A Putative Sugar-Binding Transcriptional Regulator in a Novel Gene Locus in *Enterococcus faecalis* Contributes to Production of Biofilm and Prolonged Bacteremia in Mice

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A biofilm-negative transposon mutant was created from an *Enterococcus faecalis* strain that produces a lot of biofilm. The transposon had been inserted in the second gene of a locus consisting of 4 open-reading frames, designated *bop* (biofilm on plastic surfaces). A nonpolar deletion of this gene and of parts of the 2 flanking genes was created; production of biofilm by this deletion mutant was significantly enhanced, compared with that by the wild-type strain. Expression of a downstream gene was significantly lower in the transposon mutant than in the wild-type strain and the biofilm-enhanced deletion mutant. Transformation of this gene into the transposon mutant partially restored production of biofilm. Mice challenged by intravenous injection with the biofilm-negative mutant strain showed significantly reduced numbers of colony-forming units in the blood, compared with mice challenged with the biofilm-enhanced deletion mutant and the wild-type. These results indicate that *bop* is involved in production of biofilm and probably regulates expression of biofilm in the *E. faecalis* strain tested.

Enterococci are one of the leading causes of infections in hospitalized patients and the third-most-common cause of nosocomial bloodstream infections [1]. Because of their intrinsic resistance to many clinically available antibiotics, these pathogens are associated with significant morbidity and mortality, especially among immunocompromised patients [2]. Production of biofilm is recognized as a virulence factor in many pathogens [3], and several authors have described the ability of enterococci to produce biofilm [4–8].

Native-valve endocarditis is a well documented biofilm process, and biofilms formed on heart valves are described by the medical community as vegetations [9]. Biofilms also play important roles in enterococcal infections of dental root canals [10], in the obstruction or blocking of urethral catheters and ureteral stents [11, 12], and in ocular infections [13].

Relatively little is known about the molecular mechanisms that control production and maintenance of biofilm in enterococci [3]. Baldassarri et al. [5] noted that production of biofilm by enterococci is influenced by either the presence of additional carbohydrates or the depletion of iron in growth media. Toledo-Arana et al. [4] have shown that the gene encoding enterococcal surface protein (Esp), *esp*, is involved in the primary attachment of enterococci to abiotic surfaces. However, their finding that the inactivation of *esp* has no effect on the production of biofilm by the *E. faecalis* strain analyzed that produced the most biofilm indi-
cates that additional mechanisms might be involved. The present study was performed to gain a better understanding of the molecular mechanisms involved in the establishment of enterococcal biofilms and to clarify their role in pathogenicity.

MATERIALS AND METHODS

Bacterial strains, plasmids, and media. The bacterial strains and plasmids used in the present study are shown in table 1. Enterococci were grown without agitation at 37°C in Todd-Hewitt broth (THB; Becton Dickinson) or tryptic soy broth (TSB; Becton Dickinson), with the addition of 1% glucose as indicated (THBG or TSBG, respectively). Escherichia coli strains DH5α and TOP 10 were cultured aerobically in Luria-Bertani broth on a rotor rack at 37°C. Erythromycin (10 μg/mL) was added for E. faecalis, kanamycin was added for enterococci (2000 μg/mL) and E. coli (50 μg/mL), and spectinomycin was added for enterococci (500 μg/mL) and E. coli (250 μg/mL) (all from Sigma Chemical).

Biofilm plate assay. Enterococci were tested for production of biofilm according to the protocol described by Baldassarri et al. [5]. In brief, bacteria were grown in TSBG overnight at 37°C. Polystyrene 96-well tissue-culture plates (Costar) were filled with 180 μL of fresh TSBG, and 20 μL of the culture grown overnight was added to each well. The plates were incubated for either 8 or 18 h at 37°C and read in an ELISA reader (BIO-TEK Instruments) at an optical density at 595 nm, to assure homogeneous growth in all wells. The culture medium was discarded, and the wells were washed carefully 3 times with 200 μL of PBS without disturbing the biofilm on the bottom of the wells. The plates were dried for 1 h at 60°C and were stained with 2% Hucker’s crystal violet for 2 min. Excess stain was removed by rinsing the plates under tap water, and plates were dried for 10 min at 60°C. The optical density at 595 nm was determined in an ELISA reader. Each assay was performed at least in triplicate and repeated at least twice. The optical density values were analyzed by analysis of variance (ANOVA) with Newman-Keuls multiple comparisons test. Bartlett’s test for equal variances was done to ensure that variances between groups did not differ significantly (PRISM software, version 3; GraphPad).

DNA manipulations. Chromosomal DNA from enterococci was prepared by use of the Qiagen DNeasy Tissue Kit, according to the manufacturer’s instructions. Plasmid DNA was prepared from enterococci and E. coli by use of the Wizard Plus Mini or Midipreps kit (Promega). DNA was purified from agarose gels and from polymerase chain reactions (PCRs) by use of the QIAquick Gel Extraction Kit or the PCR Purification Kit (Qiagen), according to the manufacturer’s instructions. Restriction enzymes and modifying enzymes were obtained from Invitrogen or New England Biolabs. Custom primers were ordered from Invitrogen. Electrocompetent enterococci were prepared according to the method of Fiedler and Wirth [14], and electroporation was performed in a Bio-Rad Gene Pulser II by use of the parameters given by Fiedler and Wirth [14]. Southern hybridization was performed by use of the ECL direct nucleic acid labeling and detection system (Amersham). All other methods (DNA ligations, electrophoresis, and transformation of competent E. coli) were performed by use of standard techniques [15].

Transposon mutagenesis. Plasmid pTV1-OK carrying transposon Tn917 was used for transposon mutagenesis [16]. The plasmid was electroporated into E. faecalis type 9 [17], and the bacteria were grown with kanamycin and erythromycin at 30°C to maintain the plasmid. After a temperature shift to the nonpermissive temperature (42°C), the plasmid was cured, and the transposon was forced to integrate into the chromosomal DNA. Bacteria were replica-plated onto erythromycin-containing Todd-Hewitt agar (THA) plates with or without kanamycin.

<table>
<thead>
<tr>
<th>Table 1. Enterococcus faecalis strains and plasmids.</th>
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<tbody>
<tr>
<td>Strain or plasmid</td>
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<tr>
<td>-------------------</td>
</tr>
<tr>
<td>E. faecalis type 9</td>
</tr>
<tr>
<td>E. faecalis 12030</td>
</tr>
<tr>
<td>E. faecalis 10D5</td>
</tr>
<tr>
<td>E. faecalis 10D5-pEU327</td>
</tr>
<tr>
<td>E. faecalis 10D5-pSBR</td>
</tr>
<tr>
<td>E. faecalis T9-TDM</td>
</tr>
<tr>
<td>Escherichia coli DH5α and TOP 10</td>
</tr>
<tr>
<td>Staphylococcus aureus ATCC 35566</td>
</tr>
<tr>
<td>Plasmid</td>
</tr>
<tr>
<td>pTV1-OK</td>
</tr>
<tr>
<td>pTEX4577</td>
</tr>
<tr>
<td>pEU327</td>
</tr>
<tr>
<td>pCRII-TOPO</td>
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<tr>
<td>pTDM</td>
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<td>pSBR</td>
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NOTE. ORFs, open-reading frames.
Only erythromycin-resistant colonies that had lost kanamycin resistance were processed. Approximately 1500 colonies were analyzed in a biofilm plate assay, as described above. The presence of a single transposon insertion was verified by Southern hybridization, using Tn917 as a probe, in 6 mutants with significantly reduced production of biofilm. One mutant, designated E. faecalis 10D5, was chosen for further analysis.

The gene interrupted by the transposon insertion was identified by use of a modified single-primer PCR protocol [18]. Primer 1 (table 2) was used, and the PCR product was sequenced by use of primer 2. A homology search was performed in the National Center for Biotechnology Information database and the TIGR database (available at: http://www.ncbi.nlm.nih.gov/BLAST/) and by automated sequencing of the PCR product. Primer 1 (table 2) was used, and the PCR product was sequenced by use of primer 2. A homology search was performed in the National Center for Biotechnology Information database and the TIGR database (available at: http://www.ncbi.nlm.nih.gov/BLAST/) and by automated sequencing of the PCR product.

**Construction of a nonpolar deletion mutant.** A nonpolar deletion of the bopB gene and parts of the 2 neighboring genes, bopA and bopC, was created by use of the method of Qin et al. [19, 20]. Primers 3 and 4 were used to amplify a 623-bp fragment in the bopA gene, and primers 5 and 6 yielded a 622-bp fragment in the bopC gene (figure 1). Primers 4 and 6 contain a 21-bp complementary sequence (underlined in table 2). Overlap-extension PCR was used to create a PCR product containing a 21-bp complementary sequence (underlined in table 2). The resulting PCR product was digested with HindIII and ligated into pEU327, which had been digested with HindIII and dephosphorylated. The chimeric plasmid pSBR was transformed into E. coli DH5α, and the correct insert and orientation were confirmed by automated sequencing. pEU327 (without insert) and pSBR were transformed into E. faecalis 10D5 by electroporation, and transformants were selected on THA plates containing spectinomycin. The presence of the plasmid in E. faecalis was confirmed by plasmid preparations and subsequent restriction digestion.

**Preparation of RNA.** Bacteria were inoculated from a fresh plate in 10 mL of TSBG and incubated for 12 h at 37°C (E. faecalis type 9, E. faecalis 10D5, and E. faecalis T9-TDM were

**Table 2.** Oligonucleotide primers used to sequence Enterococcus faecalis strains in the present study.

<table>
<thead>
<tr>
<th>Primer</th>
<th>Description</th>
<th>Sequence, 5′→3′</th>
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<tbody>
<tr>
<td>1</td>
<td>SP-PCR primer Tn917 left</td>
<td>AGAGAGATCACGTCGTAAG</td>
</tr>
<tr>
<td>2</td>
<td>SP-PCR sequencing primer</td>
<td>AATGTACAAATATACAGCGAA</td>
</tr>
<tr>
<td>3</td>
<td>bopA left</td>
<td>CGGGGAAATTTTGAAGAACA</td>
</tr>
<tr>
<td>4</td>
<td>bopA right</td>
<td>ACTAGCGCGCCGGCTTGCAGCCAGCAAGGCCTTGTGTAT</td>
</tr>
<tr>
<td>5</td>
<td>bopC right</td>
<td>CCCCCCACTGAGATGATGAAAC</td>
</tr>
<tr>
<td>6</td>
<td>bopC left</td>
<td>GGAGCAAGGCCGCCGCTAGTGAGCCCTTTGAAGAAGGA</td>
</tr>
<tr>
<td>7</td>
<td>bopA left-2</td>
<td>TCCAAATGACCTTTGGAAA</td>
</tr>
<tr>
<td>8</td>
<td>bopC right-2</td>
<td>CCCTTTGTCAGTTCTT</td>
</tr>
<tr>
<td>9</td>
<td>bopD HindIII left</td>
<td>CCCAAACGTTATGGCAATTACAAGTAAAAGATG</td>
</tr>
<tr>
<td>10</td>
<td>bopD HindIII right</td>
<td>CCCAAAGCTTTTATAGAAAATAATAGGCAAATCTGTTT</td>
</tr>
<tr>
<td>11</td>
<td>bopD left</td>
<td>ACGGCAGCAATTGGTGAAAC</td>
</tr>
<tr>
<td>12</td>
<td>recA left</td>
<td>GCAACGAAATGGTGGAAAC</td>
</tr>
<tr>
<td>13</td>
<td>bopD right</td>
<td>GGCCTCTCGTGTACGGCTTC</td>
</tr>
<tr>
<td>14</td>
<td>recA right</td>
<td>AAGGCATCGGCAATCTAAG</td>
</tr>
<tr>
<td>15</td>
<td>bopD right-2</td>
<td>TCACGGCTATTTATTGAGGA</td>
</tr>
</tbody>
</table>

**NOTE.** Underlined nucleotides in primers 4 and 6 represent the 21-bp overlap used in the overlap-extension single-primer (SP) polymerase chain reaction (PCR). Underlined nucleotides in primers 9 and 10 represent the HindIII site introduced into the bopD gene.
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Figure 1. Schematic representation of the gene locus in *Enterococcus faecalis* involved in production of biofilm. All 4 genes are expressed on a single mRNA transcript. The insertion of the transposon in *E. faecalis* 10D5 is indicated by a triangle, and the gene deletion of *E. faecalis* T9-TDM is shown by the bracket. Arrows, primers; nos. correspond to the nos. used in table 2. Primers 1, 2, 12, and 14 are not shown.

grown in TSBG without antibiotics; *E. faecalis* 10D5-pEU and *E. faecalis* 10D5-pSBR were grown with 500 μg/mL spectinomycin). A volume of 400 μL of this culture was used to inoculate 20 mL of TSBG with or without the above-mentioned antibiotics and was incubated for 3 h at 37°C without aeration. Cells (5 × 10⁸; calculated after measurement of optical density at 650 nm) were mixed with a 2× volume of RNAprotect Bacteria reagent (Qiagen), and RNA was isolated by use of the RNasey Midi Kit (Qiagen), according to the manufacturer’s recommendations, which included digestion with DNase I on the spin column. The concentration of RNA was calculated after measurement of optical density at 260 nm, and equal amounts were used as starting material in subsequent experiments. To remove any remaining DNA contaminations, a second DNase I treatment (Invitrogen) of each RNA sample was performed according to the manufacturer’s instructions. The enzyme was inactivated at 65°C in the presence of EDTA. To verify the absence of residual genomic DNA in each sample, the RNA was amplified in a PCR with *Taq* DNA polymerase and the respective primers in the presence and absence of SuperScript II Reverse Transcriptase (Invitrogen). RNA samples were used for cDNA synthesis by use of the iScript cDNA synthesis kit (Biorad), according to the manufacturer’s recommendations.

**Quantitative real-time PCR.** Quantitative real-time PCR was performed in an iCycler iQ (Bio-Rad) by use of the QuantiTect SYBR green PCR kit (Qiagen), according to the manufacturer’s recommendations. The *bopD* transcripts were amplified with the primers 11 and 13 (table 2). The constitutively expressed housekeeping gene *recA* was amplified with the primers 12 and 14 (table 2) as an internal control to normalize RNA concentrations. To monitor the specificity of the reactions, final PCR products were analyzed by melting curves showing that all specific primers resulted in only 1 specific product. The standard curves of dilutions of starting material, amplification efficiencies, and expression ratios between *bopD* and *recA* were calculated by use of Microsoft Excel. The values used for comparison of gene expression between the different strains were the numbers of PCR cycles required to reach the threshold cycle (*C*ₚ), which was set at 10× the SD of the fluorescence of the first 10 cycles. The amount of *bopD* transcript relative to the control gene *recA* was calculated by use of the standard-curve method, as described elsewhere [24, 25], and was expressed as the percentage of the amount of transcripts of the wild-type *E. faecalis* type 9.

**Reverse-transcription (RT) PCR.** RT-PCR was performed with the RNA samples, to detect cotranscription of all 4 *bop* genes by use of the SuperScript One-Step RT-PCR with Platinum *Taq* Kit (Invitrogen), according to the manufacturer’s recommendations, by use of the primers 7 and 15 (table 2).

**Scanning electron microscopy.** Bacteria were grown in TSB or TSBG in 24-well plates containing polystyrene segments. After a 12-h incubation at 37°C, polystyrene segments were rinsed twice in PBS and once in 0.1 mol/L cacodylate buffer and fixed as described elsewhere [5], to preserve extracellular polysaccharide. In brief, cells were first fixed for 20 min at room temperature with 0.1 mol/L cacodylate-buffered 2.5% glutaraldehyde containing 0.075% (wt/vol) ruthenium red (Glut-RR; Merck) and 75 mmol/L lysine. They were then fixed with Glut-RR without lysine for 2 h and finally fixed with 1% OsO₄, plus ruthenium red for an additional 1 h. Samples were
dehydrated by exposure to a graded series of ethanol, critical-point dried, gold sputtered, and examined with a Cambridge SE360 scanning electron microscope.

**Catheter adherence assay.** The ability of bacteria to adhere to polyethylene catheters was tested by use of the method described by Muller et al. [26] with modifications. In brief, bacteria were inoculated in THB and incubated at 37°C until an OD_{600} of 0.4 was reached and diluted to ∼4 × 10^7 cfu/mL. Sections of polyethylene catheter tubing (Intramedic PE tubing, diameter 0.61 mm; Becton Dickinson) were gas sterilized. Sections of 20 mm were dipped into the broth with the bacterial inoculum for 30 min at 37°C. The catheter pieces were subsequently washed 3 times for 15 seconds in PBS and vigorously rolled over tryptic soy agar (TSA) plates. The plates were incubated at 37°C overnight, and colonies were counted.

**Mouse sepsis model.** The animal studies described in the present study were reviewed and approved by the Institutional Animal Care and Use Committee at Harvard University. Female BALB/c mice were inoculated intravenously in the tail vein with 5 × 10^8 cfu of either wild-type *E. faecalis* type 9, biofilm-negative transposon mutant *E. faecalis* 10D5, or the biofilm-enhanced triple-gene deletion mutant *E. faecalis* T9-TDM. Bacteria were grown in THB overnight, centrifuged, and resuspended in sterile saline. Aliquots were shock-frozen and stored at −80°C. The concentration of the stock was verified by dilutions and viable counts on TSA, and these numbers were used to calculate the appropriate dilutions for the desired inoculum. For the experiments, aliquots were thawed, diluted in sterile saline, and injected into the tail vein; the actual diluted inoculum was once more verified by viable counts. After 3 days, the mice were killed, blood was obtained by cardiac puncture, and 100 μL was plated on TSA.

**Statistical analysis.** Statistical analysis was done by ANOVA with Newman-Keuls multiple comparison tests, and Bartlett’s test for equal variances was used to assure that variances did not differ significantly between groups (PRISM, version 3; GraphPad Software).

## RESULTS

Clinical *E. faecalis* strains and laboratory isolates were tested for production of biofilm [27]. One strain, *E. faecalis* type 9 [17], showed a very high degree of production of biofilm (OD_{595} of >2.5) after an 18-h incubation period. This value corresponded to the results obtained with a strain of *Staphylococcus aureus* (ATCC 35556) that produces a lot of biofilm [28].

Insertional inactivation of the *bopD* gene was unsuccessful in *E. faecalis* type 9 and in a different biofilm-producing *E. faecalis* strain, *E. faecalis* 12030 [29], which possesses the *bopD* gene, suggesting that the *bopD* gene is essential for production of biofilm under the growth conditions used. Using the same conditions, we were able to create deletion mutants in 2 different genes.

To test the hypothesis that the biofilm-negative phenotype
Figure 2. Scanning electron micrograph of wild-type *Enterococcus faecalis* type 9 and the mutant strain *E. faecalis* 10D5. (A) The wild-type strain shows a multilayered growth pattern, whereas the biofilm-negative mutant grows mostly in a single layer (B).
of the transposon mutant 10D5 was due to a polar effect of the transposon insertion on a gene downstream of the bopB gene, which showed similar levels for all strains (C, range, 16.43–17.1), using the standard-curve method [24, 25]. The calculated amounts of transcripts of the sugar-binding transcriptional regulator bopD showed that expression of bopD mRNA in the transposon mutant and the transposon mutant with pEU327 was significantly reduced, to 8.5% and 11.2%, respectively, compared with the expression in E. faecalis type 9, which was assumed to be 100%. The amount of bopD mRNA transcripts expressed by the biofilm-enhanced deletion mutant E. faecalis T9-TDM was 161%; the transposon mutant reconstituted with the bopD gene showed an expression of 237.7%, compared with that of the wild-type strain (table 3).

We studied the role of biofilm as a pathogenicity factor in a mouse bacteremia model. BALB/c mice were inoculated intravenously in the tail vein with cfu of either the wild-type strain ( ), the biofilm-enhanced triple-gene deletion mutant E. faecalis type strain ( ), the biofilm-enhanced triple-gene deletion mutant E. faecalis type 9 to adhere to plastic catheters was compared with that of the biofilm-negative transposon mutant. After a 30-min incubation period, no difference in adherence could be observed between the wild-type and the transposon mutant (P = .001, Mann-Whitney U test; figure 4).

We used quantitative analysis of mRNA transcripts by real-time PCR to investigate whether the decrease in biofilm production observed in the transposon mutant 10D5 was indeed caused by a polar effect of the transposon on the transcription of the downstream bopD gene. Isolation of total RNA was performed under 2 different conditions: the wild-type, the transposon mutant, and the triple-deletion mutant were grown without antibiotics; and the transposon mutant supplemented with the expression vector pEU327—–with and without the insertion of the bopD gene—–was grown in the presence of the selective antibiotic spectinomycin. The samples were DNase treated, reverse transcribed, and amplified with primers inside the bopD gene (primers 11 and 13; table 2 and figure 1) using quantitative real-time PCR. The levels of expression of bopD were normalized to the expression of the constitutively expressed housekeeping gene recA, which showed similar levels for all strains (C, range, 16.43–17.1), using the standard-curve method [24, 25]. The calculated amounts of transcripts of the sugar-binding transcriptional regulator bopD showed that expression of bopD mRNA in the transposon mutant and the transposon mutant with pEU327 was significantly reduced, to 8.5% and 11.2%, respectively, compared with the expression in E. faecalis type 9, which was assumed to be 100%. The amount of bopD mRNA transcripts expressed by the biofilm-enhanced deletion mutant E. faecalis T9-TDM was 161%; the transposon mutant reconstituted with the bopD gene showed an expression of 237.7%, compared with that of the wild-type strain (table 3).

The ability of E. faecalis type 9 to adhere to plastic catheters was compared with that of the biofilm-negative transposon mutant. After a 30-min incubation period, no difference in adherence could be observed between the wild-type and the transposon mutant (P = .001, Mann-Whitney U test; figure 4).

We studied the role of biofilm as a pathogenicity factor in a mouse bacteremia model. BALB/c mice were inoculated intravenously in the tail vein with 5 × 10⁴ cfu of either the wild-type strain (n = 10), the biofilm-enhanced triple-gene deletion mutant E. faecalis T9-TDM (n = 8), or the biofilm-negative transposon mutant strain E. faecalis 10D5 (n = 8). In mice that received the wild-type strain E. faecalis type 9, significantly less

![Graph](https://academic.oup.com/jid/article-abstract/189/3/420/817938)
bacteria growth was seen ($P<.05$) than in mice challenged with the biofilm-enhanced triple-gene deletion mutant *E. faecalis* T9-TDM, and significantly more bacteria growth was seen ($P<.05$) than in mice challenged with the biofilm-negative transposon mutant *E. faecalis* 10D5 (figure 5).

**DISCUSSION**

Production of biofilm plays a major role in the pathogenesis of many clinically important pathogens [9]. The occurrence of biofilm in enterococcal infections has frequently been reported [10, 12, 13, 30, 31]; however, only a few studies have attempted to elucidate the underlying molecular mechanisms [4, 5].

We have described a novel gene locus, designated as *bop*, that is involved in production of biofilm. The observed phenotype in the triple-gene deletion mutant and the complementation studies indicate that the biofilm-negative phenotype of the transposon mutant is due to a polar effect on a downstream gene (i.e., *bopD*), whereas the enhanced production of biofilm in the triple-gene-deletion mutant correlates with an increased amount of *bopD* mRNA. This result may be due to the closer proximity of the ORF to the promoter and/or to an increased half-life of the mRNA transcript. Alternative explanations include the creation of a new promoter that is secondary to the deletion or the possible lack of negative feedback of 1 or all of the first 3 gene products of the transcripts. From the results of the present study, we conclude that production of biofilm may be a virulence factor in enterococci that leads to prolonged bacteremia. The ability of the strain tested to produce biofilm in vitro is correlated with its persistence in the mouse bacteremia model in vivo. A reduction or increase in production of biofilm by the 2 mutants leads to decreased or increased bacteremia, respectively. Possible mechanisms leading to increased bacterial colony counts in the blood of the biofilm-enhanced mutant are resistance to natural surfactants [32] and chemical biocides [33], resistance to phagocytes or better survival in macrophages [5, 9, 34, 35], or resistance to antibodies [9, 33].

Shankar et al. [36] described Esp, which has homology to the α-C and rib proteins in streptococci. This protein has been shown to be associated with the colonization of the urinary tract [37], and Willems et al. [38] and Baldassarri et al. [39] discovered that epidemic enterococcal isolates causing nosocomial infections carried the *esp* gene more frequently than did fecal isolates.

Toledo-Arana et al. [4] examined 200 strains of enterococci and found a high correlation between the presence of the *esp* gene and the ability of a given strain to produce a biofilm. Deletion mutants in the *esp* gene were created in several biofilm-producing *E. faecalis* strains; 2 strains lost the ability to form biofilm, whereas, in 1 strain that produce a lot of biofilm, disruption of the *esp* gene did not result in a significant decrease in production of biofilm. Toledo-Arana et al. [4] concluded that *esp* is responsible for the primary attachment of enterococci to abiotic surfaces but that additional surface adhesins were involved in this process, especially in strains that produce a lot of biofilm. Because *E. faecalis* type 9, the strain used in the present study, is an extremely potent producer of biofilm, it seems likely that different mechanisms exist for greater biofilm production, compared with the establishment of a weak-to-moderate biofilm.

Toledo-Arana et al. [4] reported that 93.5% of the biofilm-producing strains possessed and expressed the *esp* gene, whereas none of the biofilm-negative strains possessed the *esp* gene. However, we could not verify this strong association between the
production of biofilm and the presence of esp in the clinical E. faecalis isolates tested [5]. Thirty-five (44%) of 79 strains tested negative for the presence of esp by PCR, but were nevertheless able to produce a lot of biofilm (authors’ unpublished data). Although this phenomenon may be related to different methods to test production of biofilm, it may also represent different characteristics in the strain collections analyzed. Toledo-Arana et al. [4] used an assay adapted by O’Toole et al. [40] for the study of production of biofilm by Pseudomonas fluorescens. In that assay, the crystal-violet is dissolved in ethanol-acetone before optical density is measured, whereas the method used in the present study [41] uses readings of the dried microtiter plates. In the present study, the ethanol-acetone method produced less-consistent results than did the method used by Christensen et al. [41]. Because the procedure proposed by Christensen et al. [41] was developed for gram-positive bacteria (i.e., Staphylococcus epidermidis) and has been used successfully by many researchers to study the production of biofilm, we feel confident that this method is also applicable to enterococci.

Differences between the biofilm assays exist also with regard to the concentration of glucose in the medium used (0.25–0.5% used by Toledo-Arana et al. [4] vs. 1% used in the present study). No systematic comparison that may explain the conflicting results between the 2 different methods has been performed.

The development of biofilm is a multistep procedure [42], with phase 1 involving the primary attachment of planktonic microorganisms to biotic and abiotic surfaces. Toledo-Arana et al. [4] speculate that Esp is one of the mediators of primary attachment in enterococci. Phase 2 of production of biofilm is the molecule-mediated secondary attachment of microorganisms to surfaces. Adhesins, such as the polysaccharide intercellular adhesin in staphylococci [43], mediate the interaction between the microorganisms and the surface and between individual bacterial cells. This phase is characterized by the formation of microcolonies [33]. Phase 3 involves the maturation of the biofilm. The microorganisms change their metabolic state, produce different extracellular products (such as exopolysaccharides) to form a glycocalyx, and divide within the biofilm. Phase 4 is marked by the detachment of planktonic cells from the biofilm to colonize further surfaces. On the basis of findings from scanning electron microscopy studies, we hypothesize that our transposon mutant is defective in phase 2 of production of biofilm. The transposon mutant grew in a monolayer on polystyrene segments, whereas the wild-type strain and the biofilm-enhanced triple deletion mutant grew in a multilayer, with a 3-dimensional pile-up and the formation of microcolonies, which were noticeably absent in the transposon mutant. The monolayer represents the primary attachment, whereas the formation of a multilayer with microcolonies requires the machinery of the secondary attachment. Comparison of the initial attachment in a catheter adherence model [26] showed no difference in the attachment to a polyethylene catheter of the transposon mutant and the wild-type strain. We therefore assume that the secondary attachment, and not the primary attachment, is impaired in our transposon mutant. On the other hand, Toledo-Arana et al. [4] speculate that esp is involved in the initial adherence of the bacteria to abiotic surfaces. This may explain the results by Toledo-Arana et al. [4] that strains that produce a lot of biofilm were not affected in their adherence by the inactivation of esp. Another possibility might be that bopD up-regulates expression of esp and possibly other virulence factors involved in adhesion of the bacteria to surfaces. The residual production of biofilm by our transposon mutant may also be related to the intact primary attachment of the bacteria mediated by esp that is not affected by the reduction of bopD expression.

We are aware that the creation of a deletion mutant in the bopD gene would be the definitive proof that the bopD gene causes the observed phenotype in the transposon mutant. Despite numerous attempts with different suicide vectors, flanking regions, and bacterial strains (data not shown), we were unable to delete the bopD gene by targeted mutagenesis. One possible explanation is that bopD is essential in the biofilm-positive strains tested. We screened a collection of 18 unrelated E. faecalis strains by use of PCR for the presence of the bopD gene and found that all strains carried the bopD gene, supporting the hypothesis that the gene is essential (data not shown). Furthermore, this hypothesis is supported by the fact that the transposon insertion did not completely inactivate bopD and that the mutant strain still expresses a residual amount of bopD mRNA (8.5% of the wild type). Depending on the incubation period, the amount of biofilm produced by the mutant is 16%–36% of that produced by the wild-type, suggesting a close relationship between the expression of bopD and production of biofilm.

Baldassarri et al. [5] found that, of 73 strains of clinical E. faecalis isolates analyzed, 66% were strong producers of biofilm, 14% were weak producers, and 20% did not produce any biofilm. The formation of biofilm in these strains was strongly affected by the presence of additional carbohydrates in the growth medium.

The dependence of production of biofilm on the presence of specific carbohydrate sources in the growth medium has been described by a number of investigators [3–5, 9]. The attributed function (sugar-binding transcriptional regulator) of the bopD-encoded protein responsible for the biofilm-negative phenotype in the present study might explain this observation. This gene shows significant sequence homology (29% identity and 50% similarity) with the ccpA gene of E. faecalis [44], which is involved in carbohydrate metabolism. The gene also shows significant homology with the ccpA gene of Listeria innocua.
(30% identity and 55% similarity), Listeria monocytogenes (30% identity and 54% similarity), Lactococcus lactis (30% identity and 54% similarity), Bacillus subtilis (29% identity and 54% similarity), Strepotococcus pyogenes (28% identity and 51% similarity), Strepotococcus pneumoniae (29% identity and 52% similarity), and with a putative maltose operon transcriptional repressor in S. pyogenes (45% identity and 65% similarity) and S. aureus (31% identity and 53% similarity).

O’Toole et al. [45] found that a gene with a similar function to bopD (i.e., carbon catabolite regulation), the global carbon metabolism regulator crc, is part of a signal transduction pathway required for production of biofilm by Pseudomonas aeruginosa. A crc mutant created by O’Toole et al. [45] showed, in scanning electron microscopy, a morphologic pattern similar to that of our mutant, growing only as a dispersed monolayer. The phenotype of their strain was associated with a defective type IV pilus–mediated twitching motility caused by decreased pilA transcription.

Carbon catabolite repression proteins, such as CcpA, are known to regulate transcription of hundreds of promoters [46] and might therefore be involved in the regulation of different genes probably associated with production of biofilm, such as esp, aggregation substance, and others. Further studies are under way to identify proteins that are expressed under the control of the bopD gene in our prototype strain.

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