Enterotoxigenic Escherichia coli secretes a highly conserved mucin-degrading metalloprotease to effectively engage intestinal epithelial cells

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Department of Medicine, Division of Infectious Diseases, and Molecular Microbiology and Microbial Pathogenesis Program, Division of Biology and Biomedical Sciences, Washington University School of Medicine, St. Louis, Missouri, USA; Medicine Service, Veterans Affairs Medical Center, St. Louis, Missouri, USA; Institute for Genome Sciences, Department of Microbiology and Immunology, University of Maryland School of Medicine, Baltimore, Maryland, USA

Enterotoxigenic *Escherichia coli* (ETEC) is a leading cause of death due to diarrheal illness among young children in developing countries, and there is currently no effective vaccine. Many elements of ETEC pathogenesis are still poorly defined. Here we demonstrate that YghJ, a secreted ETEC antigen identified in immunoproteomic studies using convalescent patient sera, is required for efficient access to small intestinal enterocytes and for the optimal delivery of heat-labile toxin (LT). Furthermore, YghJ is a highly conserved metalloprotease that influences intestinal colonization of ETEC by degrading the major mucins in the small intestine, MUC2 and MUC3. Genes encoding YghJ and its cognate type II secretion system (T2SS), which also secretes LT, are highly conserved in ETEC and exist in other enteric pathogens, including other diarrheagenic *E. coli* and *Vibrio cholerae* bacteria, suggesting that this mucin-degrading enzyme may represent a shared virulence feature of these important pathogens.

Enterotoxigenic *Escherichia coli* (ETEC) bacteria are a diverse group of organisms that share the ability to secrete and effectively deliver heat-stable toxin (ST) and/or heat-labile toxin (LT) enterotoxins (1). Collectively, these organisms cause millions of deaths following moderate to severe diarrhea in young children (2–4). In the classical paradigm for ETEC pathogenesis, these organisms adhere to the small intestinal mucosa via plasmid-encoded antigens known as colonization factors (CFs). At this site, ETEC bacteria deliver toxins to receptors on epithelial cells. Bound toxin increases host cell cyclic nucleotide concentrations, activating the cystic fibrosis transmembrane regulatory channel (CFTR) and ultimately culminating in fluid efflux into the intestinal lumen (1).

Most ETEC vaccine development has focused on a subset of antigens, including CFs and LT (5). Unfortunately, lack of ST immunogenicity, incomplete protection afforded by LT immunization, and substantial antigenic heterogeneity of the CFs (6) have hindered the development of a broadly protective ETEC vaccine. However, the recent discovery of novel ETEC antigens (7, 8), the complex nature of immune responses to infection (9), and the modulation of many bacterial genes during infection (10) suggest that neither molecular pathogenesis nor the nature of the protective immune response following infection with these pathogens is completely understood.

For instance, while direct engagement of intestinal epithelial cells is essential for efficient toxin delivery by ETEC (11), the virulence features contributing to this process are still poorly defined. Interestingly, in the intestine, access of pathogens to enterocytes is largely limited by intestinal mucins, including MUC2 (12), the major mucin secreted into the lumen of the intestine, as well as cell-surface-bound mucins, including MUC3 (13). While many enteric pathogens, including *Vibrio cholerae* and other diarrheagenic *E. coli*, secrete enzymes that degrade mucin, these enzymes had not previously been identified in ETEC.

The present studies suggest that YghJ, a conserved (14, 15) secreted molecule highlighted in recent immunoproteomic (9) and transcriptome (10) analysis of ETEC, is a mucin-binding metalloprotease that degrades intestinal mucins, including MUC2 and MUC3 to promote access of ETEC to enterocytes, thereby accelerating efficient delivery of the heat-labile toxin to cognate receptors on the epithelial surface.

**MATERIALS AND METHODS**

**Maintenance and propagation of human cell lines.** LS174T cells (American Type Culture Collection [ATCC] CL-188) were propagated in Eagle’s minimum essential medium supplemented with 10% (final concentration) of fetal bovine serum (FBS). Caco-2 intestinal epithelial cells were maintained in Eagle’s minimum essential medium containing FBS (20% vol/vol). Jurkat cells were propagated in RPMI 1640 medium supplemented with FBS (10%). All cells were maintained at 37°C in 5% CO₂.

**Bacterial strains and growth conditions.** Bacterial strains used are listed in Table 1. In most experiments, ETEC bacteria were grown in Luria broth at 37°C overnight from frozen glycerol stocks. To optimize secretion of YghJ via the type II secretion system (T2SS), bacteria were grown in Casamino Acids-yeast extract medium (CAYE) (11).

**Cloning, expression, and purification of recombinant YghJ.** yghJ was amplified from *E. coli* H10407 genomic DNA using primers jf031912.1 (5’-tccgagctctgattgtgggctctcgggtgtc-3’) and jf031912.2 (5’-ttggatccattgtaaggacatc-3’). The amplified fragment was cloned into pET28a(+) and transformed into BL21 (DE3) pLysS E. coli. Recombinant YghJ was purified using His-tag affinity chromatography.

**Supplemental material.** Supplemental material for this article may be found at http://dx.doi.org/10.1128/IAI.01106-13.

**Conflict of interest.** The authors declare no conflict of interest.

**Funding.** This work was supported by National Institutes of Health grants AI078430, AI101061, AI070046, AI107223, and AI106741 (to J.M.F.) and AI107332 (to W.G.L.).
an ongoing project to sequence multiple clinical isolates (http://gscid.igs.uma
tisera against rYghJ-myc-His6 were produced in rabbits as previously de-
used to identify potential functional domains within YghJ (16). Protein
enhanced lookup time accelerated BLAST (Delta-BLAST) searches were
grade; GE Life Sciences) (10). Recombinant proteins with mutations in
allowed by gel filtration chromatography (HiLoad 16/60 Superdex 200 prep
clarified lysates to homogeneity by nickel affinity chromatography, fol-

<table>
<thead>
<tr>
<th>Strain or plasmid</th>
<th>Description</th>
<th>Reference(s) or source</th>
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<tr>
<td>H10407</td>
<td>Wild-type ETEC strain O78:H11; CFA/1; LT+ /ST+ ; EtpA+</td>
<td>56, 57</td>
</tr>
<tr>
<td>E24377A</td>
<td>WT ETEC strain O139:H28</td>
<td>58</td>
</tr>
<tr>
<td>B7A</td>
<td>WT ETEC strain O148:H28</td>
<td>59</td>
</tr>
<tr>
<td>Nissle 1917</td>
<td>O6:H1 probiotic strain originally isolated from an asymptomatic German soldier</td>
<td>32</td>
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<tr>
<td>HS</td>
<td>Isolated from a healthy adult scientist at WRAIR; O9:H4; motile</td>
<td>31</td>
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<tr>
<td>jf1123</td>
<td>H10407 derivative with isogenic deletion of gpgE</td>
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<tr>
<td>jf1124</td>
<td>H10407 derivative with isogenic deletion of gpgM</td>
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<td>H10407 derivative with isogenic deletion of gpgG</td>
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<tr>
<td>TOP10</td>
<td>F- mcrA Δ(mcr-mrsRMS-mcrBC) Δ800lacZΔM15 ΔlacX74 recA1 araD139 Δ(ara leu)7697 galU galK rpsL (Str')</td>
<td>Invitrogen</td>
</tr>
<tr>
<td>yghJ mutant</td>
<td>Isogenic insertion in yghJ; Km' Cm'</td>
<td>14</td>
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Plasmids

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<tr>
<th>Plasmid</th>
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<tr>
<td>pBAD/Myc-HisA</td>
<td>Arabinose-inducible expression plasmid</td>
<td>Invitrogen</td>
</tr>
<tr>
<td>pQL001</td>
<td>yghJ cloned into XhoI and HindIII sites of pBAD/myc-HisA in frame with myc-His tags</td>
<td>This study</td>
</tr>
<tr>
<td>pQL117*</td>
<td>Site-directed mutation of yghJ in codon corresponding to E1309(D)</td>
<td>This study</td>
</tr>
<tr>
<td>pQL114*</td>
<td>Site-directed mutation of yghJ in codon corresponding to E1309(A)</td>
<td>This study</td>
</tr>
<tr>
<td>pQL150*</td>
<td>Site-directed mutation of yghJ in codon corresponding to H1308(A)</td>
<td>This study</td>
</tr>
<tr>
<td>pQL152*</td>
<td>Site-directed mutation of yghJ in codon corresponding to H1312(A)</td>
<td>This study</td>
</tr>
<tr>
<td>pQL124*</td>
<td>66-nucleotide in-frame deletion in yghJ</td>
<td>This study</td>
</tr>
</tbody>
</table>

a Mutagenized yghJ plasmids (indicated by asterisks) used plasmid pQL001 as a template for mutagenesis.

b WRAIR, Walter Reed Army Institute of Research; Str', streptomycin resistant; Km', kanamycin resistant; Cm', chloramphenicol resistant.

tive ETEC sequence is capitalized; XhoI site underlined) and jf031912.2
(5'-cccaagcttgaattTCGCACGATCTCATTGCTC-3' [HindIII site
underlined]) for directional cloning into XhoI and HindIII sites in
pBAD/myc-HisA to create pQL001. E. coli TOP10/pQL001 (5
= 1) was then in-
duced with arabinose to express recombinant YghJ tagged with myc and
polyhistidine (rYghJ-myc-His6), and the fusion protein was purified from
clarified lysates to homogeneity by nickel affinity chromatography, fol-

Bioinformatic analysis of YghJ and T2SS sequences. Domain en-
chanced look-up time accelerated BLAST (Delta-BLAST) searches were
used to identify potential functional domains within YghJ (16). Protein
homology/analogy recognition engine (Phyre2) was then used to com-
pare regions of YghJ with libraries of known protein structures to further
elucidate potential functional residues (17).

BLASTN was used to query multiple draft ETEC genomes emerging from
comparative genome analysis of enterotoxigenic

Mutagenesis of the putative M60/pf13402 metallopeptidase do-
main. Site-directed mutagenesis of the native yghJ gene fragment carried
on pQL001 was performed by high-fidelity PCR using mutagenic primer
sets as indicated in Table 2. Mutagenized plasmids were then used to
transform E. coli TOP10 to ampicillin resistance. Mutations were con-
firmed by sequencing using primers jf101812.3 (5'-CCGAGAAGAACC
GAATGTC-3') and jf101812.4 (5'-TTACCCTTTGAACTGACCA-3').

Production and purification of polyclonal antibody. Polyclonal an-
tiserum against rYghJ-myc-His6, were produced in rabbits as previously de-
scribed (8). Antibodies to YghJ were prepared by cross absorption of
resulting antiserum against an immobilized E. coli lysate column (Thermo
Scientific) followed by affinity purification using the recombinant protein
immobilized on nitrocellulose membranes (18, 19).

Purification of MUC2. MUC2 was purified from supernatants of tis-

**TABLE 1** Bacterial strains and plasmids used in these studies

<table>
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<td>yghJ cloned into XhoI and HindIII sites of pBAD/myc-HisA in frame with myc-His tags</td>
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TABLE 2 Oligonucleotides used in these studies

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<tr>
<th>Primer</th>
<th>Sequence (5’→3’a)</th>
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<tr>
<td>jf031912.1</td>
<td>TCCGAGCTCGAGATCTCTTGTCACCTCTGAGTTATATTAAATGAATAAG (XhoI site underlined)</td>
<td>yghj forward cloning primer</td>
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<tr>
<td>jf031912.2</td>
<td>CGCACTGGATCCATCTCTGAGACATCTTTATGCTC (HindIII site underlined)</td>
<td>yghj reverse cloning primer</td>
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<td>jf082312.1</td>
<td>GCTGATTGCACTGGTGCTGCTGATCTGACCGAGGCC (GAA→GAT mutation underlined)</td>
<td>Site-directed mutagenesis (E1309D) forward</td>
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<tr>
<td>jf082312.2</td>
<td>GGCGTTATGACCGACATGTCGCAGATCGACGCC (GAA→GAT mutation underlined)</td>
<td>Site-directed mutagenesis (E1309D) reverse</td>
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<tr>
<td>jf082312.3</td>
<td>GGCGTTATGACCGAGCTGATCTGACCGAGGCC (GAA→GAT mutation underlined)</td>
<td>Site-directed mutagenesis (H1308A) forward</td>
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<td>jf082312.4</td>
<td>GGCGTTATGACCGAGCTGATCTGACCGAGGCC (GAA→GAT mutation underlined)</td>
<td>Site-directed mutagenesis (H1312A) forward</td>
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<td>jf112612.1</td>
<td>ACGACTGGTCGATCTGCGTGAGATGCTGTAACCGCCGAGAAAAAG (CAT→GCT mutation underlined)</td>
<td>Site-directed mutagenesis (H1312A) reverse</td>
</tr>
<tr>
<td>jf112612.2</td>
<td>CGGTATGACCGAGCTGATCTGACCGAGGCC (GAA→GAT mutation underlined)</td>
<td>Site-directed mutagenesis (H1312A) forward</td>
</tr>
<tr>
<td>jf112612.3</td>
<td>CGGTATGACCGAGCTGATCTGACCGAGGCC (GAA→GAT mutation underlined)</td>
<td>Site-directed mutagenesis (H1312A) reverse</td>
</tr>
<tr>
<td>jf101712.1</td>
<td>GACTGGTGATCCTGGAAGTCGGCTATAACGCCGGAGAAAAAG (CAT→GCT mutation underlined)</td>
<td>Mutagenesis primer to construct 22-amino-acid internal deletion of Yghj residues H13108 to N1329</td>
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<tr>
<td>jf101712.2</td>
<td>CGCCGCGACGAGCTGCTGGCAGACGTG (−66)CCAGATCGGCGAGTCAAGAGATGAGTCTGCAAGAGG (GAA→GAT mutation underlined)</td>
<td>Reverse complement of jf101712.1</td>
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<tr>
<td>jf101812.1</td>
<td>CGGAAGAAGAACCTGAATGC</td>
<td>Forward sequencing primer yghj from nt 3616 to 3635</td>
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<tr>
<td>jf101812.2</td>
<td>TTACCGTTGGATTCAGCACA Reverse sequencing primer</td>
<td>Reverse sequencing primer yghj from nt 4319 to 4300</td>
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(a) (−66) indicates the position of the 66-nucleotide in-frame deletion in yghj extending from nucleotide (nt) 3904 to 3969.

X-100, 0.1 mM phenylmethylsulfonyl fluoride [PMSF], and complete EDTA-free protease inhibitor cocktail [Roche®]. Following incubation on ice for 30 min and repeated freeze (dry ice)-thaw (37°C) cycles, the lysates were centrifuged at 10,000 x g (4°C) to pellet debris. Clarified lysates were then separated on gradient (3 to 8% Tris-acetate; Invitrogen) PAGE. Following transfer to nitrocellulose membranes, Caco-2 lysates were immobilized with anti-MUC3A/B goat polyclonal IgG antibodies (F-19 [catalog no. sc-13314; Santa Cruz]) that recognize an internal region of mucin 3A of human origin (gene identification [ID] 4584).

To examine degradation of purified MUC2, 0.1 μg of protein was treated for at least 30 min with 5 μg of Yghj-myc-His, at 37°C. Reaction products were resolved by SDS-PAGE, and MUC2 digests were examined by western blotting with anti-MUC2 rabbit polyclonal (IgG) (H-300 [catalog no. sc-15334; Santa Cruz]) that recognize an internal region of mucin 2 of rat origin (gene identification [ID] 4583). The remaining after treatment was detected by immunofluorescence confocal microscopy as described below, and images were saved as z-stacks. Image data were then analyzed using Velocity three-dimensional (3D) image analysis software (version 6.2; PerkinElmer, Inc.).

To determine whether Yghj degrades the mucin-like CD43 glycoprotein on the surfaces of human T lymphocytes, we followed a protocol similar to that outlined by Szabady et al. (23). Briefly, 1 x 10⁶ Jurkat cells were incubated for 3 h at 37°C in 5% CO₂ and 5% CO₂, with 5 μg of Yghj suspended in a total volume of 100 μl of RPMI 1640 medium. The cells were pelleted at 400 x g for 5 min, washed with PBS, and blocked with 1% BSA in PBS, and then cell surface CD43 was labeled with phycoerythrin-conjugated anti-CD43 (mouse anti-human CD43 monoclonal clone L10; Invitrogen) and analyzed by flow cytometry.

To test the activity of Yghj in degrading other substrates, we examined the hydrolysis of fluorescein-labeled proteins (24). Quenched substrates, including IgG, gelatin, and bovine submaxillary mucin (BSM) were prepared by labeling with fluorescein isothiocyanate (FITC) [Sigma] as previously described (24). Casein-FITC was purchased from Sigma. Briefly, 10 μl of Yghj (50 μg) was added to 90 μl of 0.1 mg/ml substrate in 100 mM Tris (pH 7.5) in black 96-well U-bottom polypropylene plates. The plates were sealed with optically clear film (TempPlate; USA Scientific) and incubated at 37°C, and fluorescence was measured every 5 min for several hours on a Tecan F200 plate reader using an excitation filter at 485 nm and an emission filter at 535 nm. Increase in fluorescence due to release of quenched FITC upon proteolysis was tested using the protease subtilisin as a positive control (0.1 to 1 mg/ml stock).

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In vitro assessment of toxin delivery and binding. Caco-2 epithelial cell monolayers were infected with ETEC H10407. yghj mutants, or complemented mutants at multiplicities of infection of approximately 100 (bacteria/cell). Cultures of bacteria were grown overnight in Luria broth from frozen glycerol stocks, diluted 1:100, and grown for 1 h. One micro-liter of each culture with or without antibodies as indicated in the figures was then added to confluent Caco-2 monolayers seeded into 96-well plates. Cultures of mutants complemented with pBAD-based expression plasmids were supplemented with 0.0002% arabinose. Two hours after inoculation, the monolayers were washed 3 times with tissue culture medium, and the medium was replaced with 100 μl of medium and the medium was replaced with 100 μl of medium/well and returned to the incubator (37°C, 5% CO₂) for 2.5 h. As previously described, we used a cyclic AMP (cAMP) enzyme immunoassay (EIA) (Arbor Assays, Ann Arbor, MI) to examine the efficiency of toxin delivery.

To examine the effect of Yghj on toxin access to cell surface receptors on enterocytes, cells were treated with fluorescein-conjugated cholera toxin B subunit. Briefly, Caco-2 or LS174T cells grown on coverslips were treated with Yghj at a final concentration of 25 μg/ml for 3 h at 37°C and 5% CO₂. Following treatment, cell membranes were stained with Cell-Mask (catalog no. C10046; Life Technologies) and then fixed with 2% paraformaldehyde for 10 min. After the cells were blocked with 1% BSA, they were labeled with cholera toxin subunit B conjugate (catalog no. C34775; Life Technologies). Images were acquired by fluorescence confocal microscopy with z-stacks, and signal data were then analyzed using Velocity 3D image analysis software (version 6.2; PerkinElmer, Inc.).

Mouse intestinal colonization and competition assays. Colonization of the ileum of infected mice was assessed using the CD-1 mouse intestinal colonization model (25). Briefly, mice were pretreated with streptomycin; the mice were given streptomycin (5 g/liter) in drinking water for 24 h, followed by drinking water alone for 12 h. After the administration of famotidine (50 mg/kg of body weight) to reduce gastric acidity, mice were challenged with approximately 10⁷ CFU of either the lacZYA::Kmr mutant by oral gavage. Twenty-four hours later, the mice were sacrificed, and dilutions of saponin intestinal lysates were plated...
FIG 1 YghJ is a highly conserved type II secretion system (T2SS) effector molecule that facilitates delivery of heat-labile toxin (LT). (a) The product of the yghJ gene, located upstream of the T2SS genes responsible for secretion of the heat-labile toxin as shown in panel a is secreted by ETEC strains with an intact T2SS. (b) Immunoblot demonstrating YghJ in trichloroacetic acid (TCA) precipitates of overnight cultures of ETEC strains H10407, B7A, and E24377A, but not the yghJ mutant, T2SS mutants (gspG, gspE, and gspM), or strain MG1655 (E. coli K-12), which has a truncated version of yghJ and lacks most T2SS genes. Commensal strains HS and Nissle 1917 secrete comparatively little YghJ. (c) Flow cytometry data demonstrating that some YghJ remains associated with the surface of strain H10407 (serotype O78:H11; top right panel) but not with the yghJ mutant (bottom right panel). The regions enclosed in rectangles show the areas gated for surface expression, and the number in the top right-hand corner of each panel represents the percentage of positive cells for the respective antigen under consideration. Anti-O78 (α-O78) data are included as positive controls for surface expression. 1° Ab, primary antibody; 2° Ab, secondary antibody; α-YghJ, anti-YghJ antibody; AF488, Alexa Fluor 488. (d) Secretion of heat-labile toxin by ETEC is not affected by yghJ antisera obtained from the recombinant YghJ (YghJΔ) mutant (pQL001) relative to the LT mutant (eltAB) are shown. OD450, optical density at 450 nm. (e) cAMP production by target Caco-2 cells following infection with wild-type ETEC H10407, yghJ mutant, or complemented mutant. The LT deletion mutant (eltAB) is included here as a negative control. (f) Affinity-purified polyclonal antibodies (α) against YghJ (YghJΔ), but not antibody preabsorbed with recombinant YghJ (YghJΔ) impair delivery of LT to target epithelial cells. Values that are significantly different (P < 0.05) from each other are indicated by a bar and asterisk (n = 4; two-tailed Mann-Whitney analysis).
**RESULTS**

YghJ Is a Conserved Mucin-Degrading Metalloprotease

**FIG 2** YghJ is required for efficient access to the surfaces of enterocytes. (a) Total ETEC recovered from intestinal lysates following infection with either the wild-type (wt) strain bearing a Km\(^+\) cassette insertion in the lacZYA locus (lacZYA::Km\(^+\)) or the yghJ::Km\(^+\) mutant. The bars show the geometric mean number of CFU/ml. Each symbol shows the value for an individual mouse. (b) Competition assay between the lacZYA mutant and the yghJ mutant showing total bacteria recovered from intestinal lysates (the bar represents the average competitive index). (c) Bacteria intimately associated with the surfaces of intestinal villi (n = 100) from intestinal segments of mice (n = 2) following challenge with either H10407 (wt) (blue open circles), or the yghJ mutant (open squares) (P values reflect two-tailed Mann-Whitney nonparametric analysis). (d to f) ETEC H10407 (serotype O78:H11) intimately associated with enterocyte surfaces of intestinal villi. Bacteria identified by anti-O78 (red) immunofluorescence imaging are shown in the insets and in panel g. (h and i) Trapping of the yghJ mutant in luminal mucus (MUC2 is shown in red; bacteria identified by anti-O78 antibodies appear green). H10407 also appears in the lumen (j), but it is also present in close association with the enterocyte surface (k and l).

agel (v1.47) was used to measure the mean fluorescence per pixel (http://rsbweb.nih.gov/ij/docs/menus/analyze.html#measure). These values were then normalized for the number of epithelial cells present in the image.

**FACS analysis and mucin accumulation studies.** Fluorescence-activated cell sorting (FACS) analysis was used to determine the presence of YghJ on the surfaces of ETEC (26). Briefly, bacteria suspended in phosphate-buffered saline (pH 7.2) were first fixed with 2% paraformaldehyde for 15 min, washed twice in PBS, and blocked with 1% BSA in PBS for 30 min. The resulting cell suspensions were incubated with affinity-purified anti-YghJ antibody in blocking solution for 1 h at room temperature, washed three times, and then incubated with anti-rabbit antibody–Alexa Fluor 594 conjugate.

To study binding of MUC2 to the surfaces of ETEC, supernatants from overnight cultures of LS174T cells grown in confluent monolayers were sterilized by filtration through a 0.22-μm filter and then concentrated through a 100-kDa-molecular-weight-cutoff centrifugal filter to concentrate MUC2 secreted into culture supernatants. Following inoculation with bacteria, the infected MUC2-positive (MUC2\(^+\)) retentate was incubated at 37°C and 5% CO\(_2\), and aliquots were retrieved at various time points. Following centrifugation at 10,000 × g and 4°C, the bacterial pellets were washed with PBS, fixed with 2% paraformaldehyde for 15 min, washed again in PBS to remove the fixative, blocked with 1% BSA in PBS, incubated with rabbit polyclonal anti-MUC2 (1:50), and detected with goat anti-rabbit fluorescent (Alexa Fluor 488; Invitrogen) antibody conjugate. MUC2 binding to bacteria was then examined by flow cytometry (26). Flow cytometry data were processed in FlowJo v10.0.5 (Tree Star, Inc.).

**RESULTS**

YghJ is required for efficient delivery of heat-labile toxin. YghJ, encoded immediately upstream of the genes encoding the type II secretion system (T2SS) that is responsible for export of the heat-labile toxin (Fig. 1a) (27) was found in abundance in culture supernatants of several ETEC strains, including H10407, B7A, and...
E24377A (Fig. 1b). However, in keeping with earlier studies suggesting that YghJ is secreted by the T2SS in other E. coli pathotypes (28), we did not find YghJ in culture supernatants of ETEC strains with mutations in T2SS genes gspE, gspG, and gspM or in cultures of E. coli MG1655 that lacks an intact T2SS (27). YghJ and the T2SS proteins were also found on the chromosomes of nonpathogenic E. coli strains (29, 30) (see supplemental material) including HS, an intestinal commensal strain previously isolated from a healthy adult (31), and Nissle 1917, originally obtained from an asymptomatic German soldier (32). However, relative to ETEC strains, the amount of YghJ secreted by these strains was quite small. Because we had previously detected YghJ in association with outer membrane vesicles (9), we also examined the surface of ETEC for YghJ by flow cytometry (Fig. 1c), revealing that some YghJ also remains associated with the surface of wild-type strain H10407. While YghJ export is dependent on T2SS, conversely, mutation of yghJ had no impact on secretion of LT (14), and likewise, trans-complementation of the mutant with a recombinant YghJ expression plasmid (pQL001) did not affect toxin secretion (Fig. 1d), suggesting that this molecule does not compete with LT or facilitate its secretion. However, we noted that the yghJ mutant was appreciably deficient in the ability to deliver LT as determined by the diminished activation of cAMP in target epithelial cells (Fig. 1e). Likewise, affinity-purified antibodies against YghJ significantly impaired delivery of LT by ETEC (Fig. 1f). Together, these studies suggest that these type II secretion effectors, YghJ and LT, act in concert to intoxicate enterocytes, leading to activation of cyclic nucleotides that drive chloride secretion that results in diarrhea.

**Intimate enterocyte engagement requires YghJ.** YghJ shares homology with accessory colonization factor D (AcfD), a lipoprotein (33) important for intestinal colonization of *Vibrio cholerae* (34). Curiously, relative to ETEC (H10407) carrying a mutation in the lacZYA locus, which does not affect intestinal colonization (25), we actually recovered slightly more yghJ mutant organisms from small intestinal lysates regardless of whether mice were challenged with the individual strains (Fig. 2a) (P/H11005 0.6) or together in competition assays (Fig. 2b). Interestingly, however, microscopic examination of ileal sections from mice challenged with either strain H10407 or the yghJ mutant demonstrated many WT organisms intimately associated with the surfaces of enterocytes (Fig. 2c and Fig. 2d to g), while we could identify few if any yghJ mutant organisms, suggesting that YghJ is required for bacteria to gain efficient access to the intestinal epithelial cells (P < 0.0001).

To gain access to the enterocyte surface, enteric pathogens must transit through complex glycoproteins known as mucins. Because there were few yghJ mutant organisms on the enterocyte surface, we questioned whether these organisms have lost the ability to traverse the mucous layer in the small intestine. In the small intestine, the major luminal mucin is MUC2 (13). In sections fixed to retain luminal mucus (Fig. 2h to l), we identified many...
**YghJ Is a Conserved Mucin-Degrading Metalloprotease**

**YghJ** mutant bacteria within the MUC2⁺ luminal mucous layer (Fig. 2h and i), while WT organisms appeared both in the lumen (Fig. 2i) and at the enterocyte surface (Fig. 2k and l).

**Deletion of yghJ accelerates accumulation of mucin on the surface of ETEC.** In sections of intestine from mice challenged with WT ETEC, we identified MUC2-coated bacteria intimately associated with the mucosal surface by immunohistochemistry (Fig. 3a) or by confocal microscopy where organisms appeared labeled with both MUC2 and anti-O78 (Fig. 3b). Similarly, for both the H10407 strain and the yghJ mutant, luminal bacteria could be identified where MUC2 appeared in close association with the surfaces of organisms (Fig. 3c). In intestinal sections where efforts were made to preserve luminal mucin, we observed both wild-type and yghJ mutant bacteria (Fig. 3d) in plumes of MUC2 deposited over goblet cells. Because the yghJ mutant appeared to have limited access to the mucosal surface, we questioned whether the kinetics of ETEC association with MUC2 might differ. Following short incubation (1 h) with MUC2-containing conditioned medium, the yghJ mutant was more frequently coated with MUC2 relative to the wild-type ETEC strain (Fig. 3e). Collectively, these data suggest that ETEC colonization of the small intestine relates in
part to its interactions with intestinal mucins and that YghJ modulates these interactions.

**YghJ specifically binds and degrades intestinal mucins.** Comparison of the predicted YghJ protein sequence to known proteins demonstrated several potential functional domains or motifs (Fig. 4a) including a N-terminal signal peptide, followed by a putative lipoprotein (L-X-G-C) motif, a domain of unknown function found in *Proteobacteria* (DUF4092) located at amino acid residues 422 to 591 of YghJ, and finally an enhancin/M60-like peptidase domain (pfam13402) at residues 1090 to 1386. Included within the predicted peptidase domain is a putative HEXXH metallopeptidase motif at positions 1308 to 1312. Enhancin (35) and other members of this family bind to and degrade mucins or mucin-like glycoproteins; therefore, we examined the ability of YghJ to degrade mucins. YghJ bound to purified MUC2 (Fig. 4b), and YghJ degraded this intestinal mucin in a dose-dependent fashion (Fig. 4c). As predicted by the putative metalloprotease motif within the peptidase domain, this activity was at least partially inhibited by EDTA. Similarly, we found that YghJ degradation of MUC2 was affected by mutating the canonical metalloprotease motif. Further comparisons (17) suggested that a 22-amino-acid region extending from H1308 to N1329 contained a potential peptidase domain, this activity was at least partially inhibited by EDTA. Further, we demonstrated that mutating the predicted HEXXH motif partially prevented mucin degradation. To further examine activity of YghJ, we studied LS174T cells, which make abundant MUC2 (20). Treatment of cells with rYghJ significantly reduced the amount of extracellular MUC2 (Fig. 4e) relative to mock-treated controls (Fig. 4f). YghJ also appeared to interact with the predominant cell-bound mucin in the small intestine, MUC3 (Fig. 4g). In addition, YghJ degraded MUC3 on the surfaces of intestinal epithelial cells in vitro (Fig. 4h), and degradation at least partly depended on an intact HEXXH motif. Similarly, chelation of metal from the recombinant protein by dialysis against phenanthroline abolished mucinase activity, while supplementation of divalent cations restored activity to the chelated protein (Fig. 4i). Together, these data suggested that YghJ is a member of a family of metalloproteases that degrade mucins.

In contrast, YghJ was inactive against the mucin-like CD43 molecule expressed by Jurkat cells (Fig. 5a), bovine submaxillary mucin, gelatin, or IgG (Fig. 5b). Collectively, these data suggest that YghJ has specific activity for the major mucins in the vertebrate lumen and on the surfaces of cells in the small intestine.

**Conservation of YghJ features in peptides from *E. coli* and *V. cholerae*.** Interestingly, we found that YghJ and genes encoding the downstream T2SS were highly conserved in ETEC and commensal strains that have been sequenced (see Table S1 in the supplemental material), as well as more recently sequenced O104:H4 Shiga toxin-producing enteroaggregative *E. coli* (36) (see Fig. S1a and S1b in the supplemental material). In contrast to commensal strains however, both the ETEC strains and the O104 strains secreted significant amounts of YghJ (Fig. S1c). The YghJ peptide is currently annotated as a homologue of the *Vibrio cholerae* protein AcfD. Alignments of YghJ and AcfD from *Vibrio cholerae* classical 6th pandemic and El Tor 7th pandemic strains demonstrated extensive homology (Fig. S1a and S1b); multiple common features include the putative lipoprotein (LXGC) motif at their amino termini, the domain of unknown function, and the M60-like peptidase domain where the metalloprotease motif sequence HEVGH was completely conserved (Fig. 6).

**YghJ is required for efficient toxin delivery to intestinal epithelia.** Because earlier studies showed that direct interaction with epithelial cells is required for efficient delivery of heat-labile toxin by ETEC (11), we postulated that degradation of mucins would promote access of toxin to surface receptors. Accordingly, we found that treatment of epithelial cells with YghJ significantly enhanced binding of labeled cholera toxin to the epithelial surface (Fig. 7). Likewise, we reasoned that degradation of mucin in the intestinal lumen would permit direct access of the bacteria to enterocytes and enhance LT-stimulated cAMP activation in target epithelial cells. Indeed, we found substantial increases in cAMP content of small intestinal epithelial cells following infection with wild-type ETEC relative to those infected with the YghJ mutant or unchallenged (PBS-challenged) control mice (Fig. 8).

As MUC2 forms a critical barrier that limits access of both pathogens and commensal organisms to the epithelial surface of the intestine (13), it has been suggested that MUC2 contributes to elimination of pathogens loosely associated with tissue, as they become trapped in luminal mucin that is removed by peristaltic flow (12). Therefore, we reasoned that in the absence of MUC2 mucinase activity provided by YghJ, mutant bacteria would be more rapidly shed in stools. However, we did not observe consistent differences in fecal shedding fol-
lowing oral challenge with wild-type or yghJ mutant bacteria (data not shown), perhaps suggesting that YghJ plays a more complex role than simply degrading luminal gel-forming mucins or that it shares this ability with other enzymes.

Collectively, however, these studies support the concept that YghJ contributes significantly to the pathogenesis of ETEC, in part by degrading intestinal mucin, thereby permitting these organisms to overcome this important host defense mechanism. By degrading mucin, these organisms gain direct access to epithelial cells required for efficient delivery of their toxin payload.

**FIG 6** Alignment of sequences surrounding the putative metalloprotease motifs (shown in bold type) of YghJ from ETEC and similar proteins from other enteric organisms. Individual strain designations are shown to the right of the sequences. These strains include Shiga toxin-producing *E. coli* serotype O104:H4 and commensal *E. coli* strains HS, SE-11, and Nissle 1917. AcfD proteins from *V. cholerae* O1 strains include strain 2010 EL-1786 (El Tor biotype, 2010 Haiti isolate), CP1030 (3) (Mexico), N16961 (prototypical 7th pandemic El Tor biotype), O395 classical O1 serotype (prototypical 6th pandemic, Ogawa biotype). (b) YghJ is secreted by ETEC and *E. coli* O104 isolates, as shown by the immunoblot of TCA precipitates. The small black arrow at the top indicates the migration of YghJ. The positions of molecular mass markers (in kilodaltons) are shown to the right of the gel.

**FIG 7** YghJ enhances toxin access to enterocytes. (a) Quantitative immunofluorescence data demonstrating binding of fluorescently labeled cholera toxin B-subunit (AF488-CTB) obtained following treatment of Caco-2 cells with rYghJ compared to mock-treated (ø) cells. (b) AF488-CTB binding to LS174T cells is enhanced following rYghJ treatment. *P* < 0.0001 by Mann-Whitney nonparametric comparison of treated and untreated cell populations. The fluorescence data are normalized to the number of cell nuclei present in each field. (c and d) Images of CTB binding to LS174T cells are shown in panels c (untreated) and d (YghJ treated). Figures represent merged images of membrane (CellMask [red]), and Alexa Fluor 488-conjugated CTB-green. Membrane images were deconvolved in ImageJ, and brightness and contrast were adjusted for clarity, while AF-CTB images were not enhanced following acquisition.
DISCUSSION

Fundamentally, the ETEC pathovar is defined by the ability to produce and effectively deliver heat-labile toxin (LT) and/or heat-stable toxin (ST) enterotoxins to epithelial receptors where they then cause net fluid secretion and diarrhea (1). Most pathogenic *Escherichia coli*, including ETEC, have relatively few pathovar-specific genes (30). Consequently, it has been suggested that little more than acquisition of genes encoding the known toxins LT and ST, which are invariably carried on plasmids, may be sufficient for *E. coli* to effectively deliver these toxins to enterocytes (37). Similarly, it has been suggested that commensal *E. coli* may act as “genetic sinks” for pathogen evolution (30). The results of the present studies support these hypotheses.

By assimilating the *yghJ* gene and downstream elements encoding the type II secretion system (T2SS) from commensal strains, ETEC strains have ensured both the secretion of LT via the T2SS and its ultimate delivery to epithelial receptors through the mucinase activity of a second T2SS effector, YghJ. Interestingly, while commensal strains produce and secrete small amounts of YghJ, only ETEC exported this protein in abundance. Therefore, ETEC might gain competitive access to enterocytes by optimizing export of this mucin-degrading protein.

FIG 8 YghJ leads to enhanced cAMP activation in target intestinal epithelial cells. (a to l) Confocal immunofluorescence images of cAMP produced in small intestinal epithelial cells of mice challenged with wild-type (wt) ETEC H10407 (a to d), the *yghJ* mutant (e to h), or mock-infected, PBS-challenged control mice (i to l). (m) Quantification of cAMP fluorescence per epithelial cell. The dotted horizontal lines and the solid horizontal line represent geometric mean levels. The values for the wt and *yghJ* groups were statistically significant by Mann-Whitney (two-tailed) nonparametric comparison (*P < 0.02*).
YghJ belongs to a large and diverse family of eukaryotic and prokaryotic proteins containing putative metalloprotease domains (38). Interestingly, enhacin, the prototype molecule of the family of proteases most closely related to YghJ, was isolated from an insect virus and targets insect intestinal mucins (35, 39). It bears a canonical HEXXH metalloprotease motif within a domain (M60-like pfam13402) that is strongly associated with pathogens and commensal organisms that colonize mucosal surfaces (40).

The significant homology between YghJ and V. cholerae AcfD (34) is worthy of comment. AcfD has antibacterial activity (33) and is required for efficient intestinal colonization of Vibrio cholerae (34). Given the presence of an enhacin-like protease domain, it has been suggested that AcfD is a mucinase (40). To our knowledge, this has not been tested experimentally. AcfD, along with two other lipoproteins encoded by V. cholerae, TcpC, and ToxR-activated gene A (TagA), are regulated by the ToxR virulence regulon (33). Interestingly, TagA (23), encoded on the same V. cholerae pathogenicity island (VPI) that encodes AcfD (41), also is a secreted mucinase. Notably, the hemagglutinin protease of V. cholerae is also a mucinase that is secreted via the T2SS (42, 43), responsible for secretion of cholera toxin (CT). Therefore, V. cholerae appears to be equipped with multiple enzymes with the ability to degrade intestinal mucins, and similar to ETEC, it uses the T2SS to export both an enterotoxin and one or more mucinases that facilitate the delivery of toxin.

The identification of YghJ homologues in a variety of enteric pathogens with known mucinases might suggest that multiple mucin-degrading enzymes could contribute cooperatively to virulence. A variety of different diarrheagenic E. coli produce mucinases (44–46), and the recent O104:H4 outbreak strain, also carries the gene that encodes Pic, an established mucinase shared by enteropathogenic E. coli and Shigella flexneri (44, 47, 48). Interestingly, mucinase activity of Pic and other molecules was established initially with readily available bovine submaxillary mucin (44). However, YghJ had no demonstrable activity against this material, suggesting structural and functional differences in mucinases. Finding other mucinases with different substrate specificities in these pathotypes raises the possibility that other molecules in addition to YghJ that degrade mucin exist in ETEC.

This concept is supported by our accompanying paper (60), which demonstrates that many ETEC strains which secrete the YghJ metalloprotease also secrete EatA, a plasmid-encoded serine protease (7) with MUC2-degrading enzymatic activity.

These enzymes are part of a dynamic complex between ETEC and the mucosa. Interestingly, elevations in intracellular cAMP have been associated with commensurate increases in mucin secretion by enterocytes (49), suggesting that LT, which exerts its toxic effect by stimulating production of this cyclic nucleotide, may itself be a mucin secretagogue. In addition, a wide variety of microbial products or pathogen-associated molecular patterns stimulate production, release, or altered glycosylation of mucins (50). Therefore, it is not surprising that some enteric pathogens make multiple enzymes to subvert this dynamic barrier.

Both intestinal commensal organisms and enteric pathogens must interact with mucins to thrive in their intestinal niche. E. coli (51) and other enteric pathogens such as Yersinia enterocolitica (52) can bind to intestinal mucus and isolated mucus-derived proteins (53), and this may be mediated in part by lipopolysaccharide (LPS) on the surfaces of the organisms. The present studies suggest that ETEC bacteria interact specifically with MUC2, the major intestinal mucin, and that MUC2 appears to colocalize with oligosaccharide of LPS on ETEC. The apparent coating of organisms with MUC2 raises questions regarding the role it could play in modulating both innate and adaptive immune responses to these organisms. YghJ and other mucin-degrading enzymes may allow ETEC and other pathogens to exploit these interactions.

As our understanding of ETEC pathogenesis evolves, new approaches to vaccine development emerge (5, 54, 55). Likewise, current information regarding the nature of E. coli commensalism in the intestine is inadequate, illustrated by the very limited number of “commensal” genomes presently available. Given the apparent paucity of pathotype-specific vaccine targets, it will be important to determine whether highly conserved antigens such as YghJ could be effectively targeted as vaccine candidates.

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