Identification of a novel cationic glycolipid in *Streptococcus agalactiae* that contributes to brain entry and meningitis

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Short title: GBS MprF synthesizes a novel glycolipid that contributes to meningitis

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Abstract

Bacterial membrane lipids are critical for membrane bilayer formation, cell division, protein localization, stress responses, and pathogenesis. Despite their critical roles, membrane lipids have not been fully elucidated for many pathogens. Here, we report the discovery of a novel cationic glycolipid, Lysyl-Glucosyl-Diacylglycerol (Lys-Glc-DAG) that is synthesized in high abundance by the bacterium *Streptococcus agalactiae* (Group B *Streptococcus*, GBS). To our knowledge, Lys-Glc-DAG is more positively charged than any other known lipids. Lys-Glc-DAG carries two positive net charges per molecule, distinct from the widely described lysylated phospholipid Lysyl-phosphatidylglycerol (Lys-PG) which carries one positive net charge due to the presence of a negatively charged phosphate moiety. We use normal phase liquid chromatography (NPLC) coupled with electrospray ionization (ESI) high-resolution tandem mass spectrometry (HRMS/MS) and genetic approaches to determine that Lys-Glc-DAG is synthesized by the enzyme MprF in GBS, which covalently modifies the neutral glycolipid Glc-DAG with the cationic amino acid lysine. GBS is a leading cause of neonatal meningitis, which requires traversal of the endothelial blood-brain barrier (BBB). We demonstrate that GBS strains lacking *mprF* exhibit a significant decrease in the ability to invade BBB endothelial cells. Further, mice challenged with a GBS∆*mprF* mutant developed bacteremia comparably to Wild-Type infected mice yet had less recovered bacteria from brain tissue and a lower incidence of meningitis. Thus, our data suggest that Lys-Glc-DAG may contribute to bacterial uptake into host cells and disease progression. Importantly, our discovery provides a platform for further study of cationic lipids at the host-pathogen interface.

Introduction

Bacterial cellular membranes are dynamic structures that are critical for survival under varying environmental conditions and are essential for host-pathogen interactions. Phospholipids and glycolipids within the membrane have varying chemical properties that alter the physiology of the membrane, which bacteria can modulate in response to environmental stresses such as pH (1), antibiotic treatment (2), and human metabolites (3). Despite their critical roles in the survival and pathogenesis, membrane lipids have not been carefully characterized using modern lipidomic techniques for many important human pathogens, including *Streptococcus agalactiae* (Group B *Streptococcus*; GBS). GBS colonizes the lower genital and gastrointestinal tracts of ~30% of healthy women (4, 5). However, GBS can cause sepsis and pneumonia in newborns and is a leading cause of neonatal meningitis, resulting in long-lasting neurological effects in survivors (6-8). Due to the severity of the resulting diseases, intrapartum antibiotic prophylaxis is prescribed for colonized pregnant women (7, 9). Even with these measures, a more complete understanding of GBS pathogenesis and new therapeutic and preventive measures are needed to mitigate the devastating impact of GBS neonatal infection.

Research on the pathogenesis of the GBS has mainly focused on cell wall-anchored or secreted proteins and polysaccharides that aid in the attachment to and invasion of host cells. The numerous attachment and virulence factors possessed by the GBS are summarized in a recent review by Armistead *et al* 2019 (10). Comparatively little is known about GBS cellular membrane lipids. To our knowledge, the only characterization of GBS lipids prior to our current study was the identification of the phospholipids

70 phosphatidylglycerol (PG), cardiolipin (CL), and lysyl-phosphatidylglycerol (Lys-PG) in
71 GBS (11, 12). Similarly, investigation into the glycolipids of the GBS membrane has
72 focused on di-glucosyl-diacylglycerol (Glc_2-DAG), which is the lipid anchor of the Type I
73 lipoteichoic acid, and its role in pathogenesis (13).
74
75 In this study, we utilized normal phase liquid chromatography (NPLC) coupled with
76 electrospray ionization (ESI) high-resolution tandem mass spectrometry (HRMS/MS) to
77 characterize the GBS membrane lipid composition, and identified a novel cationic
78 glycolipid, lysyl-glucosyl-diacylglycerol (Lys-Glc-DAG), which comprises a major portion
79 of the GBS total lipid extract. While Lys-PG has been reported in a range of bacterial
80 species (14), Lys-Glc-DAG represents, to our knowledge, the first example of lysine
81 modification of a neutral glycolipid. By gene deletion and heterologous expression, we
82 show the GBS MprF enzyme is responsible for the biosynthesis of both the novel Lys-
83 Glc-DAG and Lys-PG. Most strikingly, using an *in vivo* hematogenous murine infection
84 model, we demonstrate that MprF does not contribute to GBS bloodstream survival. This
85 distinguishes the GBS MprF from the well-known *Staphylococcus aureus* MprF, which
86 synthesizes only Lys-PG (15, 16). Rather, GBS MprF contributes specifically to meningitis
87 and penetration of the blood-brain barrier. These results greatly expand our knowledge
88 of naturally occurring lipids and MprF functionality and reveal insights into the
89 pathogenesis of meningitis caused by GBS.
90
91 **Results**
92 **Identification of Lys-Glc-DAG, a novel cationic glycolipid in GBS**

93 The membrane lipids of three GBS clinical isolates of representative serotypes were
94 characterized: COH1 (17), A909 (18), CNCTC 10/84 and CJB111 (serotypes III, 1a, and
95 V, respectively) (19). Common Gram-positive bacterial lipids were identified by normal
96 phase LC coupled with negative ion ESI/MS/MS, including diacylglycerol (DAG),
97 monohexosyldiacylglycerol (MHDAG), dihexosyldiacylglycerol (DHDAG),
98 phosphatidylglycerol (PG), and lysyl-phosphatidylglycerol (Lys-PG), as shown by the
99 negative total ion chromatogram (TIC) (Fig. 1A).
100
101 Surprisingly, the positive TIC (Fig. 1B, Supplemental Figure S1) shows highly abundant
102 peaks of unknown identity at the retention time ~25-29 min. The mass spectra (Fig. 1C)
103 and LC retention times of this lipid do not match with any other bacterial lipids we have
104 analyzed or exact masses in lipidomic databases. Tandem MS (MS/MS) in the positive
105 ion mode (Fig. 1D), negative ion mode (Fig. 1E), and high-resolution mass measurement
106 (Fig. 1C) allowed us to propose lysyl-glucosyl-diacylglycerol (Lys-Glc-DAG) (Fig. 1F) as
107 the structure of this unknown lipid. Observed and exact masses of Lys-Glc-DAG are
108 shown in Table S1. The assignment of glucose was based on the observation that
109 glucosyl-diacylglycerol (Glc-DAG) is a major membrane component of GBS and other
110 streptococci (13), and results from an isotopic labeling experiment using ^{13}C-labeled
111 glucose (Glucose-$^{13}C_6$). The assignment of lysine modification was supported by an
112 isotopic labeling experiment with deuterated lysine (lysine-*d4*). The expected mass shifts
113 (+4 Da) were observed in both molecular ions and MS/MS product ions (Supplemental
114 Figure S2). Comparison of both MS/MS spectra of labeled (Glucose-$^{13}C_6$) and unlabeled
115 Lys-Glc-DAG indicates the lysine residue is linked to the 6-position of glucose

116 (Supplemental Figure S2). Lys-Glc-DAG consists of several molecular species with
117 different fatty acyl compositions resulting in different retention times and multiple,
118 unresolved TIC peaks (~25-29 min).
119
120 **GBS MprF synthesizes Lys-Glc-DAG**
121 The enzyme MprF (multiple peptide resistance factor) catalyzes the aminoacylation of PG
122 with lysine in some Gram-positive pathogens (15, 20). We determined that GBS MprF is
123 responsible and sufficient for synthesizing Lys-Glc-DAG as well as Lys-PG. Deletion of
124 *mprF* from both COH1 and CJB111 abolishes Lys-Glc-DAG and Lys-PG synthesis, which
125 are restored by complementation (Fig. 1G, Supplemental Figure S3). Deletion of GBS
126 *mprF* does not confer a growth defect in Todd-Hewitt broth or tissue culture medium. The
127 oral colonizer *Streptococcus mitis* does not encode *mprF* or synthesize Lys-PG but
128 synthesizes Glc-DAG and PG (2, 3). Heterologous expression of GBS *mprF* in *S. mitis*
129 results in Lys-Glc-DAG and Lys-PG production (Fig. 1H), while expression of
130 *Enterococcus faecium mprF* results in only Lys-PG production (Fig. 1H), as expected (1).
131 Biosynthetic pathways involving MprF are shown in Fig. 1I.
132
133 **MprF contributes to GBS pathogenesis**
134 We investigated whether MprF contributes to GBS invasion into brain endothelial cells
135 and development of meningitis. To mimic the human blood-brain barrier (BBB), we utilized
136 the human cerebral microvascular endothelial cell line hCMEC/D3. *In vitro* assays for
137 adhesion and invasion were performed as described previously (13, 21, 22). There was
138 no significant difference in the ability of Δ*mprF* compared to WT and complement cells to

139 attach to hCMEC/D3 cells (Fig. 2A). However, we observed a significant decrease in the
140 amount of Δ*mprF* recovered from the intracellular compartment of hCMEC/D3 cells (Fig.
141 2A). The reduced invasion phenotype was confirmed in the hypervirulent serotype V
142 strain, CJB111 (23, 24) (Supplemental Figure S4). Intracellular survival requires GBS to
143 survive low pH conditions in lysosomes (pH 4.5 – 5.5) (25), and Δ*mprF* is unable to survive
144 low pH conditions (Fig. 2B). This suggests that MprF promotes GBS invasion and possibly
145 intracellular survival in brain endothelial cells.
146
147 We hypothesized that these *in vitro* phenotypes of Δ*mprF* would translate into a
148 diminished ability to penetrate the BBB and produce meningitis *in vivo*. Using our
149 standard model of GBS hematogenous meningitis (13, 21) mice were challenged with
150 either WT GBS or Δ*mprF*. Mice were sacrificed at 72 h to determine bacterial loads in
151 blood and brain tissue. We recovered significantly less CFU in the brains of Δ*mprF*-
152 infected mice compared to the WT-infected mice (Fig. 2C). However, there was no
153 significant difference in CFU recovered from the bloodstream (Fig. 2D), demonstrating
154 that Δ*mprF* does not have a general *in vivo* growth defect. Furthermore, mice challenged
155 with WT GBS had significantly more leukocyte infiltration, meningeal thickening and
156 neutrophil chemokine, KC, in brain homogenates compared to Δ*mprF* mutant-infected
157 animals (Fig. 2E-G). Taken together, *mprF* contributes to GBS penetration into the brain
158 and to the pathogenesis of meningitis *in vivo*.
159
160 **Discussion**

161 Lipid nanoparticles are essential for mRNA vaccine delivery. Engineered cationic lipids
162 are utilized in lipid nanoparticles for vaccine and drug delivery and are required for uptake
163 of particles into cells (26, 27). Substantial effort has been dedicated to the synthesis of
164 cationic lipids with low toxicity and efficient delivery properties. Here, we report the
165 discovery of Lys-Glc-DAG, a naturally occurring cationic glycolipid synthesized in high
166 abundance by GBS, which in conjunction with Lys-PG aids in invasion of human
167 endothelial cells. We discovered that GBS MprF uniquely synthesizes the novel and
168 highly abundant Lys-Glc-DAG, as well as Lys-PG. This establishes that GBS capitalizes
169 on MprF to modulate charges of both glycolipids and phospholipids at the membrane.
170
171 MprF catalyzes the aminoacylation of the anionic phospholipid PG in a range of Gram-
172 positive and Gram-negative bacteria (15, 20). MprF is a membrane-bound enzyme
173 comprised of a N-terminal lipid flippase domain (28) and a C-terminal catalytic domain
174 that catalyzes the aminoacylation of the glycerol group of PG by using aminoacyl-tRNAs
175 as the amino acid donors (29-31). An important function of PG aminoacylation is
176 proposed to be lowering the net negative charge of the cellular envelope to confer
177 protection from cationic antimicrobial peptides (CAMPs) produced by host immune
178 systems and bacteriocins produced by competitor bacteria (15, 20). However, a previous
179 study observed no contribution of *mprF* to GBS *in vitro* susceptibility to commonly studied
180 CAMPs, which is unlike the well-characterized *S. aureus mprF* (32), thus highlighting the
181 unique differences between the extracellular surface of these bacteria.
182

183 Based on our tissue culture and mouse infection experiments, we propose that GBS have
184 an MprF enzyme and corresponding cellular lipid properties that are adapted for efficient
185 invasion of mammalian cells. Deletion of *mprF* impacts GBS virulence, but only for
186 meningitis, and not for bacteremia. This demonstrates that MprF plays a specific role in
187 BBB penetration, but not *in vivo* survival in general. It is unknown how lysinylated lipids
188 in the GBS membrane, which is covered by a layer of peptidoglycan, mechanistically
189 impact invasion. Because Lys-Glc-DAG is abundantly synthesized by GBS MprF, with
190 Lys-PG a comparatively minor product, it is likely that Lys-Glc-DAG is the most relevant
191 lipid for meningitis pathogenesis. Speculatively, Lys-Glc-DAG may contribute to
192 membrane vesicle (MV) formation by GBS. MVs have previously been shown to be pro-
193 inflammatory and result in preterm birth and fetal death in mice (33), but have not been
194 studied during meningitis progression. In future studies, it will be key to investigate this,
195 as well as the specific host inflammatory and signaling responses to the GBS *mprF*
196 mutant.
197
198 Our identification of the novel Lys-Glc-DAG glycolipid rationalizes further study of the
199 lipidomes of human pathogens. First, lipids contribute to virulence, and understanding
200 these virulence mechanisms and the mechanisms for lipid synthesis may identify novel
201 antimicrobial drug targets. The decreased *in vivo* pathogenicity of the Δ*mprF* mutant
202 identifies GBS MprF as a candidate for targeting by antimicrobial strategies. Moreover,
203 Lys-Glc-DAG could be utilized as a specific molecular biomarker for GBS diagnostics.
204 Second, pathogens use lipids to modulate their surface charges and interact with their
205 hosts, and they innovate lipids to meet their specific needs. Lys-Glc-DAG is a naturally

206 occurring, strongly cationic lipid with potential for use in lipid nanoparticles for vaccine
207 and drug delivery. Importantly, our discovery suggests that lipidome analysis of human
208 pathogens is likely to reveal novel lipids of biotechnological utility.
209

210 **Materials and methods**

211 **Bacterial strains, media, and growth conditions**

212 See Table S2 for strains used in this study. GBS strains were grown statically at 37°C in
213 Todd-Hewitt Broth (THB) and *S. mitis* strains were grown statically at 37°C and 5% CO_2,
214 unless otherwise stated. Streptococcal chemically defined medium (34) was diluted from
215 stock as described (35) with 1% w/v glucose (referred to as DM), slightly modified from
216 (36), unless otherwise stated. *Escherichia coli* strains were grown in Lysogeny Broth (LB)
217 at 37°C with rotation at 225 rpm. Kanamycin and erythromycin (Sigma-Aldrich) were
218 supplemented to media at 50 µg/mL and 300 µg/mL for *E. coli,* respectively, or 300 µg/mL
219 and 5 µg/mL, respectively, for streptococcal strains.
220

221 **Routine molecular biology techniques**

222 All PCR reactions utilized Phusion polymerase (Thermo Fisher). PCR products and
223 restriction digest products were purified using GeneJET PCR purification kit (Thermo
224 Fisher) per manufacturer protocols. See Table S3 for primers. Plasmids were extracted
225 using GeneJET plasmid miniprep kit (Thermo Fisher) per manufacturer protocols.
226 Restriction enzyme digests utilized XbaI, XhoI, and PstI (New England Biolabs) for 3 h at
227 37°C in a water bath. Ligations utilized T4 DNA ligase (New England Biolabs) at 16°C
228 overnight or Gibson Assembly Master Mix (New England Biolabs) per manufacturer

229 protocols where stated. All plasmid constructs were sequence confirmed by Sanger
230 sequencing (Massachusetts General Hospital DNA Core or CU Anschutz Molecular
231 Biology Core).
232
233 **Deuterated lysine and $^{13}C_6$-D-glucose isotope tracking**
234 A GBS COH1 colony was inoculated into 15 mL of DM containing 450 μM lysine-*d4*
235 (Cambridge Isotopes Laboratories) or a single COH1 colony was inoculated into 10 mL
236 DM supplemented with 0.5% w/v $^{13}C_6$D-glucose (U-13C6, Cambridge Isotopes
237 Laboratories) for overnight growth for lipidomic analysis described below.
238
239 **Construction of MprF expression plasmids**
240 Genomic DNA was isolated using the Qiagen DNeasy Blood and Tissue kit per the
241 manufacturer's protocol with the exception that cells were pre-treated with 180 μL 50
242 mg/mL lysozyme, 25 μL 2500 U/mL mutanolysin, and 15 μL 20 mg/mL pre-boiled RNase
243 A and incubated at 37°C for 2 h. The *mprF* genes from GBS COH1, (GBSCOH1_1931),
244 GBS CJB111 (ID870_10050), and *E. faecium* 1,231,410 (EFTG_00601) were amplified
245 and either Gibson ligated into pABG5Δ*phoZ* (37) or ligated into pDCErm (38). Plasmid
246 constructs were transformed into chemical competent *E. coli*. Briefly, chemically
247 competent cells were incubated for 10 min on ice with 5 μL of Gibson reaction before heat
248 shock at 42°C for 70 sec, then placed on ice for 2 min before 900 μL of cold SOC medium
249 was added. Outgrowth was performed at 37°C, with shaking at 225 rpm, for 1 h. Cultures
250 were plated on LB agar plates containing 50 μg/mL kanamycin. Colonies were screened
251 by PCR for presence of the *mprF* insert.

252

253 **Expression of *mprF* in *S. mitis***

254 Natural transformation was performed as previously described (3). Briefly, precultures
255 were thawed at room temperature, diluted in 900 µL of THB, further diluted 1:50 in
256 prewarmed 5 mL THB, and incubated for 45 min at 37°C. 500 µL of culture was then
257 aliquoted with 1 µL of 1 mg/ml competence-stimulating peptide (EIRQTHNIFFNFFKRR)
258 and 1 µg/mL plasmid. Transformation reaction mixtures were cultured for 2 h at 37°C in
259 microcentrifuge tubes before being plated on THB agar supplemented with 300 µg/mL
260 kanamycin. Single transformant colonies were cultured in 15 mL THB overnight. PCR
261 was used to confirm the presence of the *mprF* insert on the plasmid. Plasmids were
262 extracted and sequence confirmed as described above. Lipidomics was performed as
263 described below in biological triplicate.

264

265 **Construction of *mprF* deletion plasmids**

266 Regions ~2 kb upstream and downstream of the GBS COH1 *mprF* (GBSCOH1_1931) or
267 CJB111 (ID870_10050) were amplified using PCR. Plasmid, pMBSacB (39), and the
268 PCR products were digested using appropriate restriction enzymes and ligated overnight.
269 7 µL of the ligation reaction was transformed into chemically competent *E. coli* DH5α as
270 described above, except that outgrowth was performed at 28°C with shaking at 225 rpm
271 for 90 min prior to plating on LB agar supplemented with 300 µg/mL erythromycin. Plates
272 were incubated at 28°C for 72 h. Colonies were screened by PCR for correct plasmid
273 construction. Positive colonies were inoculated into 50 mL LB media containing antibiotic
274 and incubated at 28°C with rotation at 225 rpm for 72 h. Cultures were pelleted using a

275 Sorvall RC6+ centrifuge at 4,280 x *g* for 6 min at room temperature. Plasmid was
276 extracted as described above except the cell pellet was split into 5 columns to prevent
277 overloading and serial eluted into 50 µL. Plasmid construction was confirmed via
278 restriction digest using XhoI and XbaI, and the insert was PCR amplified and sequence-
279 verified.
280

281 **Generation of electrocompetent GBS cells for *mprF* knockout**

282 Electrocompetent cells were generated as described (39) with minor modifications.
283 Briefly, a GBS COH1 or CJB111 colony was inoculated in 5 mL M17 medium (BD Bacto)
284 with 0.5% glucose and grown overnight at 37°C. The 5 mL was used to inoculate a second
285 overnight culture of 50 mL pre-warmed filter-sterilized M17 medium containing 0.5%
286 glucose, 0.6% glycine, and 25% PEG 8000. The second overnight was added to 130 mL
287 of the same medium and grown for 1 h at 37°C. Cells were pelleted at 3,200 x *g* in a
288 Sorvall RC6+ at 4°C for 10 min. Cells were washed twice with 25 mL cold filter-sterilized
289 GBS wash buffer containing 25% PEG 8000 and 10% glycerol in water, and pelleted as
290 above. Cell pellets were re-suspended in 1 mL GBS wash buffer and either used
291 immediately for transformation or stored in 100 µL aliquots at -80°C until use.
292

293 **Deletion of GBS COH1 and CJB111 *mprF***

294 Electrocompetent cells were generated as described (39) with minor modifications. The
295 double crossover homologous recombination knockout strategy was performed as
296 described previously (22, 39, 40) with minor modifications. 1 µg of plasmid was added to
297 electrocompetent GBS cells and transferred to a cold 1 mm cuvette (Fisher or BioRad).

298 Electroporation was carried out at 2.5 kV on an Eppendorf eporator. 1 mL of THB
299 containing 12.5% PEG 8000, 20 mM $MgCl_2$, and 2 mM $CaCl_2$ was immediately added
300 and then the entire reaction was transferred to a glass culture tube. Outgrowth was at
301 28°C for 2 h followed by plating on THB agar supplemented with 5 µg/mL erythromycin.
302 Plates were incubated for 48 h at 28°C. A single colony was cultured overnight in 5 mL
303 THB with 5 µg/mL erythromycin at 28°C. The culture was screened via PCR for the
304 plasmid insert with the initial denaturing step extended to 10 min. The overnight culture
305 was diluted 1:1000 THB containing 5 µg/mL erythromycin and incubated overnight at
306 37°C to promote single cross over events. The culture was then serial diluted and plated
307 on THB agar plates with antibiotic and incubated at 37°C overnight. Colonies were
308 screened for single crossover events by PCR. Single crossover colonies were inoculated
309 in 5 mL THB at 28°C to promote double crossover events. Overnight cultures were diluted
310 1:1000 into 5 mL THB containing sterile 0.75 M sucrose and incubated at 37°C. Overnight
311 cultures were serial diluted and plated on THB agar and incubated at 37°C overnight.
312 Colonies were patched onto THB agar with and without 5 µg/mL erythromycin to confirm
313 loss of plasmid. Colonies were also screened by PCR for the loss of *mprF*. Colonies
314 positive for the loss of *mprF* were inoculated into 5 mL THB at 37°C. Cultures were
315 stocked and gDNA extracted as described above, with minor modifications. Sequence
316 confirmation of the *mprF* knockout was done via Sanger sequencing (Massachusetts
317 General Hospital DNA Core or CU Anschutz Molecular Biology Core). The mutant was
318 grown overnight in 15 mL THB at 37°C and pelleted at 6,150 x *g* for 5 min in a Sorvall
319 RC6+ centrifuge at room temperature for lipid extraction as described. Genomic DNA of
320 COH1Δ*mprF* was isolated as described above and whole genome sequencing was

321 performed in paired-end reads (2 by 150 bp) on the Illumina NextSeq 550 platform at the
322 Microbial Genome Sequencing Center (Pittsburgh, PA). Illumina sequence reads are
323 deposited in the Sequence Read Archive, accession PRJNA675025.
324

325 **Complementation of *mprF* in COH1Δ*mprF* and CJB111Δ*mprF***

326 Electrocompetent GBS strains were generated as previously described (41). Briefly,
327 GBSΔ*mprF* was inoculated into 5 mL THB with 0.6% glycine and grown overnight. The
328 culture was expanded to 50 mL in pre-warmed THB with 0.6% glycine and grown to an
329 OD_{600} nm of 0.3 and pelleted for 10 min at 3200 x *g* at 4°C in a Sorvall RC6+ floor
330 centrifuge. The pellet was kept on ice through the remainder of the protocol. The pellet
331 was washed twice with 25 mL and once with 10 mL of cold 0.625 M sucrose and pelleted
332 as above. The cell pellet was resuspended in 400 µL of cold 20% glycerol, aliquoted in
333 50 µL aliquots, and used immediately or stored at -80°C until use. Electroporation was
334 performed as described above, with recovery in THB supplemented with 0.25 M sucrose,
335 and plated on THB agar with kanamycin at 300 µg/mL.
336

337 **Acidic Bligh-Dyer extractions**

338 Centrifugation was performed using a Sorvall RC6+ centrifuge. Cultures were pelleted at
339 4,280 x *g* for 5 min at room temperature unless otherwise stated. The supernatants were
340 removed, and cell pellets were stored at -80°C until acidic Bligh-Dyer lipid extractions
341 were performed as described (3). Briefly, cell pellets were resuspended in 1X PBS
342 (Sigma-Aldrich) and transferred to Coring Pyrex glass tubes with PTFR-lined caps
343 (VWR), followed by 1:2 vol:vol chloroform:methanol addition. Single phase extractions

344 were vortexed periodically and incubated at room temperature for 15 minutes before 500
345 x *g* centrifugation for 10 min. A two-phase Bligh-Dyer was achieved by addition of 100 µL
346 37% HCl, 1 mL $CHCl_3$, and 900 µl of 1X PBS, which was then vortexed and centrifuged
347 for 5 min at 500 x *g.* The lower phase was removed to a new tube and dried under nitrogen
348 before being stored at -80°C prior to lipidomic analysis.
349

350 **Liquid Chromatography/Electrospray Ionization Mass Spectrometry**

351 Normal phase LC was performed on an Agilent 1200 quaternary LC system equipped
352 with an Ascentis silica HPLC column (5 µm; 25 cm by 2.1 mm; Sigma-Aldrich) as
353 described previously (42, 43). Briefly, mobile phase A consisted of chloroform-methanol-
354 aqueous ammonium hydroxide (800:195:5, vol/vol), mobile phase B consisted of
355 chloroform-methanol-water-aqueous ammonium hydroxide (600:340:50:5, vol/vol), and
356 mobile phase C consisted of chloroform-methanol-water-aqueous ammonium hydroxide
357 (450:450:95:5, vol/vol). The elution program consisted of the following: 100% mobile
358 phase A was held isocratically for 2 min, then linearly increased to 100% mobile phase B
359 over 14 min, and held at 100% mobile phase B for 11 min. The LC gradient was then
360 changed to 100% mobile phase C over 3 min, held at 100% mobile phase C for 3 min,
361 and, finally, returned to 100% mobile phase A over 0.5 min and held at 100% mobile
362 phase A for 5 min. The LC eluent (with a total flow rate of 300 µl/min) was introduced into
363 the ESI source of a high-resolution TripleTOF5600 mass spectrometer (Sciex,
364 Framingham, MA). Instrumental settings for negative-ion ESI and MS/MS analysis of lipid
365 species were: IS = -4,500 V, CUR = 20 psi, GSI = 20 psi, DP = -55 V, and FP = -150V.
366 Settings for positive-ion ESI and MS/MS analysis were: IS = +5,000 V, CUR = 20 psi, GSI

367 = 20 psi, DP = +55 V, and FP = +50V. The MS/MS analysis used nitrogen as the collision
368 gas. Data analysis was performed using Analyst TF1.5 software (Sciex, Framingham,
369 MA).
370
371 **pH-adjusted THB growth**
372 Approximately 30 mL of fresh THB were adjusted to different pH values, measured using
373 a Mettler Toledo FiveEasy pH/MV meter, and sterile-filtered using 0.22 µM syringe filters.
374 A final volume of 200 µL culture medium was aliquoted per well in a flat-bottom 96 well
375 plate (Falcon); culture media were not supplemented with antibiotics. Overnight cultures
376 of GBS strains were used to inoculate the wells to a starting OD_{600nm} 0.02 per well. Plates
377 were incubated for 24 h at 37°C before OD_{600nm} was read using a BioTek MX Synergy 2
378 plate reader. This experiment was performed in biological triplicate.
379
380 **hCMEC cell adherence and invasion assays**
381 Human Cerebral Microvascular Endothelial cells hCMEC/D3 (obtained from Millipore)
382 were grown in EndoGRO-MV complete media (Millipore, SCME004) supplemented with
383 5% fetal bovine serum (FBS) and 1 ng/ml fibroblast growth factor-2 (FGF-2; Millipore).
384 Cells were grown in tissue culture treated 24 well plates and 5% CO_2 at 37°C.
385
386 Assays to determine the total number of bacteria adhered to host cells or intracellular
387 bacteria were performed as described previously (21, 22). Briefly, bacteria were grown to
388 mid log phase (OD_{600nm} 0.4-0.5) and normalized to 1 x 10^8 to infect cell monolayers at a
389 multiplicity of infection (MOI) of 1 (1 x 10^5 CFU per well). The total cell-associated GBS

390 were recovered after 30 min incubation. Cells were washed slowly five times with 500 μL
391 1X PBS (Sigma) and detached by addition of 100 μL of 0.25% trypsin-EDTA solution
392 (Gibco) and incubation for 5 min before lysing the eukaryotic cells with the addition of 400
393 μL of 0.025% Triton X-100 (Sigma) and vigorous pipetting. The lysates were then serially
394 diluted and plated on THB agar and incubated overnight to determine CFU. Bacterial
395 invasion assays were performed as described above except infection plates were
396 incubated for 2 h before incubation with 100 μg gentamicin (Sigma) and 5 μg penicillin
397 (Sigma) supplemented media for an additional 2 h to kill all extracellular bacteria, prior to
398 being trypsinized, lysed, and plated as described. Experiments were performed in
399 biological triplicate with four technical replicates per experiment.
400

401 **Murine model of GBS hematogenous meningitis**

402 All animal experiments were conducted under the approval of the Institutional Animal
403 Care and Use Committee (#00316) at the University of Colorado Anschutz Medical
404 Campus and performed using accepted veterinary standards. The murine meningitis
405 model was performed as previously described (22, 44, 45). Briefly, 7-week-old male
406 CD1 (Charles River) mice were challenged intravenously with 1×10^9 CFU of WT COH1
407 or the isogenic Δ*mprF* mutant. At 72 h post-infection, mice were euthanized and blood
408 and brain tissue were harvested, homogenized, and serially diluted on THB agar plates
409 to determine bacterial CFU.
410

411 **Histology and ELISA**

412 Mouse brain tissue was frozen in OCT compound (Sakura) and sectioned using a
413 CM1950 cryostat (Leica). Sections were stained using hematoxylin and eosin (Sigma)
414 and images were taken using a BZ-X710 microscope (Keyence). Images were analyzed
415 using ImageJ software. Meningeal thickening was quantified from sections taken from
416 three different mice per group, and six images per slide. Meningeal thickening was
417 quantified across two points per image. KC protein from mouse brain homogenates was
418 detected by enzyme-linked immunosorbent assay according to the manufacturer's
419 instructions (R&D systems).
420

421 **Conflict of interest**

422 The authors have declared that no conflict of interest exists.
423

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427 *E. faecium* 1,231,410 DNA.
428

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Figure legends

Fig 1. Lipidomic profiling of GBS and identification of Lys-Glc-DAG synthesized by MprF. Total ion chromatogram (TIC) of LC/MS in A) negative ion mode, B) positive ion mode shows a major unknown lipid eluting at ~25-29 min. C) Positive ESI/MS showing the $[M+H]^+$ ions of the unknown lipid. D) Positive ion MS/MS spectrum of $[M+H]^+$ at *m/z* 885.6 and E) negative ion MS/MS spectrum of $[M-H]^-$ at *m/z* 883.6 of the unknown lipid. F) Lys-Glc-DAG (16:0/18:1) is proposed as the structure of the unknown lipid. G) TIC showing loss of Lys-Glc-DAG and Lys-PG in COH1Δ*mprF* which is present when *mprF* is complemented *in trans*. H) Lys-Glc-DAG and Lys-PG is only present in *S. mitis* when expressing GBS *mprF* compared to Lys-PG only when expressing *E. faecium mprF*. "*" denotes methylcarbamate of Lys-Glc-DAG, an extraction artifact due to the use of chloroform. I) Biosynthetic pathways involving MprF.

Fig 2. Contribution of lysine lipids to meningitis pathogenesis. A) *In vitro* assays for adherence and invasion of hCMEC cells indicates *mprF* contributes to invasion but not adherence to brain endothelium (mean of 3 replicate experiments with 4 technical replicates, mean and SEM). B) pH-adjusted medium growth indicates Δ*mprF* cannot survive in low pH conditions, mean and SD. Groups of CD-1 mice were injected intravenously with COH1 WT or COH1Δ*mprF* strains and bacterial counts were assessed in the C) brain and D) blood after 72h. Representative data from 2 independent experiments are shown (WT, $n = 20$; Δ*mprF,* $n = 19$). E) Hematoxylin-eosin-stained brain sections from representative mice infected with WT (top) or Δ*mprF* mutant (bottom); arrows indicate meningeal thickening and leukocyte infiltration. F) Quantification of meningeal thickening using ImageJ. G) KC chemokine production measured by ELISA. Panels C, D, F, and G) median indicated. Statistical analyses performed using GraphPad Prism: A) One-way ANOVA with Tukey's multiple comparisons test; C, D, F) unpaired two-tailed t-test; G) Mann-Whitney U test; p-values indicated; ns, no significance (p-value > 0.05).

Supplemental files

Supplemental Figure S1. Detection of Lys-PG and Lys-Glc-DAG in *S. agalactiae* A909 and *S. agalactiae* CNCTC 10/84.

Supplemental Figure S2. Isotopic incorporation of deuterated lysine and ^{13}C-labeled glucose into Lys-Glc-DAG and Lys-PG.

Supplemental Figure S3. Positive ion mass spectra of retention time 27-29 minutes of hypervirulent CJB111 strain.

Supplemental Figure S4. *In vitro* hCMEC adhesion and invasion of CJB111 strains.

Supplemental Table S1. Observed and calculated exact masses of the $[M+H]^+$ ions of Lys-Glc-DAG molecular species in *S. agalactiae* COH1.

Supplemental Table S2. Strains and plasmids used in this study.

614 Supplemental Table S3. Primers used in this study.
615

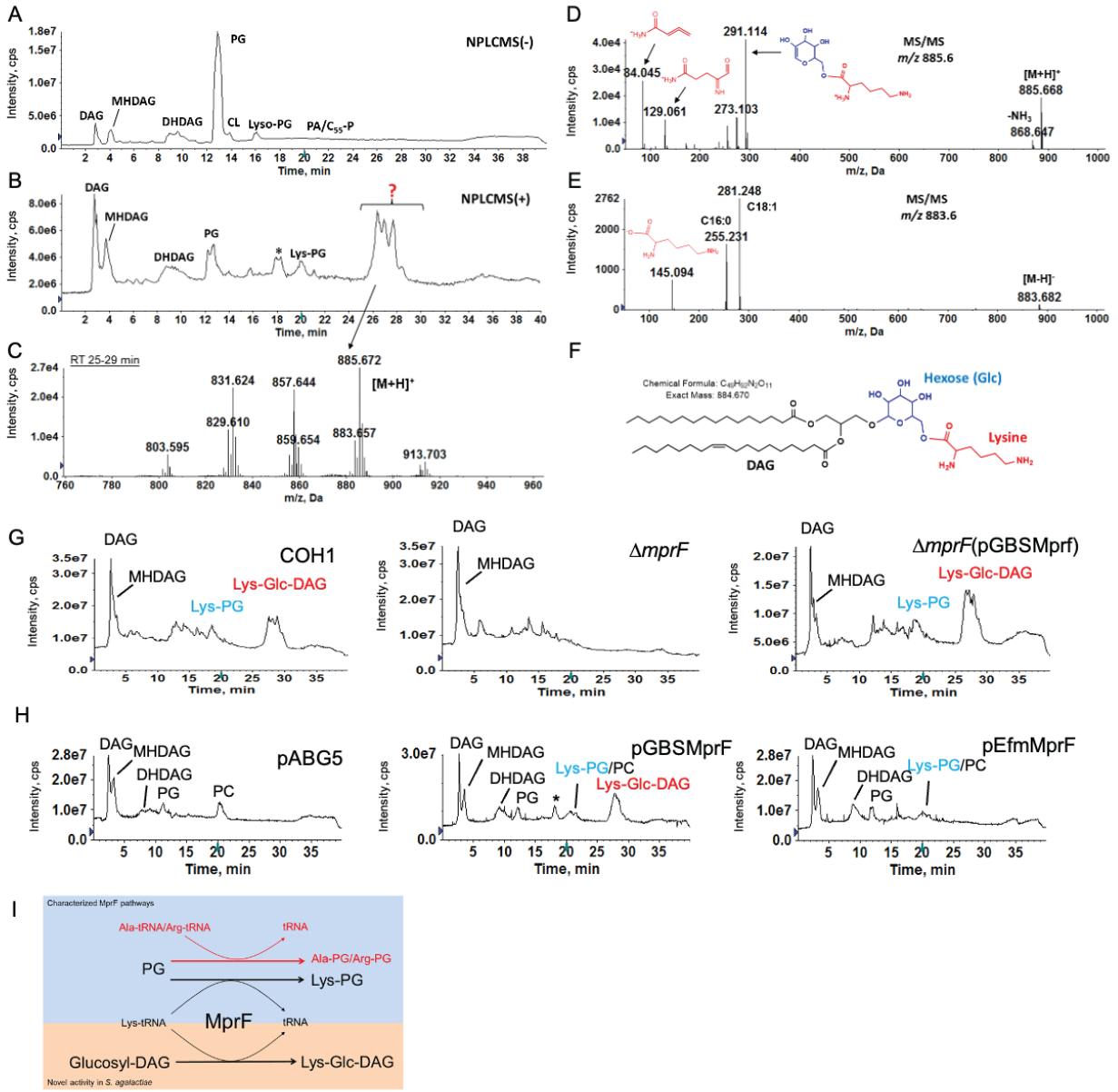

Fig 1. Lipidomic profiling of GBS and identification of Lys-Glc-DAG synthesized by MprF. Total ion chromatogram (TIC) of LC/MS in A) negative ion mode, B) positive ion mode shows a major unknown lipid eluting at ~25-29 min. C) Positive ESI/MS showing the $[M+H]^+$ ions of the unknown lipid. D) Positive ion MS/MS spectrum of $[M+H]^+$ at *m/z* 885.6 and E) negative ion MS/MS spectrum of $[M-H]^-$ at *m/z* 883.6 of the unknown lipid. F) Lys-Glc-DAG (16:0/18:1) is proposed as the structure of the unknown lipid. G) TIC showing loss of Lys-Glc-DAG and Lys-PG in COH1Δ*mprF* which is present when *mprF* is complemented *in trans*. H) Lys-Glc-DAG and Lys-PG is only present in *S. mitis* when expressing GBS *mprF* compared to Lys-PG only when expressing *E. faecium mprF*. "*" denotes methylcarbamate of Lys-Glc-DAG, an extraction artifact due to the use of chloroform. I) Biosynthetic pathways involving MprF.

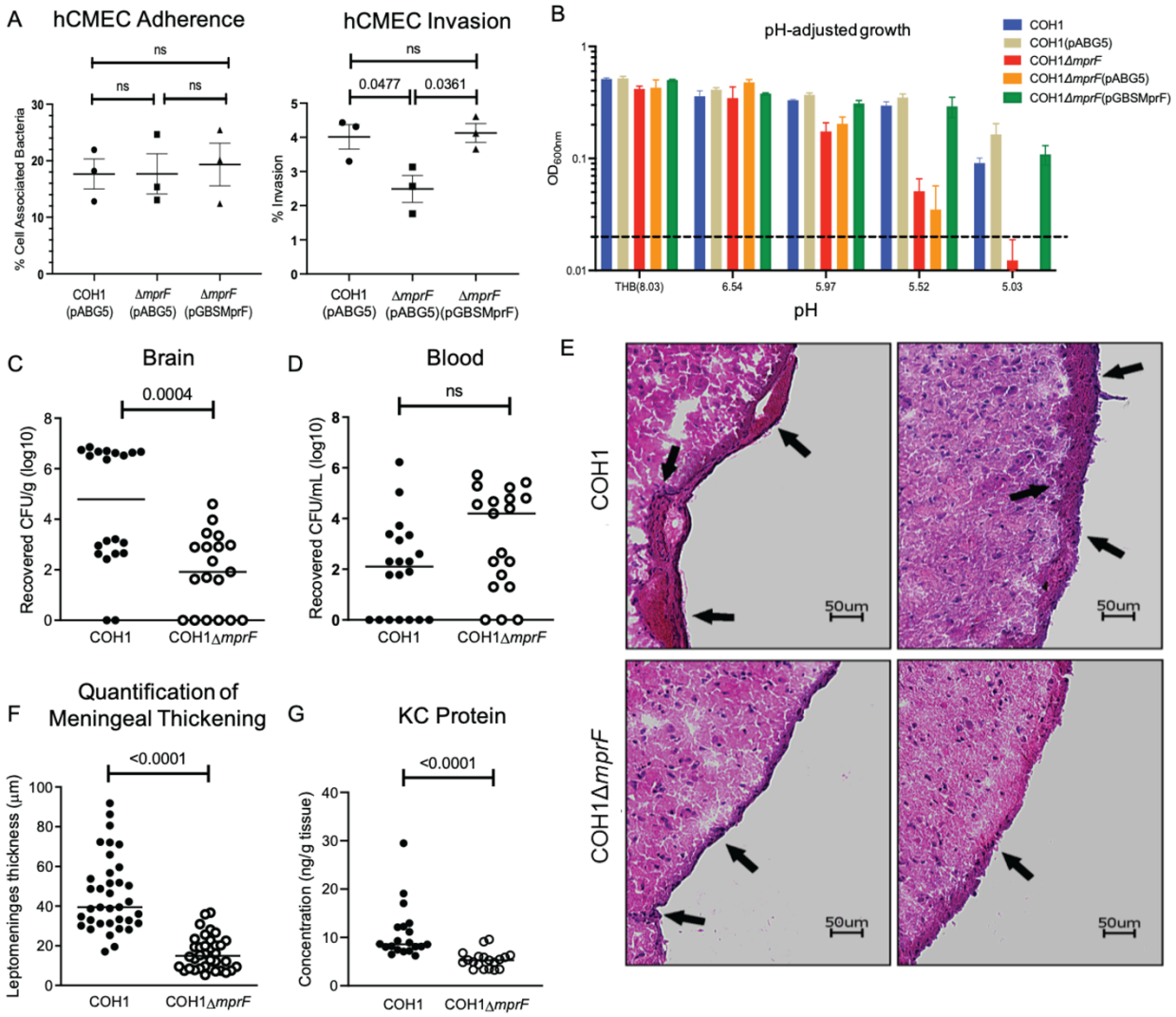

Fig 2. Contribution of lysine lipids to meningitis pathogenesis. A) *In vitro* assays for adherence and invasion of hCMEC cells indicates *mprF* contributes to invasion but not adherence to brain endothelium (mean of 3 replicate experiments with 4 technical replicates, mean and SEM). B) pH-adjusted medium growth indicates Δ*mprF* cannot survive in low pH conditions, mean and SD. Groups of CD-1 mice were injected intravenously with COH1 WT or COH1Δ*mprF* strains and bacterial counts were assessed in the C) brain and D) blood after 72h. Representative data from 2 independent experiments are shown (WT, $n = 20$; Δ*mprF*, $n = 19$). E) Hematoxylin-eosin-stained brain sections from representative mice infected with WT (top) or Δ*mprF* mutant (bottom); arrows indicate meningeal thickening and leukocyte infiltration. F) Quantification of meningeal thickening using ImageJ. G) KC chemokine production measured by ELISA. Panels C, D, F, and G) median indicated. Statistical analyses performed using GraphPad Prism: A) One-way ANOVA with Tukey's multiple comparisons test; C, D, F) unpaired two-tailed t-test; G) Mann-Whitney U test; p-values indicated; ns, no significance (p-value > 0.05).

644 **Supplemental Figures, and Tables**

645 **Identification of a novel cationic glycolipid in *Streptococcus agalactiae* that**

646 **contributes to brain entry and meningitis**

647

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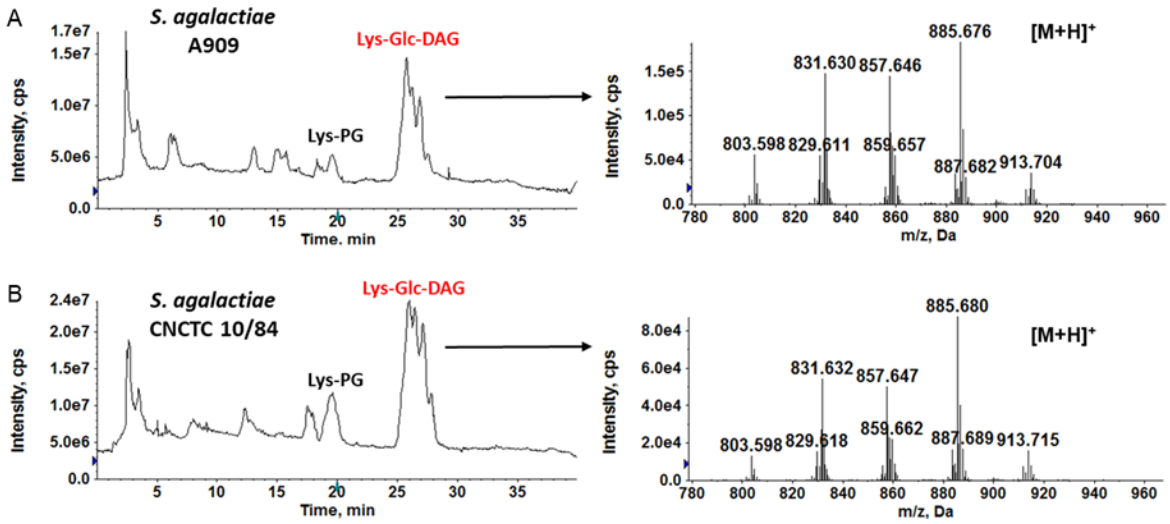
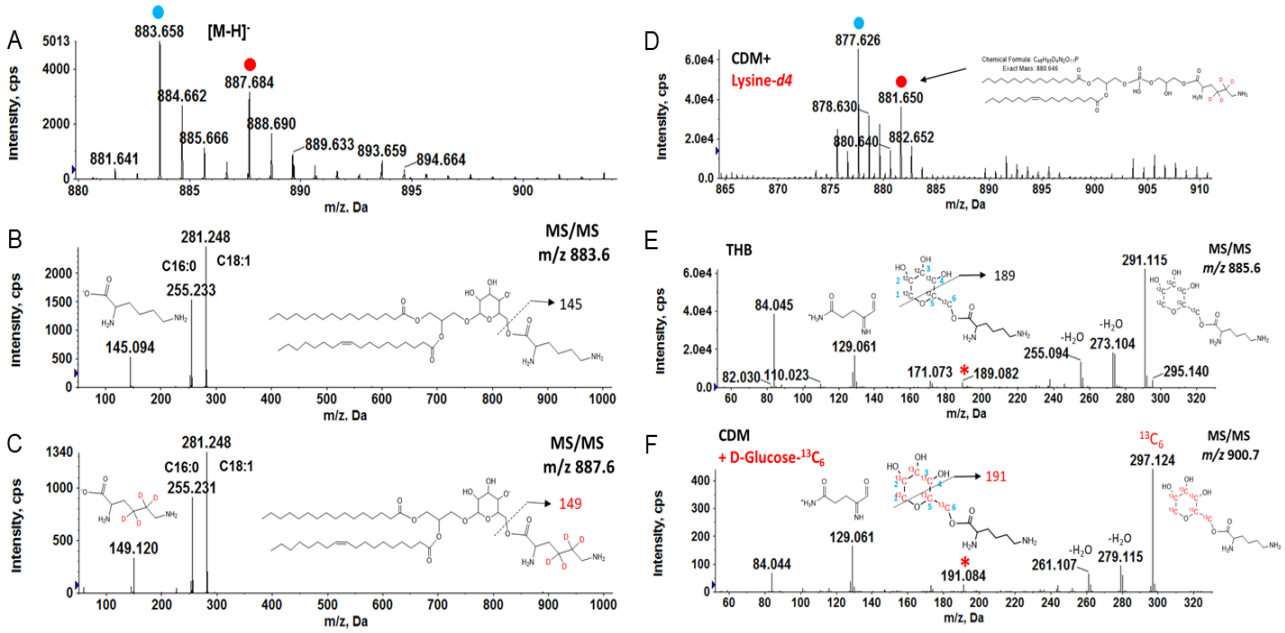
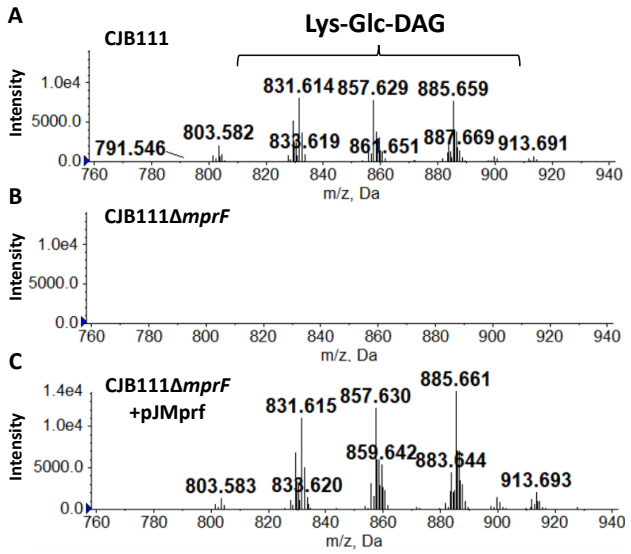


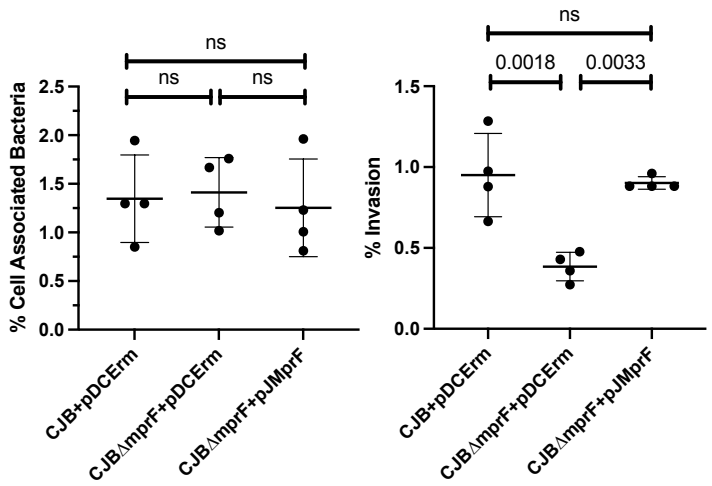
Supplemental Figure S1. Detection of Lys-PG and Lys-Glc-DAG in *S. agalactiae* A909 and *S. agalactiae* CNCTC 10/84. Positive TICs (left panels) showing the presence of Lys-PG and Lys-Glc-DAG in S. *agalactiae* A909 and S. *agalactiae* CNCTC 10/84. Mass spectra (right panels) show the $[M+H]^+$ ions of Lys-Glc-DAG.



Supplemental Figure S2. Isotopic incorporation of deuterated lysine and ^{13}C-labeled glucose into Lys-Glc-DAG and Lys-PG. The lipid extracts of *S. agalactiae* COH1 cultured in DM, DM supplemented with 450 µM L-lysine-*d4* (4,4,5,5-D4), or in DM containing 0.5% w/v D-Glucose (U-$^{13}C_6$) were analyzed by LC-ESI/MS in the positive ion mode. A) Negative ESI/MS of [M-H]$^-$ ions of major Lys-Glc-DAG species in *S. agalactiae* COH1 when cultured in DM supplemented with lysine-*d4*. The incorporation of lysine-*d4* into Lys-Glc-DAG is evidenced by an upward *m/z* shift of 4 Da of the [M-H]$^-$ ion (from *m/z* 883 to *m/z* 887). B) MS/MS of [M-H]$^-$ at *m/z* 883.6 produces a deprotonated lysine residue at *m/z* 145. C) MS/MS of [M-H]$^-$ at *m/z* 887.6 produces a deprotonated lysine-*d4* residue at *m/z* 149. D) [M+H]$^+$ ions of major Lys-PG species in *S. agalactiae* COH1 cultured in DM supplemented with lysine-*d4.* The incorporation of lysine-*d4* in Lys-PG is evidenced by an upward *m/z* shift of 4 Da from unlabeled Lys-PG (blue dot) to labeled Lys-PG (red dot). E) MS/MS of 885.6. A major product ion at *m/z* 291.1 is derived from glucose-lysine residue. F) MS/MS of *m/z* 900.7 (containing fifteen ^{13}C atoms). The presence of *m/z* 297.1 (with 6 Da shift) is consistent with glucose in Lys-Glc-DAG is replaced with D-Glucose (U-$^{13}C_6$). The other nine ^{13}C atoms are incorporated into the DAG portion of Lys-Glc-DAG. Furthermore, MS/MS data indicate that lysine is linked to the C6 position of glucose by the fragmentation schemes for forming *m/z* 189 ion from the unlabeled Lys-Glc-DAG and *m/z* 191 ion from the ^{13}C-labeled Lys-Glc-DAG.



Supplemental Figure S3. Positive ion mass spectra of retention time 27-29 minutes of hypervirulent CJB111 strain. Lys-Glc-DAG is present in the membrane of WT CJB111 (A). Deletion of *mprF* from CJB111 genome results in loss of Lys-Glc-DAG from the membrane (B). *MprF* complemented *in trans* reestablishes Lys-Glc-DAG back into the membrane (C).



Supplemental Figure S4. *In vitro* hCMEC adhesion and invasion of CJB111 strains. *In vitro* assays for adherence and invasion of hCMEC cells indicates *mprF* contributes to invasion but not adherence to brain endothelium. Data indicates the percentage of the initial inoculum that was recovered. Experiments were performed three times with each condition in quadruplicate. Data from one representative experiment is shown, mean and standard deviation indicated. One-Way ANOVA with Tukey's multiple comparisons statistical test was used. P-values indicated; ns, not significant.

704 **Supplemental Table S1. Observed and calculated exact masses of the $[M+H]^+$ ions**
705 **of Lys-Glc-DAG molecular species in *S. agalactiae* COH1.**

Lys-Glc-DAG[1]	$[M+H]^+$	
	Observed mass	Exact mass
C28:1	801.575	801.583
C28:0	803.595	803.599
C30:1	829.610	829.615
C30:0	831.624	831.630
C32:2	855.623	855.630
C32:1	857.644	857.646
C34:2	883.657	883.622
C34:1	885.672	885.677
C36:2	911.686	911.693
C36:1	913.703	913.709

706

707 [1]The numbers before and after colons indicate the total acyl chain carbon atoms and
708 double bonds, respectively.

709 **Supplemental Table S2. Strains and plasmids used in this study.**

Organism	Strain	Description	Ref
S. agalactiae	ATCC BAA-1176 (COH1)	Wild-type *S. agalactiae* strain, serotype III	(1)
	COH1Δ*mprF*	*mprF* (GBSCOH1_1931) deletion strain	This work
	COH1Δ*mprF(*pABG5)	Empty vector control strain	This work
	COH1Δ*mprF*(pGBSMprf)	Expresses GBS *mprF* from P_{prtF} in pABG5Δ*phoZ*	This work
	COH1(pABG5)	Empty vector control	This work
	CJB111	Wilt-type *S. agalactiae* strain, serotype V	(2, 3)
	CJB111Δ*mprF*	*mprF* (ID870_10050) deletion strain	This work
	CJB111Δ*mprF*(pDCErm)	Empty vector control strain	This work
	CJB111Δ*mprF*(pJMprF)	Expresses GBS *mprF* in pDCErm	This work
	ATCC BAA-1138 (A909)	Wild-type *S. agalactiae* strain, serotype Ia	(4)
	CNCTC 10/84	Wild-type *S. agalactiae* strain, serotype V. Obtained from Dr. K Patras, UCSD	(5, 6)
S. mitis	ATCC 49456	Wild-type *S. mitis* type strain, also known as NCTC 12261	(7)
	ATCC 49456(pABG5)	Empty vector control	This work
	ATCC 49456(pGBSMprF)	Expresses GBS *mprF* from P_{prtF} in pABG5Δ*phoZ*	This work
	ATCC 49456(pEfmMprF1)	Expresses *E. faecium mprF1* from P_{prtF} in pABG5Δ*phoZ*	This work
	ATCC 49456(pEfmMprF2)	Expresses *E. faecium mprF1* from P_{prtF} in pABG5Δ*phoZ*	This work
E. coli	DH5α	Plasmid cloning host; F^-, φ80*lac*ZΔM15, *rec*A1, *end*A1, *hsd*R17, *pho*A, *sup*E44, λ^- *thi*-1, *gyr*A96, *rel*A1	(8)
	DH5α(pABG5)	Empty vector control	This work
	MC1061	Plasmid cloning host; F^-, araD139, Δ(araABC-leu)7696, Δ(lac)X74, galU, galK, hsdR2, (r_K^- m_K^+), mcrB1, rpsL, (Str^r)	(9)

	MC1061(pDCErm)	Empty vector control	This work
	DH5α(pGBSMprF)	Expresses COH1 *mprF* (GBSCOH1_1931) from P_{prtF} in pABG5Δ*phoZ*	This work
	DH5α(pEfmMprF1)	Expresses *E. faecium mprF1* from P_{prtF} in pABG5Δ*phoZ*	This work
	DH5α(pEfmMprF2)	Expresses *E. faecium mprF1* from P_{prtF} in pABG5Δ*phoZ*	This work
	DH5α(pMBMprFKO)	Allelic exchange plasmid containing ~2 kb sequence flanking GBSCOH1_1931	This work
	MC1061(pJMprFKO)	Allelic exchange plasmid containing ~2 kb sequence flanking ID870_10050	This work
	MC1061(pJMprF)	Expresses CJB11 *mprF* from $P_{tetM/erm}$ in pDCErm	This work
E. faecium	1,231,410	Wild type *E. faecium* strain	(10)

Plasmid	**Description**	**Ref**
pABG5Δ*phoZ*	Constitutive expression vector for streptococci with the P_{prtF} promoter. Confers kanamycin resistance. Referred to as pABG5 throughout the text	(11)
pGBSMprF	pABG5Δ*phoZ* expressing COH1 *mprF* (GBSCOH1_1931) from P_{prtF}	This work
pEfmMprF1	pABG5Δ*phoZ* expressing *E. faecium* 1,231,410 *mprF1* (EFTG_00601) from P_{prtF}	This work
pMBSacB	Allelic exchange plasmid for *S. agalactiae*. Confers erythromycin resistance and sucrose sensitivity	(12)
pMBMprFKO	Knockout plasmid containing ~2 kb sequence flanking GBSCOH1_1931	This work
pJMprFKO	Knockout plasmid containing ~2 kb sequence flanking ID870_10050	This work
pDCErm	Consitituitive expression vector for streptococcus from $P_{tetM/erm}$	(13)
pJMprF	pDCErm expressing CJB111 *mprF* (ID870_10050)	This work

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712 **Supplemental Table S3. Primers used in this study.**

Primer	5' – 3' sequence	Use
GBS_MprF_F	GAGAGGTCCCTTTCCTTGAAAAAGCTAATTGAAAAAGTC	Amplify GBSCOH1_1931 for Gibson assembly
GBS_MprF_R	ACCAATACCTTTATCTTATTTAACAATCTTAATTTTACTATC	Amplify GBSCOH1_1931 for Gibson assembly
Faec_MprF1_F	GAGAGGTCCCTTTCCTTGTTAAAAAATACCATACAATG	Amplify EFTG_00601 for Gibson assembly
Faec_MprF1_R	ACCAATACCTTTATCTTAATACTTTCTTCGTATCC	Amplify EFTG_00601 for Gibson assembly
MpF_SacII	ACGTCACCGCGGTTGAAAAAGCTAATTGAAAAAGTC	Amplify CJB111 *mprF* ID870_10050 for ligation
MpR_BamHI	ACGTCAGGATCCTTATTTAACAATCTTAATTTTACTATC	Amplify CJB111 *mprF* ID870_10050 for ligation
pABG5-5'	GGAAAGGGACCTCTCTTCCTAAAC	Linearize pABG5Δ*phoZ* for Gibson assembly
pABG5-3'	GATAAAGGTATTGGTAAATAACAAA	Linearize pABG5Δ*phoZ* for Gibson assembly
	Expression plasmid sequencing	
GBS_S1	GAATGGAATAATATAGTAGGCT	For sequencing pGBSMprF/pJMprF, amplifies with pABG5_Fup2/ pF
GBS_S2	GATTGTATCCCTTATTCC	For sequencing pGBSMprF/pJMprF, amplifies with GBS_S3
GBS_S3	CGATTCAATAGCTTCAC	For sequencing pGBSMprF/pJMprF, amplifies with GBS_S2
GBS_S4	GATAAAAGGCTCTACTGG	For sequencing pGBSMprF/pJMprF, amplifies with pABG5_FDwn/pR
pABG5_FDwn	CCAATAATAATGACTAGAGAAG	For pABG5 plasmid insert sequencing
pABG5_Fup2	CAAAAGGTTTCGACTTTTCACC	For pABG5 plasmid insert sequencing
EF1_S1	GAATAACGCTGATCAAAAGT	For sequencing pEfmMprF1, amplifies with pABG5_Fup2
EF1_S2	TGCCAAGAGAAATAGTC	For sequencing pEfmMprF1, amplifies with EF1_S3
EF1_S3	ACAATCTCTTCGCTTG	For sequencing pEfmMprF1, amplifies with EF1_S2
EF1_S4	CCAACTGTTCTTCTCCAA	For sequencing pEfmMprF1, amplifies with pABG5_FDwn
pF	AGCGCTAGGAGGAAAC	For pDCErm plasmid insert sequencing
pR	CCCATGCCATCTCCAATC	For pDCErm plasmid insert sequencing
GBSCOH1_1931 knockout plasmid construction, sequencing, and integration screening		
Mp1F_PstI	ACGTCACTGCAGTTCAATTAGCTTTTTCAACAATTTC	Amplifies upstream fragment from within GBSCOH1_1931/ID870_10050 leaving 6 codons, with Mp1R_XhoI
Mp1R_XhoI	ACGTCACTCGAGGCTGTTTATGGTGCTTTG	5' most primer of upstream fragment, amplifies with Mp1F_PstI
Mp2F_XbaI	ACGTCATCTAGAGAAAAGGCTAGATTACGAAC	3' most primer of downstream fragment, amplifies with Mp2R_PstI
Mp2R_PstI	ACGTCACTGCAGGTTAAATAAGCTTTATTTGGCA	Amplifies downstream fragment leaving 2 codons and stop codon of GBSCOH1_1931/ID870_10050, with Mp2F_XbaI
T7 promoter	TAATACGACTCACTATAGGG	Amplifies with MpS5F below to sequence plasmid, amplifies with T3 promoter for insert screening and plasmid presence
T3 promoter	AATTAACCCTCACTAAAGGG	Amplifies with MpS3R below, amplifies with T7 promoter for insert screening and plasmid presence
Int_F	GCTAATTGAACTGCAGGTTAAATAAG	Anneals at *mprF* knockout site, amplifies with Out_R for single integration screening

Out_R	GCTATTATATTTAGTGGTTTAATTGG	Anneals outside recombination arms, amplifies with Int_F, for single integration screening
Genomic knockout region sequencing		
MpS3F	CATTAGCTAGTCTTATCGGAG	Anneals outside integration arms, amplifies with MpS3R
MpS3R	ACAGCTACTTGGTAGTTCA	Amplifies with MpS3F
MpS4F	GCTACTAAGGCAAGATACG	Amplifies with MpS4R, knockout screening and plasmid sequencing primer
MpS4R	ATGGTCAGCGATGGTG	Amplifies with MpS4F, knockout screening and plasmid sequencing primer
MpS5F	CATAAGCGAAATAACTTGAG	Amplifies with MpS5R
MpS5R	GTATACAACGGCTTGATTGG	Anneals outside integration arms, amplifies with MpS5F

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