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Loop Mediated Isothermal Amplification (LAMP) assay for Rapid detection of *Streptococcus agalactiae* (Group B Streptococcus - GBS) in vaginal swabs - A Proof of Concept Study

McKenna, J., Cox, C., Fairley, D. J., Burke, R., Shields, M. D., Watt, A., & Coyle, P. V. (2017). Loop Mediated Isothermal Amplification (LAMP) assay for Rapid detection of *Streptococcus agalactiae* (Group B Streptococcus - GBS) in vaginal swabs - A Proof of Concept Study. *Journal of Medical Microbiology*, 66(3), 294-300. DOI: 10.1099/jmm.0.000437

Published in:

Journal of Medical Microbiology

Document Version:

Peer reviewed version

Queen's University Belfast - Research Portal:

[Link to publication record in Queen's University Belfast Research Portal](#)

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1 **Loop-Mediated Isothermal Amplification (LAMP) assay for Rapid detection of**
2 ***Streptococcus agalactiae* (Group B Streptococcus - GBS) in vaginal swabs – A Proof of**
3 **Concept Study**

4

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14

15 **Abstract**

16 Neonatal infection with *Streptococcus agalactiae* (Group B streptococcus – GBS) is a life
17 threatening condition which is preventable if colonised mothers are identified and given
18 antibiotic prophylaxis during labour. Conventional culture is time consuming and unreliable,
19 and many available non-culture diagnostics are too complex to implement routinely at point
20 of care. Loop-mediated isothermal amplification (LAMP) is a method which enables the
21 rapid and specific detection of target nucleic acid sequences in clinical material without any
22 requirements for extensive sample preparation. A prototype LAMP assay targeting the GBS
23 *sip* gene is described. The assay was 100% specific for GBS with a Limit of Detection of 14
24 genome copies per reaction. The clinical utility of the prototype LAMP assay for rapid direct
25 molecular detection of GBS was determined by testing a total of 157 vaginal swabs with

26 minimal sample processing using a rapid lysis solution. Compared to a reference qPCR assay
27 the direct LAMP protocol had a sensitivity and specificity of 95.4% and 100% with a Positive
28 Predictive Value (PPV) and Negative Predictive Value (NPV) of 100% and 98.3%. Positive
29 (LR+) and negative (LR-) likelihood ratios were infinity and 0.05 respectively. The direct
30 LAMP method took a mean of 45 minutes from receipt of a swab to generation of confirmed
31 result compared to 2 hours 30 minutes for the reference qPCR test. The direct LAMP
32 protocol described is easy to perform facilitating rapid and accurate detection of GBS in
33 vaginal swabs. This test has potential for use at point of care.

34

35 **Introduction**

36 *Streptococcus agalactiae* (Group B streptococcus - GBS) is the leading cause of early onset
37 neonatal sepsis [1-5]. Asymptomatic GBS colonisation of the vagina and lower
38 gastrointestinal tract occurs in 10-30% of pregnant women and is the most significant risk
39 factor for neonatal GBS disease as transmission can occur from the recto/vaginal area during
40 childbirth [4,6-9]. The implementation of culture based antepartum screening programmes for
41 all pregnant women at 34-38 weeks and initiating intrapartum antibiotic prophylaxis has
42 helped to reduce but not eliminate neonatal early onset disease (EOD) in many industrialised
43 countries [4,10,11]. Despite technological advances the primary method for detection of GBS
44 colonisation remains selective laboratory based culture of vaginal and/or rectal swab
45 specimens followed by ancillary confirmation tests. This approach demonstrates variable
46 sensitivity [12-14] and is associated with long turnaround times of 18-72 hours rendering
47 culture unfeasible as an intrapartum test. Thus, women who give birth prematurely are not
48 screened, and women who become colonised after screening are not identified [7,8]. A
49 sensitive screening assay which could rapidly determine GBS status during labour would be

50 beneficial as it would facilitate targeted therapy whilst reducing the risks associated with
51 antibiotic use in non-colonised women [15].

52 Quantitative Polymerase Chain Reaction (qPCR) assays can provide test results in a few
53 hours [15-20]. However, requirements for expensive equipment, intricate sample preparation,
54 skilled staff and/or support precludes the use of PCR at point of care (POC) [21-23].

55 Loop-mediated isothermal amplification (LAMP) is an isothermal molecular amplification
56 technique which offers simple qualitative detection combined with exceptional sensitivity and
57 specificity [24-26]. The single reaction temperature (60 – 65⁰C) employed by LAMP means
58 there are no requirements for thermocycling resulting in a need for less complex equipment
59 making it amenable to use at POC [22,27]. Furthermore compared to PCR, LAMP is also
60 demonstrably more resistant to inhibitors found in clinical material indicating potential for
61 direct application to clinical specimens and/or crude sample preparations [21,28,29]. This is
62 advantageous as one of the issues frequently hampering application of Nucleic acid
63 amplification tests (NAAT) at POC are requirements to perform dedicated multistep nucleic
64 acid extraction steps which add to test complexity, cost and turnaround time [21-23]. Whilst a
65 number of LAMP assays for GBS detection have been developed previously, they are not
66 amenable for POC use having requirements for an 18-24 hr pre-enrichment culture step [20],
67 require multiple time consuming manipulations prone to contamination [30] or have
68 unproven clinical efficacy [31,32].

69 Here we describe a newly designed GBS LAMP assay targeting *S. agalactiae sip* gene. As a
70 proof of concept the LAMP assay was applied to residual vaginal swabs which had
71 undergone minimal sample processing (Direct detection – no extraction protocol) with a rapid
72 lysis solution containing the bacteriolytic enzyme achromopeptidase (ACH). ACH
73 demonstrates high lytic activity against a range of gram positive cocci including GBS [23,33-
74 35].

75 **Materials and Methods**

76

77 *Clinical Specimens:* The study was approved by the Office for Research Ethics committee
78 Northern Ireland (reference 09/NIR02/43). A total of 157 residual vaginal swabs from
79 pregnant women submitted to Department of Microbiology, Belfast Health and Social Care
80 Trust (BHSCT) for bacterial investigations between March – July 2013 were
81 opportunistically collected and utilised for the clinical validation study. The sample set
82 consisted of 153 High Vaginal swabs (HVS) and 4 Low Vaginal Swabs (LVS). All vaginal
83 swabs were collected on plastic rayon tipped swabs (Sterilin Ltd., Newport, UK) and
84 transported to laboratory in AMIES transport medium. Culture of all swab specimens was
85 carried out according to BHSCT Standard Operating Procedure by laboratory staff unaware
86 that the samples were to be subsequently included in a study. Briefly, each swab was plated
87 onto Columbia Blood agar (CBA) and differential Granada™ agar (bioMérieux, Basingstoke,
88 UK). CBA plates were incubated in 10% CO₂ atmosphere with Granada™ plates incubated
89 anaerobically at 37⁰C. Plates were examined at 18-24 hours and again at 48 hours with
90 presumptive positive GBS colonies on Granada™ agar identified by production of orange
91 pigment. Presumptive GBS colonies on CBA were identified on the basis of haemolysis. All
92 suspect colonies were appropriately identified by a combination of standard tests including
93 Gram stain, catalase activity and latex agglutination using SLIDEX® Strepto Plus kit
94 (bioMérieux, Basingstoke, UK) to identify the presence of Group B antigen. Following
95 routine bacteriological culture all residual swabs were stored at +4⁰C for a maximum of one
96 week until required for processing and molecular analysis.

97

98 *Rapid Sample preparation method for direct LAMP:* Lysis solution consisted of 10 U/L of
99 achromopeptidase (ACH) (Sigma-Aldrich, Dorset, UK) in 10 mmol/L Tris-HCL pH8.0, 1

100 mmol/L EDTA (Sigma-Aldrich, Dorset, UK). Residual swab specimens were removed from
101 AMIES transport medium tubes with ~2 cm end physically broken off into 400 µl pre
102 aliquoted lysis solution [ACH] by firmly pressing the swab against the side of a microfuge
103 tube (Sarstedt, Leicester, UK). Tubes were capped and swabs incubated at ambient 'room
104 temperature' (22 - 24⁰C) for 5 minutes before boiling at 95⁰C for 5 minutes in a dedicated
105 heat block to simultaneously deactivate ACH and denature any target DNA for LAMP
106 analysis. Samples were immediately cooled by placing directly on ice. A 5µl aliquot of lysis
107 supernatant was used for GBS direct LAMP testing as outlined below. Remaining lysis
108 supernatant was stored at 4⁰C.

109

110 *Nucleic acid (NA) extraction for qPCR and indirect LAMP:* GBS reference and clinical
111 isolates were pre-treated with ACH before undergoing total nucleic acid extraction using
112 QIAamp blood DNA mini extraction kit (Qiagen, Crawley, UK). A 200 µl saline suspension
113 of each GBS isolate was prepared and added to an equal volume of ACH 20 U/L for a final
114 working concentration of ACH of 10 U/L. The suspension was incubated at room
115 temperature for 5 minutes before being boiled at 95⁰C/5 minutes. 200 µl aliquot of each
116 lysate was then added to AL lysis buffer (Qiagen, Crawley, UK) and processed as per
117 manufacturer's instructions to produce 100 µl of genomic extract.

118 Bacterial and fungal genomic DNA for specificity evaluation was obtained using QIAamp
119 blood DNA mini extraction kit (Qiagen, Crawley, UK). 200 µl saline suspensions of each
120 target organism were added to AL lysis buffer and processed as per manufacturer's
121 instructions to produce 100 µl of genomic extract.

122 Vaginal swab lysates were extracted as follows; A 200 µl aliquot of ACH lysis supernatant
123 (produced as indicated in previous section) was removed from each clinical swab specimen
124 and extracted using MagNA Pure 96 viral NA small volume kit and MagNA Pure instrument

125 (Roche Diagnostics, Mannheim, Germany) as per manufacturer's instructions. Resultant 100
126 μ l genomic extract aliquots were stored at -80°C until required for qPCR and LAMP
127 (indirect) analysis.

128

129 *LAMP primers and reaction:* LAMP primers targeting a highly conserved region of *S.*
130 *agalactiae sip* gene (HiberGene Diagnostics, Ireland) were employed throughout. The LAMP
131 primer set consisted of forward (sip_FIP) and reverse (sip_BIP) 'inner' primers, forward
132 (sip_F3) and reverse (sip_B3) 'outer' primers and forward (sip_FL) and reverse (sip_BL)
133 'loop' primers. Optimised GBS LAMP consisted of 5 μ l of template DNA, 12.5 μ l of LAMP
134 isothermal Master Mix ISO 001 (OptiGene Ltd., Horsham, UK) containing novel strand
135 displacing DNA polymerase (*GspSSD*), propriety thermostable inorganic pyrophosphatase,
136 reaction buffer, MgCl, dNTP's, DNA intercalating dye, 2 μ M each of FIP and BIP, 0.2 μ M
137 each of F3 and B3, 1 μ M each of FL and BL and Nuclease Free Water (Promega,
138 Southampton, UK) for a final reaction volume of 25 μ l. The GENIE® II (OptiGene Ltd,
139 Horsham, UK) real time fluorometer was utilised for concurrent target isothermal
140 amplification and detection. LAMP reactions were performed at a previously identified
141 optimal reaction temperature of 62°C for 30 minutes followed by a heating and cooling step
142 to $98-80^{\circ}\text{C}$ (0.05°C/s) which allows re-annealing of amplified DNA and display of a
143 specific annealing curve. Positive and negative controls were included for each run and
144 stringent precautions undertaken to prevent cross contamination. Positive LAMP reactions
145 were identified by GENIE® II (OptiGene Ltd, Horsham, UK) instrument software. In the
146 results section each positive reaction had a Time to positivity (T_T) value in minutes and
147 seconds and a specific melting point temperature (T_m) in degrees centigrade ($^{\circ}\text{C}$).

148

149 *Real Time PCR (qPCR)*: qPCR was employed as the reference molecular detection method.
150 Primer and hybridisation probe sequences targeting *S. agalactiae sip* gene were as previously
151 described [17]. Primer sequences as follows: Forward primer 5'–
152 ATCCTGAGACAACACTGACA–3', and reverse primer 5'–
153 TTGCTGGTGTCTATTTTCA–3'. The hybridisation probe 5'–
154 ATCAGAAGAGTCATACTGCCACTTC3' contained a FAM label on 5' end with a Black
155 Hole Quencher 1 (BHQ1) on 3' end. Primers and hybridisation probe were synthesised by
156 Eurogentec (Eurogentec, Liège Belgium). The final qPCR reaction mix contained 1X
157 Platinum® UDG Mastermix (Life Sciences, Paisley, UK), 0.2 µM Bovine serum albumin
158 (Sigma, Dorset, UK), total of 4 mmol/L MgCl₂, 0.4 µM forward and reverse primers, 0.2 µM
159 hybridisation probe, Nuclease Free Water (Promega, Southampton, UK) and 3 µl of target
160 template for a final reaction volume of 12 µl. qPCR was performed using a Light Cycler 480
161 (LC480) instrument (Roche Diagnostics, Mannheim, Germany). A No Template Control
162 (NTC) consisting of Nuclease Free Water (Promega, Southampton, UK) and a plasmid
163 reference standard containing 3.50E06 *sip* genome copies per ml were included for all qPCR
164 runs. The qPCR run parameters consisted of an initial step of 95°C for 10 minutes followed
165 by an amplification program for 45 cycles of 10 seconds at 95°C, 30 seconds at 60°C, 1
166 second at 72°C with fluorescence acquisition at the end of each extension. Data was analysed
167 using LC480 software and GBS genome copy number for positive specimens determined
168 from crossing point threshold (Cp) relative to an external positive control curve.

169

170 *Specificity & sensitivity*: Specificity of GBS LAMP was evaluated using total genomic
171 extracts (containing approximately 10E07 genome copies) derived from a range of bacteria
172 (n=55) and fungi (n=1). These included a number of GBS reference, clinical and veterinary
173 isolates (n=17). Reaction mix without DNA template was included as a negative control.

174 The following organisms were tested; *Streptococcus agalactiae* (NCTC 11360, NCTC 8187,
175 NCTC 11078, NCTC 11079, NCTC 11080, NCTC 11930, NCTC 9829, ATCC 12386, ID:
176 603532, ID: 603535, ID: 605872, RVH2419/12, RVH2543/12, RVH60/13, RVH524/13,
177 VSD04988, VSD04946), *Streptococcus pneumoniae* (ATCC 49619, RVH59/07),
178 *Streptococcus parasanquis* (RVH74/07), *Streptococcus intermedius* (RVH305/07),
179 *Streptococcus pyogenes* (ATCC 19615), *Streptococcus salivarius* (RVH557/13),
180 *Streptococcus vestibularis* (RVH527/13), *Streptococcus mitis/oralis* (RVH508/13),
181 *Streptococcus dysgalactiae* (RVH497/13), *Streptococcus anginosus* (RVH452/13),
182 *Staphylococcus aureus* (ATCC 25923), MRSA (NCTC 10442), *Staphylococcus epidermidis*
183 (ATCC 12228), *Staphylococcus lugdunensis* (RVH isolate), *Staphylococcus capitis* (RVH
184 isolate), *Enterococcus faecalis* (ATCC 29212, RVH009/07), *Micrococcus luteus*
185 (RVH290/07), *Brevibacillus brevis* (RVH381/13), *Bacillus cereus* (RVH299/13), *Neisseria*
186 *meningitidis* (NCTC 10791 serogroup Y, RVH531/07 serogroup B), *Neisseria sicca*
187 (RVH920/06), *Klebsiella pneumoniae* (RVH45/07), *Klebsiella oxytoca* (RVH135/07),
188 *Enterobacter aerogenes* (NCTC 10006, RVH001/07), *Enterobacter cloacae* (NCTC 9394),
189 *Serratia marcescens* (RVH287/07), *Acinetobacter baumannii* (RVH36/07), *Acinetobacter*
190 *lwoffii* (RVH98/07), *Escherichia coli* (NCTC 9001, ATCC 25922), *Citrobacter freundii*
191 (NCTC 9750), *Haemophilus influenzae* (NCTC 4560), *Sphingobacterium spiritivorum*
192 (ATCC 33861), *Stenotrophomonas maltophilia* (ATCC 17666), *Pseudomonas aeruginosa*
193 (ATCC 27853), *Gardnerella vaginalis* (ATCC 49145), *Candida albicans* (ATCC 10028).
194 LAMP analytical sensitivity (limit of detection - LOD) was determined using tenfold serial
195 dilutions of *S. agalactiae* ATCC 12386 nucleic acid extracts analysed in duplicate containing
196 2.8E07 to 2.8E02 genome copies per ml respectively. A No Template Control (NTC)
197 consisting of Nuclease Free Water (Promega, Southampton, UK) was included with all
198 LAMP runs.

199 *Statistical analysis:* For purposes of validation the reference molecular method was defined
200 as achromopeptidase (ACH) pre-treatment of a clinical swab specimen followed by Nucleic
201 Acid (NA) extraction and qPCR testing. A specimen was considered a true positive if: (i)
202 GBS was obtained following culture; or (ii) Specimen was identified as GBS qPCR positive.
203 All qPCR and LAMP results were compared with routine culture results. Sensitivity,
204 specificity, positive predictive value (PPV), negative predictive values (NPV), positive (LR+)
205 and negative (LR-) likelihood ratios for each test method were calculated. The level of
206 agreement between LAMP and qPCR assays was assessed using Kappa (κ) coefficient with
207 95% confidence levels. κ was calculated using the formula $\frac{\text{Pr}(o) - \text{Pr}(e)}{1 - \text{Pr}(e)}$, where
208 $\text{Pr}(o)$ is the observed agreement and $\text{Pr}(e)$ is the hypothetical probability of chance
209 agreement.

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224 **Results**

225

226 *Analytical reactivity, specificity and sensitivity:* The LAMP assay successfully amplified
227 DNA from all GBS reference, clinical and veterinary strains analysed with Time to positivity
228 (T_T) values of less than 20 minutes and specific melt point temperature values (T_m) ranging
229 from 85.5 – 86.21⁰C obtained. No amplification was recorded for any other bacterial or
230 fungal species tested. This confirmed 100% specificity of the GBS LAMP assay.

231 Employing tenfold serial dilutions of a known concentration (2.8E07 to 2.8E02 copies per
232 ml) of GBS ATCC 12386 nucleic acid extracts in duplicate the LAMP assay consistently
233 detected 2.80E03 *sip* genome copies per ml corresponding to an analytical Limit of Detection
234 (LOD) of 14 genome copies per reaction (for 5 μ l input volume and final reaction volume of
235 25 μ l). The mean GBS LAMP T_T and T_m for 2.80E03 *sip* genome copies per ml were
236 determined as 11 minutes and 85.98⁰C respectively. The LAMP LOD was slightly higher
237 than that achieved for qPCR which in our laboratory had a previously determined LOD of
238 1.00E03 genome copies per ml equating to 2 genome copies per reaction.

239

240 *Clinical Validation:* Routine bacteriological culture was compared to the reference qPCR
241 molecular method, direct LAMP and indirect LAMP methods. Summary of findings are
242 outlined in Tables 1 and 2. A total of 36/157 (22.9%) specimens analysed were confirmed as
243 GBS culture positive. All 36 culture positive GBS specimens were correctly identified as
244 positive by qPCR and by the direct and indirect LAMP methods. An additional 7 specimens
245 were identified as GBS positive by qPCR giving a total of 43/157 (27.4%) ‘true’ positive
246 specimens. Comparison of difference between qPCR and culture results was statistically
247 significant ($p=0.0005$). The loads of GBS determined by qPCR (genome copies per ml) for
248 positive clinical specimens were as follows: Mean = 1.23E+08; Max= 2.50E+09; Min=

249 1.90E+03; Median= 2.40E+06. Compared to culture qPCR had a sensitivity and specificity of
250 100% and 94.2% with a PPV and NPV of 83.7% and 100%. Positive (LR+) and negative
251 (LR-) likelihood ratios were infinity and 0.16 respectively. The mean genome copies per ml
252 of the seven identified specimens missed by culture but positive by qPCR was 1.09E06
253 (Range 1.90E03 – 7.60E06; Median 5.50E03) compared to 1.47E08 (Range 4.60E03 -
254 2.50E09; Median 3.65E06) for specimens identified as both culture and qPCR positive. This
255 difference in mean genome copies per ml was statistically significant ($p < 0.0001$).

256 The direct LAMP method took a mean of 45 minutes from receipt of a swab to generation of
257 confirmed result compared to 1 hour 45 minutes for indirect LAMP (extraction protocol) and
258 2 hours 30 minutes for reference qPCR test.

259 There was a very high level of agreement between LAMP (Indirect and direct) methods and
260 reference qPCR assay. Compared to qPCR agreement ranged from 100% for indirect LAMP
261 (Kappa = 1.0; Strength of agreement = perfect) to a level of agreement of 98.7% for direct
262 LAMP (Kappa = 0.968; Strength of agreement = very good). Indirect LAMP method
263 identified 43/157 (27.4%) specimen extracts as GBS positive with the direct LAMP method
264 identifying a total of 41/157 (26.1%) of crude specimen ACH lysates as GBS positive.
265 Compared to qPCR the indirect LAMP method had a sensitivity and specificity of 100% and
266 a PPV and NPV of 100%. Positive (LR+) and negative (LR-) likelihood ratios were infinity
267 and 0.00 respectively. Compared to qPCR the direct LAMP had a sensitivity and specificity
268 of 95.4% and 100% with a PPV and NPV of 100% and 98.3%. Positive (LR+) and negative
269 (LR-) likelihood ratios were infinity and 0.05 respectively. Two specimens (405 & 453 see
270 Table 2) were identified as false negative after analysis by direct LAMP method. Following
271 nucleic acid extraction and analysis by qPCR these specimens tested GBS positive with
272 genome copy loads of 1.90E+03 per ml (9.5 copies per 5µl addition) and 1.91+E03 per ml
273 (9.6 copies per 5µl addition) respectively. Additionally following nucleic acid extraction both

274 of the specimens tested LAMP positive returning T_T values of 12.15 and 29.00 minutes
275 respectively. Overall the mean time to achieve positivity (T_T) for direct LAMP method was
276 higher compared to indirect LAMP method; 14.83 minutes (range 8.15 – 26.00 minutes)
277 compared to 9.60 minutes (range 5.00 – 29.00 minutes). Testing performance comparison is
278 displayed in Table 1 with all specimens identified as positive by either culture, qPCR and/or
279 LAMP is presented in Table 2.

280

281

282 **Discussion**

283 Screening for maternal GBS colonisation at 35-37 weeks via selective culture is a time
284 consuming and inadequate method which fails to identify all cases of GBS [12,13,20]. There
285 is a recognised clinical need for rapid, highly sensitive and specific methods to detect GBS
286 which can be used at POC before or during labour to identify women for prophylactic
287 antibiotic treatment. Currently qPCR offers the required specification to achieve these goals
288 however technical obstacles including requirements for stringent sample preparation,
289 complex instrumentation and skilled personnel have restricted their introduction at POC [21-
290 23]. The robust chemistry, ease of operation, rapidity, low cost, and modest equipment
291 requirements associated with LAMP represent significant advantages over existing molecular
292 methods for detection of pathogens [22,27,29,36].

293 The primary objective of this proof of concept study was to validate the effectiveness of a
294 prototype LAMP assay (HiberGene diagnostics, Ireland) in combination with a simple rapid
295 specimen lysis protocol (without extraction) for direct detection of GBS in residual vaginal
296 swabs. Pre-lysis with ACH at a concentration of 10 U/L for 5 minutes at room temperature
297 has been previously shown in our laboratory to be a highly effective method to significantly
298 increase the available yield of GBS nucleic acid for molecular analysis [35]. Eliminating the

299 requirement for nucleic acid extraction not only simplified the test procedure but also resulted
300 in significant time savings with direct LAMP taking 45 minutes from receipt of swab to
301 definitive GBS result compared to 60 minutes and >2 hrs for indirect LAMP and qPCR
302 respectively. The GBS LAMP assay had an analytical LOD of 2.80E03 genome copies per ml
303 which compared favourably with the determined reference qPCR analytical LOD of 1.00E03
304 genome copies per ml. Crucially when applied to clinical specimens, qPCR and both direct
305 and indirect LAMP methods resulted in identification of additional GBS positives (n=7)
306 missed by culture. These findings were not unexpected and are consistent with previous
307 studies demonstrating an increase in GBS positivity rate when Nucleic acid amplification
308 tests (NAAT's) are directly compared to culture [13,16,18,19,20]. Higher detection rates of
309 NAAT's have been claimed to be due to the inability of culture to detect low numbers of
310 GBS bacteria but may also be attributed to the presence of antagonistic flora and/or the
311 detection of non-culturable cells [19,37].

312 Compared to the reference qPCR method the direct LAMP had a sensitivity of 95.4% and
313 specificity of 100%. High specificity is an intrinsic feature of LAMP and reflects the
314 presence of six specific LAMP primers recognising eight target regions on *sip* gene. The
315 direct LAMP assay returned higher mean T_T values for identified positive specimens
316 compared to the indirect LAMP assay applied to the same samples which had undergone
317 nucleic acid extraction (14.69 minutes versus 9.61 minutes respectively - difference of 5.08
318 minutes). Additionally the direct LAMP assay failed to detect GBS in two specimens
319 subsequently shown to contain low genomic loads by qPCR. These findings indicate that the
320 presence of component(s) in crude lysate matrices can impede LAMP and in conjunction
321 with low initial GBS loads may have contributed to the two false negative results. Solution(s)
322 to combat this could include prior centrifugation and/or a dilution step(s) although this would
323 complicate the assay protocol and make application less attractive at POC. At present the

324 clinical significance of specimens containing a low GBS burden remains to be determined
325 [16]. The excellent performance of qPCR and LAMP in this study must also be taken in
326 context as ‘second hand’ residual vaginal swabs post bacteriological culture as described
327 would certainly benefit from further field evaluation employing dedicated recto/vaginal
328 swabs in order to fully establish diagnostic and analytical characteristics. Efforts are currently
329 underway to address this.

330 Whilst this study utilised a GENIE® II fluorometer (cost £5000) to conduct isothermal
331 amplification and specific detection of GBS in real time it would be entirely feasible to
332 perform GBS LAMP testing using a simple heating block in conjunction with simple visual
333 endpoint interpretation. This represents a commonly applied and valid approach for LAMP
334 testing particularly in resource limited settings [27,38,39].

335 In conclusion the data presented demonstrates the efficacy of employing LAMP on minimally
336 processed vaginal swabs for rapid direct molecular detection of GBS. The simplicity of the
337 direct LAMP protocol combined with described sensitivity and specificity are desirable
338 characteristics amenable to POC use in resource limited settings.

339

340 **Acknowledgments**

341 This project was funded by Northern Ireland Public Health Agency. RB was funded by an
342 Academic Research Fellowship (Queen’s University Belfast). JPMcK, PVC, and DJF hold
343 share options in HiberGene Diagnostics Ltd.

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495 **Table 1** LAMP (Indirect & direct) and culture testing performance for clinical swabs (n=157)
 496 compared to reference GBS qPCR method. For LAMP the mean, maximum, minimum and
 497 median time to achieve LAMP positivity in minutes: seconds (T_T) and specific melt
 498 temperatures (T_m) in degrees centigrade are shown.

GBS qPCR	LAMP (INDIRECT)		LAMP (DIRECT)		Culture	
	Positive	Negative	Positive	Negative	Positive	Negative
Positive	43	0	41	2	36	7
Negative	0	114	0	114	0	114
Sensitivity	100%		95.4%		100%	
Specificity	100%		100%		94.2%	
PPV	100%		100%		83.7%	
NPV	100%		98.3%		100%	
(LR+)	Infinity		Infinity		Infinity	
(LR-)	0.00		0.05		0.16	
Mean T _T (T _m)	09.61 mins (86.66 ⁰ C)		14.69 mins (86.68 ⁰ C)		NA	
Max T _T (T _m)	29.00 mins (87.60 ⁰ C)		26.00 mins (87.60 ⁰ C)		NA	
Min T _T (T _m)	05.00 mins (85.86 ⁰ C)		08.15 mins (85.75 ⁰ C)		NA	
Median T _T (T _m)	08.30 mins (86.39 ⁰ C)		14.00 mins (86.40 ⁰ C)		NA	

499 NA; Not applicable

500

501 **Table 2** Individual vaginal swab specimens identified either as GBS positive by culture,
 502 qPCR, indirect and/or direct LAMP methods. For qPCR genome copies per ml detected are
 503 shown. For LAMP the time to achieve positivity in minutes T_T and specific melt temperatures
 504 (T_m) in degrees centigrade are shown

Specimen Code	Culture Result	qPCR Result copies/ml	Indirect LAMP Result T _T mins (T _m)	Direct LAMP Result T _T mins (T _m)
334	+	+ 2.4E06	+ 08.20 (87.20 ⁰ C)	+ 17.50 (87.60 ⁰ C)
337	+	+ 5.6E03	+ 11.50 (87.60 ⁰ C)	+ 22.20 (87.60 ⁰ C)

354	+	+ 1.1E09	+ 05.30 (87.30 ⁰ C)	+ 09.51 (87.40 ⁰ C)
355	-	+ 4.2E03	+ 10.30 (87.11 ⁰ C)	+ 21.00 (87.10 ⁰ C)
370	+	+ 9.0E04	+ 09.30 (87.60 ⁰ C)	+ 19.00 (87.25 ⁰ C)
372	-	+ 6.3E03	+ 15.15 (87.41 ⁰ C)	+ 16.00 (86.00 ⁰ C)
373	+	+ 2.2E06	+ 08.00 (87.10 ⁰ C)	+ 14.50 (87.10 ⁰ C)
374	+	+ 2.5E09	+ 05.00 (87.30 ⁰ C)	+ 09.30 (87.41 ⁰ C)
376	+	+ 3.6E04	+ 09.30 (87.43 ⁰ C)	+ 20.15 (87.60 ⁰ C)
380	+	+ 2.8E04	+ 12.00 (87.09 ⁰ C)	+ 24.15 (87.20 ⁰ C)
382	+	+ 4.6E03	+ 17.15 (87.55 ⁰ C)	+ 21.00 (87.40 ⁰ C)
392	-	+ 5.5E03	+ 12.00 (87.40 ⁰ C)	+ 14.50 (86.61 ⁰ C)
395	+	+ 2.4E04	+ 11.45 (87.35 ⁰ C)	+ 20.30 (87.55 ⁰ C)
403	+	+ 1.1E04	+ 09.45 (86.04 ⁰ C)	+ 22.45 (87.38 ⁰ C)
405	-	+ 1.9E03	+ 12.15 (86.12 ⁰ C)	-
408	+	+ 1.7E05	+ 09.00 (86.09 ⁰ C)	+ 26.00 (87.44 ⁰ C)
425	+	+ 5.6E07	+ 07.00 (85.86 ⁰ C)	+ 08.45 (85.75 ⁰ C)
426	-	+ 3.7E04	+ 12.15 (86.14 ⁰ C)	+ 15.45 (86.12 ⁰ C)
427	+	+ 2.8E06	+ 08.30 (86.11 ⁰ C)	+ 11.30 (85.92 ⁰ C)
446	+	+ 1.5E08	+ 08.00 (87.00 ⁰ C)	+ 17.45 (87.11 ⁰ C)
448	-	+ 7.6E06	+ 09.45 (86.91 ⁰ C)	+ 20.00 (87.02 ⁰ C)
451	+	+ 1.3E08	+ 07.15 (87.00 ⁰ C)	+ 15.45 (87.21 ⁰ C)
453	-	+ 1.9E03	+ 29.00 (87.14 ⁰ C)	-
685	+	+ 2.2E08	+ 07.00 (86.30 ⁰ C)	+ 12.30 (86.50 ⁰ C)
687	+	+ 1.0E08	+ 07.20 (86.30 ⁰ C)	+ 11.00 (86.51 ⁰ C)
695	+	+ 9.0E04	+ 11.15 (86.49 ⁰ C)	+ 17.45 (86.39 ⁰ C)
711	+	+ 1.1E08	+ 06.50 (86.20 ⁰ C)	+ 10.30 (86.38 ⁰ C)
729	+	+ 5.6E07	+ 07.21 (86.20 ⁰ C)	+ 13.15 (86.43 ⁰ C)
732	+	+ 2.6E04	+ 11.50 (86.50 ⁰ C)	+ 18.15 (86.40 ⁰ C)
736	+	+ 9.4E05	+ 08.00 (86.30 ⁰ C)	+ 11.30 (86.30 ⁰ C)
755	+	+ 5.2E07	+ 07.00 (86.28 ⁰ C)	+ 10.45 (86.40 ⁰ C)
782	+	+ 2.4E06	+ 08.45 (86.49 ⁰ C)	+ 11.10 (86.30 ⁰ C)
789	+	+ 1.6E04	+ 17.00 (86.39 ⁰ C)	+ 19.00 (86.20 ⁰ C)
793	+	+ 2.3E07	+ 08.00 (86.49 ⁰ C)	+ 11.00 (86.40 ⁰ C)
825	+	+ 4.5E06	+ 08.15 (86.29 ⁰ C)	+ 10.45 (86.26 ⁰ C)
826	+	+ 1.1E07	+ 08.30 (86.29 ⁰ C)	+ 09.45 (86.30 ⁰ C)
831	+	+ 9.3E07	+ 06.45 (86.39 ⁰ C)	+ 09.00 (86.40 ⁰ C)

843	+	+ 4.2E08	+ 06.15 (86.29 ⁰ C)	+ 08.15 (86.36 ⁰ C)
864	+	+ 2.0E08	+ 06.30 (86.29 ⁰ C)	+ 08.15 (86.33 ⁰ C)
870	+	+ 7.0E05	+ 09.30 (86.39 ⁰ C)	+ 14.00 (85.80 ⁰ C)
872	+	+ 8.5E06	+ 08.00 (86.00 ⁰ C)	+ 10.15 (85.80 ⁰ C)
876	+	+ 5.2E07	+ 07.15 (86.29 ⁰ C)	+ 11.00 (86.42 ⁰ C)
891	+	+ 1.8E06	+ 08.30 (86.29 ⁰ C)	+ 11.00 (86.39 ⁰ C)
Totals	36	43	43	41

505