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Differences in Genetic and Transcriptional Organization of the glpTQ Operons between Haemophilus influenzae Type b and Nontypeable Strains

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The glpTQ operon of Haemophilus influenzae type b (Hib) and nontypeable H. influenzae (NTHi) strains is highly conserved, except for a 1.4-kb glpTQ intergenic region that was found in most Hib strains. The presence of this intergenic region results in divergent glpTQ transcriptional profiles for Hib and NTHi where Hib strains appear to have evolved an alternative promoter for glpQ expression. Based on the intergenic region’s low G+C content, we speculate that this DNA fragment was acquired by lateral transfer.

Haemophilus influenzae is a common pathogen, especially among children, but the clinical manifestations are largely type specific. The encapsulated H. influenzae serotype b (Hib) usually causes invasive infections, such as meningitis and sepsis-mia (2), whereas the much more common nonencapsulated, or nontypeable, H. influenzae (NTHi) is a major cause of otitis media, sinusitis, and pneumonia (8). General vaccination against Hib has reduced the incidence of Hib infection to a near minimum (10), while attempts to construct a vaccine against the costly NTHi infections have as yet been unsuccessful due to a high genetic heterogeneity among NTHi strains (20). An extensively studied virulence factor and potential vaccine candidate in H. influenzae is protein D, a 42-kDa conserved lipoprotein expressed on the bacterial surface (1, 13, 21, 24). An isogenic protein D-negative mutant has been shown to be less effective than its wild-type parental strain in its ability to (i) cause experimental otitis media in rats (14), (ii) cause damaged to ciliated human respiratory epithelium (15), and (iii) promote internalization into human monocyte cells (17). The mechanism behind the virulence properties of protein D is unknown but may involve choline decoration of H. influenzae lipoooligosaccharides (LOS), since protein D expression allows H. influenzae to obtain choline from cocultured host cells and subsequently incorporate this molecule into its LOS (6).

The ability of protein D to promote the incorporation of choline into LOS comes from its glycerophosphodiester phosphodiesterase activity, catalyzing the hydrolysis of glycerophosphodiester into glycerol-3-phosphate (G3P) and an alcohol (14, 18). The gene encoding protein D (hpd) is homologous to glpQ of Escherichia coli (16) and other bacteria. The glpQ gene belongs to the glp regulon that is involved in the utilization of glycerol and of G3P and its precursors as energy sources and to supply precursors for phospholipid biosynthesis. In E. coli and Bacillus subtilis (19), glpQ is transcribed together with glpT, which is located upstream of glpQ and encodes a G3P per-

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FIG. 1. Schematic genetic map of the glpABC, glpTQ, and glpFK operons in H. influenzae Rd (7) and genetic map and RNA transcript analysis results of the glpTQ operons of Hib HK695, Hib Eagan, Eagan-derived 1.4-kb glpTQ intergenic region mutant Ekm1, and NTHi 772. Arrows labeled with gene names and ORFs denote transcriptional orientations. Potential transcriptional termination loop structures are marked with circles. Conserved restriction endonuclease sites are indicated. RNA transcripts detected by Northern blotting or RT-PCR are marked under the respective genes or ORFs with thick and fine lines, respectively.

M13-u and M13-r (Table 1) by using an Applied Biosystems 377 automatic sequencer. The DNA sequences of glpT and the glpTQ intergenic region of NTHi 772 were determined from a 2.0-kb PCR product amplified with primers glpA-1 and hpd-10 (Table 1) and sequenced with primers specific for the glpT gene of Hib Eagan (25). The DNA sequence upstream of glpT of Hib Eagan was obtained from a PCR amplicon by using primers glpA-1 and glpT-9 (Table 1).

The glpT sequences of Hib Eagan and NTHi 772 were almost as highly conserved as the previously sequenced glpQ gene (13, 24). The glpT genes from the two strains differed in 15 bp and displayed identical deduced amino acid sequences of the same length. The regulatory region upstream of the NTHi 772 glpT gene was also identical to the corresponding region of Eagan, except that 772 contained one extra base pair located 91 bp upstream of the glpT start codon (Fig. 2). Potential catabolic and transcriptional regulation sites with homology to consensus sequences upstream of glpT in E. coli were also found upstream of glpT in Eagan and 772. They include two catabolic activator protein binding sites (4), two operator sites with the potential of binding to the E. coli GlpR repressor protein (29), and a sequence homologous to the integration host factor (IHF) (9) (Fig. 2). The binding of IHF to this site may bend the DNA to facilitate the formation of a complex structure that is involved in the inhibition of GlpT expression, mediated by the GlpR repressor in E. coli (28). However, despite the existence of two GlpR homologues, no homologues of hfdA and hfdB (R. A. Weisberg, M. Freundlich, D. Friedman, J. Gardner, N. Goosen, H. Nash, A. Oppenheim, and J. Rouvière-Yaniv, Letter, Mol. Microbiol. 19:642, 1996) have been identified in the H. influenzae Rd genome (7).

In the glpTQ intergenic region, both Hib strains contained practically identical 1,428-bp sequences, except that HK695 contained one more tetrameric repeat (TTTA) in addition to the five repeats present in Eagan. The repeats were localized in a putative open reading frame (ORF) of 414 bp in HK695, designated ORF1 for these Hib strains (Fig. 1). The lack of one tetramer in Eagan caused a frameshift that led to a stop codon after 228 bp and resulted in two smaller ORFs (Fig. 1). Most tetrameric DNA repeats in H. influenzae have been associated with the regulation of potential virulence factors such as iron acquisition factors, adhesion molecules, and LOS biosynthesis (11, 27), but the function of ORF1 is unknown. Another putative 390-bp ORF (ORF2) of the Hib glpTQ intergenic region was found immediately upstream of glpQ (Fig. 1). The glpTQ intergenic region of the two Hib strains was highly homologous to the corresponding region of H. influenzae Rd (7). Two ORFs with unknown functions, HI0687 and HI0688, correspond to ORF1 and ORF2 of the Hib strains with the exception that HI0687 of H. influenzae Rd exhibits a larger size than ORF1 (Fig. 1). The G+C contents of the 1.4-kb glpTQ intergenic region of the Hib strains was approximately 26%, which is much lower than the average of 38% for the glpT and glpQ genes and 39% for the H. influenzae Rd genome in general. Although no typical insertion-like sequences were found in this region, the 1.4-kb fragment might have been acquired by lateral transfer from an organism with a lower G+C content. The glpTQ intergenic region of NTHi 772 was only 103 bp long, out of which the first 52 bp was homologous to the glpTQ intergenic regions of the Hib strains Eagan and HK695. This homologous part contains an inverted repeat sequence with the ability to form a typical hairpin loop structure exhibiting a lowest free energy value of −9.8 kcal/mol (23) that may function as a potential transcription terminator for glpT expression. A similar conserved inverted repeat sequence was also identified immediately downstream of the glpQ stop codon in both Hib and NTHi strains (Fig. 1). This potential glpQ transcriptional terminator exhibited a lowest free energy value of −16.8 kcal/mol (23).

Construction of a 1.4-kb mutant in H. influenzae. Reverse PCR with a Pwo PCR kit (Roche Diagnostics) was used to amplify the fragment flanking the 1.4-kb intergenic region of pXME10 with primers Hibup-3 and Hibup-4 (Table 1), resulting in a 1.2-kb deletion of the 1.4-kb intergenic region. The PCR product was ligated to the 1.3-kb kanamycin resistance (Km' ) cassette excised from pUC4K (Amersham Pharmacia Biotech) with HincII, and the ligation mixture was transformed into E. coli DH5α. Following the excision of the vector backbone by BamHI-SphI cleavage, the 3.5-kb linear DNA fragment was transformed into Eagan for homologous recombination (14). The chromosomal DNA of five Km' colonies was examined by Southern hybridization with digoxigenin (Roche Diagnostics)-labeled probes. The glpT and glpQ probes were labeled by PCR using a pXME10-derived nested deletion and
pHIC348 (12) as templates with M13-u-glpTx1 and hpd-6B–hpdl-4 (Table 1) (24) as primer pairs, respectively. The kanamycin probe was labeled by random priming from the gel-purified Km' cassette that had been excised from pUC4K with HincII. Southern blot analysis (data not shown) of EcoRI- or HaeIII-digested chromosomal Hib DNA revealed that the Km' cassette had been inserted just downstream of the glpT coding region (Fig. 1) in all tested Km' clones. The growth rate of one such mutant, Ekml, was compared to that of the parent strain Eagan, and metabolic fingerprints were analyzed with GN MicroPlate and ES MicroPlate kits (Biolog, Hayward, Calif.) either in brain heart infusion broth supplemented with NAD and hemin or in the chemically defined BCM1 medium (25). No significant difference in cell densities, generation times, or metabolic properties was observed for triplicate experiments (data not shown).

**Characterization of promoter positions of the glpTQ operons.** Primer extension analysis (22) was applied to identify potential transcriptional start positions by using antisense DNA primers (Table 1) that bound just downstream of the respective start codons. Primers were labeled with [γ-32P]ATP by T4 polynucleotide kinase (Amersham Pharmacia Biotech) and were used for the extension of 40 μg of total RNA, prepared with an RNeasy kit (QIAGEN) from cultures grown in supplemented brain heart infusion broth. Labeled products were analyzed on a 6% polyacrylamide gel containing 7 M urea in a Sequi-Gen sequencing cell (Bio-Rad Laboratories). The signal in the gel was measured either by exposure to X-ray film or by a PhosphorImager and analyzed with ImageQuant software (Molecular Dynamics). A total of four bands, designated P1 to P4, corresponding to potential transcriptional start positions of glpT were detected in NTHi 772, whereas only three bands were detected in Hib Eagan (P1, P2, and P4) (Fig. 2). The lack of P3 in Hib Eagan was unexpected since potential corresponding −10 and −35 promoter sequences were found in both strains. The existence of one more promoter (P3) in 772 suggests that the regulation conditions and expression levels of glpT might differ for NTHi and Hib strains. This hypothesis was supported by the observation that glpT of NTHi 772 that was cloned into the pACYC184-based vector pSU18 (3) failed to complement the G3P uptake levels in the Hib Eagan glpT rec-1 double mutant ETM22r2 (unpublished data), although both strains contain almost identical glpT genes. We further analyzed the total RNA of ETM22r2 that had been transformed with pXMS1 (25), carrying Eagan glpT plus a partial regulatory region ending 156 bp upstream of the glpT start codon cloned into pSU18. Only one band corresponding to position P1 was found (data not shown), although the P2 site and its putative −10 promoter sequence plus the region where a −35 consensus sequence normally is found (Fig. 2) was included in pXMS1. This result suggests that the P1 site may be essential for glpT transcription in Eagan since pXMS1 is able to complement the glpT mutant ETM22r2 to a higher level of GlpT expression than that of the wild-type strain, Eagan (25).

**TABLE 1. Oligonucleotides used in this study**

<table>
<thead>
<tr>
<th>Primer</th>
<th>Nucleotide sequence</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>glpT-1</td>
<td>5'-TTGCAGatCCACCGATAATGTAC-3'</td>
<td>Reverse primer annealing to nt 85–60 of Rd glpA, used for amplification and sequencing</td>
</tr>
<tr>
<td>glpT-9</td>
<td>5'-ATGCGetGCaGGTTTAGAATGGTCA-3'</td>
<td>Reverse primer annealing to nt 29–6 of Eagan glpT, used for amplification, sequencing, and primer extension</td>
</tr>
<tr>
<td>Hibup-1</td>
<td>5'-AAAAAGGGCaGGCAATTTGCTTAGTC-3'</td>
<td>Forward primer annealing to nt 8–35 of downstream glpT stop codon of Eagan, used for RT-PCR</td>
</tr>
<tr>
<td>Hibup-2</td>
<td>5'-CCTATCAAaggTCCAATGCAACATCTTG-3'</td>
<td>Reverse primer annealing to nt 264–234 of downstream ORF1 stop codon of HK695, used for RT-PCR</td>
</tr>
<tr>
<td>Hibup-3</td>
<td>5'-AAAGGCCACTAAGCAATTGCCCACCACGCTTTTTAAG-3'</td>
<td>Reverse primer annealing to nt 41–5 of downstream glpT stop codon of Eagan, used for construction of 1.4-kb mutant</td>
</tr>
<tr>
<td>Hibup-4</td>
<td>5'-TGCTGGAATGATTATAAAT-3'</td>
<td>Forward primer annealing to nt 98–117 of Eagan ORF2, used for construction of 1.4-kb mutant and RT-PCR</td>
</tr>
<tr>
<td>Hibup-5</td>
<td>5'-AATGGGTTAGATTCCTATT-3'</td>
<td>Forward primer annealing to nt 41–63 of Eagan ORF1, used for RT-PCR</td>
</tr>
<tr>
<td>Hibup-6</td>
<td>5'-AAATCCTCAGATAAAAAATCTAACA-3'</td>
<td>Reverse primer annealing to nt 130–107 of Eagan ORF1, used for primer extension</td>
</tr>
<tr>
<td>Hibup-7</td>
<td>5'-GGCATAGCAAGTATTTCCAAAGATAC-3'</td>
<td>Reverse primer annealing to nt 328–303 of HK695 ORF1, used for RT-PCR</td>
</tr>
<tr>
<td>Hibup-8</td>
<td>5'-TTCCGTGAATTTAATTAGT-3'</td>
<td>Reverse primer annealing to nt 267–246 of Eagan ORF2, used for RT-PCR</td>
</tr>
<tr>
<td>Hibup-9</td>
<td>5'-CTCAGCCCTTTCCAAAATCTAATT-3'</td>
<td>Reverse primer annealing to nt 35–8 of Eagan ORF2, used for primer extension</td>
</tr>
<tr>
<td>Hibup-10</td>
<td>5'-GTTGACTACTGCTCTACTATG-3'</td>
<td>Reverse primer annealing to nt 185–156 of Eagan ORF2, used for primer extension</td>
</tr>
<tr>
<td>Hibup-11</td>
<td>5'-ATTTTgATCCCTTATACATTTGCTGA-3'</td>
<td>Reverse primer annealing to nt 52–28 of glpQ, used for amplification and primer extension</td>
</tr>
<tr>
<td>hpd-10</td>
<td>5'-CCTGCTATCTGCAGCTGTAATA-3'</td>
<td>M13 universal primer for pBluescript II vectors, used for sequencing</td>
</tr>
<tr>
<td>M13-u</td>
<td>5'-GTTTCCCCATGCACGAC-3'</td>
<td>M13 reverse primer for pBluescript II vectors, used for sequencing</td>
</tr>
<tr>
<td>M13-r</td>
<td>5'-AACAGCTATGACATCG-3'</td>
<td></td>
</tr>
</tbody>
</table>

*a Lowercase letters indicate nucleotides substituted for the creation of restriction sites.

b nt, nucleotide.
It also indicates that the signal at the P2 site in primer extension analysis may be a degradation product of a glpT mRNA initiated from the upstream promoter site P4. Since ETM22r2 is a glpT mutant that was created by the selection of spontaneous fosfomycin-resistant Hib Eagan clones (25), it is likely that the P4 promoter site probably exists in ETM22r2. No signal from P4 could be detected in ETM22r2(pXMS1), which may be due to the fact that this potential signal is too weak in comparison to the P1 signal from the medium-copy-number plasmid pXMS1. When potential promoter sites for glpQ were analyzed, only one band was identified 28 bp upstream of the glpQ start codon in Hib Eagan as well as in E. coli (pXME10), which contains glpQ from Eagan. A primer extension product was found 64 bp upstream of the glpQ start codon in NTHi 772 and from E. coli (pHIC348), which contains glpQ from 772 (data not shown). The transcriptional start of Hib Eagan ORF1 in the glpTQ intergenic region was mapped to 59 bp upstream of the glpQ start codon in NTHi 772 and from E. coli (pHIC348), which contains glpQ from 772 (data not shown). The transcriptional start of Hib Eagan ORF1 in the glpTQ intergenic region was mapped to 59 bp upstream of the ORF1 start codon in Hib Eagan and E. coli harboring pXME10 (data not shown). Since the glpQ intergenic region of NTHi 772 is only 103 bp, the potential transcriptional starts of NTHi 772 glpQ and Hib Eagan ORF1 must be located within 1 bp from each other in relation to the ends of their respective glpT genes. Both promoters share the same putative −10 and −35 sequences, which are situated within the loop structure downstream of glpT. Furthermore, in spite of the divergent sequences immediately upstream of the glpQ start codons of Eagan and 772 (24), the two strains appear to share the same putative ribosomal binding site. Attempts to locate a transcriptional start for ORF2 of the 1.4-kb region were unsuccessful, but two bands were found within the ORF2 coding region for both Eagan and E. coli harboring pXME10 (Fig. 3). These were located 85 and 89 bp, respectively, downstream of the ORF2 start codon. Shared putative −10 and −35 sequences were also found upstream of these sites.

**RNA transcript analysis.** glpT (1.4 kb) and glpQ (1.1 kb) transcripts from the total RNAs of NTHi 772, Hib Eagan, and ETM22r2 were visualized by using Northern hybridization (Fig. 4). Hib Eagan and ETM22r2 were visualized by using Northern hybridization (Fig. 4). Hib Eagan and ETM22r2 were visualized by using Northern hybridization (Fig. 4). Hib Eagan and ETM22r2 were visualized by using Northern hybridization (Fig. 4). Hib Eagan and ETM22r2 were visualized by using Northern hybridization (Fig. 4).

![Diagram](image-url)

**FIG. 2.** Nucleotide sequence alignment of the glpT promoter region of *H. influenzae* Rd (7), Hib Eagan, and NTHi 772. The numbered positions of nucleotides refer to the Rd genome. A sequence gap is indicated with the symbol ∥. The glpT and glpA start codons are indicated in boldface and italics, and arrows mark the transcriptional directions. Putative −10 and −35 sequences are underlined with double and single solid lines, respectively. Proposed catabolic activator protein (CAP), IHF, and operator binding (O) sites are indicated with dashed arrows above the sequences. Potential promoter sites (P) for the glpT genes of Eagan and 772, based on the primer extension assay, are marked with vertical arrows.
to the 1.1-kb glpQ transcript, the 3.9-kb fragment was also found when the same blot was reprobed with a glpQ probe, suggesting that glpT transcription could continue downstream once the loop structure was removed. However, the practically identical loop structure downstream of 772 glpT only partially terminated glpT transcription because a cotranscribed glpTQ transcript was found in this strain. We therefore conclude that a complete interruption of the glpTQ cotranscript requires the existence of the 1.4-kb glpTQ intergenic region.

As we failed to detect any signals by using ORF1 or ORF2 probes in Northern hybridization (data not shown), RNA transcripts of the 1.4-kb intergenic region of Eagan were further characterized with reverse transcription (RT)-PCR by using Ready-To-Go beads (Amersham Pharmacia Biotech) and different combinations of RT-PCR primers (Table 1). An RNA transcript that covered the entire ORF1 and the ORF1-ORF2 intergenic region was identified, whereas another was found covering most parts of ORF2 (Fig. 1), corresponding to the potential promoter positions found 85 to 89 bp within ORF2 in our primer extension assay. This latter ORF2 transcript appeared to be cotranscribed with the downstream glpQ. This result is in contrast to the 1.1-kb glpQ transcript previously identified by Northern hybridization and to the potential promoter positions of glpQ obtained by the primer extension assay, but as we could detect the transcriptional signal only by RT-PCR and not by Northern blotting, it is assumed that the transcription level of this alternative glpQ promoter situated within ORF2 is low. ORF2 may act as a transcription regulatory region for glpQ in Hib, since it is located immediately upstream of the glpQ coding region, separated by only 11 bp. No apparent catabolic regulation sequence homologues were found in this region. We could not find any putative catabolic regulation sites upstream of NTHi 772 glpQ either, but its putative promoter, found in the primer extension analysis, is located at practically the same position as the potential promoter of ORF1 in Hib Eagan. We therefore speculate that Hib strains that contain the 1.4-kb fragment between glpT and glpQ have evolved an alternative promoter region for glpQ transcription and that the old glpQ promoter now serves as a promoter for ORF1. The transcriptional level of Hib ORF1 appears to be low, since an ORF1 mRNA was detected only by RT-PCR analysis, whereas an NTHi 772 glpQ mRNA was detectable by Northern blot analysis. The promoters are located 1 bp apart within the potential transcriptional terminator loop for glpT (Fig. 1), but it is unlikely that this difference would be the explanation for the observed differences in transcriptional levels between these promoters. The regulation of the Eagan glpQ gene is unknown because it transcribed independently of glpT, whereas the regulation of the glpQ gene in NTHi 772 might be dependent upon the cotranscribed upstream glpT gene.

Overall, this study shows the effect the presence of the 1.4-kb glpTQ intergenic region that exists only in Hib and other encapsulated H. influenzae strains has on glpT and glpQ transcription in these strains compared with their transcription in NTHi 772. For NTHi strains, the glpQ gene (encoding the virulence factor protein D) was in part cotranscribed and possibly coregulated with the upstream glpT gene, encoding G3P per-
mease, and in part transcribed by a promoter that is situated within a hairpin loop structure. In Hib strains, the same promoter appears to transcribe at least one unique ORF (ORF1) that may have the ability to phase vary its expression due to the variation of the number of tetramer repeats situated within the ORF. It would be very interesting to further study and determine how the regulation of genes in the intergenic region of NTHi strains differs from that in Hib strains and to investigate what role the ORFs in the 1.4-kb intergenic region of Hib strains have in pathogenesis.

Nucleotide sequence accession numbers. The entire DNA sequences of the glpT gene of NTHi 772, as well as the 1.4-kb intergenic region of Hib Eagan and HK695 (26), were determined in this study and submitted to GenBank with the following accession numbers: for the 1.4-kb intergenic region of Eagan, accession no. AF132899; for the 1.4-kb intergenic region of HK695, accession no. AF132900; and for glpT of NTHi 772, accession no. AF132901.

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REFERENCES


