Encounters with oxygen: Aerobic physiology and H₂O₂ production of Lactobacillus johnsonii

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Chapter 2

Hydrogen peroxide production in species of the *Lactobacillus acidophilus* group, a central role for a novel NADH dependent flavin reductase.

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Summary
Hydrogen peroxide production is a well-known trait of many bacterial species associated with the human body. In the presence of oxygen, the probiotic lactic acid bacterium Lactobacillus johnsonii NCC 533 excretes up to 1 mM H$_2$O$_2$, inducing growth stagnation and cell death. Disruption of genes commonly assumed to be involved in H$_2$O$_2$ production, e.g. pyruvate oxidase, NADH oxidase and lactate oxidase, did not affect this. Here we describe the purification of a novel NADH-dependent flavin reductase, encoded by two highly-similar genes (LJ_0548 and LJ_0549) that are conserved in lactobacilli belonging to the Lactobacillus acidophilus group. The genes are predicted to encode two 20 kDa proteins containing FMN_red conserved domains. Reductase activity requires FMN, FAD or riboflavin and is specific for NADH, and not NADPH. The $K_m$ for FMN is 30 ± 8 µM in accordance with its proposed in vivo role in H$_2$O$_2$ production. Deletion of the encoding genes in L. johnsonii led to 40-fold reduced H$_2$O$_2$ formation, which could only be restored by in trans complementation of both genes. Our work identifies a novel, conserved NADH-dependent flavin reductase that is prominently involved in H$_2$O$_2$ production in L. johnsonii.
Introduction
Hydrogen peroxide ($\text{H}_2\text{O}_2$) production is a well-known capacity of several bacterial species that are associated with the human body. Some of these $\text{H}_2\text{O}_2$-forming species are opportunistic-pathogens or pathobionts, such as *Streptococcus pyogenes* (86), *Streptococcus mutans* (74, 189), and *Streptococcus pneumoniae* (91, 190). Other $\text{H}_2\text{O}_2$ producing species or strains have been proposed to have probiotic properties, such as *Bifidobacterium bifidus* (69) and *Lactobacillus johnsonii* (38), or are prevalent in the commensal vaginal microbiota such as *Lactobacillus crispatus, Lactobacillus jensenii* and *Lactobacillus gasseri* (94).

Accumulation of $\text{H}_2\text{O}_2$ mainly occurs in species that lack the main $\text{H}_2\text{O}_2$-scavenging enzymes, such as catalase and NADH peroxidase. Analogously, when the genes encoding these enzymes are deleted from the *Escherichia coli* genome, $\text{H}_2\text{O}_2$ is generated upon oxygenation and accumulates in the extracellular growth medium (95, 191). Hydrogen peroxide is mainly produced in central carbon and energy metabolism by oxidases, including pyruvate oxidase (Pox), lactate oxidase (Lox) and NADH oxidases (Nox) (32). For example, activity of lactate oxidase encoded by *S. pyogenes* is primarily responsible for $\text{H}_2\text{O}_2$ production in cells that are depleted for glucose (192, 193), whereas $\text{H}_2\text{O}_2$ production by *S. pneumoniae* is due to pyruvate oxidase activity (91). In several species, $\text{H}_2\text{O}_2$-producing NADH oxidases have been identified: for instance in *Thermus thermophilus* (194), *S. mutans* (74) and *Amphibacillus xylanus* (72).

Species that accumulate $\text{H}_2\text{O}_2$ or other reactive oxygen species (ROS) upon exposure to molecular oxygen generally have an energy metabolism that is adapted to anaerobic environments. The proteins that catalyze the low-potential redox reactions in anaerobic energy metabolism, such as fumarate and nitrate respiration, commonly carry low-potential metal clusters and solvent-exposed flavin cofactors that readily react with oxygen and contribute to the generation of ROS. $\text{H}_2\text{O}_2$ and superoxide ($\text{O}_2^-\text{)}$ belong to the strongest oxidant-species and can accelerate the rate of ROS generation, the chemistry of which has been reviewed previously (6).

This study focuses on the $\text{H}_2\text{O}_2$ producing species *L. johnsonii*. This organism is applied as a probiotic supplement in the food industry (176). The strain was isolated from the human intestine, where it interacts with the host epithelium as well as with other microbes (170, 171, 195). The gastro-intestinal (GI) tract is predominantly an anaerobic niche, but the presence of oxygen gradients in the proximity of the mucosal surfaces is well established (40, 41, 196). Hydrogen peroxide derived from species like
*L. johnsonii* may play a role in these environments. Several studies have speculated on the effect that H$_2$O$_2$ may exert on the host as well as on the microbiome. Some authors propose that it can directly damage the epithelium (62, 197) and cause cell death of other bacteria (38, 190). Others suggest that H$_2$O$_2$ accumulation may contribute to the maintenance of a normal and homeostatic microbiota. Especially for the vaginal microbiota, strong evidence exists that women carrying H$_2$O$_2$-producing lactobacilli are less prone to develop bacterial vaginosis (187, 198), which is a very common disease and an independent risk factor for the acquisition of sexually transmitted disease and preterm birth (199, 200).

Despite the data that support this hypothesis, the mechanism for the proposed homeostatic effect of H$_2$O$_2$ producing lactobacilli in the microbiota remains largely unknown. It has been suggested that H$_2$O$_2$ can contribute to the anti-inflammatory effect of commensal and probiotic bacteria through its influence on the peroxisome proliferator activated receptor-γ (PPAR-γ) which plays a central role in regulation of intestinal inflammation and homeostasis (201, 202). Expression of PPAR-γ is induced *in vivo* and *in vitro* by the presence of *L. crispatus* and is inhibited by the addition of either catalase or glutathione, pinpointing H$_2$O$_2$ as the responsible factor for the observed induction (50). A recent study on development of type 1 diabetes in rats substantiated the role in immune modulation by bacterially derived H$_2$O$_2$. Here, H$_2$O$_2$ directly affected the activity of indoleamine 2,3-dioxygenase which is an important immune modulator (203).

Members of the *L. acidophilus* group are frequently encountered a the important microbial groups involved in H$_2$O$_2$ production in the vaginal and GI-tract microbiota. This group of lactobacilli encompasses several closely related species (168, 204), including those that are proposed to confer probiotic effects to consumers (*L. johnsonii*, *L. gasseri*, and *L. acidophilus*) as well as several important organisms in food fermentations (*Lactobacillus delbruecki* subsp. *bulgaricus*, *Lactobacillus kefiranofaciens* and *Lactobacillus helveticus*). Although many studies have reported on the H$_2$O$_2$ production by species of the *L. acidophilus* group, our understanding of the enzymatic reactions and mechanisms underlying these observations remains limited to the notion that NADH and flavin are involved in the reaction (37, 93) and that it is catalyzed by a protein that is constitutively expressed (94). The enzymes that catalyze the H$_2$O$_2$-generating reactions remain uncharacterized, to date.

In this study, we identify a novel NADH-dependent flavin reductase as the primary source
for H₂O₂ in anaerobically grown *L. johnsonii* NCC 533, a member of the *L. acidophilus* group, upon exposure to oxygen. The enzyme is encoded by two small consecutive genes that show high similarity and are conserved throughout the *L. acidophilus* group. Mutation of these genes in *L. johnsonii* NCC 533 led to a strain that failed to produce H₂O₂ upon exposure to molecular oxygen.

**Materials & Methods**

**Bacterial strains and culture conditions**

*L. johnsonii* NCC 533 was obtained from the Nestec Culture Collection and cultured in commercial MRS medium (Merck, Whitehouse Station, NJ, USA) (205) at 37°C under static conditions, with minimal headspace for 16 hours. The deletion strains NCC 9333, NCC 9334, NCC 9337 and NCC 9359 were precultured in MRS containing 5 µg ml⁻¹ erythromycin, while 5 µg ml⁻¹ chloramphenicol was added for the NCC 9359 strains carrying plasmid pDP1016, pDP1017 or pDP1019.

**Growth and H₂O₂ production**

Cells were grown overnight in closed static tubes at 37°C in LAPtg medium. (20 g L⁻¹ glucose, 10 g L⁻¹ yeast extract, 10 g L⁻¹ bacto peptone 10 g L⁻¹ bacto tryptone plus 1 g L⁻¹ Tween 80). This medium was used instead of the regular MRS medium for lactobacilli, because the meat extract in MRS was found to interfere with the enzymatic assay for H₂O₂. Cell density was determined by measurement of the optical density at 600 nm. H₂O₂ concentrations were determined using the phenol red assay (described below).

**Cell extracts**

Bacterial cultures were grown in 1 L bottles that were filled to the top with MRS medium, to minimize the headspace volume. Cultures were inoculated with 5 mL overnight precultures in the same medium and incubated for 24 hours at 37°C with continuous stirring. Cells were harvested by centrifugation (5’, 2600 x g, 4°C) and the cell pellets were suspended in 50 mL of 50 mM potassium phosphate buffer (pH 7.0) with 2 mM EDTA and 25 mM NaCl. Lysozyme (Sigma-Aldrich, St. Louis, MO, USA) was added to a final concentration of 1 mg mL⁻¹ and incubated for 30 minutes at 37°C. Subsequently, cells were disrupted by 3 rounds of 1 minute sonication at 100W (Branson Ultrasonics, Danbury, CT, USA) and cooled on ice water. Crude cell debris was removed from the disrupted cell suspension by low-speed centrifugation (5’, 2600 x g, 4°C), followed
by ultracentrifugation of the supernatant (60’, 165000 x g, 4°C), generating the cell extract (supernatant) that was used in subsequent purification steps and enzyme assays. Protein concentrations of cell extracts were determined using the MicroBCA (microbicinchoninic acid) assay kit (Thermo Fisher, Scientific Inc., Waltham, MA, USA).

Alternatively, 50 mL overnight anaerobic cultures in MRS were centrifuged, suspended in 50 mM potassium phosphate buffer (pH 7.0) and transferred to screw-cap tubes with 100 mg zirconium beads. Cells were disrupted in 3 rounds for 20 seconds and cell debris was removed by centrifugation (10’, 21500 x g, 4°C). Protein concentrations of cell extracts were determined using the MicroBCA assay kit (Thermo Fisher Scientific Inc). These extracts showed a 2-fold lower enzyme activity overall. They were employed for analysis of the activity, $K_m$ determination and SDS-gel.

Protein purification: ammonium sulfate precipitation, Q column, gel filtration and SDS gel

Cell extracts were placed in a beaker at 4°C and ammonium sulfate was added slowly under continuous stirring until reaching intermediate steps (30, 50, 70 and 90%) of saturation. Next, the cell extract was left without stirring on ice for 20 min and subsequently spun down (10’ min, 12000 x g, 4°C). The precipitate was suspended in 50 mM potassium phosphate buffer (pH 7.0) and dialyzed overnight at 4°C against 3 L 20 mM Tris buffer, pH 8.0.

Anion-exchange chromatography was carried out with an Äkta FPLC system (GE Healthcare, Little Chalfont, Buckinghamshire, United Kingdom) fitted with a Hi-Trap Q HP 5 mL column (GE Healthcare). As a loading buffer, 20 mM Tris, pH 8.0 was used at a rate of 4 mL min⁻¹ and a linear gradient was applied from 0 to 1 M NaCl in 20 column volumes. The fraction showing NADH oxidase activity (see below) was concentrated to 0.2 mL using a 10K Corning Spin-XUF6 column. This concentrated fraction was subjected to further fractionation by size exclusion chromatography using a Superdex 200 HR 10/30 column (GE Healthcare) in 20 mM Tris buffer (pH 8.0) with 250 mM NaCl at 0.5 mL min⁻¹.

For the SDS-gel electrophoresis, cell extracts were boiled for 5 minutes with SDS sample buffer (50 mM Tris-HCl pH 6.8, 100 mM dithiothreitol [DTT], 2% SDS, 0.1% bromophenol blue, 10% glycerol) and loaded on a 15% SDS gel with a 7% stacking gel on a Hoefer system (Thermo Scientific). The amount of sample that was applied was corrected for the variations in $OD_{600}$ of the culture. The prestained marker Pageruler Plus from Fermentas (Thermo Scientific) was used. Gels were stained with PageBlue
Protein Staining Solution (Fermentas Coomassie G-250 dye).

**Enzyme activity assay**
NADH dependent flavin reductase activity in crude extract (for preparation, see above) was analyzed by determination of the NADH dissipation, as well as through the determination of the final \( \text{H}_2\text{O}_2 \) concentration. NADH oxidation was measured by monitoring the absorption at 340 nm at 37°C in a 200 µL reaction mixture with 500 µM NADH or 500 µM NADPH. As a flavin source either 250 µM flavin adenine dinucleotide (FAD) or 25 µM FAD, flavin mononucleotide (FMN) or riboflavin was added. The reaction mixture was buffered by 50 mM potassium phosphate buffer at pH 7.0.

For \( \text{H}_2\text{O}_2 \) measurement, the same reaction mixture in 200 µL volume was used with a lower NADH concentration (250 µM) to prevent oxygen from becoming the limiting substrate. After 10 minutes of incubation, the \( \text{H}_2\text{O}_2 \) concentration was determined with a phenol red enzymatic assay by transferring 20 µL sample to 180 µL of a reaction mixture containing 5 µg mL\(^{-1}\) horseradish peroxidase (Roche, Penzberg, Germany) and 30 µM phenol red in water. After 5 minutes of reaction, pH was increased by the addition of 10 µL 1M NaOH. Absorption was determined at 620 nm.

These enzymatic activity assays were employed to detect protein activity in the fractions that were obtained from the three protein purification steps. Furthermore, the assays were used to determine the enzyme activity level in cell extracts of mutant strains. In the latter instance, 25 µM FMN was used as the flavin source. Enzyme activities are expressed as specific activity per milligram of protein in the cell extract per minute and were measured in triplicate.

The specificity constant \( K_m \) was determined by measuring NADH consumption rate of the cell extract in the presence of various concentrations of FAD, FMN and riboflavin (2.5 – 250 µM). The \( K_m \) is calculated by fitting a hyperbolic curve \( (V_{\text{max}} * C_s) / (K_m + C_s) \), with \( C_s \) for flavin concentration and optimization for \( V_{\text{max}} \) and \( K_m \) using the Solver function in Microsoft Excel. \( R^2 >0.96 \). Averages and standard deviations are calculated from technical triplicates.

**Digestion, MS analysis, and protein identification**
Semipurified protein samples were digested with an in-house protocol using 1 mg of trypsin (modified to prevent autodigestion, Promega, Madison, WI, USA) per 50 mg of
protein in a 0.1 M Tris pH 7.5 buffer following alkylation of the cysteine residues with DTT and iodoacetamide. Trypsin digestion was stopped after 16 hours by the addition of 10% trifluoroacetic acid (TFA) to a final concentration of 1%. Tryptic peptides were purified using an 80 µg capacity OMIX tip (Varian, Agilent) and collected in a volume of 30 µL 50% acetonitrile (ACN) - 0.1% TFA.

Mass spectrometry analysis of the peptide samples was performed with a Micromass Q-TOF1 (quadrupole time of flight) mass spectrometer (Micromass, Waters, Milford, MA, USA) coupled to a nano-liquid chromatography (nano-LC) system (LC Packings, Dionex, Sunnyvale, CA, USA). The peptides were separated on a nano-analytical column (75 µm i.d., 25 cm length C18 PepMap, Dionex) using a gradient of 0–50% acetonitril and 0.1% formic acid. The LC eluent flow of 300 nL min⁻¹ was directly infused into the Q-TOF1 spectrometer, operating in data-dependent MS and tandem MS (MS/MS) modes. Low-energy collision-induced dissociation (CID) of selected precursor ions was used to obtain fragmentation spectra of the peptides. After processing the raw data with the Masslynx software (Micromass, Waters) the resulting peaklist (.pkl file) was used to search in the NCBInr database with MASCOT online (Matrix Science, Boston, MA, USA).

The search parameters were: a fixed modification of carbamidomethyl for cysteine, variable modifications of oxidized methionine, trypsin with the allowance of one missed cleavage, peptide and MS/MS tolerance ±0.3 Da and peptide charge state +1. Probability based MASCOT scores were used to evaluate the protein identifications.

Construction of L. johnsonii deletion strains
An overview of the mutants and plasmids used in this study can be found in table 2.1. An overview of all primers can be found in Supplementary material Table S2.1. The genome sequence of L. johnsonii is deposited in GenBank under accession no. AE017198 (176).
Table 2.1 List of strains and plasmids used in this study.

<table>
<thead>
<tr>
<th>Strain</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>NCC 533</td>
<td><em>Lactobacillus johnsonii</em> strain from the Nestec Culture Collection</td>
</tr>
<tr>
<td>NCC 9333</td>
<td>Δ<em>pox</em> (chapter 4)</td>
</tr>
<tr>
<td>NCC 9334</td>
<td>Δ<em>LJ_1826</em> (predicted to encode lactate oxidase; Lox)</td>
</tr>
<tr>
<td>NCC 9337</td>
<td>Δ<em>LJ_1254</em> and Δ<em>LJ_1255</em> (predicted to encode NADH oxidase; Nox)</td>
</tr>
<tr>
<td>NCC 9359</td>
<td>Δ<em>LJ_0548</em> and Δ<em>LJ_0549</em> (predicted to encode NADH flavin reductase)</td>
</tr>
<tr>
<td>pDP749</td>
<td>Temperature sensitive, allele exchange plasmid for <em>L. johnsonii</em> NCC 533</td>
</tr>
<tr>
<td></td>
<td>(185)</td>
</tr>
<tr>
<td>pDP889</td>
<td>pDP749 construct for <em>lox</em> (<em>LJ_1826</em>) deletion</td>
</tr>
<tr>
<td>pDP902</td>
<td>pDP749 construct for <em>nox</em> (<em>LJ_1254</em> and <em>LJ_1255</em>) deletion</td>
</tr>
<tr>
<td>pDP1010</td>
<td>pDP749 construct for <em>LJ_0548</em> and <em>LJ_0549</em> deletion</td>
</tr>
<tr>
<td>pDP794</td>
<td>pNZ124 based expression plasmid with <em>LJ_0045</em> promoter and <em>LJ_1125</em> terminator</td>
</tr>
<tr>
<td>pDP1016</td>
<td>pDP794 with <em>LJ_0548</em> expression plasmid</td>
</tr>
<tr>
<td>pDP1017</td>
<td>pDP794 with <em>LJ_0549</em> expression plasmid</td>
</tr>
<tr>
<td>pDP1019</td>
<td>pDP794 with <em>LJ_0548</em> and <em>LJ_0549</em> expression plasmid</td>
</tr>
</tbody>
</table>

The construction of the *pox*-deletion strain NCC 9333 is described in the Materials & Methods section of chapter 4. The deletion of the gene *LJ_1826*, predicted to encode a lactate oxidase enzyme, was achieved similarly: the 5' homology region of the *LJ_1826* gene was amplified from *L. johnsonii* NCC 533 genomic DNA using primers A and B. The 1077 bp amplicon was SacI-BamHI digested and cloned in SacI-BamHI digested pDP749, yielding an intermediate plasmid. The 3' region of the *LJ_1826* gene was amplified using the primers C plus D, the 1170 bp amplicon digested with PstI-KpnI and cloned in the similarly digested intermediate plasmid to yield the *lox*-deletion plasmid pDP889. Plasmid pDP889 isolated from *L. lactis* was used to transform NCC 533 (185) and loop-in/loop-out gene replacement was achieved as described previously (206). The deletion was confirmed by PCR analysis and the deletion strain was named NCC 9334.

In *L. johnsonii* NCC 533, NADH oxidase is predicted to be encoded by the genes *LJ_1254* and *LJ_1255*. Deletion of *LJ_1254* and *LJ_1255* was achieved in the same way as for the LOX-encoding gen: the 1008 bp at the 5' end region of the *LJ_1255* gene was amplified using primers E and F, and the 993 bp at the 3' end region of the *LJ_1254* gene was amplified using primers G plus H. These amplicons were cloned into pDP749 to give plasmid pDP902 and used to produce the *nox* deletion strain NCC 9337.

The deletion of *LJ_0548* and *LJ_0549* was achieved by amplification of 1062 bp at the
5’ end region of the LJ_0548 gene with primers I plus J and the 1098 bp at the 3’ end region of the LJ_0549 gene was amplified using primers K plus L. These were cloned into pDP749 to give plasmid pDP1010 which was used to produce the LJ_0548 and LJ_0549 deletion strain NCC 9359.

Construction of the L. johnsonii overexpression strains

The L. johnsonii expression plasmid pDP794 was constructed as follows: the predicted bidirectional terminator situated between the LJ_1125 and LJ_1126 genes of NCC 533 was amplified with the primers O and P. This 359 bp amplicon was digested with the restriction enzymes HindIII and XhoI and cloned into similarly digested pNZ124 (207) to yield pNZ124-LJ_1125 trm. The LJ_0045 D-lactate dehydrogenase promoter was amplified using NCC 533 chromosomal DNA as a template using the primers R plus S. This 215 bp amplicon was digested with the restriction enzymes BglII plus SacI and cloned into similarly digested pNZ124-LJ_1125 trm to produce plasmid pDP794. This plasmid, with the promoter region of the LJ_0045 lactate dehydrogenase gene and a bidirectional terminator, was used for overexpression of the LJ_0548 and LJ_0549 genes.

For the construction of these overexpression plasmids the following cloning steps were performed: For pDP1016 the gene LJ_0548 was amplified using primers T plus V. The 597 bp amplicon was digested with SphI and HindIII and cloned into SphI plus HindIII digested pDP794 to give plasmid pDP1016. For pDP1017, the LJ_0549 gene was amplified using primers U plus W. The 583 bp amplicon was digested with SphI and HindIII and cloned into SphI plus HindIII digested pDP794 to give plasmid pDP1017. For pDP1019 the genes LJ_0548 and LJ_0549 were amplified using primers T plus W, the 1132 bp amplicon was digested with SphI and HindIII and cloned into SphI plus HindIII digested pDP794 to give plasmid pDP1019. These cloning procedures yielded plasmids on which expression of LJ_0548 and/or LJ_0549 is controlled by the strong ldh promoter. Genetic maps of plasmids pDP1016, pDP1017 and pDP1019 were created using Clone Manager (Supplementary materials Figure S2.1).

Growth in batch culture

Aerotolerance of NCC 9359 was compared to wildtype L. johnsonii in continuously stirred vessels with 400 mL MRS medium. Batches were sparged with specific gas mixtures containing 5% CO₂ and either no oxygen (0% oxygen, anaerobic) or normal
oxygen levels (20% oxygen, aerobic). Cultures were grown at 37°C with continuous mixing (ca. 200 rpm) and pH was maintained at 6.5 by automated 4M NaOH titration. Cell densities were determined by measuring the optical density at 600 nm (OD$_{600}$). Maximum specific growth rate was determined by fitting an exponential trend line through the data points with a minimal R$^2$ of 0.99.

Organic acid measurement by HPLC
Extracellular metabolite concentrations were determined as described previously (208) using high pressure liquid chromatography (HPLC, LKB and Pharmacia, Oregon City, OR, USA) fitted with a Rezex organic acid analysis column (Phenomenex, Torrance, CA, USA) at 45°C and an RI 1530 refractive index detector (Jasco, Easton, MD, USA). The mobile phase consisted of a 7.2 mM H$_2$SO$_4$ solution. Chromatograms were analyzed using AZUR chromatography software (St. Martin D’Heres, France).

Statistical analysis
Statistical significance was determined using a Student’s two tailed t-test for unequal or equal variance. An F-test was employed to verify whether variances could be considered equal (p>0.05) or unequal (p<0.05).

Results
H$_2$O$_2$ accumulation results in premature growth stagnation during aerobic growth of L. johnsonii NCC 533
To assess the growth behavior of L. johnsonii NCC 533 in anaerobic and aerobic conditions, LAPTg medium was inoculated with an overnight culture and incubated at 37°C either in a static tube with minimal headspace (anaerobic) or under continuous shaking with 10 volumes headspace (aerobic). Growth rates of aerobic and anaerobic cultures were similar up to an OD$_{600}$ of 1.0 (Figure 2.1A). However, aerobic cultures accumulated up to 1 mM H$_2$O$_2$ during growth (Figure 2.1B), leading to growth stagnation at an approximate density of OD$_{600}$ 1.5. This growth stagnation could be completely abolished by the addition of 0.5 mg mL$^{-1}$ catalase to the medium, which prevented the accumulation of H$_2$O$_2$. These findings show that oxidative stress resulting from endogenous H$_2$O$_2$ production is the main cause for the observed growth arrest of L. johnsonii NCC 533 under aerobic conditions.
H$_2$O$_2$ production is not dependent on predicted pyruvate oxidase, lactate oxidase or NADH oxidase encoding genes.

The main contributor to H$_2$O$_2$ production in lactic acid bacteria (LAB) has been proposed to be the oxygen dependent lactate utilization pathway, which oxidizes lactate via pyruvate and acetyl-phosphate to acetate, generating CO$_2$, ATP, NADH and H$_2$O$_2$ (83, 86). The redox balance in this pathway is proposed to be restored by dissipation of the NADH via an NADH-oxidase dependent reaction that generates either H$_2$O$_2$ or water. The oxygen-dependent lactate utilization pathway thereby encompasses three potential H$_2$O$_2$ producing reactions: (i) pyruvate oxidation (catalyzed by the Pox enzyme), (ii) lactate oxidation (catalyzed by the Lox enzyme) and (iii) NADH oxidation (catalyzed by the Nox enzyme).

To assess the contribution to the observed H$_2$O$_2$ production of the genes predicted to encode these enzymes in L. johnsonii, mutant derivatives of the wild-type strain were constructed that lack the lactate oxidase encoding gene LJ_1826 (NCC 9334), the pyruvate oxidase encoding gene LJ_1853 (NCC 9333) or the NADH oxidase encoding genes LJ_1254 and LJ_1255 (NCC 9337). The H$_2$O$_2$ production capacity of the mutants was compared to that of the wild-type strain. To this end, all strains were grown anaerobically (static cultures) in LAPTg medium to an OD$_{600}$ of ~0.7 and subsequently transferred to aerobic conditions (shake flask incubation). H$_2$O$_2$ production was measured after 1 and 2 hours of incubation. Deletion of the predicted pox, lox, or nox genes did not significantly affect the level of H$_2$O$_2$ production after 1 hour in these

Figure 2.1: Growth and H$_2$O$_2$ concentration of L. johnsonii NCC 533 in LAPTg medium under anaerobic (square symbols), aerobic conditions (circular symbols) or aerobic conditions with 0.5 mg ml$^{-1}$ catalase added to the medium (triangular symbols). Culture densities were determined by optical density measurement at 600 nm (Panel A) and H$_2$O$_2$ concentrations were determined by the phenol red enzymatic assay (Panel B). The data represent duplicate experiments ± standard error of the mean.
strains in comparison with the level produced by the parental strain NCC 533 (Figure 2.2, all p-values >0.05). Exposure to oxygen for two hours resulted in small differences between H$_2$O$_2$ levels between the strains: the pox mutant produced less (0.48 mM vs 0.53 mM in the wild type, p<0.05) and the Δnox produced more H$_2$O$_2$ (0.56 mM, p<0.05). It appears justified to conclude that the oxidative lactate-utilization pathway is not responsible for the greater part of the H$_2$O$_2$ production, suggesting that an alternative metabolic conversion may account for the H$_2$O$_2$ production. This suggestion is in agreement with the observation that in the presence of oxygen, no substantial production and excretion of acetate occurs (chapter 4).

Previously, it has been suggested that *L. delbrueckii*, a close relative of *L. johnsonii*, produces H$_2$O$_2$ via an NADH dependent reaction that is enhanced by the addition of a flavin source (37, 93, 94). To identify the protein and gene involved in such proposed enzymatic reaction in *L. johnsonii* we initiated its purification, using enzyme activity assays to track the enzyme during purification.

Cell extracts of *L. johnsonii* NCC 533 contain NADH-dependent flavin reductase activity. Cell extracts of *L. johnsonii* NCC 533 contain NADH consumption activity when a flavin compound is added as a supplement to the assay's reaction mixture (Figure 2.3A). The activity requires the addition of either FAD, FMN or riboflavin and does not show any activity with NADPH instead of NADH. Addition of 10-fold lower FMN concentration resulted in a significantly lower enzymatic rate (0.21 and 0.12 µmol / mg protein / min, p<.05). Following this observation, we further explored enzyme kinetics with different flavin sources at various concentrations. Michaelis-Menten-like kinetics were observed.
when the flavin concentration is varied (see Materials & Methods for method of $K_m$ calculation), indicating that flavin is a direct substrate for the enzyme. The $K_m$ of free flavin does not significantly differ for the various flavins used: 30 µM ± 8 for FMN, 64 µM ± 21 for FAD and 41 µM ± 10 for riboflavin (p<.05).

The reaction is likely to involve a two electron transfer reaction since a considerable amount of H$_2$O$_2$ is formed as an end product, regardless of the flavin form that is added. When the FMN level in the assay is lowered to 25 µM, the H$_2$O$_2$ concentration exceeds the flavin concentration more than five fold (135 µM H$_2$O$_2$ ± 33 µM), indicating that the free flavin is recycled during the reaction (Figure 2.3B). Altogether, these observations allow the classification of the protein(s) responsible for the measured activity as an NADH-dependent flavin reductase.

**Figure 2.3A and B:** Typical NADH dependent flavin reductase activity in *L. johnsonii* cell extract. NADH consumption rates were measured by absorption at 340 nm (Panel A). Endpoint H$_2$O$_2$ concentrations were determined using the phenol red assay (Panel B). Either 500 µM NADH was used, substituted by 500 µM NADPH where indicated (panel A) or 250 µM NADH substituted by 250 µM NADPH where indicated (Panel B). 250 µM or 25 µM of either FAD, FMN or riboflavin was added as a flavin source. Protein concentration in the cell abstracts was determined by the MicroBCA assay. Data represent the average of technical triplicates ± standard deviation and are representative of cell extracts derived in comparable experiments.

The reaction is likely to involve a two electron transfer reaction since a considerable amount of H$_2$O$_2$ is formed as an end product, regardless of the flavin form that is added. When the FMN level in the assay is lowered to 25 µM, the H$_2$O$_2$ concentration exceeds the flavin concentration more than five fold (135 µM H$_2$O$_2$ ± 33 µM), indicating that the free flavin is recycled during the reaction (Figure 2.3B). Altogether, these observations allow the classification of the protein(s) responsible for the measured activity as an NADH-dependent flavin reductase.

Purification and identification of the NADH-dependent flavin reductase activity.

In order to identify the protein(s) responsible for the NADH-dependent flavin reductase activity, cell extract of wild type *L. johnsonii* NCC 533 was subjected to the following purification steps; (i) ammonium sulfate precipitation, (ii) Q column chromatography and (iii) gel filtration (see Materials & Methods for details). After the ammonium sulfate precipitation, the 50%-70% fractions clearly display most NADH consumption. After the subsequent fractionation of this fraction using anion exchange chromatography, highest activity clearly eluted after 83 an 86 ml (see Supplementary materials, Figure S2.2). These fractions were combined and were subsequently further separated by
size exclusion chromatography (Superdex2000). Only a single fraction eluted during this chromatography step that displayed clear H₂O₂ production in the enzymatic assay (Figure 2.4). The size of the enzymes in this fraction were, based on its elution time, estimated to be ~18kDa. The enzyme(s) in this fraction that showed NADH flavin reductase activity were only partially purified, since multiple bands were apparent when it was loaded on SDS-gel (results not shown). The active fraction obtained was digested with trypsin and analyzed using LC-MS/MS, using the fraction preceding this active fraction (and containing no activity) as a comparative negative-control. In the active fraction 25 L. johnsonii proteins could be assigned with a probability based score of P<0.05. The protein that was predicted with highest probability was the hypothetical protein LJ_0548 to which 8 peptides could be assigned with a total coverage of 63%, indicating a high abundance in the fraction. Three peptides could be assigned to the hypothetical protein LJ_0549 (33% sequence coverage) which is encoded by LJ_0549, the LJ_0548 neighboring gene. Noteworthy, the predicted protein sequences of LJ_0548 (accession number Q74HL7) and LJ_0549 (accession number Q74HL8) both contain a conserved FMN reductase domain, supporting the role of these gene-products in the NADH dependent flavin reductase activity. Furthermore, no peptides belonging to these two proteins were detected in the fraction that did not show any NADH flavin reductase activity but eluted close to the active fraction (negative-control). Taken together, these observations pointed toward the involvement of the LJ_0548 and LJ_0549 genes in the NADH flavin reductase activity of cell extracts of L. johnsonii.

![Figure 2.4: Size-exclusion chromatogram (Superdex200) of final purification step. Protein concentration is determined by absorption at 280 nm (black line). The eluting proteins were collected in fractions of 1 ml and tested for NADH flavin reductase activity by addition of 500 µM NADH and 250 µM FAD. H₂O₂ concentration was determined after 10 min (symbols).](image)

A mutant derivative of L. johnsonii NCC 533 was constructed that lacks the genes LJ_0548 and LJ_0549 (NCC 9359). The cell extracts of this mutant strain completely
lacked flavin dependent NADH reductase activity that was detected in the extracts obtained from the wild-type strain, nor could any H₂O₂ be detected in the reaction mixture supplemented with the mutant strain extract. These results indicate that the \textit{LJ\_0548} and/or \textit{LJ\_0549} encode the NADH dependent flavin reductase activity. The \textit{LJ\_0548-0549} deletion strain (NCC 9359) was complemented by providing one or both of the deleted genes \textit{in trans} on a plasmid under expression control of the strong, constitutive D-lactate dehydrogenase gene promoter (\textit{LJ\_0045}; \textit{ldhDp}). Cell extracts derived from the NCC 9359 strain harboring either the \textit{LJ\_0548-} (pDP1016) or the \textit{LJ\_0549-} (pDP1017) expression plasmid did not show any additional bands on an SDS-protein gel. These cell extracts also did not show any significant NADH-dependent flavin reductase activity. Conversely, the extract derived from the strain harboring the plasmid expressing both the \textit{LJ\_0548} and \textit{LJ\_0549} genes (pDP1019) displayed an additional band of 20 kDa on an SDS-gel (Supplementary materials, Figure S2.3) and an NADH consumption rate that was more than 7-fold higher compared to the rate measured in extracts derived from the wild-type strain (Figure 2.5A). The level of H₂O₂ production driven by the extract derived from the strain overexpressing \textit{LJ\_0548} and \textit{LJ\_0549} was comparable to the level produced by the extract from the wild-type, which reflects the maximal level of H₂O₂ production that can be obtained in this assay as a consequence of the limited amount of NADH provided in the reaction mixture (Figure 2.5B). These results show that the \textit{LJ\_0548-0549} operon encodes the observed NADH-dependent flavin reductase activity.

\textit{H₂O₂} production of the \textit{LJ\_0548 and LJ\_0549} deletion strain

Having identified \textit{LJ\_0548} and \textit{LJ\_0549} as coding for the enzymes responsible for NADH-dependent flavin reductase activity in the cell extracts of \textit{L. johnsonii} NCC 533, we studied the \textit{in vivo} contribution of this activity to the aerobic physiology of this bacterium by comparing the wild type to its \textit{nfr}-deletion derivative (\textit{ΔLJ\_0548- LJ\_0549}, NCC 9359). Maximum specific growth rate of the mutant in shake flask was similar to the wild type and its metabolism remained homolactic (result not shown). However, when exposed to stronger aeration (750 ml/min, 75% N₂, 20% O₂, 5% CO₂), the \textit{nfr}-deletion derivative displayed a reduced growth rate compared to wild type strain, whereas exposure to the anaerobic gas-mixture equivalent of this regimen (750 ml/min 95% N₂, 5% CO₂) did not result in a difference between the \textit{nfr}-mutant and its wild type counterpart (Supplementary material, Figure S2.4).
To test H$_2$O$_2$ production, the wild-type strain (NCC 533) and its LJ$_{0548-0549}$ deletion derivatives were grown anaerobically to mid-logarithmic phase (OD$_{600}$ ~0.8) at 37°C and were then transferred to aerobic (shake-flask) conditions. H$_2$O$_2$ in the spent medium of each of the cultures was assessed after 1 hour of oxygen exposure (Figure 2.6). Notably, the LJ$_{0548-0549}$ deletion (strain NCC 9359) resulted in complete loss of the capacity to produce H$_2$O$_2$ under these conditions, while substantial amounts of this reactive oxygen molecule were detected in the NCC 533 culture exposed to the same conditions. Moreover, the NCC 9359 mutant strain that was in trans complemented with plasmid borne expression of either LJ$_{0548}$ (pDP1016) or LJ$_{0549}$ (pDP1017) did not produce detectable H$_2$O$_2$ levels, whereas the strain complemented with plasmid-borne expression of both LJ$_{0548}$ and LJ$_{0549}$ (pDP1019) displayed a restored H$_2$O$_2$ production capacity, comparable to that observed in the parental strain NCC 533. These data confirm that the L. johnsonii NCC 533 NADH-dependent flavin reductase is encoded by the LJ$_{0548-0549}$ cluster and that this activity is the major H$_2$O$_2$ producing system expressed under the conditions employed here.

In order to test if LJ$_{0548}$ and LJ$_{0549}$ play a role in anaerobic fumarate respiration of L. johnsonii, the external metabolite profiles of wild type NCC 533 and NCC 9359 (the
LJ_0548 and LJ_0549 deletion derivative) were compared. After 7 hours of anaerobic growth in MRS medium supplemented with 10 mM fumarate, cells were removed by centrifugation and external metabolites were analyzed using HPLC. No change in the concentration of fumarate was observed and no succinate formation was detected. Both aerobic and anaerobic metabolism of the mutant strains remained entirely homolactic (results not shown).

Sequence analysis of LJ_0548 and LJ_0549, and their conservation among bacteria

Using the wealth of genomic sequence availability, the prevalence and context of the LJ_0548 and LJ_0549 single genes as well as the combination of the two consecutive genes were analyzed using diverse genome comparison tools.

The LJ_0548 and LJ_0549 genes are predicted to encode proteins of 178 and 184 residues, respectively, that share substantial similarity (40% identity and 59% similarity at amino acid sequence level). The protein domain signature recognition module Interproscan (209) revealed that both genes have a highly conserved FMN reductase domain (PFAM domain 03358), covering the N-terminal 145 residues. In the PANTHER classification system program (210), LJ_0548 was classified as a chromate reductase, a group of enzymes that has been annotated as such due to their potential use in chromate bioremediation (211). The ortholog in Pseudomonas putida has been shown to catalyze the transfer of electrons from NADH to the quinone pool (212). The crystal structure of the E. coli gene annotated as chromate reductase clearly demonstrates the amino acids that constitute the flavin binding site (213). A ClustalW multiple sequence
alignment shows that four out of the eleven residues of this binding site are conserved in both *LJ_0548* and *LJ_0549*, i.e. Ser18, Asn20, Glu82 and Ser 117 (Supplementary Materials Figure S2.5).

The *LJ_0548-0549* locus in *L. johnsonii* NCC 533 appears to be conserved in all other members of the *L. acidophilus* group. Examination of the genetic context in more distant species using the STRING module (214) revealed that the closest homologues of *LJ_0548* and *LJ_0549* are encountered as consecutive genes in several different species (see Figure 2.7), including *L. plantarum*, and several species belonging to the *Streptococcus, Enterococcus* and *Pediococcus* genera. In these examples, the first of these two genes is similar in sequence and size to either *LJ_0548* or *LJ_0549* and is followed by a second, larger gene, of which the N-terminal residues (~200) are homologues to *LJ_0548*. This type of arrangement is also present in a more distant species from the Actinobacteria class, *Atopobium parvulum*, which is a species often found in the human oral cavity(215). In all aforementioned species, the homologues of *LJ_0548* and *LJ_0549* are annotated as fumarate reductases, NADH dehydrogenases or flavin reductases, but to the best of our knowledge there is no experimental data to support these annotations.
Figure 2.7: Genetic context conservation of LJ_0548 and LJ_0549 found using the STRING module.
Discussion

Our work has identified a novel NADH-dependent FMN reductase in *L. johnsonii* NCC 533, that is encoded by two adjacent genes (*LJ_0548* and *LJ_0549*) and acts as the major *H₂O₂* producing system in this bacterium. *L. johnsonii* is a lactic acid bacterium that belongs to the phylogenetically closely related *L. acidophilus* group (168, 216), which includes several strains of *Lactobacillus* species that are marketed as probiotic supplements like *L. acidophilus*, *L. johnsonii*, *L. jensenii*, *L. crispatus* and *L. gasseri*, but also encompasses the well-known yoghurt bacterium *L. delbrueckii*. It has been established that these species endure oxidative stress as a consequence of endogenously produced *H₂O₂* (35-37). The enzymes identified here have characteristics that are in agreement with those observed previously in strains of the *L. acidophilus* group, including that the enzyme reaction consumes NADH, uses flavin as a cofactor, is constitutively expressed and is not produced in response to molecular oxygen (37, 93, 94). In addition, the maximal reaction rate measured in cell extracts of *L. johnsonii* is in the same order of magnitude as the rate previously reported for *L. delbrueckii* (37).

Apparent Michaelis-Menten kinetics were observed when the concentration of flavin was varied in the enzymatic assay. However, the *H₂O₂* produced in the assay reaches a higher level than the total initial concentration of flavin added to the assay, indicating that free oxidized flavin serves as a substrate in this reaction but the reduced flavin is subsequently oxidized and reused. This is in agreement with the behavior of reduced flavins that spontaneously react with oxygen, yielding *H₂O₂*.

Despite the recognition of this enzyme activity in various *L. acidophilus* group species, the molecular characteristics and genetic determinant(s) of this activity have not been described to date. Therefore, our study is the first to identify and characterize this novel enzyme family and its encoding genes. The enzyme is shown to be responsible for the major *H₂O₂* production in an industrially relevant member of the *L. acidophilus* group, *L. johnsonii*. This capacity has previously been proposed to influence gut homeostasis and anti-inflammatory activity of this group of organisms (50) and the identification of the responsible genes and the construction of the corresponding deletion strain may accelerate the establishment of this presumed function *in vivo*, which is assumed to play a role in the bacterium’s protective effect against vaginal disease (187).

The *Vₘₐₓ* and *Kₘ* values of the different flavins that were tested in the enzymatic assay did not differ strongly. The *Kₘ* value for flavins were found in the range of 30-50 µM. Intracellular flavin concentrations in *E. coli* and *Shewanella oneidensis* were reported
in the order of 0.5 µmol per gram protein (217), which in combination with the “rule-of-thumb” estimate of ~200 g/l as the concentration of intracellular protein in prokaryotes (218) implies that the intracellular flavin concentration would be ~100 µM. The partitioning of flavin bound to protein and available as electron acceptor for the proteins we describe here is unknown. One study on intracellular free FAD concentration in *Amphibacillus xylanus* finds 13 µM using HPLC (219). Such a flavin concentration in *L. johnsonii* would be sufficient for its proposed *in vivo* role. Given the clear confirmation of the *in vivo* role of Nfr by the physiology of the *nfr*-deletion mutants, we consider it a valid conclusion that analogous to the previously found concentration in *A. xylanus* the free flavin levels in *L. johnsonii* suffice for significant H₂O₂ production.

Surprisingly, the genes that are considered to be responsible for H₂O₂ production in other LAB were shown to not contribute significantly to this phenotype in *L. johnsonii*, since the genes predicted to encode lactate, pyruvate or NADH oxidases could be deleted without consequences for the H₂O₂ production in this species. The homologs of *LJ_0548* and *LJ_0549* have been annotated as fumarate reductase, NADH dehydrogenase or NAD(P)H dependent FMN reductase. The *LJ_0548* and *LJ_0549* proteins are predicted to be small flavoproteins that are highly similar (40%). The size of the denatured protein components in the cell extract of the *LJ_0548-0549* overexpressing strain on the SDS-gel is 20 kDa, corresponding to the size of the gene product of either *LJ_0548* or *LJ_0549* as inferred from their gene sequence. Its elution from the gel filtration column suggests that the active protein has a size of ~18 kDa, which would mean that only one of either *LJ_0548* or *LJ_0549* would be required for activity. However, for complementation of the *LJ_0548-0549* deletion strain, both genes appear to be required, whereas in trans complementation with a plasmid harboring either one of the genes failed to result in detectable protein expression (SDS-PAGE) or functional complementation. Although we can conclude that both genes are required to produce the functional enzyme, its exact composition remains unclear.

The observation that the deletion derivative NCC 9359 produces small amounts of H₂O₂ upon prolonged exposure to oxygen indicates that besides the NADH flavin reductase identified here, other H₂O₂ producing enzymes may exist in this species. Nevertheless, the enzyme identified here appears to be the major contributor to the H₂O₂ production capacity in this species. Possibly, the additional H₂O₂ producing reactions involve oxidases, like the aforementioned pyruvate, lactate and NADH oxidase, which may contribute to H₂O₂ production upon extended oxygen exposure. However, it is unlikely that the conditions of oxygenation used in this study, both in terms of its duration and/or
oxygen tension, will be encountered in the GI-tract, which is thought to be the natural
habitat of *L. johnsonii*. We propose therefore that the constitutive flavin reductase is the
primary source of H$_2$O$_2$ in an environment where microbes predominantly encounter
anaerobic (intestinal lumen) conditions and only sporadically encounter lower and more
variable concentrations of oxygen when they are present in closer proximity to the
intestine mucosa. In contrast, prolonged exposure to aerobic conditions and/or higher
oxygen tensions can occur during industrial processing, which may elicit the activation
of alternative H$_2$O$_2$ production reactions as our preliminary observations imply.

*L. johnsonii* has been proposed to have lost numerous genes and pathways during its
adaptation to the nutrient-rich environment of the intestinal tract (176). Nevertheless,
the newly discovered NADH dependent flavin reductase appears to be constitutively
expressed, suggesting that it plays an important role in the lifestyle of *L. johnsonii* in its
natural environment. Since lactate fermentation from glucose is entirely redox-neutral,
it is unclear in what metabolic step the NADH is generated that is consumed in the
reaction catalyzed by the *LJ_0548-549* enzyme. We hypothesize that the additional
electrons are generated in the metabolism of one of the many vitamins, peptides and
amino acids that are consumed by *L. johnsonii* in addition to glucose.

Although the results presented here do not rule out that this newly identified flavin
reductase serves a metabolic purpose in which H$_2$O$_2$ is a side product, we suggest that
the production of H$_2$O$_2$ in itself has a biological function. For example, it may contribute
to the antimicrobial capacities of *L. johnsonii* that may be of great importance for the
organism to maintain its niche / position within the densely populated microbiota (38).
Moreover, H$_2$O$_2$ may serve as a chemical signal in host-microbe interactions, as it has
been proposed to influence PPAR-γ, one of the major regulators of inflammation
in the intestinal epithelium (50). Alternatively, the reduced aerotolerance of the *nfr-
deletion* derivative as compared to its wildtype counterpart suggests that the reaction
catalyzed by this enzyme may enable *L. johnsonii* to prevent or reduce oxidative stress.

If the flavins that are reduced by these proteins, form the most readily oxidized parts
in the cytoplasm and can effectively capture oxygen, the activity of these flavins may
prevent other, more damaging effects of oxygen, such as the direct oxidation of iron-
sulfur clusters (220, 221) or the formation of semiquinones (212). Also in *L. johnsonii*,
the controlled production of H$_2$O$_2$ may be preferred over the uncontrollable other
effects oxygen might exert. The role that this NADH dependent flavin reductase plays
in oxidative stress, H$_2$O$_2$ scavenging and aerotolerance of *L. johnsonii* is the subject of
further studies.
Acknowledgments
This work was supported by Nestlé Research Centre, Vers-chez-les-Blanc, Switzerland. We would like to acknowledge Anne-Cécile Pittet for her technical assistance in construction of the mutants and Filipe Branco dos Santos for his valuable input on the purification of the NADH flavin reductase activity.
Supplementary materials

Table S2.1: Primers used for construction of *L. johnsonii* mutant strains (chapter 2).

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Figure S2.1: Genetic maps of LJ_0548 and/or LJ_0549 overexpression plasmids.
Figure S2.2: Purification of NADH flavin reductase activity in cell free extract of wild type *L. johnsonii*. NADH consumption rate (in the presence of 250 µM FAD) is determined in fractions obtained during ammonium sulphate precipitation (panel A). The fraction with highest activity is subsequently used for anion exchange chromatography. All fractions eluting from the Q column (panel B) are tested for NADH flavin reductase activity. On the left axis, absorption at 280 nm is shown which is an indicator of protein concentration. On the right axis, NADH consumption rate is shown in the eluting fractions.

Figure S2.3: SDS gel of cell free extracts of *L. johnsonii* NCC 533 (wt, lane 1), NCC 9359 + pDP 1016 (∆nfr + LJ_0548, lane 2), NCC 9359 + pDP 1017 (∆nfr + LJ_0549, lane 3), NCC 9359 (∆nfr, lane 4), NCC 9359 + pDP 1019 (∆nfr + LJ_0548-LJ_0549, lane 5), PageRuler™ marker (lane 6).
Figure S2.4: Growth rate of *L. johnsonii* NCC 533 (grey bars) and its *nfr*-deletion derivative NCC 9359 (white bars) in MRS-medium in stirred pH controlled sparged with 750 ml/min of N₂ + 5% CO₂ (anaerobic) or N₂ + 20% O₂ + 5% CO₂ (aerobic). Growth rates were determined as explained in Materials & Methods. Data are average of triplicate experiments ± standard deviation.

![Growth rate graph](image)

**L. johnsonii** LJ_0549

---MKLAIVGVTNADFZRFLDPMAKETYKDQAEIEY-EIAADLPF

**L. johnsonii** LJ_0548

---MKLFASIVGNADHYNRDLNFIKHTDRELYDE-EVAKDLPMF

**E. coli** K12 ChrR

MSEKLQVTVLGLKSFENGVRATLFKIAPASMEVNLPSIDPLYD

---MKLLAIVGTNADFSYNRFLQMAKRYKDQAIEY-EIAADLPF

---MKLFASIVGNADHYNRDLNFIKHTDRELYDE-EVAKDLPMF

**L. johnsonii** LJ_0549

KEAQP----DSKVEFKNKIREADGVIFATPDKGIPSALKSAMEWTS

**L. johnsonii** LJ_0548

EGVKE----PAAASFAKVDADAVLHTEQQHLSVPSSLKSALEWLS

**E. coli** K12 ChrR

ADVQFEEGFPATVEALAEQRADGVATPTKHSVPGGLKAIDWLS

---MKLLAIVGTNADFSYNRFLQMAKRYKDQAIEY-EIAADLPF

---MKLFASIVGNADHYNRDLNFIKHTDRELYDE-EVAKDLPMF

**L. johnsonii** LJ_0549

HAQGNADVMKMPAMVLTQYGIQGASRAQEMREILLSFDQSANVLPG

**L. johnsonii** LJ_0548

AEHPI----FEDKVPPVVTQVLPQGSMGSHLLKVLSSLPSFGAKVFG

**E. coli** K12 ChrR

LDPQF----LAQKPVPTSTHGVIGARQCYHLQILVLFD--AVMK

---MKLLAIVGTNADFSYNRFLQMAKRYKDQAIEY-EIAADLPF

---MKLFASIVGNADHYNRDLNFIKHTDRELYDE-EVAKDLPMF

**L. johnsonii** LJ_0549

EVLIGHAADKFDKNTGDLQETIHAIADFNFKNVFKVEQAK

**L. johnsonii** LJ_0548

EFMQGTAPEQFDEGN------LPAKTQVDLHHDFFDSYAEVSK

**E. coli** K12 ChrR

EFMQGQTVNKDPQTFGEVQDQTLHDHLMQALGFEQVR

---MKLLAIVGTNADFSYNRFLQMAKRYKDQAIEY-EIAADLPF

---MKLFASIVGNADHYNRDLNFIKHTDRELYDE-EVAKDLPMF

**L. johnsonii** LJ_0549

EVLIGHAADKFDKNTGDLQETIHAIADFNFKNVFKVEQAK

**L. johnsonii** LJ_0548

EFMQGTAPEQFDEGN------LPAKTQVDLHHDFFDSYAEVSK

**E. coli** K12 ChrR

EFMQGQTVNKDPQTFGEVQDQTLHDHLMQALGFEQVR

Figure S2.5: ClustalW2 comparison of *LJ_0548* / *LJ_0549* to chromate reductase (ChrR) from *E. coli*. Highlighted in grey are the residues that constitute the flavin binding site, highlighted in yellow are the similarities in these residues in the *L. johnsonii* genes.