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\textit{Streptococcus pneumoniae} (pneumococcus) is a common asymptomatic commensal of the nasopharynx in healthy individuals. However, in young children, in the elderly, and in immunocompromised people, this gram-positive bacterium is a major cause of otitis media, pneumonia, and septicemia. To persist at these various sites, the pneumococcus needs to adapt and orchestrate its gene expression. Two-component signal transduction systems (TCSs) play a central role in bacterial regulation, sporulation, genetic competence, and chemotaxis, in response to environmental changes (1, 27). TCSs typically consist of a membrane-associated sensory protein called a histidine kinase (HK) and a cognate cytosolic DNA-binding response regulator (RR), which acts as a transcriptional regulator. When an external signal is sensed, a histidine residue of the histidine kinase autophosphorylates, after which this phosphogroup is transferred to the response regulator. This results in a conformational change in the regulatory protein, which can then perform its regulatory function.

The pneumococcal genome contains 13 putative complete TCSs plus one orphan response regulator (15, 28). Ten of the pneumococcal TCSs have been shown to be important for virulence (for a review, see reference 22). For instance, CiaR/CiaH has been demonstrated to contribute to virulence (25, 29), probably in part through control of expression of \textit{htrA}, which encodes a serine protease that is a major virulence factor (11, 19). Recently, TCS06 has been found to regulate the expression of \textit{cbpA}, which codes for a major adhesin that is also a protective antigen (26).

Relatively little is known about TCS09, which consists of an RR encoded by \textit{sp0661} (spr0578 in the R6 genome) and an HK encoded by \textit{sp0662} (spr0579). Amino acid sequence homology data suggest that the sensory domain of the HK is related to the extracellular part of \textit{McpA} and \textit{McpB} of \textit{Bacillus subtilis} (15). These proteins are believed to be involved in the control of chemotaxis through sensing of environmental nutrient concentrations. The extracellular stimulus of TCS09, however, is not known.

Several in vivo studies have demonstrated that RR09 has a role in virulence. Interestingly, the contribution of RR09 to virulence varies with the bacterial strain and the site of infection (3, 6, 15, 29). It has been suggested that in strain 0100993 (serotype 3)
RR09 is involved in the dissemination from the lung to the systemic circulation, since attenuation of 0100993Δrr09 was observed in a murine pneumonia model but not in a sepsis model of infection (3). In D39 (serotype 2) the lack of RR09 led to an avirulent phenotype upon intranasal, intravenous, or intraperitoneal infection (3). The genetic differences between strains are likely to have a significant impact on the repertoire of genes regulated by RR09. In line with this, TCS04 mutants were recently found to confer strain-dependent phenotypes in a murine infection model, possibly caused by differential regulation of pneumococcal surface antigen A (20).

So far, no gene targets of RR09 that could account for the observed in vivo phenotypes of rr09 mutants have been identified, although sequence homology data have suggested that TCS09 is involved in nutrient perception (3, 15). To investigate strain differences in the role of TCS09 in pneumococcal virulence further, we examined the phenotype of a TIGR4 rr09 mutant using a murine pneumonia model. In addition, we used DNA microarray technology to examine how transcriptional patterns are affected by a lack of rr09. To this end, global expression profiles of wild-type and rr09 mutants were analyzed during different stages of in vitro growth. We assessed strain-specific regulation by RR09 by comparing transcriptional profiles of mutants with two different genetic backgrounds, namely, strains D39 and TIGR4. In vitro expression experiments and data analysis were performed independently in two laboratories (Rotterdam and Glasgow) using slightly different methods, after which the data were validated and combined. Finally, we assessed expression of rr09 and three of its identified in vitro targets during experimental virulence in mice.

**MATERIALS AND METHODS**

**Pneumococcal strains.** Wild-type *S. pneumoniae* strains D39 (~ NCTC 7466; serotype 2) and TIGR4 (~ ATCC BAA-334; serotype 4) were used in this study. The Δrr09 derivative of TIGR4 was constructed by insertional inactivation using an erythromycin resistance cassette, as described previously for D39Δrr09 (3). Pneumococcal strains were grown on Columbia blood agar supplemented with 5% (vol/vol) defibrinated sheep blood (and supplemented with 1 μg/ml erythromycin for the rr09 mutant strains). For RNA isolation analyses, cultures were grown in Todd-Hewitt broth supplemented with 5 g/liter yeast extract (THY broth) or in brain heart infusion broth (BHI broth) without erythromycin until they reached the desired turbidity. For construction of the sp0036 mutant (annotated spr0062 in R6), approximately 100-hp portions of up- and downstream regions of the targeted sequence were amplified by PCR using primers 50L (TCTTATGTTGATTTCTCTGTAAG) and 50M (GGGCCGCGTCGAGTGAAGATCATGTAAGAACCC) and primers 50N (TCCTACCTCCAGGGGCGGACCTGCTCTTATCTCCTGTTGG) and 50O (CAAAATTTAGCAGTAAATCTTCTTGGTCTTGG) and 50O (CAAATTTAGCAGTAAATCTTCTTGGTCTTGG) and 50O (CAAATTTAGCAGTAAATCTTCTTGGTCTTGG). These fragments were joined by overlap extension PCR due to overlap in the 50M and 50N primers. This fusion PCR product was cloned into TOPO- 

**Microarray hybridization.** For array 1, labeled wild-type and Δrr09 cDNA were combined and dried using a SpeedVac. The cDNA was dissolved in 30 μl of 10 μM dUTP (Amersham), 0.5 mM dATP, 0.5 mM dCTP, 0.5 mM dGTP, and 3.2 μg/ml random nonamers. The synthesized cDNA was then labeled by coupling either Cy3 or Cy5 to the dUTP aminoacyl reactive group (CyScribe postlabeling kit; Amersham Biosciences) and was purified using a GFX PCR, DNA, and gel band purification kit (Amersham Biosciences).

**RNA extraction.** Five hundred milliliters of THY broth was inoculated with 10 to 20 colonies from agar plates, and the cultures were statically grown at 37°C. Samples for RNA isolation were removed when the cultures reached an optical density at 600 nm (OD600) of either 0.1 (early log phase) or 0.2 (mid-log phase), and the pneumococcal cells were harvested by centrifugation for 10 min at 3,500 × g and 4°C. Subsequently, the cells were resuspended in 400 μl of THY broth supplemented with 1.5 g of glass beads (diameter, 0.1 mm; Sigma), 500 μl of 10% (wt/vol) sodium dodecyl sulfate (SDS), and 50 μl of 3 M sodium acetate (pH 5.2). Each mixture was then snap-frozen in liquid nitrogen and stored at −80°C until it was used. The cells were lysed by vigorous shaking for 5 min at 4°C and subsequently centrifuged for 10 min at 9,300 × g and 4°C. The upper phase was mixed with an equal volume of chloroform and centrifuged for 2 min at 16,000 × g and 4°C. After this, RNA was purified using a High Pure RNA isolation kit (Roche Diagnostics). Contaminating genomic DNA was removed by treatment with RNase-free DNase I (Roche Diagnostics). RNA was isolated from three replicate cultures of D39 and TIGR4.

**Microarray construction.** Two different DNA microarray platforms were used for analysis of samples isolated at low and high OD600 these platforms are referred to below as array 1 for an OD600 of 0.1 or 0.2 and array 2 for an OD600 of 0.6. Array 1 was constructed as described previously (14, 31) and contained amplicons representing 2,087 open reading frames (ORFs) of *S. pneumoniae* TIGR4 and 184 unique *S. pneumoniae* R6 ORFs, all spotted in duplicate.

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**Microarray hybridization.** For array 1, labeled wild-type and Δrr09 cDNA were combined and dried using a SpeedVac. The cDNA was dissolved in 10 μl of Slidehyb #1 hybridization buffer (Ambion Europe Ltd.), boiled for 3 min, and kept on ice until hybridization. Primarily, 20 ng of total RNA was incubated for 16 h at 42°C in the presence of 400 U Superscript III RNase H− reverse transcriptase (Invitrogen), 0.2 mM aminoacyl dUTP (Amersham), 0.5 mM dATP, 0.5 mM dCTP, 0.3 mM dGTP, and 3.2 μg/ml random nonamers. The synthesized cDNA was then labeled by coupling either Cy3 or Cy5 to the dUTP aminoacyl reactive group (CyScribe postlabeling kit; Amersham Biosciences) and was purified using a GFX PCR, DNA, and gel band purification kit (Amersham Biosciences).

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and this was followed by two washes in 0.1× SSC–0.1% SDS for 5 min and in 0.1× SSC for 5 min. For each independent RNA sample one dye swap was performed.

Microarray data analysis. For array 1, dual-channel array images were acquired with a GeneTAC LS IV confocal laser scanner (Genomics Solutions) and were analyzed with the ArrayPro 4.5 software (Media Cybernetics Inc.). Spots were screened visually to identify the low-quality spots. Slide data were processed using MicroPreP as described previously (4, 31, 32). Prior to analysis, automatically and manually flagged spots and spots with very low background-subtracted signal intensities (5% of the weakest spots [sum of Cy3 and Cy5 net signals]) were filtered out of all data sets. Net signal intensities were calculated using grid-based background subtraction. In Prep, a grid-based Lowess transformation was performed for slide normalization, with an f value (percentage of the spots used for curve fitting) of 0.5 and an nSteps value (number of iterations) of 5. In Postprep, negative and empty values were removed, and outliers were removed by the deviation test. Further analysis was performed using a Cyber-T Student’s t test for paired data (18). This web-based program lists the ratios of all intrareplicates and standard deviations and P values assigned to these mean ratios. For identification of differentially expressed genes, only genes with a minimum of three differences with a Student’s t test value of $P < 0.05$ and a ratio change threshold of at least 2 standard deviations over the median ratio for each strain.

Isolation of pneumococcal RNA during experimental infection. Female outbred CD-1 mice (body weight, 20 to 30 g) were purchased from Harlan Olac, Bicester, United Kingdom. Nine-week-old mice were lightly anesthetized with 2.5% (vol/vol) halothane, after which 1.0 × 10^{6} CFU wild-type D39, wild-type TIGR4, or TIGR4Δrr09 resuspended in 50 μl of sterile PBS was administered in the nostrils of mice held vertically. Control mice were inoculated with sterile PBS/H9004. Isolation of pneumococci from host mouse cells, the mixtures were centrifuged for 10 min at 825 × g and 4°C. Each supernatant was transferred to a new tube and centrifuged for 5 min at 16,000 × g and 4°C. The pellet was then washed-frozen in liquid nitrogen. The lungs that were collected were homogenized in 2 ml RNAlater (QIAGEN). To confirm the absence of genomic DNA, reactions without reverse transcriptase were performed. Subsequently, 1 μl of cDNA diluted 1:10 (for the in vitro experiments) or 1:4 (for in vivo experiments) was used as the template in real-time PCR. Duplicate quantitative PCR assays were performed using a DyNaMo HS SYBR green quantitative PCR kit (Bioki) with an ABI Prism 7700 according to the manufacturer’s instructions. Primers (sequences are available on request) were designed using the Oligo 6.2 software (Molecular Biology Insights) and were used at a concentration of 300 nM for 40 cycles of amplification (15 s at 95°C and 1 min at 60°C), which was followed by a melting curve analysis to verify the product homogeneity.

Validation of selected targets from array 2 was performed in essentially the same manner, with a few minor differences. Two micrograms of RNA was reverse transcribed using 6 μg of random hexamers and SuperScript III reverse transcriptase (Invitrogen). Total cDNA was diluted 1:10 (for in vitro experiments) or 1:4 (for in vivo experiments) and used as the template in real-time PCR. Duplicate quantitative PCR assays were performed using a DyNaMo HS SYBR green quantitative PCR kit (Bioki) with an ABI Prism 7700 according to the manufacturer’s instructions. Primers (sequences are available on request) were designed using the Oligo 6.2 software (Molecular Biology Insights) and were used at a concentration of 300 nM for 40 cycles of amplification (15 s at 95°C and 1 min at 60°C), which was followed by a melting curve analysis to verify the product homogeneity.

RESULTS AND DISCUSSION

In vivo characteristics of TIGR4Δrr09. Previous studies indicated that RR09 has a strain-specific role in pneumococcal virulence, as D39 with deletion of the response regulator rr09
was found to be avirulent in all murine models tested, while 0100993Δrr09 was found to be attenuated only upon intranasal infection (3). Here, we extended these observations by analyzing a TIGR4Δrr09 mutant in a murine pneumonia model of infection. Mice infected intranasally with 10^6 CFU of TIGR4Δrr09 were found to have significantly longer survival times than mice infected with the parental strain (Fig. 1a). None of the mice infected with the wild-type strain survived longer than 30 h after inoculation. The level of survival of mice infected with Δrr09 dropped to 20% after 48 h, and none of these mice survived longer than 100 h after inoculation. Furthermore, the TIGR4Δrr09 bacterial counts in BALF, lungs, and blood showed that there were significant reductions compared to the wild-type strain (P < 0.01) (Fig. 1b). This indicated that like 0100993Δrr09, the TIGR4Δrr09 mutant was attenuated upon intranasal infection but was not avirulent like D39Δrr09.

Microarray analysis of pneumococcal mutants. To identify genes controlled by RR09, we compared the transcriptional profiles of S. pneumoniae wild-type strains D39 and TIGR4 and their isogenic mutant Δrr09 derivatives at various stages of growth. During this analysis, we used two different ampiclon-based microarrays, both designed to provide nonredundant representation of the sequenced R6 and TIGR4 genomes. Importantly, no differences in in vitro growth between the wild-type strains and the Δrr09 mutants were detected, indicating that the observed differential gene expression was not a result of altered growth rates.

Comparison of D39 and TIGR4. Little overlap was observed in the sets of genes controlled by RR09 in D39 and TIGR4, with a few notable exceptions (Fig. 2a and b and Table 1). The levels of transcription of two genes, encoding a putative lactose phosphotransferase system (PTS) repressor (sp0875) and a 1-phosphofructokinase (sp0876), were increased in both D39 and TIGR4 Δrr09 mutants in BHI broth at an OD_{600} of 0.6 (Fig. 2a and Table 1). Five genes were downregulated in both Δrr09 derivatives (Fig. 2b and Table 1). Five genes appeared to be oppositely regulated by RR09 in D39 and TIGR4 when they were grown in THY broth; these genes included glnR and pyrR, which were upregulated in D39Δrr09 and downregulated in TIGR4 when the organisms were grown in THY broth (Table 1).

Gene regulation by RR09: D39. A total of 102 genes were found to be differentially expressed in wild-type strain D39 and the Δrr09 mutant. Forty-three of these genes could be considered to be directly or indirectly repressed by RR09 as they were upregulated in the D39 Δrr09 derivative compared to the expression in the wild type (Fig. 3a; see Tables S1 to S3 in the supplemental material).

The transcription of genes involved in genetic competence, such as comAB, comDE, cinA, comX, and cglABC, increased significantly in D39Δrr09 in the early and mid-log phases of growth in THY broth. Upregulation of comDE induces competence, which in turn induces transcription of comX. Peterson et al. described genes induced by competence-stimulating peptide and described three groups of responding genes: early, common, and late.

### TABLE 1. Genes regulated by RR09 in both D39 and TIGR4

<table>
<thead>
<tr>
<th>Gene</th>
<th>Annotation</th>
<th>D39 Ratios</th>
<th>TIGR4 Ratios</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>OD_{600} = 0.1</td>
<td>OD_{600} = 0.2</td>
</tr>
<tr>
<td>Commonly regulated</td>
<td>Lactose phosphotransferase system repressor, lacR</td>
<td>−0.06</td>
<td>−0.51</td>
</tr>
<tr>
<td></td>
<td>sp0875</td>
<td>−0.12</td>
<td>−0.33</td>
</tr>
<tr>
<td></td>
<td>1-Phosphofructokinase, putative</td>
<td>−2.40</td>
<td>−2.48</td>
</tr>
<tr>
<td></td>
<td>sp0647</td>
<td>−3.26</td>
<td>−3.47</td>
</tr>
<tr>
<td></td>
<td>Beta-galactosidase, bgaA</td>
<td>−1.05</td>
<td>−0.66</td>
</tr>
<tr>
<td></td>
<td>sp1804</td>
<td>−1.55</td>
<td>−2.47</td>
</tr>
<tr>
<td></td>
<td>Dextran glucosidase dex3, putative</td>
<td>−1.19</td>
<td>−1.50</td>
</tr>
<tr>
<td></td>
<td>sp1884</td>
<td>−0.82</td>
<td>1.36</td>
</tr>
<tr>
<td></td>
<td>Pyrimidine operon regulatory protein, pyrR</td>
<td>1.45</td>
<td>1.50</td>
</tr>
<tr>
<td></td>
<td>sp2414</td>
<td>−0.05</td>
<td>0.01</td>
</tr>
<tr>
<td>Oppositely regulated</td>
<td>ABC transporter, permease protein</td>
<td>NA</td>
<td>0.36</td>
</tr>
<tr>
<td></td>
<td>sp0501</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td></td>
<td>sp0964</td>
<td>0.82</td>
<td>1.36</td>
</tr>
<tr>
<td></td>
<td>Glycosyl hydrolase-related protein</td>
<td>−0.05</td>
<td>0.01</td>
</tr>
</tbody>
</table>

<sup>a</sup> Commonly regulated genes showed the same expression pattern in D39 and TIGR4, while oppositely regulated genes were found to be upregulated in the rr09 mutant in one strain and downregulated in the other.

<sup>b</sup> The values are log(expression in Δrr09 mutant/expression in wild type) values. The values in bold type are the values for genes that are considered to be differentially expressed.

<sup>c</sup> NA, no valid data were acquired.
late, and delayed genes (24). In this study, upregulation of early genes (regulated by ComE) and late genes (gglABC and cina) may have been the result of premature development of competence caused by the lack of RR09.

A similar pattern of increased expression in the rr09 mutant was observed for genes encoding products predicted to be involved in pyrimidine and purine synthesis (e.g., sp1277 and sp1278), riboflavin kinase (sp1110), and a polypeptide deformylase (sp1549). Interestingly, the polypeptide deformylase has been suggested to be a broad-range antimicrobial target (5). In BHI broth at an OD_{600} of 0.6, the notable genes are downregulated at an OD_{600} of 0.6 in BHI broth. (a) Genes upregulated in D39Δrr09; (b) genes downregulated in D39Δrr09; (c) genes upregulated in TIGR4Δrr09; (d) genes downregulated in TIGR4Δrr09.

FIG. 3. Distribution of genes regulated by RR09 at OD_{600} of 0.1 and 0.2 in THY broth and at an OD_{600} of 0.6 in BHI broth. (a) Genes upregulated in D39Δrr09; (b) genes downregulated in D39Δrr09; (c) genes upregulated in TIGR4Δrr09; (d) genes downregulated in TIGR4Δrr09.

Several of the 41 genes found to be repressed in TIGR4Δrr09 are predicted to encode products involved in metabolism of (amino) sugars and purines or pyrimidines (e.g., sp0266 and sp1278), particularly during early growth in THY broth (Fig. 3d; see Tables S4 to S6 in the supplemental material). Later during growth in BHI broth, the downregulated genes included the gene encoding pneumococcal surface protein A (pspA), clpL, coding for the ATP-dependent ClpL protease, and various stress response genes (hrcA, dnaJ, dnaK, and dnaJ), as well as genes in an ABC transporter operon (sp0044 to sp0056) was observed in the mutant.

An interesting pattern of regulation was observed for genes located on the rlrA pathogenicity islet: the genes were strongly downregulated in THY broth but strongly upregulated in BHI broth. This 12-kb islet, which is not present in the D39 genome (2, 23, 28), encodes the transcriptional activator RlrA, three surface proteins (RrgA, RrgB, and RrgC), and three putative sortases (SrtB, SrtC, and SrtD). RlrA has been shown to positively regulate the expression of these seven genes on the pathogenicity islet by another regulator, MgrA, has been reported (8), no differential expression of mgrA was observed in this study, possibly due to a low level of expression and hence low signals. The pathogenicity islet has been shown to contribute to virulence (2, 6, 7), and thus, unbalanced regulation in TIGR4Δrr09 may have resulted in the attenuation that we observed in the murine model (Fig. 1). Although the regulatory mechanism of this pattern of expression remains unclear, the differences in regulation between the two broth media used suggest that there is indirect regulation, which might involve a number of downstream regulators controlled by RR09 in a growth-phase-dependent manner.

Real-time PCR analysis. To validate our microarray data, relative transcript levels were determined by quantitative real-time PCR for a selection of genes for all growth phases sampled. Overall, the expression ratios obtained by microarray and real-time PCR analyses were found to be strongly positively correlated for both D39 (R^2 = 0.86; n = 24) and TIGR4 (R^2 = 0.90; n = 31). For example, expression of comA was confirmed to be enriched for genes predicted to encode proteins involved in carbohydrate metabolism, particularly genes encoding enzyme II of nine sugar-specific phosphotransferase systems. These membrane-associated proteins facilitate the uptake of carbohydrates such as mannose and fructose. For instance, several genes encoding the putative mannos-specific PTS IIABC (sp0061 to sp0064), the cellobiose-specific PTS IIABC (sp0305 to sp0310), and the galactitol-specific PTS IIABC (sp0645 to sp0647) were in this group. However, genes encoding other components of these phosphotransferase systems, including enzyme I, HPr, and CcpA (global regulator of carbon metabolism) (for a review, see reference 30), did not appear to be regulated by RR09 in D39. Expression of these genes may be controlled by a different transcriptional regulator.
to be strongly upregulated in D39Δrr09, and the comA expression levels in TIGR4Δrr09 and the wild-type strain were found to be similar by both methods (not shown).

An interesting target of RR09 identified by our microarray analysis was the rlrA pathogenicity islet of TIGR4, which had an unusual, growth-phase-dependent pattern of expression. Real-time PCR analysis of two genes of this locus, rrgA and rlrA, confirmed this transcriptional profile: there was strong downregulation at the lower optical densities, and there was strong upregulation later (Fig. 4).

In addition, we validated the levels of expression of other genes (htrA, spoJ, pspA, sp1896, and sp2141 to sp2144) identified as differentially expressed by microarray analysis and found that there was agreement between the microarray and real-time PCR results (not shown).

Expression of pneumococcal genes during experimental virulence. To determine to what extent the observed in vitro gene regulation by RR09 reflected the in vivo situation, we examined expression of rr09 and three putative targets during experimental infection of mice with D39, TIGR4, and TIGR4Δrr09. Due to its avirulent phenotype, analysis of gene expression in wild-type strain TIGR4 during infection was not possible. To determine to what extent the observed in vitro gene expression was comparable for the two strains in all compartments sampled (not shown).

Strain-dependent regulation of comA does not explain the observed difference in virulence. While our analysis indicated that RR09 has a prominent role in regulation of sugar metabolism in D39, only three putative PTs were found to be regulated by RR09 in TIGR4. It seems unlikely that there is a difference in the sugar diets of D39 and TIGR4, as both genomes basically contain the same putative PTs (20 PTSs common to both strains and one PTS specific for TIGR4) (9, 28).

A clear example of a PTS locus differentially regulated by RR09 in D39 and TIGR4 was the locus comprising sp0060 to sp0066, and therefore we also examined expression of this locus by real-time PCR in a third strain, 0100993. This and previous studies showed that RR09 mutants of the three
strains used here all have different phenotypes in murine models of infection (2). While strong downregulation of sp0060 to sp0066 was confirmed to occur in D39Δrr09, no RR09-dependent regulation was observed in either TIGR4 or 0100993 (Fig. 6). The observed downregulation of this locus in D39Δrr09 may result in reduced sugar uptake and thus a smaller supply of carbohydrates for the polysaccharide capsule, which in turn might explain the avirulent phenotype of D39Δrr09. To test this hypothesis, an sp0063 mutant was constructed and tested in a murine model, and it was compared with the D39 wild-type strain and the rr09 mutant. There was no significant difference in the survival rates between wild-type strain D39- and sp0063 mutant-infected mice; all five wild-type strain-infected mice died, as did four of the five Δsp0063-infected mice. Likewise, the blood counts at 24 h postinfection were similar (Fig. 7). In agreement with our previous work (3), the rr09 mutant was essentially avirulent; all infected mice survived, and the blood counts at 24 h were below the detection limit (~83 CFU/ml). Indeed, the mice showed no overt clinical signs of infection. Thus, the gene product of sp0063 alone does not significantly contribute to virulence in D39 in this model and hence does not explain the dramatic phenotype seen after deletion of rr09 in D39. The Δrr09 derivatives of TIGR4 and 0100993 conferred a less severe in vivo phenotype. In vivo expression of sp0063 could be demonstrated for both D39 and TIGR, and the levels in TIGR4 were higher (almost fourfold) (Fig. 5a). In TIGR4, sp0063 appears to be regulated by RR09 in vivo (Fig. 5b) but not in vitro (Fig. 6), highlighting the importance of measuring gene expression in vivo. Moreover, this finding provides further evidence that the differential regulation of this operon observed in vitro does not explain the difference between D39 and TIGR4 in vivo. Also, there appears to be a redundancy of PTS in the pneumococcal genome, which could complement the lower level of expression of the PTS. This is underscored by our preliminary data, which indicate that the rr09 and sp0063 mutants are able to ferment mannose (not shown).

In conclusion, we identified several targets of RR09 in D39 and TIGR4 that could account for the phenotypes of their mutants, and we demonstrated that rr09 and three of its targets are expressed in vivo. These targets include both common and strain-specific targets of RR09. During in vitro growth, some genes were found to be controlled by RR09 at all phases of growth examined, while other genes appeared to be regulated in a growth-phase-dependent manner. Although this differential expression could have been the result of the different growth conditions and/or of the use of two different microarrays, this explanation appears less likely considering the considerable overlap between the sets of genes regulated at the different growth phases (e.g., sp0060 to sp0066, sp0645 to sp0648, and the rlrA pathogenicity island). The expression of pneumococcal genes in different broth media has been shown to differ substantially (21), but our results show that apparent putative targets can be identified with different experimental setups. The targets identified can be either directly or indirectly regulated by RR09. Further experiments, such as DNA binding assays, are necessary to distinguish between these two possibilities. DNase footprinting can be used to identify the RR09 DNA-binding sequence, and in order to obtain an initial view of the RR09 regulon in other strains, the consensus binding sequence could subsequently be used for in silico screening. Although the exact roles of most of the identified targets in pneumococcal virulence still have to be investigated, a few targets have already been studied extensively. Furthermore, predictions of the functions of many of the novel RR09 targets identified here are still based on sequence homology alone, and further studies are required to identify the exact roles in pneumococcal virulence. Pneumococci are likely to have different nutritional needs during the various stages of infection. Possibly, RR09 plays a role in this process by regulating genes required for nutrient uptake in response to various conditions characteristic of different sites in the host. The signal that triggers RR09 might be present at one site and not at another,
and particular strains might respond differently to these signals, potentially explaining the phenotype differences observed in animal studies.

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