held for 6 min to re-equilibrate the column to original conditions. Peptides were introduced to the mass spectrometer from the LC by using a Jet Stream source (Agilent Technologies) operating in positive-ion mode (3,500 V). Source parameters employed gas temp (250°C), drying gas (14 L min^{-1}), nebulizer (35 psig), sheath gas temp (250°C), sheath gas flow (11 L min^{-1}), VCap (3,500 V), fragmentor (180 V), OCT 1 RF Vpp (750 V). The data were acquired with Agilent MassHunter Workstation Software, LC/MS Data Acquisition B.06.01 operating in Auto MS/MS mode whereby the 20 most intense ions (charge states, 2–5) within 300–1,400 m/z mass range above a threshold of 1,500 counts were selected for MS/MS analysis. MS/MS spectra (100–1,700 m/z) were collected with the quadrupole set to “medium” resolution and were acquired until 45,000 total counts were collected or for a maximum accumulation time of 333 ms. Former parent ions were excluded for 0.1 min following MS/MS acquisition. The acquired data were exported as mgf files and searched against the pan proteome that is highly related to *Pseudomonas taiwanensis* VLB120 with Mascot search engine version 2.3.02 (Matrix Science). The resulting search results were filtered and analyzed by Scaffold v 4.3.0 (Proteome Software Inc.). The normalized spectral counts of each sample were exported from Scaffold, and the relative quantity changes of identified proteins in mutant samples were calculated in comparison to the wild type sample. The statistical significance of these changes and the adjusted p-values were evaluated by limma R package. The mass

spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE (65) partner repository with the dataset identifier PXD013623 and 10.6019/PXD013623.

RNA preparation and analysis

Samples for transcription analysis were taken during early-, mid- and late-exponential growth at an OD_{600nm} of approximately 0.5, approximately 2.5 and after glucose depletion, respectively. Prior to RNA isolation, the culture sample was diluted with the DNA/RNA protection reagent of the Monarch Total RNA Miniprep Kit (New England Biolabs, Ipswich, MA, USA), followed mechanical lysis with ZR BashingBead™ Lysis Tube (0.5mm) (Zymo Research, Irvine, CA, USA) for 1 min using the Mini-Beadbeater-16 (Biospec, Bartlesville, OK, USA). After a centrifugation step at 16,000 x g for 2 min the supernatant was transferred into a new tube. An equal volume of RNA lysis buffer of the Monarch Total RNA Miniprep Kit was added, and the RNA isolation was continued as described in the supplier's manual. After the last elution step, an additional in-tube DNase treatment was done using RNase-free DNaseI (New England Biolabs, Ipswich, MA, USA). The final RNA yield and purity were evaluated by the absorption ratio A_{260}/A_{280} measured with a Nanodrop (Thermo Scientific, Rockford, IL, USA). The synthesis of cDNA for reverse transcription was carried out with a Protoscript II first strand cDNA synthesis kit (New England Biolabs, Ipswich, MA, USA) using 120 ng total RNA and 60 µM random hexamers. The qPCR analyses were conducted with 5 µL of the reverse transcription reaction mixture with gene-specific primers (Supplementary Table S1) and the Luna Universal qPCR Master Mix (New England Biolabs, Ipswich, MA, USA) was used. Primers for qPCR were designed with the PrimerQuest Tool of IDT technologies. Gene expression levels for each individual sample were normalized relative to the internal reference gene, *rpoB* and the wild type in the corresponding growth phase calculated by a mathematical method based on the calculated real-time PCR efficiencies (66). The qPCR was

performed with the CFX96 Real-Time PCR Detection System (Biorad, Hercules, CA, USA). All qPCR reactions were performed in triplicates.

Inverted membrane vesicle preparation and NADH oxidation activity

Cultures were harvested at early-exponential growth phase at an optical density (OD_{600nm}) of approximately 0.5, as well as in the late-exponential growth phase (OD_{600nm}, of 3-4). Inverted membrane vesicles were prepared as described by Borisov (67). Briefly, cells were centrifuged for 8 min at 5,000 x g and resuspended in 2 mL spheroplast buffer (200 mM Tris-HCl pH 8.0, 2 mM EDTA, 30 % sucrose), centrifuged again and resuspended in 1 mL spheroplast buffer. Spheroplasts were prepared using lysozyme (0.03 g) and incubated for 30 min at room temperature. Spheroplasts were centrifuged for 10 min at 5,000 x g and resuspended in 2 mL sonication buffer (100 mM HEPES-KOH pH 7.5, 50 mM K_2SO_4, 10 mM $MgSO_4$, 2 mM DTT, 0.5 mM PMSF). The vesicles were sonicated (Bioruptor, Diadenode, Belgium) in 4 cycles à 30 sec at high intensity with an intermediate pause of 30 sec in ice water. The inverted membrane vesicles were centrifuged twice for 10 min at 5,000 x g to remove cell debris. The supernatant was centrifuged for 30 min at 120,000 x g and the resulting pellet was resuspended in the assay buffer (25 mM HEPES, 25 mM BIS-TRIS propane pH 7, 10 mM $MgSO_4$).

The freshly prepared inverted membrane vesicles were immediately used for the determination of the NADH oxidation activity as we observed a rapid activity decline when the membrane samples were stored on ice. 150 µL mL^{-1} isolated membrane fractions were added to the assay buffer, and the reaction was initiated by the addition of 125 µM NADH. The total volume of the assay was 200 µL. The NADH oxidation was monitored over 30 min at 340 nm in a Synergy™ MX microplate reader (BioTek, Winooski, VT, USA). For calculating the specific enzyme activity, we used the NADH molar extinction coefficient ε_{NADH} = 6.22 mM^{-1} cm^{-1}; one unit of activity was the quantity that catalyzed the oxidation of 1 µmol of NADH per min. The protein concentration was measured with the

reducing agent compatible Pierce BCA Protein Assay Kit (Thermo Scientific, Rockford, IL, USA).

Respiration activity monitoring

The cultivations and measurements of the oxygen transfer rate (OTR) and the carbon dioxide transfer rate (CTR) were performed in a modified RAMOS System, developed by the Chair of Biochemical Engineering (RWTH Aachen University) (33, 68). The standard RAMOS for shake flasks is commercially available from the Kühner AG (Birsfelden, Switzerland) or HiTec Zang GmbH (Herzogenrath, Germany). All cultivations were performed in 250-mL Ramos flasks with 10 % (v/v) filling volume using MSM medium supplemented with 25 mM glucose. The cultures were inoculated from liquid pre-cultures to an approximate OD_{600nm} of 0.05. The OTR and CTR were measured thrice per hour. All experiments were performed in biological duplicates.

Redox cofactor quantification

Samples for redox cofactor analysis were collected from early-, mid-, and late-exponential growth phase at OD_{600nm} of approximately 0.6, 2.2, and 4.0, respectively. The samples were rapidly transferred into 15-mL Falcon tubes containing 5 mL of quenching solution (acetonitrile:methanol:water, 40:40:20, v/v) with ^{13}C labeled cell extracts at –40℃. After three freeze-thaw cycles, the samples were centrifuged at 13,000 x g for 5 min and concentrated by evaporating the quenching solvent using a vacuum concentrator (SAVANT, SpeedVac, Thermo Fisher Scientific, San Diego, CA, USA) for 5 hours followed by lyophilization (LABCONCO, FreeZone, Kansas City, MO, USA). All dried extracts were stored −80°C until analysis or re-suspended in LC-MS grade water for LC-MS analysis. All redox cofactor metabolites were measured on an AB SCIEX Qtrap1 5500 mass spectrometer (AB SCIEX, Framingham, MA, USA) operated in negative ion and selected multiple reaction monitoring (MRM) mode. The column XSELECT HSS XP (150 mm × 2.1 mm × 2.5 µm) (Waters, Milford, MA, USA) with ion-pairing technique was used for the chromatography separation as previously described (69). Peak integration and

metabolite quantification were performed using an isotope-ratio-based approach on Multi-QuantTM 3.0.2 (AB SCIEX) software as previously described (70, 71).

ROS assay

The ROS sensitive fluorescent dye 2',7'-dichlorodihydrofluorescein diacetate (H_2-DCFA, Sigma Aldrich, St. Louis, MO, USA) was used to monitor the ROS formation in *P. taiwanensis* VLB120. Cells were harvested at multiple time points during the growth experiment and centrifuged for 5 min at 8,000 x g. The pellet was washed once in the mineral salt medium described above but lacking nitrogen (MSM-N) and centrifuged again. The cells were resuspended to an optical density of OD_{600nm} of ~0.4 in 1 mL MSM-N but supplemented with 25 mM glucose to allow respiratory activity. The ROS-sensitive H_2-DCFA dye was added to the cells to a final concentration of 20 µM. The cells were incubated in the dark for 30 min at 30°C at 250 rpm for aeration. After the incubation, the cells were immediately analyzed in the microplate reader Synergy^{TM} MX (BioTek, Winooski, VT, USA). The oxidized fluorescent DCF was measured using Ex/Em 504/529 nm. The measurement was performed in biological and technical triplicates. As a positive control, 1 mM H_2O_2 was included in all experiments and treated in the same way as the biological samples (data not shown).

Acknowledgments

This study has been conducted within the ERA SynBio project SynPath (Grant ID 031A459) with financial support of the German Federal Ministry of Education and Research and is part of the Joint BioEnergy Institute, supported by the Office of Science, Office of Basic Energy Sciences and Office of Biological and Environmental Research of the U.S. Department of Energy under Contract No. DE-AC02-05CH11231. BEE and SCN acknowledge financial support by the German Academic Exchange Service (DAAD) through the thematic network Aachen-California Network of Academic Exchange (ACalNet) funded by the German Federal Ministry of Education and Research (BMBF). BEE acknowledges partial support by the CSIRO-UQ Synthetic Biology Alliance. LMB acknowledges funding by the Cluster of Excellence "The Fuel Science Center - Adaptive Conversion Systems for Renewable Energy and Carbon Sources" (EXC 2186), which is funded by the Excellence Initiative of the German federal and state governments to promote science and research at German universities. We thank Stephani Baum and Uwe Conrath for sharing lab equipment and for technical support. We are grateful to Itay Budin for discussions and instruction on the membrane isolation and *in vitro* assays and Sophia Nölting for support with qPCR measurements. We thank Benedikt Wynands and Nick Wierckx for sharing the strain *P. taiwanensis* VLB120 pSTY^{-}, Victor de Lorenzo (Centro Nacional de Biotechnología - CNB, Madrid) for providing plasmid pEMG, and Pablo Nikel for providing plasmid pS2311·Nox.

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Figures legends

Figure 1. Physiological characterization of *P. taiwanensis* VLB120 (A) and the NADH dehydrogenase deficient mutants Δ*ndh1* (B), Δ*ndh2* (C), ΔΔ*ndh* (D), Δ*nuo* (E), and Δ*nuo*Δ*ndh1* (F). The strains were cultured in MSM with 25 mM glucose. The OD_{600nm} (black circles), glucose (blue squares), gluconate (green triangles) were measured over time. The shadowed area in (D) indicates the first growth phase. The data shown are the mean of biological triplicates; error bars show the standard deviation. μ_{recalc} is the growth rate of *P. taiwanensis* VLB120 pSTY$^-$. The wild type OD_{600nm} are plotted (grey, open circles) in graphs (B)-(F) for comparison.

Figure 2. Respiratory activity of *P. taiwanensis* VLB120 and the ΔΔ*ndh* mutant. (A) CTR and OTR date of the wild type strain, the highlighted area corresponds to the surplus of consumed oxygen. The area was calculated from the sectional integrals between the OTR (dashed line) and CTR (solid line). (B) Oxygen transfer rates (OTR, dashed line) during cultivation of *P. taiwanensis* VLB120 (black) and mutant ΔΔ*ndh* (green).

Figure 3. Relative gene expression of the NADH dehydrogenase encoding genes *ndh1*, *ndh2*, and *nuoA* in NADH dehydrogenase mutants Δ*ndh1* (A), Δ*ndh2* (B), ΔΔ*ndh* (C), Δ*nuo* (D), and Δ*nuo*Δ*ndh1* (E) at early-, mid-, and late-exponential growth phase normalized to the corresponding values of the wild type. mRNA abundance was determined by quantitative PCR. Values were normalized to the relative transcript level of *P. taiwanensis* VLB120 in the corresponding growth phase. *nuoA* was used as a proxy for the expression of the *nuo* operon. Gene deletions in the respective mutant are marked with ‘X’ and were not analyzed by qPCR. Experiments were performed in biological triplicates.

Figure 4. Quantification of the NADH/NAD^+ ratio in the *P. taiwanensis* VLB120 (black) and the NADH dehydrogenase mutants ΔΔ*ndh* (green), Δ*nuo* (orange), and Δ*nuo*Δ*ndh1* (red) in early-, mid- and late-exponential growth phase.

Figure 5. Significant changes at proteome level of *P. taiwanensis* VLB120 NADH dehydrogenase mutants in early- (A), mid- (B), and late-exponential (C) growth phase relative to the wild type. Proteins are clustered into functional categories according to the KEGG classification system (39). Each bar represents the number of proteins in the depicted category, the abundance of which was either increased or decreased in response to NADH dehydrogenase deficiency. Experiments were performed in biological triplicates.

Figure 6. Proposed metabolic changes caused by type-2 NADH dehydrogenase deficiency in *P. taiwanensis* VLB120. An increased NADH/NAD^+ ratio ***(1)*** might result in substrate inhibition of the Nuo complex as well as ROS production ***(2)*****,** which is reported for this NADH dehydrogenase (45, 46). Re-routing of the flux through the TCA cycle into the glyoxylate shunt ***(3)*** reduces redox cofactor formation (48-50) and helps to scavenge reactive oxygen species by glyoxylate (48, 52). Limited ATP provision from oxidative phosphorylation can be mitigated by upregulation of the ADI pathway, based on our proteomics data ***(4)*** (58, 72). The light representation of the Ndh dehydrogenase indicates deficiency of both isozymes. ETC, electron transport chain; ROS, reactive oxygen species; ADI, arginine deiminase pathway; Nuo, type-1 NADH dehydrogenase; Ndh, type-2 NADH dehydrogenase; Sdh, succinate dehydrogenase; bc1, cytochrome bc1 (complex III); cbb3, cytochrome cbb3 (complex IV); QH_2, ubiquinol; Q, ubiquinone; SUC, succinate, SUCCoA, succinyl-CoA; FUM, fumarate.

Tables

Table 1. Calculated carbon uptake, gluconate accumulation, oxygen formation rates, biomass, and the gluconate yield of wild type and NADH dehydrogenase mutants during exponential growth.

Strain	Carbon uptake rate[a]	Biomass [b]	Gluconate yield [c]	Gluconate accumulation [d]	Surplus O_2 consumption [e]
	[mmol g_{cdw}^{-1} h^{-1}]	[g L^{-1}]	[mmol g_{CDW}^{-1}]	[mM]	[mM]
wild type	7.3 ± 0.4	0.7 ± 0.0	13.7 ± 2.1	8.9 ± 1.1	9.2 ± 1.3
Δ*ndh1*	7.9 ± 0.2	0.7 ± 0.0	11.6 ± 1.7	8.6 ± 1.3	8.1 ± 0.1
Δ*ndh2*	7.2 ± 0.2	0.6 ± 0.0	12.8 ± 1.2	7.7 ± 0.3	6.3 ± 0.5
ΔΔ*ndh*	8.9 ± 0.5 / 3.5 ± 0.2	0.4 ± 0.0	20.7 ± 1.1	8.8 ± 0.4	7.2 ± 1.6
Δ*nuo*	7.0 ± 1.2	0.6 ± 0.1	25.3 ± 2.5	14.5 ± 0.8	12.9 ± 0.2
Δ*nuo*Δ*ndh*1	6.1 ± 0.2	0.8 ± 0.0	20.9 ± 1.4	16.1 ± 1.3	14.1 ± 3.9

[a] For ΔΔ*ndh*, separate growth rates were determined for phase 1 (2-6 h) and phase 2 (6-8 h). For all other mutants, growth rates were calculated for the exponential phase (between 3-4 h to 6-7 h after inoculation).

[b] The biomass concentration at the time point of the monitored maximum gluconate concentration according to [d]; shown is the mean of duplicate or triplicate experiments and the corresponding standard deviation

[c] The gluconate yield was calculated by dividing the monitored maximum gluconate concentration according to [d] with the corresponding biomass concentration according to [b]; shown is the mean of duplicate or triplicate experiments and the corresponding standard deviation.

[d] The gluconate accumulation was determined from offline monitored measurements; shown is the mean of duplicate or triplicate experiments and the corresponding standard deviation.

[e] The surplus oxygen consumption was calculated from the sectional integrals between the OTR (mmol L^{-1} h^{-1}) and CTR (mmol L^{-1} h^{-1}) between start of the cultivation and the timepoint of intersection of CTR and OTR (see Figure 2); shown is the mean of duplicate experiments and the corresponding standard deviation.

Table 2. Specific NADH oxidation activities of inverted membrane vesicles of *P. taiwanensis* VLB120 wild type and NADH dehydrogenase mutants in the early and late-exponential growth phase.

Strain	**Specific NADH oxidation activity[a] (U $mg_{protein}^{-1}$)**	
	Early-exponential	**Late-exponential**
Wild type	1.2 ± 0.2	0.7 ± 0.2
Δ*ndh1*	1.3 ± 0.1	0.5 ± 0.1
Δ*ndh2*	1.0 ± 0.2	0.4 ± 0.1
ΔΔ*ndh*	1.1 ± 0.1	0.5 ± 0.2
Δ*nuo*	1.2 ± 0.1	0.5 ± 0.1
Δ*nuo*Δ*ndh1*	0.8 ± 0.1	0.5 ± 0.2

[a] Mean values and standard deviations were determined from independent, biological triplicates

Table 3. Protein abundance in NADH dehydrogenase mutants relative to the wild type. Proteins marked with a diamond (◊) are discussed in the text.

			ΔΔ*ndh*			Δ*nuo*			Δ*nuo*Δ*ndh1*		
			early	mid	late	early	mid	late	early	mid	Late
	Gene name	**Gene function or product**[a]	**Log2 fold change relative to the wild type**[b]								
	Carbohydrate metabolism										
	Pgk	Phosphoglycerate kinase									
	SucC	Succinate-CoA ligase, subunit beta				0.3	0.3	0.5	0.4	0.4	0.5
	SucD	Succinate-CoA ligase, subunit alpha					0.4	1.0	0.6	0.8	1.0
	SdhB	Succinate dehydrogenase						0.8	0.5	0.5	0.8
◊	Glk	Glucokinase	-3.1	-2.8	-2.5						
	TktA	Transketolase			-1.5						
◊	AceA	Isocitrate lyase			0.8			-1.3			
	Ppc	Phosphoenolpyruvate carboxylase					1.35				
	Idh	Isocitrate dehydrogenase						0.6		0.5	-2.6
◊	Gcd	Quinoprotein glucose dehydrogenase						2.2			
	Energy metabolism										
	TsaA	Putative peroxiredoxin					0.5	0.7	0.5	0.48	0.79
	Fpr-I	Ferredoxin-NADP(+) reductase	-1.0		-1.1				-3.1	-1.7	
◊	PP_0235	Peroxidase			3.2						
◊	ChrR	Quinone reductase			2.0						
	Amino acid metabolism										
◊	ArcA	Arginine deiminase			1.1			-1.9			-1.9
◊	ArcB	Ornithine carbamoyltransferase			1.2			-2.3			-2.3
◊	ArcC	Carbamate kinase			0.8	-0.6		-2.0			-1.5
	Transporter/Carbon uptake										
◊	OprB-I	Porin	1.4		1.4			-2.5		-2.0	-2.8
◊	GntT	D-gluconate transporter	0.6		1.2				0.9		
	GtsA	Mannose/glucose ABC transporter	0.8			0.9	0.8		1.0	0.7	
	GtsD	Mannose/glucose ABC transporter	0.7								
	Stress proteins										
◊	KatG	Catalase-peroxidase			0.7			-2.3			-2.8
	TauA	Taurine ABC transporter			2.4						
	DnaK	Chaperone protein			-0.3						
	TrxA	Thioredoxin	0.9		0.6						

Color key

-3	-2	-1		1	2	3

Fold change

[a] Gene function assignment differs from Figure 5

890 [b] Numbers indicate the fold change for upregulated (+) and downregulated (-) proteins
891 relative to the wild type, and the lack of a number indicates no differential production.
892

893 **Table 4.** Bacterial strains and plasmids used in this study.

Strain	Relevant characteristics[a]	Reference
E. coli		
DH5α	*fhuA*2 *lac*(del)U169 *phoA glnV*44 Φ80' *lacZ*(del)M15 *gyrA*96 *recA*1 *relA*1 *endA*1 *thi*-1 *hsdR*17	NEB
DH5α λpir1	F−, Δlac169, rpoS(Am), robA1, creC510, hsdR514, endA, recA1uidA(ΔMluI)::pir-116; host for oriV(R6K) vectors in high copy number	Thermo Fisher Scientific
HB101 pRK2013	SmR, hsdR-M+, proA2, leuB6, thi-1, recA; bears plasmid pRK2013	(73)
DH5α pSW-2	Gm^r, DH5α bearing pSW-2	(27)
DH5α λpir1 pEMG	Km^r, DH5α λpir1 bearing plasmid pEMG	(27)
DH5α λpir1 pEMG_ko_ndh1	Km^r, PVLB_13270 deletion plasmid	This study
DH5α λpir1 pEMG_ko_ndh2	Km^r, PVLB_21880 deletion plasmid	This study
DH5α λpir1 pEMG_ko_nuo	Km^r, PVLB_15600-15660 deletion plasmid	This study
Plasmids		
pS2311·Nox	Km^r; derivative of vector pSEVA2311 with the *nox* gene from *S. pneumoniae*	(36)
P. taiwanensis		
VLB120	wild type	Prof. Dr. A. Schmid (UFZ, Leipzig, DE)
VLB120 $pSTY^-$	VLB120 devoid of megaplasmid pSTY	(29)
VLB120 Δ*ndh1*	Δ*ndh1* (PVLB_13270), $pSTY^-$	This study
VLB120 Δ*ndh2*	Δ*ndh2* (PVLB_21880), $pSTY^-$	This study
VLB120 ΔΔ*ndh*	ΔΔ*ndh* (PVLB_13270, PVLB_21880), $pSTY^-$	This study
VLB120 Δ*nuo*	Δ*nuo* (PVLB_15600-15660), $pSTY^-$	This study
VLB120 Δ*nuo*Δ*ndh1*	Δ*ndh1* (PVLB_13270), Δ*nuo* (PVLB_15600-15660), $pSTY^-$	This study
VLB120 pS2311·Nox	Km^r, VLB120 bearing pS2311·Nox	

VLB120 ΔΔ*ndh* pS2311·Nox	Km^r, ΔΔ*ndh* (PVLB_13270, PVLB_21880), pSTY$^-$ bearing pS2311·Nox	This study

894 [a] Gm^r, Km^r, gentamycin, kanamycin resistance, respectively.

895

896 **Table 5.** Primers used in this study.

Primer	Sequence (5' - 3')[a]	Description
SN019	gataacagggtaatctgCGCAGGATGAAAGCTAAACC	TS1 ndh1 forward
SN020	aacagccaTGAGTCGTTCGAATAACTAC	TS1 ndh1 reverse
SN021	acgactcaTGGCTGTTCAGCAATGATGG	TS2 ndh1 forward
SN022	cgggtaccgagctcgGCAAGGGCGAGCATGATGAC	TS2 ndh1 reverse
SN023	gataacagggtaatctgTCGACCTCAACACGCACTTC	TS1 ndh2 forward
SN024	ccggcaagCGATGCGATGAGTCATGG	TS1 ndh2 reverse
SN025	tcgcatcgCTTGCCGGCGATAAAGCCAG	TS2 ndh2 forward
SN026	cgggtaccgagctcgCGGCACTCCCAGATAACTTG	TS2 ndh2 reverse
SN027	ATACGGGCCGTTCATCAGTC	Verification cointegration ndh1 forward
SN028	GCGATCTTGCGAATGGTGTC	Verification cointegration ndh1 reverse
SN029	CCGGCTGAATGACGAATG	Verification cointegration ndh2 forward
SN030	gttacgacccggtgtatg	Verification cointegration ndh2 reverse
SN112	tcagataactTTAAGTAGAGCGGCGACTTG	TS1 nuo reverse
SN113	agggataacagggtaatctgCCTTATCGCCGCCGAATCAC	TS1 nuo forward
SN114	ctctacttaaAGTTATCTGAACGGGCTTGG	TS2 nuo forward
SN115	atccccgggtaccgagctcgGCGCTCCAGTTGGTGGATTC	TS2 nuo reverse
SN116	CTCGTCCAAGCCACCTGATG	Verification cointegration nuo forward
SN117	AGCCTCAAGGTCATGGTCTG	Verification cointegration nuo reverse
SN171	CGGACACAGACCATGCATAC	Verification cointegration, binding in *nuoA*
SN200	CTGCACACCTATGCCTACAA	qPCR ndh2 forward
SN201	TACAGCGACACATAGAACATCC	qPCR ndh2 reverse
SN214	TTGGCCCAGAGGAAATCAC	qPCR rpoB forward
SN215	GGCACCGACGTAGACAATAC	qPCR rpoB reverse
SN234	AGAACGAACCCTTCGAATCC	qPCR nuoA forward
SN235	GCATCGCGACCAGATAGAAT	qPCR nuoA reverse
SN228	CGAATACGTCGCTAGCCATAC	qPCR ndh1 forward
SN229	ATCACTTTCAGGTGCTCGTC	qPCR ndh1 forward

[a] Underlined nucleotides refer to gene-specific regions; the primer efficiency of the qPCR primer pairs for *ndh2* (SN200, SN201), *rpoB* (SN214, SN215), *nuoA* (SN234, SN235), and *ndh1* (SN228 and SN229) was 104.4%, 101.8%,104.4 % and 103.4%, respectively.