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The Regulator PerR Is Involved in Oxidative Stress Response and Iron Homeostasis and Is Necessary for Full Virulence of *Streptococcus pyogenes*

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Ferric uptake regulator (Fur) and Fur-like proteins form an important family of transcriptional regulators in many bacterial species. In this work we have characterized a Fur-like protein, the peroxide regulator PerR, in an M1 serotype of *Streptococcus pyogenes*. To determine the role of PerR in *S. pyogenes*, we inactivated the gene by allelic replacement. PerR-deficient bacteria showed 48% reduction of ⁵⁵Fe incorporation from the culture medium. Transcriptional analysis revealed that *mtsA*, encoding a metal-binding protein of an ABC transporter in *S. pyogenes*, was transcribed at lower levels than were wild-type cells. Although total iron accumulation was reduced, the growth of the mutant strain was not significantly hampered. The mutant showed hyperresistance to hydrogen peroxide, and this response was induced in wild-type cells by growth in aerobiosis, suggesting that PerR acts as an oxidative stress-responsive repressor. PerR may also participate in the response to superoxide stress, as the *perR* mutant was more sensitive to the superoxide anion and had a reduced transcription of *sodA*, which encodes the sole superoxide dismutase of *S. pyogenes*. Complementation of the mutation with a functional *perR* gene restored ⁵⁵Fe incorporation, response to peroxide stress, and transcription of both *mtsA* and *sodA* to levels comparable to those of wild-type bacteria. Finally, the *perR* mutant was attenuated in virulence in a murine air sac model of infection (*P < 0.05*). These results demonstrate that PerR is involved in the regulation of iron homeostasis and oxidative stress responses and that it contributes to the virulence of *S. pyogenes*.

Oxidative stress is generated by exposure to reactive oxygen species (ROS), such as superoxide anion (O₂⁻), hydrogen peroxide (H₂O₂), and the highly toxic hydroxyl radical (OH), which can damage nucleic acids, proteins, and cell membranes. As a defense, cells have evolved inducible responses to protect themselves against oxidative stress (18, 42, 51). In bacteria, a large body of evidence, originating mainly from studies with *Escherichia coli* and *Salmonella*, has shown that peroxide and superoxide stress responses are distinct (18). Superoxide dismutase (SOD) represents the first line of defense against superoxide stress by converting O₂⁻ into H₂O₂ and O₂, thereby protecting cells from the toxic effects of O₂⁻ (21).

There is an intimate relationship between oxidative stress and iron metabolism. Iron is both an essential cofactor and a potentially hazardous metal participating in the production of ROS (27). Lack of iron regulation may impose oxidative stress upon cells (54), and many microorganisms have evolved systems that couple control of iron homeostasis to protection against ROS (7, 9, 16, 34, 35, 53, 56, 60). Bacterial iron metabolism is regulated by Fur (ferric uptake regulator) in gram-negative bacteria and by DtxR (diphtheria toxin repressor) in most gram-positive bacteria (for reviews see references 28 and 31). More recently, Fur and Fur-like proteins have also been characterized in gram-positive species (4, 22, 34, 35, 38, 39, 58).

Both *Bacillus subtilis* and *Staphylococcus aureus* contain three distinct Fur homologues: Fur, which typically controls iron homeostasis (4, 35); the H₂O₂- and metal ion-responsive peroxide regulator PerR (4, 34); and Zur, which is involved in the regulation of zinc homeostasis (22, 39). In contrast, *Streptococcus pyogenes* seems to have a single PerR protein, which was recently reported to be involved in the resistance response to peroxides (38). Fur proteins generally act as transcriptional repressors by Fe²⁺-dependent binding to specific sequences (so-called iron boxes) in the promoters of iron-regulated genes (1, 14, 28). However, Fur can also regulate transcription of iron-activated genes (13) and can even behave as a positive regulator, either directly or indirectly (15, 20, 29, 44). Fur is now considered a pleiotropic regulator, as it can control not only iron acquisition systems but also the most diverse processes such as acid and oxidative stress responses, chemotaxis, swarming, bioluminescence, metabolic pathways, and production of virulence factors (reviewed in references 17, 28, and 48). With respect to oxidative stress, Fur regulation of SOD has been observed in several bacterial species (53). Interestingly, in *E. coli*, Fur represses transcription of manganese-dependent *sodA* (11, 52), but it is a positive regulator of iron-dependent *sodB* (15, 44).

*S. pyogenes*, or group A *Streptococcus*, is an important human pathogen causing various diseases, from mild supplicative throat and skin infections to life-threatening invasive diseases (12). *S. pyogenes* virulence determinants are often regulated in response to growth phase and environmental signals, such as temperature, osmolality, pH, iron limitation, and O₂ and CO₂ tension (5, 24, 26, 40, 41, 50, 55, 57). *S. pyogenes* is a facultative
TABLE 1. Bacterial strains and plasmids

<table>
<thead>
<tr>
<th>Strain or plasmid</th>
<th>Relevant properties</th>
<th>Source or reference</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Strains</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>E. coli</em> DH5α</td>
<td>recA1 endA1 hsdR17</td>
<td>Invitrogenb</td>
</tr>
<tr>
<td><em>S. pyogenes</em></td>
<td></td>
<td></td>
</tr>
<tr>
<td>API</td>
<td>Serotype M1, wild type</td>
<td>World Health Organization Prague collectionc</td>
</tr>
<tr>
<td>SR301</td>
<td>perR::kan Km’</td>
<td>This study</td>
</tr>
<tr>
<td>SR304</td>
<td>perR::kan/pLU21 (perR+) Km’ Sp’</td>
<td>This study</td>
</tr>
<tr>
<td>R1J</td>
<td>mtxA::kan Km’</td>
<td>37</td>
</tr>
<tr>
<td><strong>Plasmids</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>pFW13</td>
<td>Allelic replacement vector, Km’</td>
<td>46</td>
</tr>
<tr>
<td>pLZ12-Spec</td>
<td><em>E. coli</em>-Streptococcus vector, Sp’</td>
<td>36</td>
</tr>
<tr>
<td>pLU11</td>
<td>perR::kan in pFW13, Km’</td>
<td>This study</td>
</tr>
<tr>
<td>pLU21</td>
<td>perR’ in pLZ12-Spec, Sp’</td>
<td>This study</td>
</tr>
</tbody>
</table>

a Km’ and Sp’ indicate resistance to kanamycin and spectinomycin, respectively.
b Invitrogen, Life Technologies, Inc., Carlsbad, Calif.
c World Health Organization Collaborating Center for Reference and Research on Streptococci, Institute of Hygiene, Prague, Czech Republic.

anaerobe and lacks catalase. However, it has other defense mechanisms against oxidative stress, including an NADH-oxidase (25), a single Mn-dependent SOD (24), two peroxidases, and the PerR regulator (38).

Starting from a previous observation that PerR is involved in the inducible response to H2O2 in an *S. pyogenes* M6 serotype strain (38), in the present work we have characterized in more detail the phenotypes of a perR mutant in an M1 serotype. The results show that PerR affects iron metabolism and peroxide and superoxide stress responses and is necessary for full virulence.

**MATERIALS AND METHODS**

**Bacterial strains, plasmids, and growth conditions.** The bacterial strains and plasmids used in this study are described in Table 1. *E. coli* was cultured in Luria-Bertani medium (Difco, Detroit, Mich.) at 37°C under aerobic conditions. *S. pyogenes* was grown in Todd-Hewitt medium (Difco) supplemented with 0.2% yeast extract (THY) or in metal-depleted THY (Cx-THY) at 37°C in 5% CO2.

**Construction of strains.** The primers used for constructing the strains are shown in Table 2. Allelic replacement mutagenesis of *perR* was performed in two steps. First, an 878-bp fragment comprising the first 201 bp of *perR* together with a 677-bp region upstream of the gene, was amplified by PCR from *API* chromosomal DNA with the primers PerR-forward (BglII) and PerR-reverse (SacI). This PCR product was digested with BglII and SacI and inserted into the BamHI and SacI sites of plasmid pFW13 (46), generating plasmid pLU11. For the second cloning, a 999-bp PCR product, including the last 105 bp of *perR* and the following 894 bp of the region downstream of the *perR* stop codon, was generated with the primers PerR-forward (Apal) and PerR-reverse (BlnI). Following digestion with *Apal* and *BlnI*, the PCR fragment was ligated into the corresponding restriction sites of pLU10. The new plasmid was denominated pLU11 (Table 1).

**Restriction sites for subsequent cloning of the PCR products are underlined. Primer sequences were chosen by using the complete genome of the M1 serotype strain SF370 (19).**

**TABLE 2. Oligonucleotides used in this study**

<table>
<thead>
<tr>
<th>Primer</th>
<th>Sequence (5’ to 3’)</th>
<th>Target</th>
</tr>
</thead>
<tbody>
<tr>
<td>PerR-forward (BglII)</td>
<td>GCAGATCTATTTCTCATTATGGACAAC</td>
<td>perR</td>
</tr>
<tr>
<td>PerR-reverse (SacI)</td>
<td>CCUGAGCTCATAGACTTGGCGAAAGGC</td>
<td>perR</td>
</tr>
<tr>
<td>PerR-forward (Apal)</td>
<td>ATGGGCCCCATTTGCACAAAGACCC</td>
<td>perR</td>
</tr>
<tr>
<td>PerR-reverse (BlnI)</td>
<td>ATCTCTAGTTGTTAACCTGTACTTGTC</td>
<td>perR</td>
</tr>
<tr>
<td>PerR-forward (EcoRI)</td>
<td>TCCTATTCTTTTATCCTTATATTTTC</td>
<td>perR</td>
</tr>
<tr>
<td>PerR-reverse (SphI)</td>
<td>ATGGATCATGCATGGTCTTCCTTTATTATCC</td>
<td>perR</td>
</tr>
<tr>
<td>MtsA-forward</td>
<td>TACGAACATTACACGGAAGAT</td>
<td>mtsA</td>
</tr>
<tr>
<td>MtsA-reverse</td>
<td>CTCTTCTTCGTTGAATTATCCCCAG</td>
<td>mtsA</td>
</tr>
<tr>
<td>FhuD-forward</td>
<td>ATAGCGGGCCTGAAAAGATTGAGGTC</td>
<td>fhuD</td>
</tr>
<tr>
<td>FhuD-reverse</td>
<td>CAAGATTATACCACAAACAGGG</td>
<td>fhuD</td>
</tr>
<tr>
<td>SodA-forward</td>
<td>TTACCAGAACCTTCCATACGG</td>
<td>sodA</td>
</tr>
<tr>
<td>SodA-reverse</td>
<td>TCTTTTTGAGATTTGCCAAACC</td>
<td>sodA</td>
</tr>
<tr>
<td>M1-forward</td>
<td>GGCTAACCATTGATGTTATCC</td>
<td>emm1</td>
</tr>
<tr>
<td>M1-reverse</td>
<td>CCGTCTGCTTCAAGGCCTTG</td>
<td>emm1</td>
</tr>
<tr>
<td>16S-forward</td>
<td>ATGTTTAGTAAATTTAAAAAGGGG</td>
<td>16S RNA</td>
</tr>
<tr>
<td>16S-reverse</td>
<td>TTTAAGAGATATGCTTCGGT</td>
<td>16S RNA</td>
</tr>
</tbody>
</table>

SF370 (19).
including a putative promoter and a transcriptional terminator, was amplified with the primers PerR-forward (EcoRI-R) and PerR-reverse (SpeI-R). The PCR product was digested with EcoRI and SpeI and ligated to plasmid pLZ12-SpeI (36) cut with the same enzymes, resulting in plasmid pLU21 (Table 1). Plasmid pLU21 was introduced into the mutant SR301 strain, and clones were selected on THY plates containing kanamycin and spectinomycin. The presence of the plasmid was verified by using the Concert Rapid Plasmid Miniprep system (Gibco-BRL) and restriction mapping. One transcomplementation clone was chosen and designated SR304.

Total 55Fe incorporation assays. S. pyogenes strains API, SR301, and SR304 were grown on THY broth. Each ON culture was washed once in Cx-THY and inoculated 1:100 in 1 ml of fresh Cx-THY containing 0.25 µCi of 55FeCl3 (Amersham Pharmacia Biotech, Uppsala, Sweden). In parallel, 10-ml reference culture tubes were inoculated and their growth was carefully followed until the optical density at 620 nm (OD620) was ≥0.6, at which point the corresponding 1-ml samples were collected. To ensure that equivalent amounts of cells were harvested, viable counts from the reference tubes were performed. Then samples were spun down (10,000 × g, 3 min), and supernatants were collected. Bacteria were washed with 1 ml of fresh Cx-THY for a total of three washes. Finally, bacterial pellets were resuspended in 200 µl of fresh Cx-THY and mixed with 5 ml of Ready Safe scintillation cocktail (Beckman). Five milliliters of scintillation fluid was also added to the supernatants. Radioactivity was measured with a β-counter calibrated for 55Fe. The percentage of 55Fe associated with the bacterial pellet was calculated by dividing the number of counts per minute of the pellet by the number of counts per minute of the pellet plus the supernatant. The experiments were performed at least three times in duplicate or triplicate samples.

Oxidative stress assays. ON cultures of S. pyogenes API, SR301, and SR304 strains were re inoculated 1:250 in fresh THY or Cx-THY and incubated at 37°C either with 5% CO2 or under aerobic conditions. When the OD620 of the cells reached ≥0.5, a 100-µl aliquot was removed (time zero) and kept on ice, and 5 mM H2O2 was added to the bacterial cultures. Samples were collected at 15, 30, 60, and 90 min after the addition of H2O2. Catalase (5 mg/ml; Sigma) was added, and the tubes were put on ice. Appropriate bacterial dilutions were plated onto THY agar plates. The cells were counted, and the percentage of survival was calculated by dividing the number of CFU at different time points with the initial number of CFU at time zero. Experiments were performed four to five times with duplicate samples, and the results were expressed as means ± standard deviations (SD). For growth in the presence of paraquat (methyl viologen; Sigma), ON cultures of API and SR301 were inoculated 1:1,000 in fresh THY containing 2 or 10 µM paraquat. Samples with no paraquat were also used as controls. After 15 h of incubation at 37°C with 5% CO2, the OD620 was recorded. Experiments were performed five times with duplicate or triplicate samples.

Protein methods. The presence of M1 protein and C5a peptidase at the surface of API and SR301 bacteria was investigated by cleavage with cyanogen bromide (CNBr) and S. pyogenes cysteine proteinase (SCP), respectively. Digestion with CNBr was performed as described previously (10), and solubilized protein fragments were analyzed by sodium dodecyl sulfate (SDS)-10% polyacrylamide gel electrophoresis (PAGE), blotting onto polyvinylidene difluoride membranes (Immobilon-P, Millipore, Bedford, Mass.), and treated with anti-C5a peptidase rabbit serum (1:50,000). Peroxidase-conjugated protein A (1:5,000; Sigma) was used as a secondary antibody in all immunoblots. After washing, proteins were detected by chemiluminescence as previously described (43). Membranes were dried and autoradiographed with X-Omat AR films (Kodak). 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A promoter, was cloned in a plasmid able to replicate in *S. pyogenes* (36) and transformed into the SR301 strain. A complemented strain was designated SR304 [**perR**::kan/pLU21 (**perR**⁻)] (Table 1).

**PerR** affects iron metabolism in *S. pyogenes*. Fur, in the presence of Fe²⁺, generally acts as a transcriptional repressor of iron uptake systems (1, 14, 17). As a consequence, **fur** mutants often express iron import systems in a constitutive fashion (2, 28). Iron incorporation by AP1 and SR301 bacteria was investigated by measuring the amount of ⁵⁵Fe accumulated in cells grown to exponential phase in Cx-THY. Interestingly, the amount of ⁵⁵Fe detected in the mutant was reduced by 48% compared to both the wild type and the complemented SR304 strain (Fig. 1A). Little is known about metal ion uptake systems in *S. pyogenes*, and only two transporters have been annotated in the complete *S. pyogenes* genome: the MtsABC transporter with broad specificity for metal cations (37) and the putative ferrichrome uptake system FhuGBDA (19, 50). Therefore, in order to investigate whether expression of **mtsABC** and/or **fhuGBDA** was affected in **perR**-deficient bacteria, Northern blot analysis on total RNA from strains AP1, SR301, and SR304 was performed. The probes used were **mtsA**, coding for the lipoprotein of MtsABC, and **fluD**, encoding a putative ferrichrome transporter. We failed to detect any transcript in all samples when using the **fluD** probe, whereas strong hybridization occurred with the **mtsA** probe. Densitometric analysis showed a 2.4-fold reduction of **mtsA** transcription in the SR301 mutant compared to that of the wild type (Fig. 1B). These data suggest that the reduced accumulation of iron by the **perR** mutant is at least partially due to a decreased transcription of **mtsA**.

**Growth features of** **perR**-deficient *S. pyogenes*. In order to analyze whether the decreased iron accumulation in the **perR** mutant affected bacterial growth in vitro, strains AP1 and SR301 were cultivated in rich medium (THY), metal-depleted THY (Cx-THY), and iron-repleted (100 μM ferric citrate) Cx-THY. No significant difference was observed when comparing generation times in the exponential phase of wild-type and mutant strains in THY (50 ± 11 and 53 ± 9 min, respec-

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**FIG. 1.** Total iron incorporation by *S. pyogenes* strains AP1, SR301, and SR304. (A) AP1 (wild type), SR301 (**perR**), and SR304 (**perR**⁻) cells were cultured in Cx-THY in the presence of ⁵⁵Fe until the mid-exponential growth phase. Cells were spun down, and supernatants were saved. After a total of three washes, the amount of radioactivity in the bacterial pellet was measured. The fraction of ⁵⁵Fe associated with the pellet was calculated by dividing the number of counts per minute of the pellet by the number of counts per minute of the pellet plus the supernatant. Values are presented as means ± SD from at least three independent experiments with duplicate or triplicate samples. Statistical significance (P < 0.001) is indicated by three asterisks. (B) Transcriptional analysis of the **mtsABC** metal transporter operon. Total RNA was prepared from strains AP1, SR301, and SR304. Bacteria were grown until the mid-exponential phase, subjected to Northern blotting, and hybridized with an **mtsA** probe. The positions of 23S and 16S rRNA are shown to the left. Size markers (in kilobases) are indicated to the right.

**FIG. 2.** Growth of wild-type and **perR** mutant strains of *S. pyogenes*. AP1 (wild type) and SR301 (**perR**) strains were cultured in Cx-THY medium or Cx-THY medium supplemented with 100 μM ferric citrate. Experiments were performed 6 to 10 times, and results from a representative one are shown.
log phase and then subjected to peroxide stress (5 mM H2O2). Stress, strains AP1, SR301, and SR304 were grown until mid-}

S. pyogenes further characterize positive bacteria (4, 34), including described as a peroxide-responsive repressor in certain gram-

S. pyogenes (38). In order to further characterize S. pyogenes susceptibility to peroxide stress, strains AP1, SR301, and SR304 were grown until mid-log phase and then subjected to peroxide stress (5 mM H2O2). Fifteen minutes after challenge, 88.3% of the SR301 bacteria were still alive compared to 13.6% of the wild-type cells, whereas after 60 min, the percentages of surviving mutant and wild-type bacteria were 29.8 and 1.8, respectively. Sensitivity to H2O2 was completely restored in the transcomplemented wild-type bacteria. This response seems constitutive in the perR mutant, thus strengthening a role for PerR as an oxidative stress-responsive repressor in S. pyogenes.

**Response to superoxide stress in wild-type and PerR-defi-
Redox-cycling agents, such as paraquat, can cause oxidative stress by generating the superoxide radical, \(O_2^{-}\), which is converted into \(H_2O_2\) and \(O_2\) by SOD (21). In order to analyze \(S.\ pyogenes\) sensitivity to paraquat, strains AP1 and SR301 were cultured ON in the presence of 0, 2, and 10 mM paraquat. The \(perR\) mutant was more sensitive to the \(O_2^{-}\)-generating agent than AP1 bacteria. At 2 mM, a small growth defect was observed in the mutant, whereas when using 10 mM, a concentration that moderately affected growth of the wild type, SR301 bacteria were highly hampered in growth (Fig. 4A). As SOD represents the major defense against the superoxide anion, we performed transcriptional analysis of \(sodA\), which encodes the single SOD present in \(S.\ pyogenes\) (24). Total RNA was extracted from the wild type, \(perR\) mutant, and transcomplemented strains, subjected to Northern blotting, and probed with \(sodA\). A reduced transcription of \(sodA\) (3.3-fold) was observed in the \(perR\) mutant, whereas transcomplementation of the \(perR\) mutation restored \(sodA\) transcription to the levels found with wild-type bacteria (Fig. 4B). The present data indicate that SR301 bacteria are more sensitive to \(O_2^{-}\) than the wild type, and this is probably due to a decreased SOD expression in the mutant, suggesting a possible role for PerR in the regulation of SOD production in \(S.\ pyogenes\).

**PerR is required for full virulence in S. pyogenes.** Both \(fur\) and \(perR\) mutants in \(S.\ aureus\) are attenuated in virulence (34, 35). Therefore, we tested the virulence of strains AP1 and SR301 in BALB/c mice. Skin air sacs were inoculated with either \(10^6\) or \(10^5\) CFU of bacteria, and mouse survival was monitored for 10 days. When using \(10^6\) CFU, 30.8% of mice infected with the wild type were alive at the end of the experiment, compared to 76.9% of the group inoculated with the \(perR\) mutant (\(P < 0.05\)). Moreover, mice injected with the \(perR\) mutant showed delayed symptoms of infection, and the first casualty was recorded after 88 h, in comparison to wild-type streptococci, which were lethal in less than 2 days (Fig. 5A). With the lower dose, all animals inoculated with the \(perR\) mutant survived, compared to 61.5% survival observed in the group infected with the AP1 strain (Fig. 5B). Analysis of these differences showed a statistical significance (\(P < 0.05\)) and suggested that the \(perR\) mutant had an approximately 10-fold reduction of virulence. The LDs of mice infected with AP1 and SR301 bacteria were \(2.4 \times 10^6\) and \(3 \times 10^6\) CFU, respectively (data not shown).

**TABLE 3. Survival of strains AP1 and SR301 at different time points following peroxide challenge.**

<table>
<thead>
<tr>
<th>Strain (growth condition)</th>
<th>0</th>
<th>15</th>
<th>30</th>
<th>60</th>
<th>90</th>
</tr>
</thead>
<tbody>
<tr>
<td>AP1 (CO2)</td>
<td>2.5 (\times 10^6) ± 7.7 (\times 10^3)</td>
<td>3.8 (\times 10^7) ± 3.6 (\times 10^7)</td>
<td>1.5 (\times 10^8) ± 7.9 (\times 10^5)</td>
<td>5.1 (\times 10^9) ± 4.2 (\times 10^6)</td>
<td>1.2 (\times 10^7) ± 1 (\times 10^9)</td>
</tr>
<tr>
<td>SR301 (CO2)</td>
<td>2.9 (\times 10^6) ± 1 (\times 10^6)</td>
<td>2.7 (\times 10^7) ± 9.7 (\times 10^5)</td>
<td>2.1 (\times 10^8) ± 9.5 (\times 10^5)</td>
<td>7.3 (\times 10^9) ± 3.3 (\times 10^7)</td>
<td>1.8 (\times 10^7) ± 1.5 (\times 10^9)</td>
</tr>
<tr>
<td>AP1 (O2)</td>
<td>1.1 (\times 10^6) ± 8.6 (\times 10^7)</td>
<td>1.6 (\times 10^7) ± 1.5 (\times 10^8)</td>
<td>7.4 (\times 10^8) ± 6.4 (\times 10^7)</td>
<td>7.3 (\times 10^9) ± 5.6 (\times 10^8)</td>
<td>3.2 (\times 10^7) ± 2.2 (\times 10^9)</td>
</tr>
<tr>
<td>SR301 (O2)</td>
<td>1.1 (\times 10^6) ± 6.9 (\times 10^7)</td>
<td>9 (\times 10^7) ± 7.9 (\times 10^5)</td>
<td>5.5 (\times 10^8) ± 3.9 (\times 10^7)</td>
<td>4.8 (\times 10^9) ± 5 (\times 10^8)</td>
<td>2.5 (\times 10^7) ± 3.1 (\times 10^9)</td>
</tr>
</tbody>
</table>

\(a\) CFU per milliliter of AP1 (wild type) and SR301 (\(perR\)) bacteria surviving \(H_2O_2\) challenge. Bacterial dilutions were plated onto THY plates 0, 15, 30, 60, and 90 min after the addition of 5 mM \(H_2O_2\). Results are expressed as means ± SD of four to five independent assays.

\(b\) AP1 and SR301 strains were grown either under aerobic conditions \(O_2\) or in the presence of 5% \(CO_2\) prior to challenge with \(H_2O_2\).

**FIG. 4.** Sensitivity to superoxide stress in \(S.\ pyogenes\). (A) Growth of AP1 (wild type) and SR301 (\(perR\)) strains in the presence of 0, 2, and 10 mM paraquat. The \(OD_{620}\) was recorded after 15 h of incubation. The results are expressed as means ± SD of five independent experiments with duplicate or triplicate samples. Statistical significance (\(P < 0.001\)) is indicated by three asterisks. (B) Transcriptional analysis of \(sodA\). Total RNA was prepared from strains AP1 (wild type), SR301 (\(perR\)), and SR304 (\(perR^+\)) grown until the mid-exponential phase. RNA was subjected to Northern blotting and hybridized with a \(sodA\) probe. Positions of 23S, 16S, and 5S rRNA are shown on the left, and size markers (in kilobases) are presented on the right.
matches were identified in the predicted coding regions. However, some imperfect matches were found; they lacked the minimum of 14 out of 19 nucleotides identical to the consensus sequence, which could be partially explained by the observations that an Fur homologue PerR was constructed and characterized in an isogenic mutant of the gene encoding the peroxide-responsive protein, which could be potentially involved in the response to H$_2$O$_2$ stress in S. pyogenes. Iron, as a cofactor of the Fenton reaction, can potentiate oxygen toxicity by converting H$_2$O$_2$ into OH$^\cdot$. The possibility that H$_2$O$_2$ resistance was a consequence of low intracellular iron levels was excluded by the observations that an S. pyogenes mtsA mutant was more sensitive to H$_2$O$_2$ both in iron-rich and iron-depleted culture medium. Therefore, resistance to H$_2$O$_2$ relies on PerR acting as a repressor of a gene or regulon involved in the defense against peroxide stress. Resistance to H$_2$O$_2$ can be induced by different stimuli, and while King et al. used H$_2$O$_2$ or ethanol as inducers (38), we obtained a 60-fold-higher survival by growing wild-type bacteria in the presence of oxygen prior to challenge.

The present work also suggests a role for PerR in the response to superoxide stress. The perR mutant was more sensitive to O$_2^-$ than the WT strain, as it grew very poorly in the presence of 10 mM paraquat. Consistent with the fact that SOD is the main defense against superoxide stress in many bacteria, including S. pyogenes (24), we observed an approximately threefold transcriptional reduction of sodA in the perR mutant compared to that in the wild-type strain. In E. coli, SOD is not strictly necessary for aerobic survival and half of the normal enzymatic activity is generally sufficient for aerobic growth; however, SOD becomes crucial under oxidative stress.
conditions (6). Also in the present case, the growth of the perR mutant was not significantly disturbed under aerobic conditions, but the mutant was sensitive to high levels of paraquat. Thus, SR30l bacteria are probably producing enough SOD to handle moderate levels of oxidative stress. In addition, the mutant was derepressed in the peroxide stress response and had low levels of intracellular iron, which might partially compensate for a lower production of SOD. A reduced total SOD activity together with a defective iron uptake was also described in a P. aeruginosa fur mutant (32). E. coli sod mutants are generally sensitive to both $O_2^{-}$ and $H_2O_2$ (6), whereas the perR mutant in S. pyogenes was resistant to $H_2O_2$ but sensitive to $O_2^{-}$. This heterogeneity in ROS susceptibility is interesting but not unprecedented. King et al. showed that inactivation of two distinct peroxidase genes in S. pyogenes generated mutants which were more sensitive to paraquat and at the same time slightly more resistant than the wild type to $H_2O_2$ in a survival assay (38).

Fur proteins are generally operating as repressors; however, Fur-dependent positive regulation has also been reported (15, 20, 29, 44). In E. coli, sodA (Mn-SOD) is under the control of six different proteins (11), including a Fur-mediated negative regulation (52), while sodB (Fe-SOD) is subjected to positive control by Fur (15). When Fur acts as an activator, no iron boxes are identified in the promoters of target genes (53). Also in S. pyogenes, PerR may behave as a bifunctional regulator, acting as a repressor of the peroxide regulon while being a transcriptional activator of SOD. The fact that we could not find any Fur or PerR boxes upstream of sodA and mtsABC suggests that PerR might function as an enhancer of sodA and mtsABC transcription.

Analogous to Fur and PerR in S. aureus (34, 35), PerR is important for virulence in S. pyogenes. In a murine skin model of infection, we observed a statistically significant difference in survival time and $LD_{50}$ after injection of wild-type or mutant bacteria. In particular, no mortality was recorded in the group infected with the perR mutant when using the lower bacterial dose. The hypothesis that known virulence factors were affected in the mutant was investigated. However, no significant variation in the production of M protein, cysteine proteinase, and C5a peptidase was revealed. Previous reports have shown that Streptococcus pneumoniae and Streptococcus agalactiae sodA mutants are attenuated in virulence (47, 59). Whether the attenuation described here is due to inactivation of perR, as reported in S. aureus (34, 35), or is a consequence of sodA down-regulation, is unclear. Moreover, since growth of the perR mutant showed a tendency to be affected in a metal-depleted medium, we cannot completely rule out that restricted iron availability in the host might hamper the mutant, resulting in virulence attenuation.

Iron metabolism and oxidative stress defenses are strictly interconnected in bacteria (53). In B. subtilis, S. aureus, and the gram-negative bacterium Campylobacter jejuni, there is a close relationship between PerR-mediated control of peroxide stress and intracellular metal ion homeostasis (9, 33–35, 56). In particular, B. subtilis PerR requires a metal cofactor (Fe, Mn) to bind DNA, and the presence of this metal ion is responsible for regulating the PerR response towards $H_2O_2$ (33). In the present case, when the levels of intracellular $H_2O_2$ are high, S. pyogenes PerR might (i) derepress the $H_2O_2$-responsive regulon, (ii) partially repress sodA in order to limit the production of $H_2O_2$, and (iii) lower the intracellular concentration of free Fe$^{3+}$ that can participate in the Fenton reaction by down-regulation of mtsABC and possibly of other metal acquisition systems. In relation to virulence, the attenuation of the perR mutant may be a result of direct or indirect regulatory effects on virulence determinants, and/or of a disturbed balance between levels of intracellular iron and oxidative stress defenses. The effects observed in the mutant depend upon PerR, since all the phenotypes could be complemented in trans, and although the molecular mechanisms are not known, PerR appears to play a crucial role in the interplay between oxidative stress responses, metal homeostasis, and virulence of S. pyogenes.

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