Overproduction of the MtrCDE Efflux Pump in *Neisseria gonorrhoeae* Produces Unexpected Changes in Cellular Transcription Patterns


Departments of Microbiology and Immunology and Medicine, Emory University School of Medicine, Atlanta, Georgia, USA; Department of Microbiology and Immunology, F. Edward Herbert School of Medicine, Uniformed Services University of the Health Sciences, Bethesda, Maryland, USA; Laboratories of Bacterial Pathogenesis, VA Medical Center, Decatur, Georgia, USA

The global consequence of drug efflux gene overexpression in bacteria has not been specifically analyzed because strains showing high-level expression typically have mutations in genes encoding regulatory proteins that control other genes. Results from a transcriptional profiling study performed with a strain of *Neisseria gonorrhoeae* that is capable of high-level transcription of the *mtrCDE* efflux pump operon independently of control by cognate regulatory proteins revealed that its overexpression has ramifications for systems other than drug efflux.

Bacteria use efflux pumps to resist the action of antibiotics during treatment of infection or to survive in the presence of antimicrobials in their environment (1). The level of expression of efflux pump-encoding genes is modulated by a complex regulatory system of repressors and activators, but derepression due to mutation in repressor-encoding genes or their promoters can significantly decrease bacterial susceptibility to antimicrobials (2). As an example, mutation in the *mtrR* repressor gene of *Neisseria gonorrhoeae* enhanced transcription of the *mtrCDE*-encoded efflux pump and resulted in both increased resistance of gonococci to structurally diverse antimicrobials (3–5) and greater in vivo fitness in an experimental mouse model of lower genital tract infection (6, 7). MtrR also has more global action, however, as it directly or indirectly impacts expression of >65 genes involved in diverse systems such as peptidoglycan synthesis, pilin secretion, the general stress response, and glutamine metabolism (8–10).

The question asked in this study was this: does overexpression of a drug efflux pump per se have a potential impact on bacteria? Heretofore, this question could not be addressed because bacteria that overexpress efflux pump genes typically contain mutations that impact cognate gene regulators (e.g., MtrR), which would make interpretation of results difficult. Taking advantage of a unique promoter that drives high-level expression of *mtrCDE* independently of MtrR control (11) (as well as activation by MtrA [12]), we performed a transcriptional profiling study. Here, we provide data that support the hypothesis that overexpression of a bacterial efflux system may have unexpected global ramifications with respect to microbial physiology.

**Bacterial strains, culture conditions, and antimicrobial testing.** *N. gonorrhoeae* strains FA19 and FA19*mtr120* were the main strains used (Table 1). “*mtr120*” signifies a single nucleotide change (C to T) 120 nucleotides upstream of *mtrCDE* (7) that generates a new promoter for *mtrCDE* transcription (11) and increases gonococcal resistance to diverse antimicrobials (Table 1), including host defense antimicrobials (7, 13). Transformants of these strains bearing an insertionally inactivated *ccpR* gene due to the presence of the nonpolar *aphA*-3 cassette were constructed by previously described methods (12). Gonococci were routinely grown as non-piliated, opacity-negative variants on gonococcal medium base (GCB) agar or in broth, each with defined supplements I and II, as previously described (4). The MIC of antimicrobials recognized by the MtrCDE efflux pump was determined by agar dilution (4). To test gonococcal susceptibility to peroxides, a microtiter plate assay was used. Briefly, this involved exposing 10^7 gonococci in GCB broth to various concentrations of hydrogen peroxide (H_2O_2) or tert-butylhydroperoxide (tBuOOH) at 37°C for 45 min before spotting 5 μl onto GCB agar plates for assessment of viability; H_2O_2 and tBuOOH are not substrates of the MtrCDE pump (unpublished observations).

**RNA-seq and qRT-PCR studies.** A transcriptional-profiling comparison study using transcriptome sequencing (RNA-seq) and three independent RNA samples prepared from broth-grown, late-logarithmic cultures of isogenic strains FA19 and FA19*mtr120* was performed using previously described methods (14). We defined differentially expressed genes as having (i) a fold change value of ≥2, (ii) a total read number larger than 5, and (iii) a Bonferroni-corrected *P* value of ≤0.05. For quantitative reverse transcriptase PCR (qRT-PCR) analysis of gene expression, RNA samples from RNA-seq experiments were used to synthesize cDNA using random hexamers. Transcripts of the genes of interest (*ccpR* and *rpsS15*) were quantified using qRT-PCR and oligonucleotide primers (see Table S1 in the supplemental material) essentially as described previously (14); *rpsS15* was used as a reference for normalization of the results.

**Global gene expression consequences of overexpression of mtrCDE.** As expected from previous studies (7, 11), RNA-seq
analysis revealed that expression of \textit{mtrC}, \textit{mtrD}, and \textit{mtrE} was highly upregulated in strain FA19\textsubscript{mtr120} compared to wild-type strain FA19, which, based on earlier reports (4, 5, 9), served as an internal control for the results of the transcriptome comparison (Table 1); this upregulation was confirmed by qRT-PCR (see Table S1 in the supplemental material). Importantly, analysis of the RNA-seq results revealed changes in the expression levels of 13 non-	extit{mtr} genes which were widely distributed across the genome (Fig. 1) and represented a variety of functional classes (Table 1) based on annotation of the FA1090 genome (www.genome.ou.edu). Only one of these non-	extit{mtr} genes (\textit{ccpR}) was overexpressed in strain FA19\textsubscript{mtr120}. Proteins encoded by the 13 underexpressed genes included four hypothetical proteins; a protease (encoded by \textit{clpP}); a periplasmic peptidase (\textit{sohB}); a stationary-phase-survival protein (\textit{surE}); an ATP-dependent Clp protease subunit (\textit{clpP}); an ATP-dependent RNA helicase (\textit{ngo0593}); a hypothetical integral membrane protein (\textit{ngo0585}); a hypothetical ATP-dependent RNA helicase (\textit{ngo0594}); a hypothetical integral membrane protein (\textit{ngo0585}); a hypothetical ATP-dependent RNA helicase (\textit{ngo0594}); a hypothetical integral membrane protein (\textit{ngo0585}); a hypothetical ATP-dependent RNA helicase (\textit{ngo0594}); a hypothetical integral membrane protein (\textit{ngo0585}); a hypothetical ATP-dependent RNA helicase (\textit{ngo0594}); a hypothetical integral membrane protein (\textit{ngo0585}); a hypothetical ATP-dependent RNA helicase (\textit{ngo0594}); a hypothetical integral membrane protein (\textit{ngo0585}); a hypothetical ATP-dependent RNA helicase (\textit{ngo0594}); 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TABLE 2  Sensitivity of isogenic gonococci to antimicrobials

<table>
<thead>
<tr>
<th>Strain</th>
<th>Em</th>
<th>CV</th>
<th>TX-100</th>
<th>PxB</th>
<th>H₂O₂</th>
<th>tBuOOH</th>
</tr>
</thead>
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<td>FA19</td>
<td>0.25</td>
<td>0.31</td>
<td>125</td>
<td>100</td>
<td>0.002</td>
<td>0.004</td>
</tr>
<tr>
<td>FA19ccpR::kan</td>
<td>0.25</td>
<td>0.31</td>
<td>125</td>
<td>100</td>
<td>0.002</td>
<td>0.004</td>
</tr>
<tr>
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<td>2</td>
<td>1.25</td>
<td>&gt;16,000</td>
<td>400</td>
<td>0.004</td>
<td>0.016</td>
</tr>
<tr>
<td>FA19mtr120 ccpR::kan</td>
<td>2</td>
<td>1.25</td>
<td>&gt;16,000</td>
<td>400</td>
<td>0.004</td>
<td>0.008</td>
</tr>
</tbody>
</table>

5 Em, erythromycin; CV, crystal violet; TX-100, Triton X-100; PxB, polymyxin B; H₂O₂, hydrogen peroxide; tBuOOH, tert-butylhydroperoxide. For efflux pump substrates Em, CV, TX-100, and PxB, the numbers refer to MICs (µg/ml), while the numbers for H₂O₂ and tBuOOH are minimal bactericidal concentrations (MBCs) in percent (vol/vol). All determinations were performed in triplicate.

We selected ccpR, which encodes cytochrome C peroxidase (16), as a model gene to further test if overexpression of mtrCDE could have distal effects on gonococcal gene expression; ccpR was also chosen as it may contribute to gonococcal resistance to oxidative stress (16, 17). By qRT-PCR analysis, we confirmed expression changes occur is unclear but should be considered in drug efflux studies.

Nucleotide sequence accession numbers. The complete data set can be accessed through GEO accession number GSE47048 and SRA accession number SRA079863.

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REFERENCES