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The surface protein HvgA mediates group B streptococcus hypervirulence and meningeal tropism in neonates

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Streptococcus agalactiae (group B streptococcus; GBS) is a normal constituent of the intestinal microflora and the major cause of human neonatal meningitis. A single clone, GBS ST-17, is strongly associated with a deadly form of the infection called late-onset disease (LOD), which is characterized by meningitis in infants after the first week of life. The pathophysiology of LOD remains poorly understood, but our epidemiological and histopathological results point to an oral route of infection. Here, we identify a novel ST-17–specific surface-anchored protein that we call hypervirulent GBS adhesin (HvgA), and demonstrate that its expression is required for GBS hypervirulence. GBS strains that express HvgA adhered more efficiently to intestinal epithelial cells, choroid plexus epithelial cells, and microvascular endothelial cells that constitute the blood–brain barrier (BBB), than did strains that do not express HvgA. Heterologous expression of HvgA in nonadhesive bacteria conferred the ability to adhere to intestinal barrier and BBB-constituting cells. In orally inoculated mice, HvgA was required for intestinal colonization and translocation across the intestinal barrier and the BBB, leading to meningitis. In conclusion, HvgA is a critical virulence trait of GBS in the neonatal context and stands as a promising target for the development of novel diagnostic and antibacterial strategies.
significant cause of morbidity and mortality in nonpregnant adults, particularly those with underlying diseases and the elderly (Phares et al., 2008).

Two distinct GBS-associated clinical syndromes, referred to as early-onset disease (EOD) and late-onset disease (LOD) have been recognized in neonates in their first week of life (age 0–6 d) and after (age 7–89 d), respectively (Edwards and Baker, 2005). Although intrapartum antibiotic prophylaxis for parturient women at risk for GBS infection has markedly decreased the incidence of EOD, it did not change that of LOD (Poyart et al., 2008; CDC, 2009). Epidemiological data collected worldwide have shown that a substantial proportion of LOD and the majority of LOD are associated with capsular serotype III (Lin et al., 2006; Gherardi et al., 2007; Phares et al., 2008; Poyart et al., 2008; CDC, 2009). Strains of serotype III contain a limited number of clonal complexes, defined by multilocus sequence typing. Among them, the ST-17 sequence type is strongly associated with neonatal meningitis and was therefore designated as “the hypervirulent clone,” despite the absence of experimental data to support this assertion (Musser et al., 1989; Jones et al., 2003, 2006; Brochet et al., 2006; Lamy et al., 2006; Bohnsack et al., 2008; Poyart et al., 2008; Manning et al., 2009).

For LOD, the mode of transmission in newborns is thought to be vertical, by inhalation of GBS-contaminated amniotic or vaginal fluid during parturition, followed by bacterial translocation across the respiratory epithelium and subsequent systemic infection (Edwards and Baker, 2005). In contrast, for LOD, the mode of transmission and the infection route remain elusive, although mother-to-child transmission might also be involved. A plausible scenario would involve early intestinal colonization by GBS that would lead in the first days of life to its intraluminal intestinal multiplication, translocation across the intestinal epithelium, and access to the bloodstream. Indeed, an intestinal portal of entry for LOD is supported by several lines of evidence: (a) 60 and 40% of the neonates asymptptomatically colonized with GBS at birth remain positive for bacteria at the rectal level at 4 and 12 wk of life, respectively (Weindling et al., 1981); and (b) a longitudinal study of GBS vaginal and rectal colonization in women during and after pregnancy has revealed that carriers are usually colonized for up to 2 yr by a single clone, which is also frequently found in newborn feces for up to 1 yr (Hansen et al., 2004).

Once translocated in the bloodstream, GBS has the ability to cross the blood–brain barrier (BBB) and cause meningitis. Several virulence factors contribute to the pathogenesis of GBS meningitis in animal models, but nearly all of them are involved in the septicemia phase of the infection, but not in GBS adhesion to and crossing of the BBB (Maisey et al., 2008). One exception is Srr-1, a recently characterized surface glycoprotein that promotes adhesion to and invasion of human brain microvascular endothelial cells and contributes to BBB crossing in mice (van Sorge et al., 2009). This illustrates that more studies are needed to identify virulence factors of GBS, especially in regard to its meningeal tropism and its ability to trigger LOD.

Here, we have identified a novel ST-17–specific surface-anchored protein, which is highly prevalent in cases of LOD. We show that this protein which we have called hypervirulent GBS adhesin (HvgA) mediates GBS neonatal intestinal colonization and crossing of the intestinal and blood–brain barriers, leading to meningitis, which are key features of LOD.

RESULTS AND DISCUSSION

Epidemiological evidence that the ST-17 hypervirulent GBS clone is associated with LOD and neonatal meningitis

We first analyzed 651 GBS isolates referred to the French national reference center for streptococci between 2006 and 2009 from consecutive cases of invasive infection in neonates (meningitis, n = 138; bacteremia, n = 166) and in adults (meningitis, n = 16; bacteremia, n = 331). Serotype III accounts for 86.2% of strains isolated from cases of neonatal meningitis and 60.8% of neonatal bacteremia, but only 25.7% of bacteremia in adults (Table I). Serotype III is significantly associated with meningitis during EOD (79.3%; P < 0.0001) and LOD (88%; P < 0.0001; Table I). Moreover, the serotype III ST-17 clone is significantly associated with meningitis during EOD (79.3%; P < 0.0001) and LOD (82.6%; P < 0.0001), and with bacteremia during LOD (78.1%; P < 0.0001; Table I).

In contrast, the ST-17 clone represents <12% of isolates from adult patients with bacteremia (Table I). Together, these results obtained from a total of 651 clinical strains demonstrate that ST-17 GBS strains account for >80% of neonatal meningitis, strongly suggesting an enhanced virulence of the ST-17 clonal complex in the neonatal context. These epidemiological observations thus prompted us to search for specific virulence factors of the ST-17 clone that may account for its apparent higher pathogenicity in neonates, its close association with LOD, and its meningeal tropism.

Histopathological study of a fatal case of ST-17–associated LOD

A term female infant (gestational age, 39 wk; birth weight, 3,140 g) was born by spontaneous vaginal delivery without complication. Maternal vaginal swab at 37 wk of gestation was negative for GBS. There was no premature membrane rupture and neither skin nor rectal swab of the neonate was made at delivery. The mother and her breastfed baby were discharged on day 4. On day 14 of life, the neonate developed muscular hypotonia, poor suckling, hyperexcitability, and fever. Cerebrospinal fluid and blood cultures were positive for GBS, which was later shown to belong to serotype III and clonal complex ST-17. Breast milk was not cultivated. Despite adequate antimicrobial treatment associating amoxicillin, ceftriaxone, and gentamicin, she died 8 h later and an autopsy was performed. Cultures of stool, blood, and cerebrospinal fluid, as well as colonic and brain autopsic tissue samples, were all positive for GBS. Immunohistochemistry of paraffin-embedded gut tissue samples led to the detection of GBS associated with the intestinal tissue and inside the lamina propria (Fig. 1, a and b). GBS also heavily infected meningeal tissues, with intense inflammation indicated by the massive recruitment of polymorphonuclear cells (Fig. 1, c and d). GBS was also observed to be tightly associated with brain microvessel endothelial
cells and choroid plexus epithelial cells, which constitute the blood–brain parenchyma and blood–cerebrospinal fluid barriers, respectively (Fig. 1, e–l). These bacteriological and histopathological analyses of this fatal case of LOD are consistent with the hypothesis that LOD results from the ability of GBS ST-17 to efficiently colonize the intestine, cross the intestinal barrier, and cross the BBB.

Table I. Serotype and ST-17 distribution of 651 GBS strains isolated from neonatal and non-pregnant adult invasive infections in France between 2006 and 2009

| Type of infection | Serotype no. | ST-17 no. |
|------------------|-------------|-----------|
|                  | Ia | Ib | II | III | IV | V | Total | % |
| **Neonatal meningitis** | 12 (8.7) | 4 (2.9) | 0 | 119 (86.2) | 0 | 3 (2.1) | 138 (100) | 113 (81.9) |
| EOD (≤6 d) | 6 (20.7) | 0 | 0 | 23 (79.3) | 0 | 0 | 29 (100) | 23 (79.3) |
| LOD (≥7–89 d) | 6 (5.5) | 4 (3.7) | 0 | 96 (88.1) | 0 | 3 (2.7) | 109 (100) | 90 (82.6) |
| **Neonatal bacteremia** | 34 (20.5) | 5 (3) | 6 (3.6) | 101 (60.8) | 3 (1.8) | 17 (10.2) | 166 (100) | 89 (53.6) |
| EOD (≤6 d) | 27 (29) | 3 (3.2) | 5 (5.4) | 41 (44.1) | 2 (2.2) | 15 (16.1) | 93 (100) | 32 (34.4) |
| LOD (≥7–89 d) | 7 (9.6) | 2 (2.7) | 1 (1.4) | 60 (82.2) | 1 (1.4) | 2 (2.7) | 73 (100) | 57 (78.1) |
| **Adult bacteremia** | 71 (21.4) | 36 (10.3) | 37 (11.2) | 85 (25.7) | 17 (5.1) | 85 (25.7) | 331 (100) | 37 (11.2) |
| EOD (≤6 d) | 27 (29) | 3 (3.2) | 5 (5.4) | 41 (44.1) | 2 (2.2) | 15 (16.1) | 93 (100) | 32 (34.4) |
| LOD (≥7–89 d) | 7 (9.6) | 2 (2.7) | 1 (1.4) | 60 (82.2) | 1 (1.4) | 2 (2.7) | 73 (100) | 57 (78.1) |
| **Adult meningitis** | 71 (21.4) | 36 (10.3) | 37 (11.2) | 85 (25.7) | 17 (5.1) | 85 (25.7) | 331 (100) | 37 (11.2) |

HvgA is an ST-17–specific surface-anchored protein that is overexpressed in vivo

We first analyzed whether the ST-17 clone expresses specific surface-exposed molecules that could account for enhanced adhesive properties. The comparative analysis of GBS whole-genome sequences has pinpointed several genes encoding surface components specific to the ST-17 clone (Tettelin et al., 2005; Brochet et al., 2006). In particular, we have identified mosaic variants at a single genomic locus (Lamy et al., 2006) encoding a cell wall–anchored protein, with two main variants displaying 38% overall amino acid identity, namely Gbs2018A, which is also referred to as BibA (Santi et al., 2007), and Gbs2018C, which we have shown to be strictly specific to the “hyper-virulent” ST-17 clone (Lamy et al., 2006). These genes have conserved regulatory regions and encode proteins with conserved N- and C-terminal parts, but a distinct central core. Indeed, comparison of the nucleotide sequences of the two loci has revealed that only the 5' and 3' ends of the two genes are highly conserved, displaying >90% sequence identity, whereas their internal parts display low level (50–60%)
or no significant (<20%) sequence identity (Fig. 2 a). We thus investigated the contribution of Gbs2018C (hereafter named HvgA for hypervirulent GBS adhesin) to GBS neonatal infection using in vitro and in vivo approaches, with the hypothesis that it might be responsible for enhanced virulence capacities of the ST-17 clone. We first demonstrated, by immunoblotting using specific anti-HvgA antibodies that HvgA in GBS BM110, a prototype ST-17 strain, harbors an LPXTG motif that anchors it to the cell wall in a sortase A–dependent manner. As shown in Fig. 2 b, a band corresponding to HvgA was detected in cell wall extracts of the WT strain, but not of an isogenic \( \Delta \text{srtA} \) mutant strain. Analysis of the corresponding culture supernatant demonstrated that this protein is not secreted in the medium by the WT strain (unpublished data). Moreover, after incubation in SDS at high temperature (10 min at 100°C), HvgA is massively released in the culture supernatant of the \( \Delta \text{srtA} \) mutant, but not of the WT GBS BM110. Collectively, these results demonstrate that HvgA is a protein anchored to the cell wall by sortase A. Flow cytometry and immunofluorescence microscopy confirmed surface expression of HvgA in GBS WT ST-17 (Fig. 2, c and d). To investigate HvgA expression in vivo, quantitative RT–PCR (qRT–PCR) on mRNAs extracted from cecal, blood, and brain samples of orally or i.v. infected mice (see Materials and methods) were performed and demonstrated that \( hvgA \) in vivo expression, relative to that of \( rpoB \), is two- to fourfold higher than in vitro (Fig. 2 e). Moreover, in total
Whereas both strains adhere similarly to A549 pulmonary epithelial cells, the ST-17 strain adheres significantly more efficiently to the intestinal epithelial Caco-2 cell line, the BBB-constituting cells hCMEC/D3, brain primary microvessel endothelial cells (MVECs), and choroid plexus epithelial cells (CPECs; Fig. 3a).

The significance of these results was broadened by the study of 20 randomly picked invasive GBS neonatal isolates of ST-17 type (n = 10) or non–ST-17 type (n = 10; strain characteristics described in Table S2). As seen for the prototype strains, comparative cell binding assays showed that ST-17 isolates adhere significantly more to Caco-2 and hCMEC/D3 cells than non–ST-17 isolates, but not to A549 cells (Fig. 3b), thereby suggesting that bacteria expressing HvgA could display a specific enhanced capacity to adhere to cells of the intestinal and blood–brain barriers. To further investigate whether HvgA is the adhesin involved in the ST-17 interaction with intestinal and blood–brain barriers constituting cells, a GBS BM110ΔhvgA deletion mutant was constructed (Fig. 1a and Tables S1 and S3).

As expected, HvgA was not expressed in this mutant and not detected at the bacterial cell surface (Fig. 2, b–d). The growth characteristics and the viability of the mutant in various culture media (Todd-Hewitt, RPMI, or DME complemented with 10% human serum), in total human blood, as well as the morphological characteristics and the aggregative properties and BibA, respectively (Table S1). Whereas both strains adhere similarly to A549 pulmonary epithelial cells, the ST-17 strain adheres significantly more efficiently to the intestinal epithelial Caco-2 cell line, the BBB-constituting cells hCMEC/D3, brain primary microvessel endothelial cells (MVECs), and choroid plexus epithelial cells (CPECs; Fig. 3a). The significance of these results was broadened by the study of 20 randomly picked invasive GBS neonatal isolates of ST-17 type (n = 10) or non–ST-17 type (n = 10; strain characteristics described in Table S2). As seen for the prototype strains, comparative cell binding assays showed that ST-17 isolates adhere significantly more to Caco-2 and hCMEC/D3 cells than non–ST-17 isolates, but not to A549 cells (Fig. 3b), thereby suggesting that bacteria expressing HvgA could display a specific enhanced capacity to adhere to cells of the intestinal and blood–brain barriers. To further investigate whether HvgA is the adhesin involved in the ST-17 interaction with intestinal and blood–brain barriers constituting cells, a GBS BM110ΔhvgA deletion mutant was constructed (Fig. 1a and Tables S1 and S3).

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human blood, hvgA is similarly overexpressed by threefold relative to standard culture medium (unpublished data). As for gbs2018A/bibA (Lamy et al., 2004; Mereghetti et al., 2008), hvgA transcription is up-regulated 85-fold in a 2-component regulatory system CovSR mutant (BM110ΔcovR; unpublished data). Together, these data show that HvgA is expressed on GBS ST-17 surface and that its expression is up-regulated in vivo conditions.

HvgA promotes specific GBS adhesion to epithelial and endothelial cells

Because these data pointed to HvgA as a potential ST-17–specific determinant conferring selective adhesive properties to GBS, we compared the adhesion to different cell types of two reference strains, BM110 serotype III ST-17 (WT ST-17) and NEM316 serotype III ST-23 (WT ST-23) expressing HvgA

Figure 3. HvgA promotes specific hyper-adhesion to epithelial and endothelial cells. (a and b) Comparison of the adhesive properties of ST-17 and non–ST-17 GBS strains. Cells were cultured for 1 h with bacteria, washed three times, and lysed, and CFUs were enumerated after plating on TH agar plates. Values are expressed as the percentage of adhesion relative to the inoculum. (c and d) Adhesion of GBS BM110 WT (ST-17) and ΔhvgA mutant to various cell lines, primary choroid plexus epithelial cells, and brain microvessel endothelial cells. Adhesion assays were conducted as described in a and b. Streptococci were labeled with a pAb-GBS (green), nuclei were labeled with Dapi (blue) and ZO1 with an anti-ZO1 antibody, and F-actin was labeled with phalloidin (red). Bar, 20 µm. Throughout this figure, results are representative of at least three independent experiments performed in triplicate. Error bars represent the SD. Asterisks indicate significant differences relative to BM110 WT or GBS ST-17 strains, as assessed by the Mann-Whitney test (*, P < 0.05; **, P < 0.01; ***, P < 0.001). NS, a nonsignificant difference.
of the streptococcal chains, were similar to that of the parental WT strain (unpublished data). We then compared the adhesion properties of the \( \Delta hvgA \) mutant to its isogenic parent, and showed that it exhibited a significantly reduced adhesion to a series of epithelial and endothelial human cell lines and rodent primary cells (Fig. 3, c and d). The direct involvement of HvgA in bacterial adhesion to cells was further established. Indeed, trans-complementation with a plasmid-driving \( hvgA \) expression (\( \text{Ph} \text{hvgA} \)) restored BM110\( hvgA \) strain adhesion properties to a level similar to that of the WT strain (Fig. 4 a). Furthermore, introduction of \( \text{Ph} \text{hvgA} \) in \textit{Lactococcus lactis} enabled HvgA expression on the lactococcal surface, as assessed by immunofluorescence microscopy and flow cytometry(Fig. 4, b and c). Trans-complemented \textit{L. lactis} strains were used in assays as described for GBS to investigate HvgA-mediated adhesion: a strain expressing HvgA adhered significantly more efficiently to Caco-2 and hCMEC/D3 cells than \textit{L. lactis} with a vector without insert and \textit{L. lactis} expressing BibA (Fig. 4 d). The nonpathogenic species \textit{L. lactis} is intrinsically nonadhesive, yet heterologous expression of HvgA in \textit{L. lactis} confers a clear adhesive phenotype. Moreover, a \( \Delta \text{bibA} \) mutant expressing HvgA adhered 10-fold more efficiently to hCMEC/D3 cells, as compared with the WT non–ST-17 (NEM316) strain (Fig. 4 e). Thus, replacement of \( \text{bibA} \) by \( hvgA \) in GBS NEM316 confers an ST-17 adhesion phenotype to this non–ST-17 strain, and establishes the specific adhesive property conferred upon HvgA expression.

\textbf{HvgA is critical for GBS intestinal colonization and translocation across the intestinal barrier}

These in vitro data argued for a key contribution of HvgA in the ability of ST-17 GBS to adhere to cells constituting the intestinal and blood–brain barriers, which are targeted during LOD. We investigated this issue in the in vivo context and used mouse models of GBS infection closely mimicking the pathology observed in the human neonate. We first monitored fecal shedding after oral inoculation (10\( ^{10} \) CFUs) of Swiss female mice (3–4 wk old) with WT ST-17 (BM110), its isogenic mutant \( \Delta hvgA \) or WT ST-23 (NEM316), to assess their respective ability to colonize the intestine. Quantification of GBS in feces showed that: a WT ST-17 strain establishes in the intestine more than one order of magnitude better than a non–ST-17 strain (Fig. 5 a), HvgA strongly contributes to this ST-17–specific phenotype (Fig. 5 b), and the non–ST-17 allelic variant BibA has no significant impact on gut colonization (Fig. 5 c). Ex vivo experiments with cecal tissue explants also demonstrated an HvgA-mediated bacterial association to the cecal epithelium (Fig. 5 d). In addition, competition experiments for intestinal colonization in which 5 \( \times \) 10\(^{10} \) CFUs of each strain were simultaneously inoculated indicated that within <1 wk, ST-17 WT totally out-competes a non–ST-17 WT strain (Fig. 5 e), as well as an isogenic \( \Delta hvgA \) mutant (Fig. 5 f). Together, these results demonstrate that HvgA confers a selective advantage at this initial step of infection.

We next addressed whether HvgA could provide the ST-17 strain with an enhanced ability to translocate across the intestinal barrier. To test this hypothesis, we used inbred BALB/c mice, as we observed that they displayed higher susceptibility than outbred Swiss mice upon oral infection. Moreover, we also observed that 4–5-wk-old mice were more resistant upon oral challenge than preweaning (15–21-d-old) BALB/c mice. We therefore inoculated orally preweaning (15–21-d-old) BALB/c mice with 10\( ^{10} \) or 2 \( \times \) 10\(^{9} \) CFUs. Their mortality rate 12 h after infection was significantly decreased when inoculated with the \( \Delta hvgA \) mutant as compared to inoculation with the WT strain (Fig. 5 g). Furthermore, 8 h
Moreover, animals that died in the first week were examined by immunohistochemistry and confocal microscopy (Fig. S2). In mice with the highest WT-ST17 bacterial load (5 × 10⁹ CFUs) in the brain, GBS were observed adhering to the inner meningeal envelopes (pia mater, Fig. S2 a) in the brain microvessel (Fig. S2 b), in the brain parenchyma (Fig. S2 c), or in the choroid plexuses (Fig. S2 d). In contrast, no bacterium was observed in mice infected with the ΔhvgA mutant. To focus specifically on the crossing of the BBB and bypass the HvgA phenotype at the BALB/c intestinal barrier level, we developed a CNS infection model in which preweaning 3 wk mice were infected i.v. every 12 h with a relatively low inoculum (5 × 10⁶ CFUs) to avoid unspecific BBB opening caused by the massive systemic inflammation triggered by high bacterial loads, but to instead mimic bloodstream neonatal meningitis. Monitoring of bacterial loads in the blood and the CNS showed that whereas WT ST-17 and its ΔhvgA isogenic mutant induce a similar level of bacteremia 48 h after i.v. inoculation (Fig. 6 c), ΔhvgA is significantly impaired in its ability to invade the CNS (Fig. 6 d). In agreement with these quantitative data, real-time imaging of bioluminescent bacteria along the infectious process revealed a marked bioluminescence emission in the head of animals infected with WT ST-17 (4/4 animals), which was detectable 20 h after infection and is visible until the death of the animal, whereas merely no signal was detected in mice infected with the ΔhvgA mutant (Fig. 6 e). Neuropathological analysis of infected animals 48 h after i.v. inoculation disclosed an intense
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associated with ST-17 GBS isolates: (1) their close association with LOD, which can now be linked to HvgA-mediated intestinal colonization and subsequent crossing of the intestinal barrier, and (2) their close association with meningitis, which can now be linked to the HvgA-mediated crossing of the BBB. This study definitely establishes the hypervirulence of the ST-17 GBS clone and links it to enhanced intestinal colonization and barrier breaching potentials. Importantly, it illustrates how a microbial factor implicated in bacterial intestinal colonization can behave as a specific virulence factor in the neonatal context, at a time when the intestinal microflora is not yet established and cannot exert its buffering effect on potential pathogenic bacteria such as GBS. Given the burden of ST-17–associated LOD and neonatal meningitis (Poyart et al., 2008; CDC, 2009), hvgA and its gene product are now promising targets for developing diagnostic tools (Lamy et al., 2006) and vaccines (Santi et al., 2009), respectively.

**MATERIAL AND METHODS**

**Bacterial strains, genetic constructions, and growth conditions.** The main characteristics of bacterial strains and plasmids used in this study are listed in Table S1. GBS NEM316, capsular serotype III, and MLST type ST 23, and GBS BM110, capsular serotype III, and MLST sequence type ST-17 are well-characterized isolates from human with invasive infections. GBS clinical strains from invasive infection were collected by the National Reference Center for Streptococci from 2006 and 2009. GBS mutants were constructed by in-frame deletions in *bibA* (GBS NEM316), *hvgA* (GBS BM110), and *srtA* (GBS BM110), as previously described (Dramsi et al., 2006).
using primers listed in Table S3 and Fig. 2 a. The expected in-frame deletions were confirmed by PCR and sequence analysis. Complemented GBS mutant strains and L. lactis expressing BibA or HvgA were constructed as follows. bibA and hvgA genes were amplified by PCR from chromosomal DNA of GBS NEM316 and BM110, respectively, using primers O5 and O6 (Fig. 2 a and Table S3) and cloned into the pOrn23 shuttle vector. Recombinant plasmids PbibA and PhvgA were introduced by electroporation into GBS mutants and L. lactis. Unless otherwise specified, GBS and L. lactis were cultured at 37°C in Todd Hewitt (TH) broth or agar and antibiotics were used at the following concentrations: erythromycin, 10 µg·ml⁻¹; kanamycin, 1,000 µg·ml⁻¹.

Generation of anti-BibA and anti-HvgA rabbit polyclonal antibodies. Recombinant Gbs2018 segments were expressed and purified as follows. DNA fragments intragenic to bibA (nt 100–1185) and hvgA (nt 88–648) were produced by PCR using genomic DNA of GBS NEM316 and BM110, respectively, as templates, as well as the primers listed in Table S3. DNA fragments were digested with the appropriate enzymes and cloned into pET-28b(+) and pET2817, respectively. The resulting plasmids were introduced into E. coli BL21DE3/pD17 for protein expression. Recombinant proteins were purified under native conditions on Ni-NTA columns (QIAGEN), followed by Q-Sepharose anion exchange chromatography (GE Healthcare). The purified BibA or HvgA truncated proteins were injected into rabbit to produce antibodies, as previously described (Laloué et al., 2005).

RNA isolation, reverse transcription, and qRT-PCR. Total RNAs were extracted from bacteria as previously described (Lamy et al., 2004). For isolation of bacterial RNA from human blood, bacteria were grown in TH broth to the mid-logarithmic phase (OD₀.₅ 0.3–0.4), washed in PBS, and resuspended in an equal volume of freshly drawn human blood from non-immune healthy donors and incubated for 1 h at 37°C. RNA isolation from animal blood and tissues was as previously described (Oggoni et al., 2006). cDNA synthesis was performed on DNAse I-treated RNA (50 µg of two independent extracts) with specific reverse primers using SuperScript II reverse transcription (Invitrogen). qRT-PCR analysis was performed as previously described (Yamamoto et al., 2005) using primers listed in Table S3. The relative fold change of each gene was calculated from 2⁻ΔΔCt by using pO2B as an internal control gene.

Immunoblots and bacterial immunofluorescence stainings. For analysis of HvgA expression, cell wall proteins were extracted as previously described (Dramsi et al., 2006, Laloué et al., 2005). After SDS-PAGE, proteins were transferred to nitrocellulose membrane. HvgA was detected using antibodies and the ECL Reagent (GE Healthcare). Immunoblots and bacterial immunofluorescence stainings were performed as previously described (Disson et al., 2009). Acquisitions of images was realized with an upright confocal microscope (Carl Zeiss, Inc.), using a 40× water immersion objective for the whole-mount tissue or an oil immersion objective for the thick section labeling. Reconstructions were realized using Imaris software.

Online supplemental material. Fig. S1 shows the role of HvgA in the mortality induced from neonates of six U.S. Academic Centers (Granada) for CFU counts. For cecum-ligated loop experiments, animals were anesthetized. The whole cecums were closed at both ends with surgical sutures. 200 µl of the adequate bacterial dilution was injected in the lumen. 1 h after infection, the mice were sacrificed; thececum-ligated loops were excised and opened longitudinally. For competitive assay, both WT and isogenic mutants were mixed in a 1:1 ratio oral infection experiments. At the indicated times, stools were collected and serial dilutions were plated on selective medium. i.v. infections were performed by i.v. injection every 12 h for 36 h. All of the procedures were in agreement with the guidelines of the European Commission for the handling of laboratory animals, directive 86/699/EEC (http://ec.europa.eu/environment/chemicals/lab_animals/home_en.htm) and were approved by the Animal Care and Use Committees of the Institut Pasteur.

Bioluminescence real-time imaging. GBS WT-ST17 strain and the ΔhvgA isogenic mutant were made bioluminescent after introduction plasmid pTCVlux by electroporation (Table S1). After i.v. infection, BALB/c mice bioluminescence was monitored each day, as previously described (Disson et al., 2009). 12 h before infection and every 12 h during the infection, animals were treated with erythromycin (20 mg/kg⁻¹).

Tissue labeling. Thin sections, thick sections, and whole-mount tissue labeling were performed as previously described (Disson et al., 2009). Acquisition of images was realized with an upright confocal microscope (Carl Zeiss, Inc.), using a 40× water immersion objective for the whole-mount tissue or an oil immersion objective for the thick section labeling. Reconstructions were realized using Imaris software.

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