The vapA co-expressed virulence plasmid gene vcgB (orf10) of the intracellular actinomycete Rhodococcus equi

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The virulence plasmid of the pathogenic actinomycete Rhodococcus equi is essential for proliferation of this pathogen in macrophages and the development of disease. The pathogenicity island of this plasmid encodes a family of virulence-associated proteins (Vap), one of which (VapA) is a virulence factor. This paper describes the vcgAB operon (vapA co-expressed gene), located upstream of the vapA operon. Transcription of the vcgAB operon gave rise to transcripts with a half-life similar to those determined for other virulence plasmid genes (1.8 min). Transcription started at a promoter similar to the vapA promoter, and proceeded through an inefficient terminator into the downstream vcgC gene. In addition, vcgC is also transcribed from a promoter downstream of vcgB. The vcgAB and vapA operons were coordinately regulated by temperature and pH in a synergistic manner. The latter parameter only affected transcription at higher growth temperatures, indicating that temperature is the dominant regulatory signal. Transcription of the vcgAB operon increased 10-fold during the late exponential and stationary growth phases. Transcription was also upregulated during the initial hours following phagocytosis by phagocytic cells. In contrast to vcgA and vcgC, the vcgB gene is conserved in the porcine VapB-encoding plasmid, as well as in pathogenic mycobacteria. The coordinated regulation of vcgB and vapA, transcription of vcgB following phagocytosis and conservation of vcgB in pathogenic mycobacteria indicate a role for vcgB and the vcg genes in the virulence of R. equi.

INTRODUCTION

Although Rhodococcus equi was originally identified as a major pathogen of foals, it sporadically infects other animals and is increasingly recognized as an opportunistic pathogen of predominantly, but not exclusively, immunocompromised humans (Meijer & Prescott, 2004; Muscatello et al., 2007). R. equi belongs to a group of actinomycetes that is characterized by a hydrophobic cell envelope containing mycolic acids, which includes Mycobacterium, Corynebacterium and Nocardia species. The majority of R. equi infections are associated with pyogranulomatous cavitating pneumonia, although systemic manifestations also occur, including osteomyelitis and cerebral infections (Meijer & Prescott, 2004; Muscatello et al., 2007). R. equi is a pathogen of alveolar macrophages that is able to prevent endosomal maturation and the accompanying acidification of the phagolysosome (Hondalus & Mosser, 1994; Toyooka et al., 2005). Proliferation of the pathogen in the endosomal compartment eventually results in the necrotic death of the host cell (Fernandez-Mora et al., 2005; Lührmann et al., 2004). Genomic analysis suggests that
evolution of virulence occurred through cooption of existing virulence genes and also by gene acquisition via lateral gene transfer (Letek et al., 2010).

All equine and the majority of porcine and human isolates harbour a large plasmid consisting of a highly conserved backbone required for replication and conjugation that is also present in a plasmid harvested by the non-pathogenic *Rhodococcus erythropolis* (Letek et al., 2008; Sekine et al., 2006; Takai et al., 2000). The equine and porcine plasmids differ in a variable region of lower G+C content than the remainder of the plasmid that corresponds to a pathogenicity island. It encodes a family of virulence-associated proteins (Vap), including the virulence factor VapA in equine isolates and its VapB homologue in pig isolates (Byrne et al., 2001; Letek et al., 2008; Ocampo-Sosa et al., 2007; Takai et al., 2000). VapA has been shown to be essential, but not sufficient, for proliferation of *R. equi* in macrophages and development of disease (Giguère et al., 1999; Jain et al., 2003). The vapA gene is located in the four-cistronic vapAICD operon, which is transcribed from a single promoter that is induced during growth at high temperature and low-to-neutral pH, conditions which resemble the host environment (Byrne et al., 2008; Russell et al., 2004). Interestingly, mRNA processing and the differential mRNA stability of the vapAICD transcript result in a greater abundance of the vapA transcript relative to that of the three downstream genes (Byrne et al., 2008). The activity of the vapA promoter (P vapA) is dependent on the presence of the LysR-type transcriptional regulator VirR, which is encoded within the five-cistronic virR operon (virR-orf5-vapH-orf7-orf8; Fig. 1) located upstream of the vapAICD operon (Byrne et al., 2007; Russell et al., 2004). In addition, evidence to date indicates that a response regulator encoded by orf8 is also required for expression of the vapAICD operon (Russell et al., 2004). The activity of the virR operon promoter (P virR) is negatively autoregulated by VirR, resulting in low-level constitutive transcription. A second promoter (P orf5), located within the virR gene (Fig. 1), becomes active during growth at high temperature and low pH, resulting in increased transcription of the four genes located downstream of virR, including orf8 (Byrne et al., 2007).

Located in between the virR and vapA operons are three genes, *vcgABC* (orf9, orf10, orf11), encoding small proteins of unknown function (Fig. 1). Only one of these, *vcgB*, is conserved in the vapB plasmid; *vcgA* is present as a pseudogene, and *vcgC* is absent (Letek et al., 2008). A DNA microarray analysis has shown that *vcgB* and the two non-conserved genes are transcribed following uptake of *R. equi* in macrophages, suggesting they may play a role in virulence (Ren & Prescott, 2003). Here we show that the *vcgB* gene belongs to a gene family conserved in pathogenic mycobacteria that infect phagocytic cells. Its induction upon phagocytosis, synergistic regulation by temperature and pH, coordinated regulation with the vapA operon, and conservation in the vapB plasmid strongly suggest a role for *vcgB* in pathogenesis.

**METHODS**

**Bacterial strains and growth conditions.** Bacterial strains and plasmids used in this study are listed in Table 1. *R. equi* 103, its plasmid-cured derivative and *E. coli* DH5α were grown in Luria-Bertani (LB) medium (Sambrook & Russell, 2001) or in minimal medium supplemented with 20 mM lactate (LMM), as previously described (Kelly et al., 2002). *R. equi* was routinely grown at 37 °C, pH 5.5 (vapA-inducing conditions), or at 30 °C and pH 8.0 (vapA non-inducing conditions). Where appropriate, ampicillin at 50 μg ml⁻¹, and apramycin at 30 μg ml⁻¹ (E. coli) or 80 μg ml⁻¹ (R. equi), were added. For solid media, agar was added to 1.5 % (w/v).

**Plasmid construction.** Promoter probes were constructed using preV6, as described by Byrne et al. (2007). Briefly, serially shortened DNA fragments from the 5’ end were produced by PCR using a common reverse primer, VCgCREV, with 8C 2089F, VCG_771F or VCG_389F, and were ligated into the ClaI site of pREV6 to produce pP1, pP2 and pP3, respectively. Construct orientation was checked by digestion with appropriate restriction enzymes and confirmed by double-strand sequencing.

pVcgABC, containing the t-tag downstream of *vcgC*, was used for the generation of a deleted version to locate the t-tag within vapA. For this, 1 μg pVcgABC was double-digested with Apal and Ndel restriction enzymes (New England Biolabs). Non-compatible overhanging ends were repaired with the Klenow fragment of DNA polymerase I. Thirty femtomoles of repaired product was digested with T4 DNA ligase and transformed into *E. coli* DH5α. Deletions were checked by PCR using primers 8C 2089F and VCgCREV, by digestion with relevant restriction enzymes and sequencing. In this case, the t-tag was used as a reporter for the comparison of the expression levels of vapA and vapC.

Reverse transcriptase quantitative PCR (RT-qPCR) analysis was performed as above but using the specific primer t-tag167R for the reverse-transcription step.

pUO95 was constructed by cloning an 872 bp PCR product containing *pVcgA*, the 3’ end of *orfB* and the 5’ end of *vcgA* into the EcoRV site of pBluescript KSII +.

**RNA isolation.** RNA was isolated from *R. equi* grown in vitro as described previously (Russell et al., 2004). *R. equi* RNA was isolated from macrophages following phagocytosis of the pathogen using a guanidine thiocyanate-based lysis buffer [4 M guanidine thiocyanate, 0.5 % (w/v) sodium N-lauryl sarcosine, 25 mM sodium citrate, 0.1 M β-mercaptoethanol] as described elsewhere (Butcher et al., 1998; Rohde et al., 2007). Samples were vortexed and passed through a needle to shear macrophage DNA and to reduce viscosity. Intracellular bacteria were recovered by centrifugation. Pelleted bacteria were lysed using TRIzol (Sigma), and physically disrupted with zirconia beads in a Magna Lyser instrument (Roche). Total RNA was isolated by chloroform extraction, followed by DNA digestion with Turbo DNase (Ambion) and application to a Qiagen RNeasy column with a second, in-column, DNA digestion with the RNase-free DNase, as previously described (Miranda-CasoLuengo et al., 2005).

**Reverse transcription and PCR.** Reverse-transcriptase reactions using hexameric random primers (Promega) were performed with 1 U ImProm-II reverse transcriptase (Promega) following the manufacturer’s recommendations with 100 ng total RNA as template in a final volume of 20 μl. The resulting product was used in either an end point PCR or an RT-qPCR. For the former, 2 μl of the reaction mixture was used as template for GoTaq Flexi DNA polymerase (Promega), as described by the manufacturer. For RT-qPCR, the product was amplified using the QuantiTect SYBR Green real-time kit following the manufacturer’s instructions (Qiagen). Reaction mixtures were subjected to 40 cycles of 95 °C for 15 s,
60 °C for 30 s and 72 °C for 30 s in a LightCycler (Roche) with temperature transition rates of 20 °C s⁻¹. Melting curve analysis was performed at 50–95 °C (temperature transition 0.2 °C s⁻¹), with continuous fluorescence detection following amplification. Cycle threshold (C_T) values were obtained and used to calculate the number of RNA copies per microgram of total RNA using a standard curve of known amounts of DNA target with r² coefficients greater than 0.997 in the range of 5×10³ to 5×10⁸ molecules per reaction. 16S rRNA was used as a control to compare the amount of RNA in each reaction. A relative approach was used for the quantification of intramacrophage R. equi transcript levels. Normalization of gene expression was performed by the (1/E)^ΔΔCT method (Pfaffl, 2004) using 16S rRNA as an internal control. Efficiencies (E) of amplification were determined for each pair of primers by running standard curves with r² coefficients greater than 0.99 in the range of 10² to 10⁵ R. equi genomic equivalents using the formula E = 10^[−1/mPCR − 1], where mPCR is the slope of the standard curve. E values for 16S rRNA, vcgA, vcgB and vcgC were 1.03, 1.03, 0.87 and 0.93, respectively. The data reported in this paper represent the results of three independent

Fig. 1. Transcriptional organization of the vcgABC gene cluster and flanking virR (Byrne et al., 2007) and vapA (Byrne et al., 2008) operons of the VapA virulence plasmid of R. equi. Promoter location is shown by hooked arrows and by 'P'. The grey boxes downstream of orf8 and vapI represent a vap pseudogene (Russell et al., 2004) and the frame-shifted 5' end of vapI (Polidor & Haas, 2006), respectively. The nucleotide sequence of a 17 bp inverted repeat downstream of vcgB and partially overlapping the 5' end of vcgC is delineated by arrows. The insert shows the results of the reverse transcriptase analysis of the vcgAB operon using the oligonucleotide pairs 08F/09R (predicted size 1880 bp) complementary to orf8 and vcgA (lanes 1–3), 09F/010R (predicted size 477 bp) complementary to vcgA and vcgB (lanes 4–6), and 010F/011R (predicted size 738 bp) complementary to vcgB and vcgC (lanes 7–9). Lanes 1, 4 and 7, 2 μl of the reverse transcriptase reaction (cDNA); lanes 2, 5 and 8, reaction without reverse transcriptase; lanes 3, 6 and 9, reaction using genomic DNA as template.

Table 1. Bacterial strains and plasmids used in this study

<table>
<thead>
<tr>
<th>Strain or plasmid</th>
<th>Genotype or characteristics</th>
<th>Source or reference</th>
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<tbody>
<tr>
<td><strong>Strains</strong></td>
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<tr>
<td>E. coli DH5α</td>
<td>supE44 lacU169 (φ80lacZ M15) hsdR17 recA1 endA1 gyrA96 thi-1 relA1</td>
<td>Bethesda Research Laboratories</td>
</tr>
<tr>
<td>R. equi 103</td>
<td>Virulent strain, 81 kb virulence plasmid</td>
<td>De La Peña-Moctezuma et al. (1996)</td>
</tr>
<tr>
<td><strong>Plasmids</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>pREV6</td>
<td>Promoter probe vector containing a t-tag located within two transcriptional terminators</td>
<td>Byrne et al. (2007)</td>
</tr>
<tr>
<td>pDrive</td>
<td>TA cloning vector</td>
<td>Qiagen</td>
</tr>
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<td>pP1</td>
<td>pREV6 with a 2089 bp DNA fragment containing promoters P_vcgA and P_vcgC, orf8, vcgA, vcgB and vcgC</td>
<td>This study</td>
</tr>
<tr>
<td>pP2</td>
<td>pREV6 with a 771 bp DNA fragment containing P_vcgA, vcgB and vcgC</td>
<td>This study</td>
</tr>
<tr>
<td>pP3</td>
<td>pREV6 with a 389 bp DNA fragment containing 'vcgC</td>
<td>This study</td>
</tr>
<tr>
<td>pVcgA</td>
<td>pREV6 with an 893 bp DNA fragment containing P_vcgA, orf8 and vcgA</td>
<td>This study</td>
</tr>
<tr>
<td>pUO9S</td>
<td>pDrive with an 872 bp DNA fragment containing the upstream sequence and the 5' end of vcgA</td>
<td>This study</td>
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</tbody>
</table>
experiments in which each sample was analysed in duplicate. The sequences of oligonucleotides used for RT-qPCR are listed in Table 2.

**mRNA half-life determination.** The rate of mRNA decay was determined as described previously (Byrne et al., 2008). Briefly, transcription was halted during mid-exponential growth by addition of rifampicin (200 μg ml⁻¹). The half-life of specific transcripts was determined by RT-qPCR followed by linear regression.

**Fluorescent primer extension and DNA sequencing.** WellRED D4-labelled oligonucleotide D4-ORF9PEx (Table 2), complementary to sequences 20–39 bp downstream of the initiation codon of vgcA, was used in the primer extension reaction to find the transcriptional start site of the vgcAB operon, as previously described (Byrne et al., 2007). Briefly, 2 μg total RNA was reverse-transcribed using ImProm-II reverse transcriptase (Promega), and the RNase-treated product was combined with DNA Size Standard kit 600 (Beckman Coulter) and analysed with a Beckman CEQ 8000 Genetic Analysis System following the manufacturer's directions (Beckman Coulter). In parallel, a dideoxy sequencing reaction with the ORF9PEx primer was carried out using Nhel-digested pUO9S as template and the GenomeLab DTCS kit as directed by the manufacturer (Beckman Coulter). 200 μl of the sequencing products prior to analysis with the Beckman CEQ 8000 Genomic Analysis System to identify the transcriptional start site.

**VapA quantification.** *R. equi* was harvested by centrifugation (10 min, 4000 g, 4 °C) and resuspended in 100 mM Tris/HCl (pH 8.0) and 10 mM EDTA (pH 8.0). Cells were lysed by three passages through a French press and cell debris was removed by centrifugation (10 min, 14 000 g, 4 °C). Soluble cell extracts were boiled for 10 min in SDS [62.5 mM Tris/HCl (pH 6.8), 10 % (v/v) glycerol, 2 % SDS, 5 % 2-mercaptoethanol, 0.02 % bromophenol blue], and applied to a denaturing polyacrylamide gel. Proteins were subsequently transferred onto a PVDF membrane (Immobilon-P, Millipore) according to the manufacturer’s instructions. Immunoblot analysis was performed with a chemiluminescent Western blot analysis system (Lumi-Light Western Blotting Substrate, Roche). Monoclonal antibody against VapA (Mab 10G5; provided by S. Takai, Kitasato University, Towada, Japan) was used for immunoblotting procedures. Protein was quantified using the Bio-Rad Multi-Imaging system and the Bio-Rad Quantity One software package.

**Infection of J774A.1 cells.** Bacteria grown in LMM were centrifuged (10 min, 3220 g) and washed twice with cation-free PBS (Sigma). Murine macrophage-like cells J774A.1 were seeded at 6 × 10⁵ cells ml⁻¹ in 6 cm tissue culture plates (Sarstedt) and cultured at 37 °C in 5 % CO₂ overnight. Monolayers were washed once with pre-warmed phagocytosis buffer [0.1 % (w/v) gelatin, equal amounts of Medium 199 and Dulbecco’s modified Eagle’s medium (DMEM)] (Hondalus et al., 1993), and the medium was replaced with phagocytosis buffer containing 5 % mouse serum (Sigma) as a source of complement. J774A.1 cells were infected with *R. equi* at an m.o.i. of 20. Infections were initiated by centrifugation (160 g, 3 min) of bacteria onto confluent monolayers to synchronize the internalization. Plates were incubated for 45 min at 37 °C in 5 % CO₂. Monolayers were washed three times with warm phagocytosis buffer (37 °C) to remove unbound bacteria and incubated for a further 15 min to allow internalization of the attached bacteria. Monolayers were washed again with warm phagocytosis buffer. Phagocytosis buffer was subsequently replaced with DMEM supplemented with 10 % (v/v) fetal calf serum, 4 mM l-glutamine, 1 % non-essential amino acids and 10 μg gentamicin ml⁻¹ (this time point was denoted t=0). Infected monolayers were harvested at different time points between 2

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

<table>
<thead>
<tr>
<th>Oligonucleotide</th>
<th>Sequence (5’ to 3’)</th>
<th>Purpose</th>
<th>Reference or source</th>
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<td>16SrRNA200F</td>
<td>AGCAACGCGATGTCAGGTA</td>
<td>Quantification of 16S rRNA gene</td>
<td>Miranda-CasoLuengo et al. (2005)</td>
</tr>
<tr>
<td>16SrRNA200R</td>
<td>TCTATCGTGAGTCGGAAAG</td>
<td>Quantification of 16S rRNA gene</td>
<td>Miranda-CasoLuengo et al. (2005)</td>
</tr>
<tr>
<td>08F</td>
<td>GAACACCTGGGAAATGTTGA</td>
<td>RT-PCR</td>
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<tr>
<td>09F</td>
<td>GCCTGTGCGTTGATCCGTTT</td>
<td>RT-PCR/quantification of vgcA</td>
<td>This study</td>
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<td>09R</td>
<td>TACAAAGCGACGGCGTAGAACAG</td>
<td>RT-PCR/quantification of vgcA</td>
<td>This study</td>
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<tr>
<td>010F</td>
<td>GAGCGCAGCCATGAAAGTA</td>
<td>RT-PCR/quantification of vgcB</td>
<td>This study</td>
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<tr>
<td>010R</td>
<td>CCGCTAGCAGAAATCTGAAAG</td>
<td>RT-PCR/quantification of vgcB</td>
<td>This study</td>
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<td>011F</td>
<td>TTAGAGATGCTGTCTGGC</td>
<td>RT-PCR/quantification of vgcC</td>
<td>This study</td>
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<tr>
<td>011R</td>
<td>GATGGCTATGCGTTGACA</td>
<td>RT-PCR/quantification of vgcC</td>
<td>This study</td>
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<tr>
<td>012F</td>
<td>CAGTACGACGTCGCGAGCA</td>
<td>Quantification of vapA</td>
<td>Byrne et al. (2008)</td>
</tr>
<tr>
<td>012R</td>
<td>CAGCGCCTGGTGGTCGAAAC</td>
<td>Quantification of vapA</td>
<td>Byrne et al. (2008)</td>
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<td>VGCREV*</td>
<td>GACTATCGGACTAAGGCGGCTCCTACGAAG</td>
<td>Construction of pP plasmids</td>
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<td>t-tag167R</td>
<td>ACGGCTAGAATCGTTGCTT</td>
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<td>This study</td>
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<td>t-tag167F</td>
<td>CAGCGGAAGCACATCGACTTC</td>
<td>Quantification of t-tag</td>
<td>This study</td>
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<td>8C_2089F*</td>
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<td>Construction of pP1</td>
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<td>VCG_771F*</td>
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<td>Construction of pP2</td>
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<td>VCG_389F*</td>
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<td>Construction of pP3</td>
<td>This study</td>
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<tr>
<td>ORF9PEx†</td>
<td>AACCAGATGAAACCCACAAGC</td>
<td>Primer extension of vgcA, and construction of pUO9S</td>
<td>This study</td>
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<tr>
<td>VP9445F</td>
<td>TGTATCGGTGCGTGAATGCT</td>
<td>Construction of pUO9S</td>
<td>This study</td>
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*Underlined sequences show ClaI restriction sites for cloning into pREV6.
†This oligonucleotide was used unmodified and fluorescently labelled with WellRed D4 dye for sequencing and primer extension, respectively.
and 48 h. Medium was replaced after 24 h with fresh medium containing 10 μg gentamicin ml⁻¹.

Enumeration of intracellular *R. equi*. The intracellular proliferation of *R. equi* was assessed by quantitative PCR (qPCR). Monolayers washed twice with PBS were scraped at indicated times post-infection (t=0, 2, 24 and 48 h), spun down, and resuspended in 10 mM Tris/HCl, pH 8.0. Harvested samples were heated at 99 ºC for 10 min, and then spun down briefly to pellet cellular debris. qPCR amplifying 16S rRNA was performed as described above. Ct values were used to calculate the *R. equi* cell number using a standard curve of known amounts of bacteria with r² coefficients greater than 0.9952 in the range of 1 × 10⁵ to 1 × 10⁹ bacteria per reaction.

Phylogenetic analysis. An alignment of the VcgB (Orf10) proteins and their mycobacterial homologues (Supplementary Fig. S1) was constructed using CLUSTAL_X (Larkin et al., 2007), and subsequently used to infer phylogenetic relationships using the programs supplied in the PHYLIP v3.68 software suite (Felsenstein, 1989). A distance matrix was calculated with PROTDIST using the Jones–Taylor–Thornton model (Jones et al., 1992). An unrooted phylogenetic tree was subsequently constructed via neighbour joining as implemented in the NEIGHBOR program.

RNA structure analyses. RNA structure and minimum free energy of prediction were done using the RNAfold of the Vienna RNA Server (http://rna.tbi.univie.ac.at/).

Statistical analyses. Statistical analyses were performed by Student’s t test for paired values. Differences were considered significant at P<0.05.

Gene nomenclature. The vapB-containing plasmid pVAPB1539 (accession no. AM947676) was recently annotated and the vapA plasmid pVAPA1037 (accession no. AM947677) was reannotated (Letek et al., 2008). The orf9 and orf11 genes of the latter plasmid were denoted pVAPA_0560 and pVAP_0580. The orf10 genes on the two plasmids were denoted pVAPB_0570 and pVAPA_0570, respectively. Since the orf9, 10 and 11 genes are regulated in a manner similar to the virulence gene vapA, we propose to rename these genes to *vcgA*, *vcgB* and *vcgC*, respectively (*vapA* co-expressed gene).

RESULTS

**vcgB is conserved in pathogenic Mycobacterium species**

A hallmark of the pathogenicity island of the *R. equi* virulence plasmid is the large proportion of genes that are unique to this pathogen, including the *vcgA* and *vcgC* genes. However, comparison by BLASTP and PSI-BLAST of VcgB with protein sequences deposited in GenBank revealed extensive similarities to a family of small mycobacterial proteins (Supplementary Fig. S1). In addition to these, VcgB homologues are also present, but not annotated, in the genomes of *Mycobacterium tuberculosis* H37Rv, *Mycobacterium bovis* BCG and *Mycobacterium abscessus*. The last species contains two *vcgB* homologues, which are separated by 3 kb. Interestingly, *vcgB* homologues were not found in species other than in the genus *Mycobacterium*, and, with the exception of *Mycobacterium smegmatis*, all are pathogenic *Mycobacterium* species.

A phylogenetic analysis showed that the VcgB homologues grouped into two clusters (Fig. 2). Cluster 1 contained the *Mycobacterium avium*, *M. avium* subsp. *paratuberculosis*, *Mycobacterium intracellulare*, *Mycobacterium ulcerans*, *Mycobacterium marinum*, *Mycobacterium kansasi* and *M. tuberculosis* proteins, whereas the *R. equi* proteins grouped with those of *M. smegmatis* and *M. abscessus*. Cluster 1 represents slow-growing mycobacterial species, whereas the species present in the second cluster are fast-growing. The topology of the VcgB phylogenetic tree closely matches that of the 16S rRNA genes of these species (Devulder et al., 2005).

**The *vcgAB* genes form an operon**

The conservation of the *vcgB* gene in pathogenicity islands of *R. equi* strains with different host specificities as well as in pathogenic mycobacteria suggests that this gene may play a role in the interaction with the host. The regulation and transcriptional organization of this gene was therefore analysed in greater detail. The *vcg* gene cluster is located between the *virR* and *vapA* operons (Fig. 1). The close proximity of *vcgA* to *vcgB* (68 bp) suggests that they may be cotranscribed. In contrast, *vcgB* is separated by 203 bp from *vcgC*. This relatively large intergenic region between *vcgB* and *vcgC* contains a 17 bp inverted repeat that may form a stable RNA structure with a free energy of −39 kcal mol⁻¹ (−163 kJ mol⁻¹), which masks the initiation codon and ribosome-binding site of *vcgC* (Fig. 1). This RNA structure is followed by three uridines, thus resembling an intrinsic terminator (Platt, 1986). To investigate the transcriptional organization of these genes, mRNA was isolated and reverse-transcribed from *R. equi* grown under *vapA*-inducing conditions. The resulting cDNA was amplified by PCR using oligonucleotide primers (Table 2) complementary to sequences in adjacent genes (Fig. 1). Strong amplification was observed when the *vcgA–vcgB* pairs were used, whereas only a weak signal was detected when the *vcgB–vcgC* primer pair was deployed. These data demonstrate that the *vcgAB* genes form an operon, with probable read-through into *vcgC*. An amplicon was not observed when oligonucleotides were used that were complementary to *orf8*, the last gene of the *virR* operon, and *vcgA*, showing that the *vcg* gene cluster is not dependent on promoters in the *virR* operon (Fig. 1).

**The *vcgABC* cluster contains an internal promoter**

The RT-PCR experiments clearly showed that *vcgA* and *vcgB* are cotranscribed, whereas the weak signal obtained following RT-PCR using the *vcgB–vcgC* primer pair suggested that read-through from *vcgB* into the downstream *vcgC* gene might occur. To examine whether this was the case, the ability of sequences upstream of *vcgC* to drive transcription of *vcgC* was examined using the promoter probe vector pREV6 (Fig. 3a). This vector contains a small DNA fragment (t-tag) located in between two transcriptional terminators that is absent in the *R. equi*
genome and virulence plasmid (Byrne et al., 2007). Introduction of the complete vcgABC cluster and the orf8–vcgA intergenic region in pREV6 resulted in transcription of the t-tag, demonstrating the presence of an active promoter. Deletion of the orf8–vcgA intergenic region, as well as vcgA and the 5’ end of vcgB, reduced transcription twofold. Further deletion of vcgB and the 5’ end of vgcC abolished transcription of the t-tag completely (Fig. 3b). These data show that read-through from a promoter (PvcgA) upstream of vgcA into vgcC does occur, despite the presence of a putative terminator, since deletion of this promoter reduced transcription of the t-tag by 50%. The fact that transcription was not abolished completely demonstrates the presence of a second promoter (PvcgC) that drives transcription of the vgcC gene.

Transcriptional termination occurs between vcgAB and vgcC

The vgcAB–vcgC intergenic region contains a putative terminator structure, although read-through past this putative terminator occurs. To examine the relative transcription levels of vgcAB and vgcC and to determine whether there is termination in between the former and latter, the transcript levels of vgcA relative to vgcC were determined. Using primers complementary to vgcA and vgcC, a 20-fold difference in transcript level was detected (Fig. 3c). To rule out that this difference was due to a difference in reverse transcription efficiency, the t-tag in pREV6 was placed either behind the PvcgA promoter (pVcgA) or behind both PvcgA and PvcgC (pP1). In this case, the effects of differential reverse transcription are negated since the same template for reverse transcription is used. As before, a 20-fold difference in transcription was observed when comparing the former with the latter (Fig. 3c). These data thus demonstrate that the vgcAB transcripts are at least 20-fold more abundant than the vgcC transcript. In addition, they show that the putative terminator downstream of vgcAB is approximately 90% effective.

Growth phase-dependent transcription of the vgc genes

R. equi was grown under vapA-inducing conditions, and vgcABC transcript levels were determined during the exponential (0–12 h) and stationary (12–48 h) growth phases (Fig. 4). The transcript levels of vgcAB increased approximately 10-fold during the late exponential and stationary growth phases compared with early exponential growth. Similarly, vgcC levels increased approximately 10-fold during the late exponential phase, but subsequently fell to levels similar to those at the start of the experiment. The half-lives of the vgcA (1.7 ± 0.2 min), vgcB (1.8 ± 0.2 min) and vgcC (1.7 ± 0.4 min) transcripts were similar to those reported for the genes of the virR operon (1.8 min) (Byrne et al., 2007) and the vapICD genes of the vapA operon (Byrne et al., 2008). In contrast, the vapA transcript is more stable, with a reported half-life of 7.5 min (Byrne et al., 2008). The short half-lives of the vgc transcripts show that the 10-fold increase in vgcAB and vgcC transcript levels was not due to accumulation of a relatively stable transcript during growth, but instead was
due to an increased transcription of the vcg operon during the mid- to late-exponential growth phase that continued into the stationary phase for the vcgAB genes, but not for vcgC (Fig. 4).

Co-regulation of the vcgAB and vapA operons: synergistic effect of high temperature and low pH

Transcription of the vapA operon, which is located downstream of the vcg genes, is induced during growth at low pH and high temperature, resembling the conditions encountered by R. equi in the host (Takai et al., 1996). To compare the regulation of the vcgAB and vapA operons, their transcription was determined following growth under vapA-inducing (pH 5.5, 37 °C) and non-inducing growth conditions (pH 8.0, 30 °C) by determining the mRNA levels of vcgB and vapA (Fig. 5). The vcgB and vapA mRNA levels under the former growth conditions were, respectively, 20- and 100-fold higher compared with the latter, demonstrating that transcription of the vcg operon is also induced by low pH and high growth temperature (Fig. 5a). To determine the relative contributions of each environmental parameter, temperature and pH were varied individually. Changing the pH of the medium from pH 8.0 to pH 5.5 while keeping the temperature at 30 °C resulted in relatively little change in the transcription level of either operon compared with non-inducing growth conditions. In contrast, an increase in growth temperature from 30 to 37 °C, while keeping the pH at 8, had a more significant, yet modest, effect (respectively, eight- and 32-fold increases in vcgB and vapA mRNA levels). The data thus show that pH only significantly affected transcription of the vcg and vapA operons at 37 °C but not at 30 °C, whereas growth temperature affected transcription at both low and high pH. However, it is clear that a simultaneous reduction in pH and increase in temperature had a synergistic effect on the transcription of the vcgAB and vapA operons.

To further validate these results, the expression levels of VapA protein were determined using monoclonal antibodies directed against VapA (Fig. 5b). The VapA expression pattern was the same as the vapA transcription pattern. As was observed for the vapA transcript levels, VapA protein levels increased by approximately 100-fold when comparing non-inducing with inducing growth conditions. Furthermore, a decrease in pH and increase in temperature at the growth medium had a synergistic effect on the VapA protein expression levels, while pH did not significantly affect expression at 30 °C.
The vcgAB operon and vcgC are transcribed in macrophages

A DNA microarray study has shown that the genes of the pathogenicity island, including the vcg genes, are transcribed in macrophages, although these microarray data have not been validated by other techniques (Ren & Prescott, 2003). To date, no temporal transcription profile of these genes, or of any other genes, following uptake of R. equi by macrophages, has been determined. To examine the regulation of the vcg genes in vivo, macrophages were infected with virulent and avirulent R. equi pregrown on minimal medium supplemented with lactate at 37 °C, pH 7. As expected, virulent R. equi proliferated within macrophages, whereas the avirulent plasmid-free strain did not (Fig. 6a). RNA was extracted over a 48 h period, and the relative transcription levels of vcgA, vcgB and vcgC were determined (Fig. 6b). Transcript levels increased two- to fivefold in the initial 8 h following infection and declined to the initial levels in the subsequent 40 h.

The promoter of the vcgAB operon is similar to the vapA and virR operon promoters

Since the vcgAB operon is regulated in a similar manner to the vapA operon, it seems likely that the promoters of the two are similar. To compare the vcgAB promoter with previously identified R. equi promoters (Byrne et al., 2007; Russell et al., 2004), the transcriptional start site of the vcgAB operon was determined by primer extension using the fluorescently labelled oligonucleotide D4-ORF9PEx, which was hybridized to mRNA isolated from R. equi grown under vapA-inducing conditions. Reverse transcription resulted in a major primer extension product with an estimated size of 331 bp (Fig. 7a). The transcriptional start site inferred from the major extension product mapped to a cytidine 292 bp upstream of the vcgA start codon (C292).

In addition, a shorter, minor extension product was observed with an estimated size of 257 bp, which...
corresponded to a thymidine 219 bp (T219) upstream of the vapA initiation codon (Fig. 7b, c).

The −10 region upstream of C292 shares significant sequence similarity (Fig. 7d) with the promoter recognized by the principal sigma factor $\sigma^{inhB}$ of Streptomyces coelicolor (Buttner et al., 1990; Kang et al., 1997). In addition, this region is similar to those of the previously identified P_virR and P_vapA Promoters (Fig. 2) of the virR and vapA operons (Byrne et al., 2007; Russell et al., 2004). As was observed previously for the P_virR and P_vapA promoters, the −35 region upstream of C292 does not share significant similarity with that of the $\sigma^{inhB}$ promoter. However, the −35 region of the vapA promoter and that of C292 are 56% identical, with three out of the four mismatches being transitions (89% similarity). In contrast, the region upstream of the minor extension product (T219) does not share any similarities with previously identified R. equi promoters.

**DISCUSSION**

The vapAB operon is, after the virR and vapA operons, the third operon of the pathogenicity island to be described in detail (Byrne et al., 2007, 2008). Transcription of this operon terminates in an inefficient terminator downstream of vapB, allowing some read-through from vapAB into the downstream vapC gene, which also has its own promoter. The RNA structure forming the vapAB terminator obscures both the vapC start codon and ribosome-binding site. This, together with the 20-fold lower vapC mRNA levels compared with vapAB, suggests that vapC is very poorly expressed.

The transcriptional regulation of the vapAB operon was identical to that of the vapA operon. Although both temperature and pH control their transcription, the latter only had a significant effect at high temperatures. In contrast, a temperature increase induced transcription of both operons, regardless of pH. Temperature therefore seems to be the primary environmental parameter that controls transcription of vapAB and vapA, and, based on the VapA protein profiles, expression of the pathogenicity island genes. The role of temperature as the primary determinant to control virulence gene expression is common to many pathogens. Although the mechanisms to detect temperature are diverse, they often rely on detection of perturbation of the conformation of biomolecules such as RNA or lipids (Klinkert & Narberhaus, 2009). The mechanism used by R. equi to control temperature-dependent virulence gene expression remains unknown. Interestingly, the effect of pH and temperature on transcription of the vapA and vapAB operons is not independent, but is clearly synergistic. This strongly suggests a common, as-yet-unidentified, denominator in the transduction of these unrelated signals to the transcriptional apparatus.

The transcript levels of the vapAB operon increased 10-fold at the end of the growth phase and remained high throughout the stationary phase. This suggests that the growth phase may be an important trigger for virulence gene expression, as has been observed in other pathogens, including Vibrio cholerae, Legionella pneumophila and Yersinia enterolitica (Hovel-Miner et al., 2009; Iriarte et al., 1995; Nielsen et al., 2006). R. equi grows rapidly in minimal media supplemented with, for example, volatile fatty acids, or in manure-enriched soils (Hughes & Sulaiman, 1987; Kelly et al., 2002), whereas in macrophages, growth is relatively slow, which may be due to a restriction of nutrients such as iron (von Bargen et al., 2011). Furthermore, populations of slow-growing or stationary phase bacteria are more vulnerable to being wiped out by phagocytic cells or predatory protozoa than fast-growing bacterial populations. Increased transcription
of virulence genes during periods of slow or impaired growth may therefore be an adaptation to survive phagocytosis.

The similarity in transcriptional regulation of the vapA and vcgAB operons is borne out in the similarity of the P_vapA and P_vcgA promoter sequences, which resemble promoters dependent on the principal sigma factor HrdB of S. coelicolor (Buttner et al., 1990; Kang et al., 1997). The promoter of the virR operon is also similar to these sequences, albeit to a lesser extent (Byrne et al., 2007; Russell et al., 2004). This suggests that these three R. equi promoters are dependent on the principal sigma factor of R. equi. Interestingly, the internal P_orfs promoter located within the virR operon (Fig. 2) is completely different, suggesting the involvement of an alternative sigma factor (Byrne et al., 2007).

The pathogenicity islands of the equine vapA and porcine vapB plasmids have undergone extensive rearrangements. These are probably associated with the host tropism of strains harbouring the plasmids following acquisition of the pathogenicity island by an ancestral rhodococcal plasmid (Letek et al., 2008). The vcgB gene, located downstream of the virR operon, is conserved in both the vapA plasmid and the vapB plasmid (Letek et al., 2008). Unlike vcgA, vcgC and the vap genes, vcgB has homologues in other bacterial species, which, with the exception of M. smegmatis, are all pathogenic mycobacteria that infect phagocytic cells. A recent analysis of the genome of M. abscessus, a fast-growing pathogenic species, revealed that in addition to the presence of mycobacterial virulence genes, the genome has acquired genes associated with pathogenicity from non-mycobacterial species, most notably from other actinobacteria, including Rhodococcus sp. (Ripoll et al., 2009). The presence of near-identical plasmids in M. marinum and M. abscessus indicates that lateral gene transfer between fast- and slow-growing mycobacteria may occur (Ripoll et al., 2009). However, the phylogeny of the mycobacterial vcgB genes resembles that of the 16S rRNA gene (Devulder et al., 2005), indicating a vertical transmission of vcgB from a common mycobacterial progenitor species. In contrast, the rhodococcal vcgB genes are within a pathogenicity island that is located on a conjugative plasmid. As is the case for the pathogenicity island itself, the rhodococcal vcgB genes were most likely acquired via a lateral gene transfer event (Letek et al., 2008, 2010; Takai et al., 2000).
With the exception of \textit{M. smegmatis}, \textit{vcgB} has only been identified in mycobacterial species that infect phagocytic cells of a wide diversity of hosts, ranging from fish to mammals. The \textit{vcgB} genes in these species survived reductive evolution of the genome that, for example, drove the emergence of \textit{M. ulcerans} from \textit{M. marinum} (Demangel et al., 2009). The \textit{R. equi} genome appears to be genetically stable, and not subject to extensive rearrangement or reductive evolution (Letek et al., 2010). In contrast, the \textit{R. equi} pathogenicity island has been subjected to extensive recent genetic rearrangements and gene corruption; for example, seven of the 23 pseudogenes in \textit{R. equi} are located in the pathogenicity island, which represents only 0.5\% of the total genome (Letek et al., 2008, 2010). While \textit{vcgB} is conserved in both the \textit{vapA} plasmid and the \textit{vapB} plasmid, the flanking \textit{vcgA} and \textit{vcgC} genes are only present in the \textit{vapA} plasmid. This conservation of \textit{vcgB} in the \textit{R. equi} pathogenicity islands, and within pathogenic mycobacterial species, suggests that this gene may play a role in the intracellular lifestyle of this group of pathogens important enough to resist corruption. This notion is strengthened by the observation that \textit{vcgB} is induced following phagocytosis and remains transcribed at least 48 h following phagocytosis, during which \textit{R. equi} proliferates. Furthermore, the coordinated regulation of the \textit{P}_{\text{vcgA}} and \textit{P}_{\text{vcgB}} promoters supports a role for \textit{vcgB} in infection. However, an \textit{R. equi} \textit{vcgB} mutant is not attenuated in a BALB/c mouse model (Ren & Prescott, 2004), indicating that under these experimental conditions, \textit{vcgB} is not critical. The circumstances during the infection process that require \textit{VcgB} therefore remain to be determined. Our current research aims to establish a function for \textit{vcgB} and other pathogenicity island genes, and to elucidate the signal transduction pathways governing their expression.

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