Significance of tagI and mfd genes in the virulence of non-typeable Haemophilus influenzae

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Summary. Non-typeable Haemophilus influenzae (NTHi) is an opportunist pathogen well adapted to the human upper respiratory tract and responsible for many respiratory diseases. In the human airway, NTHi is exposed to pollutants, such as alkylating agents, that damage its DNA. In this study, we examined the significance of genes involved in the repair of DNA alkylation damage in NTHi virulence. Two knockout mutants, tagI and mfd, encoding N3methyladenine-DNA glycosylase I and the key protein involved in transcription-coupled repair, respectively, were constructed and their virulence in a BALB/c mouse model was examined. This work shows that N3-methyladenine-DNA glycosylase I is constitutively expressed in NTHi and that it is relevant for its virulence. [Int Microbiol 2014; 17(3):159-164]

Keywords: Haemophilus influenzae · alkylating agents · virulence · genes tagI and mfd

Introduction

Non-typeable Haemophilus influenzae (NTHi) is a commensal gram-negative bacterium well adapted to the human upper respiratory tract [7]. It has been implicated in the etiology of otitis media, conjunctivitis, sinusitis, pneumonia, and chronic bronchitis, and in the progression of chronic obstructive pulmonary disease (COPD) [19]. However, within its human host, this opportunistic pathogen is exposed to high levels of genotoxic stress in the form of airway pollutants. In a study based on proteomic expression profiling of H. influenzae grown in pooled sputum from adults with COPD, both the expression of antioxidant activity and stress responses were shown to be important for NTHi survival in the Airways [13]. DNA-damaging agents are ubiquitous. They are generated endogenously during cell metabolism and are present in the environment—in air, water and foods—although generally in low concentrations. For example, tobacco smoke contains a mixture of alkylating agents, some of which act directly (alkyl halides, acrolein, crotonaldehyde, ethylene oxide, propylene oxide, acrylonitrile, and acrylamide), while others act indirectly (requiring metabolic transformation to form reactive species) [15]. Moreover, human airway pollutants such as tobacco smoke damage not only eukaryotic cells but also the DNA of the respiratory tract microbiota.

The repair of DNA alkylation damage in bacterial cells has been mainly studied in Escherichia coli. As in other
bacteria, *E. coli* has two specific mechanisms to remove alkyl radicals from its DNA: (i) via the constitutive expression of genes encoding the necessary repair enzymes and (ii) via the alkyl-induced expression of these proteins [16]. This adaptive response to the repair of DNA alkylation damage is regulated by the Ada protein, a positive transcriptional regulator that stimulates the expression of the *ada, alkA, alkB*, and *aidB* genes [5,16]. Bacteria also have two additional enzymes involved in the specific repair of DNA alkylation damage: Ogts (*O^6^-meG-DNA methyltransferase*) [10] and TagI (*N^3^meA-DNA glycosylase I*) [2]. In addition, two other systems are involved in the repair of DNA alkylation damage: the nucleotide excision repair (NER) [20] and the transcription-coupled repair (TCR) [17] systems. The latter system mediates the bulk repair of DNA damage via the Mfd protein, followed by the engagement of NER.

The aim of the present work was to determine the significance of *tagI* and *mfd* genes involved in the repair of DNA alkylation damage in NTHi virulence. Accordingly, knockout mutants in *tagI*, specific for DNA alkylation damage, and *mfd*, involved in bulk DNA repair, were constructed and their virulence in a BALB/c mouse model was studied.

### Materials and methods

**Bacteria, media, and growth conditions.** *Haemophilus influenzae* NTHi375, an otitis media isolate [4], was grown on chocolate agar + PolytiteX plates (PVX, BioMerieux), on brain heart infusion (BHI) medium with or without agar supplemented with 10 μg hemin ml⁻¹ and 10 μg NAD ml⁻¹ (sBHI). The cultures were grown at 37 °C for 18 h in an atmosphere of 5 % CO₂. *Escherichia coli* DY380 strain was grown in LB (Luria–Bertani) broth or on agar plates at 37 °C for 18 h. When necessary, 50 μg ampicillin ml⁻¹ and 50 μg spectinomycin ml⁻¹ were added.

**Construction of *tagI* and *mfd* knockout mutants.** The *tagI* knockout mutant was constructed from strain NTHi375 using a previously described method [18]. Briefly, the entire gene targeted for deletion was PCR-amplified from the genomic DNA of NTHi375 strain (Table 1, Fig. 1A), cloned into pGEM-T (Promega), and electroporated into *E. coli* DY380. Strain DY380 harboring the plasmid with the *tagI* gene was selected by plating onto LB agar plates supplemented with 50 μg ampicillin ml⁻¹. Then, with plasmid pRSM2832 [18] as template, PCR was used to generate an amplicon

### Table 1. Oligonucleotide primers used in this study

<table>
<thead>
<tr>
<th>Primer</th>
<th>Sequence (5′-3′)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Primer used to obtain the mutants</strong></td>
<td></td>
</tr>
<tr>
<td>TagI_F</td>
<td>cggtgtgcgcgaacaatca</td>
</tr>
<tr>
<td>TagI_R</td>
<td>tcgtgaaaccttattggaactc</td>
</tr>
<tr>
<td>Mfd_F</td>
<td>tacactatgecctaattttaacaca</td>
</tr>
<tr>
<td>Mfd_R</td>
<td>acaatgatcgggcttctttttatg</td>
</tr>
<tr>
<td>P1-TagI</td>
<td>gtttgccgaacaatacatattatatattatatgatcagcagcaggaaggggagaacgtgaatttcgcaccaaaacagctatttgtccgaggggtacgtgcac</td>
</tr>
<tr>
<td>P2-TagI</td>
<td>aatcatttaaatgtcgctgcaccaaccaacccatataattcattagcataaagccatcaacagctgattttgcccaataaagacagacaaacacctgttaggcgtgagctgtctgg</td>
</tr>
<tr>
<td>P1-Mfd</td>
<td>catttttaagaattatgtactgttttcggtggagacggaaggtcgccgagagactttgcttgatttgctttcaccgttaaaattccggggatccgtcgacc</td>
</tr>
<tr>
<td>P2-Mfd</td>
<td>tatattggcttccgagaaatggcctgtaccgaatctgaacatgtctatggagtggacgagctgttggtctgagtttaccgttgagctgtctgg</td>
</tr>
<tr>
<td><strong>Primers used for RT-qPCR assays</strong></td>
<td></td>
</tr>
<tr>
<td>trpA F</td>
<td>cttcggtgcgttcgtaac</td>
</tr>
<tr>
<td>trpA R</td>
<td>tgcgacgaatttttccaatagt</td>
</tr>
<tr>
<td>Tag F</td>
<td>cgccaaataaagctctgcat</td>
</tr>
<tr>
<td>Tag R</td>
<td>cggggtgctccgggattta</td>
</tr>
<tr>
<td>recA F</td>
<td>cagttggcaggaaggct</td>
</tr>
<tr>
<td>recA R</td>
<td>cgccaaataaagctctgcat</td>
</tr>
</tbody>
</table>

Forward primer, up; reverse primer, dw. Underlined text corresponds to the 80 nucleotides of the 5′ and 3′ ends (H1 and H2) of the NTHi gene to be deleted.
containing a cassette with both the \( rpsL \) and the spectinomycin resistance genes, flanked by FRT (FLP recombinase target) sites. In addition, the design of the primers produced an amplicon that contained 80 nucleotides (nt) of the 5′ and 3′ ends of the \( tagI \) gene to be deleted, flanking each of the FRT regions (Table 1, Fig. 1B). The amplicon was electroporated into \( E. coli \) strain DY380 harboring pGEM-T carrying the \( tagI \) gene. After induction of the recombinase genes of strain DY380 by heat shock at 42°C, spectinomycin-resistant clones were isolated by plating the transfectants onto LB agar plates supplemented with 50 \( \mu \)g spectinomycin ml –1. One of these positive clones was chosen for further use after PCR and sequencing to confirm that it harbored a plasmid with the correct insertion. This plasmid was digested with \( NcoI \) and \( NsiI \) restriction enzymes, and the fragment with the appropriately sized insert was recovered and used to transform NTHi375 strain by the MIV method, as previously described [12], to obtain the desired construct (Fig. 1C). Spectinomycin-resistant clones were isolated by plating onto BHI agar plates supplemented with 200 \( \mu \)g spectinomycin ml –1 followed by incubation at 37°C. One of these clones was isolated for further use after PCR and DNA sequencing to confirm that it contained the desired mutation and that it did not harbor any remnants of the plasmid. The same procedure was used to obtain the \( mfd \) mutant. Afterwards, pRSM2947, a temperature-sensitive replicon appropriate for NTHi and harboring both the FLP recombinase under the control of the \( tet \) regulatory system and a kanamycin resistance marker, was transformed by electroporation into the knockout mutants, to remove the cassette containing both \( rpsL \) and the spectinomycin resistance genes.

**NTHi infection BALB/c model.** To infect the mice, the bacteria were recovered with 1 ml of PBS from a chocolate-agar plate grown for 16 h, yielding a bacterial suspension of \( \approx 5 \times 10^9 \) colony-forming units (CFU)/ml. Twenty microliters of bacteria (\( \approx 10^7 \) CFU) were inoculated into the nares of 5- to 7-week-old female BALB/c mice (Harland Iberica). After 48 h of infection, the mice were killed by cervical dislocation and their lungs were rapidly dissected for the determination of bacterial load. The dissected lungs were homogenized on ice in 500 \( \mu \)l of PBS using an Ultra-Turrax T10 basic homogenizer (IKA). Bacteria from the homogenates and from serial dilutions thereof were recovered on chocolate-agar plates. The results are reported as log CFU per gram of tissue. In each case, clones recovered from the mice were confirmed by PCR.

The mice were treated in accordance with the Directive of the European Parliament and of the Council on the protection of animals used for scientific purposes (Directive 2010/63/EU) and in agreement with the Bioethical Committee of the University of the Balearic Islands. This study was approved by the Bioethical Committee of the University of the Balearic Islands under authorization number 1748.

**Reverse transcription–quantitative real-time PCR.** RNA from strain NTHi375 grown in sBHI and treated or not with 1.5 \( \mu \)g N-methyl-N′-nitro-N-nitrosoguanidine (MNNG) ml –1 for 1 h was extracted using the RNeasy minikit (Qiagen) and DNase treatment (Ambion). Reverse transcription–quantitative real-time PCR (RT-qPCR) was performed in a 20-\( \mu \)l reaction mixture with Lightcycler RNA Master SYBR Green I (Roche) on a...
Lightcycler 480 instrument (LC480; Roche), following the manufacturer’s instructions and using suitable oligonucleotide primer pairs for each gene (Table 1). The relative mRNA concentration obtained from the tag gene was determined according to a standard curve generated by amplifying an internal fragment of the trpA gene, which is not affected by MNNG treatment. Similarly, the recA gene served as the positive control for the induction of gene expression by MNNG. The expression factor was calculated as the ratio between the mRNA concentrations obtained from genes expressed in MNNG-treated NTHi 375 cells with respect to those from untreated cells.

Statistical analysis. Statistical analyses were performed using one-way analysis of variance (ANOVA) with Bonferroni contrasts. P < 0.05 was considered statistically significant. The analyses were performed using Prism4 for PC (GraphPad Software).

In silico analysis. To identify the proteins of *H. influenzae* involved in DNA alkylation repair, *E. coli* protein sequences implicated in this system were scanned for homologues by using BLASTP [http://blast.ncbi.nlm.nih.gov/Blast.cgi] against the published genomes of *H. influenzae* strains.

### Results and Discussion

The present work was designed to determine the significance of DNA alkylation damage repair in NTHi virulence. *In silico* analysis revealed that the adaptive response to the repair of DNA alkylation damage was missing in *H. influenzae* because Ada, AlkA, AlkB, and AidB proteins were absent. However, this bacterium contains the genes encoding ogt and tagl as well as the genes involved in the NER and TCR systems. Based on these results, we studied the importance of AlkA, TagI has a very high specificity for 3-MeA binding pocket and the absence of the catalytic aspartate that is present in all other helix-hairpin-helix family members, including AlkA, Tagl has a very high specificity because it almost exclusively cleaves 3-methyladenine [2,6]. This specificity probably arises from the enzyme’s unique aromatic-residue-rich 3-MeA binding pocket and the absence of the catalytic aspartate that is present in all other helix-hairpin-helix family members, including AlkA [6].

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DNA injuries induced by alkylating agents present in the environment [1]. By contrast, _H. influenzae_ is a human obligate pathogen well adapted to the human upper respiratory tract, and with a low persistence outside the host [8], which would explain why it does not have the full complement of repair mechanisms needed to repair alkylation-type damage. Consequently, the deletion of a key protein in the repair of alkylation injuries must be more relevant for this species than it is for _Salmonella_. In this context, the role of _N³-meaA-DNA glycosylase I_ in _NTHi_ survival in human airways must be emphasized, because this enzyme catalyzes the specific removal of _N³-methyladenine_, a mainly lethal insult that blocks DNA replication [3,9]. In the setting of tobacco smoke and _NTHi_ respiratory infections [10], the bacterial TagI protein would thus be critical in repairing DNA damage caused by the alkylating agents in cigarette smoke during the infective process of _NTHi_.

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Competing interests. None declared.

References