

1 *Salmonella* Typhi Lipopolysaccharide O-antigen Modifications Impact on Serum Resistance
2 and Antibody Recognition

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4 Erica Kintz^{a##}, Christian Heiss^b, Ian Black^b, Nicholas Donohue^a, Naj Brown^a, Mark R.

5 Davies^{a**}, Parastoo Azadi^b, Stephen Baker^{c, d}, Paul M. Kaye^a, Marjan van der Woude^{a#}

6

7 ^aCentre for Immunology and Infection, Hull York Medical School and the Department of
8 Biology, University of York, York, UK

9 ^bComplex Carbohydrate Research Center, The University of Georgia, Athens, Georgia, USA

10 ^c The Hospital for Tropical Diseases, Wellcome Trust Major Overseas Programme, Oxford
11 University Clinical Research Unit, Ho Chi Minh City, Vietnam

12 ^dCentre for Tropical Medicine, Oxford University, Oxford, United Kingdom

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15 Running Head: *S. Typhi* O-antigen Modification and Host Defence

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17 #Address correspondence to Marjan van der Woude, Marjan.vanderwoude@york.ac.uk or

18 Erica Kintz, E.Kintz@uea.ac.uk

19

20 * Current address Norwich Medical School, University of East Anglia. Norwich, United
21 Kingdom

22 **Current address Department of Microbiology and Immunology, Peter Doherty Institute for
23 Infection and Immunity, University of Melbourne, Australia

24

25 **Abstract**

26 *Salmonella* Typhi is a human restricted Gram-negative bacterial pathogen, responsible for
27 causing an estimated 27 million cases of typhoid fever annually leading to 217,000 deaths,
28 and current vaccines do not offer full protection. The O-antigen side chain of the
29 lipopolysaccharide is an immunodominant antigen, can define host-pathogen interactions,
30 and is under consideration as a vaccine target for some Gram-negative species. The
31 composition of the O-antigen can be modified by activity of glycosyltransferase (*gtr*) operons
32 acquired by horizontal gene transfer. Here we investigate the role of two *gtr* operons we
33 identified in the *S. Typhi* genome. Strains were engineered to express specific *gtr* operons.
34 Full chemical analysis of the O-antigen of these strains identified *gtr*-dependent glucosylation
35 and acetylation. The glucosylated form of the O-antigen mediated enhanced survival in
36 human serum and decreased complement binding. A single nucleotide deviation from an
37 epigenetic phase variation signature sequence rendered expression of this glucosylating *gtr*
38 operon uniform in the population. In contrast, expression of the acetylating *gtrC* is controlled
39 by epigenetic phase variation. Acetylation did not affect serum survival, but phase variation
40 can be an immune evasion mechanism and thus this modification may contribute to
41 persistence in a host. In murine immunization studies, both O-antigen modifications were
42 generally immunodominant. Our results emphasize that natural O-antigen modification
43 should be taken into consideration when assessing responses to vaccines, especially O-
44 antigen based vaccines, and that the *Salmonella gtr* repertoire may confound the protective
45 efficacy of broad ranging *Salmonella* lipopolysaccharide conjugate vaccines.

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48

49 **INTRODUCTION**

50 *Salmonella enterica* subspecies *enterica* serovar Typhi (*S. Typhi*) is responsible for an
51 estimated 27 million new cases of typhoid fever and 217,000 deaths annually (1). Infection
52 with *S. Typhi* occurs via the fecal-oral route; after ingestion, bacteria cross the intestinal
53 epithelium, enter the bloodstream and spread systemically (2). In some cases, *S. Typhi* is
54 capable of colonizing the gall bladder, leading to chronic asymptomatic shedding and
55 contributing to the infection cycle. Two vaccines are currently licensed for use against *S.*
56 *Typhi*: the parenterally administered Vi capsular polysaccharide subunit vaccine and the
57 orally administered live-attenuated Ty21a vaccine. Neither vaccine offers complete
58 protection (3) and there is on-going research into new vaccine formulations against *S. Typhi*
59 and other *Salmonella* infections (3, 4). Conjugate vaccines, combining carrier proteins with
60 the Vi polysaccharide antigen are under development. However, Vi expression can be up- or
61 down-regulated and Vi-negative isolates have been isolated from typhoid patients (5, 6).
62 Lipopolysaccharide (LPS) is a Gram-negative bacterial virulence factor, a component of the
63 outer membrane and, in the absence of Vi, is the predominant *S. Typhi* surface carbohydrate.
64 Notably, the efficacy of the *S. Typhi* Ty21 vaccine is associated in part to expression of LPS
65 (7).

66

67 LPS is composed of a lipid A tail, which anchors the LPS into the membrane, a core
68 oligosaccharide and O-antigen side chain. The surface-exposed O-antigen side chain protects
69 the bacterial cell from the actions of the innate immune system (8). The O-antigen is
70 immunogenic, and may be a functional target for novel vaccines (9, 10). The *S. enterica*
71 subspecies is comprised of over 2,600 serovars, which is based on differences in the antigenic
72 properties of the O and H (flagellar) antigens, and forms the basis of the Kauffman-White

73 serotyping system (11). Antibodies are raised during natural infection against the LPS and the
74 detection of *S. Typhi* O-antigen antibodies forms the basis of the diagnostic Widal test for
75 typhoid (12). Furthermore, significant cross-reactivity between serovars sharing certain O-
76 antigen epitopes exists, which may be exploited in developing pan-*Salmonella* vaccines (13).
77 Therefore, gaining insight into occurrence and significance of variation in *S. Typhi* O-antigen
78 composition may enhance understanding of *S. Typhi* pathogenesis, and support the
79 development of diagnostic and intervention tools and therapies.

80

81 Modifications in LPS, including those in the O-antigen, play a role in many chronic bacterial
82 infections (14). O-antigen structures can be modified through several processes, and recently
83 we identified and characterised numerous *Salmonella gtr* (glycosyltransferase) operons (15).
84 Using the amino acid sequence identity of the GtrC O-antigen modifying proteins we were
85 able to group the *gtr* operons into ten different “families” and proposed that each family
86 performs a different O-antigen modification (15). We additionally noted that a single
87 *Salmonella* isolate may harbour multiple *gtr* operons and several families of these *gtr* operons
88 can undergo phase variation (15, 16), thus generating further potential complexity of the O-
89 antigen presented by a population. If, as a result, clonal bacterial populations have a non-
90 uniform O-antigen composition, this could serve as a means of immune evasion (17-19).

91

92 The significance of *gtr*-mediated O-antigen modification for *Salmonella* biology is not fully
93 understood. In *S. Typhimurium* specific modifications have been implicated in gut
94 colonization (20) and in phage resistance (21). To better understand the extent and impact of
95 O-antigen variation, we aimed to characterize the activity and expression of the *gtr* repertoire
96 in *S. Typhi*. Given that *S. Typhi* causes a systemic infection and that evading the innate

97 immune response can contribute to persistence, we measured the effect of *gtr* modification on
98 serum sensitivity. Further, we assessed the antibody response towards each O-antigen
99 modification in serum from a murine immunization model.

100

101 **MATERIALS AND METHODS**

102 **Bacterial strains and culture conditions**

103 Strains were grown in LB unless mentioned otherwise. For *S. Typhi* BRD948, medium was
104 supplemented with an Aro mix (final concentrations: 40 μ M L-phenylalanine, 40 μ M L-
105 tryptophan, 1 μ M para-aminobenzoic acid, and 1 μ M 2,3-dihydroxybenzoic acid, tyrosine 40
106 μ M). Antibiotic were used at the following concentrations: tetracycline (15 μ g/ml),
107 ampicillin (100 μ g/ml), chloramphenicol (34 μ g/ml for vectors or 8 μ g/ml for chromosomal
108 inserts) or kanamycin (30 μ g/ml). *S. Typhi* BRD948 and its derivatives were confirmed to be
109 Vi+ by serum agglutination (Vi antiserum, Serum Statens Institute). For analysis of LacZ
110 expression, strains were grown on minimal M9 media (Sigma, Gillingham, UK) with 0.2%
111 glucose (*S. Typhimurium*) or LB (*S. Typhi*) with 40 μ g/ml X-gal (5-Bromo-4-chloro-3-
112 indolyl- β -D-galactoside, Melford). Strains are listed in Supplemental Table S1.

113

114 **Molecular biology, strain construction and mutagenesis**

115 Standard molecular biology techniques were used (22). Details on vectors and primers used
116 in these studies are provided in Supplemental Table S1. Strains containing a *lacZ* reporter
117 fusion on the chromosome at the *attB* site were generated using the CRIM system (23) using
118 vector pMV243 (24). Allelic replacement was used to introduce mutations to the
119 chromosome (25). Antibiotic resistance cassettes were obtained from Tn10 for TcR and
120 pKD4 for KmR (25). Unmarked strains were generated by removal of the pKD13 derived

121 KmR cassette by Flp recombinase expressed from pCP20 (26). Vectors, and primer details
122 are provided in Table S1.

123

124 **Analysis of gene expression.**

125 β -galactosidase assays on strains with *lacZ* reporter fusions were performed as described by
126 Miller (27). Cultures derived from two independent colonies were grown in M9 minimal
127 media with glucose. Samples were collected at least in triplicate between OD₆₀₀ 0.3-1.5 for
128 measurement of β -galactosidase activity, given in Miller Units. The switch frequency of
129 phase variation was calculated for two independent colonies each for a Lac⁺ or Lac⁻
130 phenotype as described (28). The switch frequency is expressed as number of cells that have
131 changed expression state (M) over total number of cells (N), divided by the number of
132 generations (g).

133

134 **LPS extraction and visualization**

135 Crude LPS extracts were prepared as described (15), separated on a Tricine SDS-PAGE and
136 O-antigen visualized using a silver stain (15) or Western blot. These crude extracts can
137 incidentally contain contaminating macromolecules that are apparent on the gels or Westerns.
138 For Western blots, the samples were transferred to PVDF and blocked with 5% milk PBS-T.
139 O12, OMA polyvalent antiserum mixture to salmonella O-antigen from Group A, B, D, E, L
140 (Serum Statens Institute) or O12₂ sera were used to probe blots as indicated using secondary
141 goat anti rabbit IgG-HRP [Sigma (A0545)]. When mouse serum was used, goat anti-mouse
142 IgG-HRP (A1068) served as secondary. Millipore's Luminato Western HRP substrate was
143 used for detection.

144

145 **Serum sensitivity assay**

146 Human serum was purchased from Sigma (H4522). This serum failed to agglutinate the *S.*
147 Typhi strains. *S.* Typhi strains were grown over night and then diluted to an $OD_{600} = 0.5$ in
148 PBS. 5ul of bacteria were added to 45ul of serum diluted in PBS and incubated one hour at
149 37°C. Dilutions were performed to determine colony-forming units. Survival was determined
150 by comparing counts to those obtained from a control that was incubated in 45ul PBS.
151 Experiments were performed in duplicate and repeated at least three times.

152

153 **C3 binding to bacterial surface**

154 Experiments were performed using stationary phase bacteria. Methods were adapted from
155 MacClennan et al. (29), following quantities similar to the serum sensitivity experiments.
156 Briefly, bacteria were incubated with full strength human serum followed by incubation with
157 Dako's polyclonal rabbit anti-human C3c complement FITC antibody (F-0201). A Beckman
158 Coulter CyAn ADP analyser was used to collect data. Bangs FITC-5 MESF kit (Cat# 555)
159 allowed for standardization of fluorescence across experiments.

160

161 **Generation of murine immune serum**

162 Female *Slc11a1*^{D169} (*Nramp1*^s) C57BL/6 CD45.1 mice were obtained from Charles River
163 UK, housed under specific pathogen-free conditions and used at 6–10 weeks of age. All
164 experiments were approved by the University of York Animal Welfare and Ethical Review
165 Body and performed under UK home Office license. For immunizations, bacteria from
166 overnight cultures was diluted to an $OD_{600} = 1.0$ in PBS. 200ul was given IP, resulting in an
167 inoculum ranging from 8.12×10^7 to 2.56×10^8 CFU. 28 days after immunization mice were
168 exsanguinated by cardiac puncture under terminal anaesthesia. Serum was obtained by

169 allowing the collected blood to coagulate overnight at 4°C, then centrifuging at 2000rpm for
170 2 minutes. The serum layer could then be removed and stored at -20°C until use. Nine mice
171 were immunised with the STy-basal strain and seven immunised with the STy- FM strain.
172

173 RESULTS

174 The genomes of the *S. Typhi* strains Ty2, CT18 and P-stx-12 (isolated from a chronic carrier
175 in India) (30) each contain two different *gtr* operons (15). These share sequence identity
176 between the *S. Typhi* strains. One operon is a family 3 *gtr* type with high identity (99%
177 amino acid) to the *S. Typhimurium* family 3 operon (STM0557-0559) that mediates α 1->4
178 glucosylation of the O-antigen galactose sugar (20). The second *gtr* operon could be grouped
179 with the family 2 GtrCs and shared 77% amino acid identity with a similar operon in the
180 invasive *S. Typhimurium* isolate D23580. This GtrC operon has been hypothesised to
181 acetylate the rhamnose residue of the O-antigen (21); the *S. Typhi* O-antigen has a rhamnose
182 residue, but no acetylation has been described.
183

184 To assess the role of the *S. Typhi gtr* operons, we generated a set of four otherwise isogenic *S.*
185 *Typhi* strains with a defined *gtr* expression pattern: STy-Basal (both *gtr* operons deleted);
186 STy-Acetyl (expressing only family 2); STy-Gluc (expressing only family 3); and STy-FM
187 (both *gtr* operons expressed). LPS from these isogenic strains was extracted and compared by
188 Western blotting (Fig 1; Fig S1). The O-antigen of all strains reacted with commercial
189 *Salmonella* serum, confirming all strains expressed O-antigen (Fig. 1A) and that production
190 of the long antigen structure was not affected. Factor O12₂ serum targets the α 1-4
191 glucosylation of the galactose (31), and the O-antigens of the parent *S. Typhi* strain, STy-
192 Gluc and STy-FM reacted with this serum; strains lacking expression of family 3 *gtr* did not

193 react with this serum (Fig. 1A). Silver staining showed that strains expressing family 3 *gtr*
194 had a distinct O-antigen laddering pattern compared to isolates that lacked family 3 *gtr* (Fig.
195 S1). These data indicate the family 3 *gtr* operon of *S. Typhi* performs the same O-antigen
196 modification as the family 3 *gtr* operon of *S. Typhimurium*, namely α 1-4 glucosylation of
197 the galactose. However, no visible shift in the O-antigen pattern for STy-Acetyl compared to
198 STy-Basal was observed, providing further evidence the family 2 GtrC does not act as a
199 glucosyltransferase.

200

201 **Chemical analysis of the O-antigen from *S. Typhi* strains**

202 To define the composition and linkages of the *gtr*-dependent modifications various chemical
203 analyses were performed on LPS isolated from the *S. Typhi* parent strain and isogenic
204 variants. Full details are available with Supplemental Figures S2 and S3, and Tables S2-S4. A
205 methylation analysis of the LPS of these strains showed only minor differences in the
206 proportion of the linkages present in the polysaccharide (Table 1). The *S. Typhi* parent strain
207 and both STy-Gluc, STy-FM showed glucosylation on *O*-4 of galactose, at 62.3%, 82.4% and
208 82.5%, respectively, deduced from the galactose linkages. Nuclear magnetic resonance
209 (NMR) analysis revealed that the extent of glucosylation was comparable to that derived
210 from the methylation analysis (Table S2, Fig. S2) [parent (55.9%), STy-Gluc (72.8%) and
211 STy-FM (71.2%)].

212

213 In contrast to the methylation analysis, in which *O*-acetyl groups are removed during the acid
214 hydrolysis, NMR on untreated LPS (no lipid A removal) permits identification of acetylation.
215 We recorded an *O*-acetylation signal from both parent *S. Typhi* and STy-FM untreated LPS
216 (both encode family 2*gtr*) (Fig. S2), but this signal was absent in the spectra from STy-Gluc.

217 A further evaluation identified a 4-linked 3-*O*-acetyl rhamnose and a 4-linked 2-*O*-acetyl-
218 rhamnose (Fig. S3, Table S4). The two states likely reflect a single modification event, with
219 subsequent migration of the acetyl group (32). The parent *S. Typhi* strain exhibited the same
220 pattern of peaks in all NMR spectra as the STy-FM strain, with only slight disparities in
221 intensity of the acetylated positions (50% and 67%, respectively), with *O*-2 and *O*-3 of
222 rhamnose in approximately equal abundance. Taken together we confirm that the *S. Typhi*
223 family 3 *gtr* operon mediates α 1>4 glucosylation of the galactose and show that the family 2
224 *gtr* operon acts as a rhamnose acetyltransferase (Fig. 1C.)

225

226 **The expression patterns of the two *S. Typhi gtr* operons differ**

227 The expression of multiple *gtr* operons in *S. enterica* is controlled by phase variation (16).
228 This regulation is associated with a signature sequence in the regulatory region of *gtrA*
229 comprised of two binding sites for the transcriptional regulatory protein OxyR and four
230 GATC sites. The GATC sites are the target sequence for Dam, a “maintenance” adenine
231 DNA methyltransferase. DNA methylation-dependent interaction of OxyR at the *gtr* binding
232 sites leads to epigenetic phase variation of *gtr* expression (15, 16). In *S. Typhi*, this signature
233 sequence is present in the regulatory region of the family 2 *gtr* regulatory region and,
234 therefore, we predicted this operon to undergo phase variation. In contrast, the family 3
235 operon has the OxyR binding sequences but only three GATC sequences, with GAAA at the
236 fourth, promoter proximal, GATC sequence (Fig. 2).

237

238 The expression of both *gtr* operons was assessed using single copy transcriptional *lacZ*
239 fusions. In *S. Typhimurium* and *S. Typhi* backgrounds, family 2 expression was controlled by
240 phase variation. The switch frequency of the ON phase to the OFF phase was similar to that

241 for the reverse switch (Table 2). Therefore, in the absence of selective pressure, a clonal
242 population should consist of similar numbers of cells with and without the family 2-mediated
243 modification. In contrast, the strain with the *lacZ* reporter for the family 3 *gtr* operon gave
244 rise to only Lac⁺ colonies, indicating the *S. Typhi* family 3 *gtr* operon is expressed but not
245 controlled by phase variation. Mutating GAAA back to GATC restored phase variation to
246 this family 3 *gtr* operon (data not shown). These data indicate that a clonal *S. Typhi*
247 population is likely to have a uniform O-antigen glycosylation pattern, but heterogeneous at
248 the single cell level with respect to O-antigen acetylation.

249

250 **Effect of *gtr* modifications on serum sensitivity**

251 *S. Typhi* spreads systemically during typhoid fever; therefore the infecting organisms must
252 have reliable mechanisms for survival in the presence of components of the innate immune
253 system. The O-antigen can contribute to serum survival. We next assessed whether *gtr*
254 expression and its effects on O-antigen composition affects serum resistance in *S. Typhi*.

255

256 Serum sensitivity of the various isogenic *S. Typhi* was measured using a commercially
257 available human serum (Fig. 3A). The two strains containing the family 3-mediated
258 glucosylation had greater resistance to serum killing than the STy-Basal or STy-Acetyl
259 strains that both lack glucosylation. Acetylation of the O-antigen did not afford any
260 significant survival benefit compared to STy-basal in any of the conditions tested. Taken
261 together, these results imply that complement-mediated killing of *S. Typhi* is altered by the
262 *gtr*-dependent glucosylation of the O-antigen.

263

264 To corroborate differences in serum sensitivity between glucosylated and non-glucosylated
265 strains, we next assessed C3 complement protein binding to the strains. C3 initiates alternate
266 pathway activation, leading to the formation of membrane attack complex (MAC). After
267 incubation in naïve human serum, cells were exposed to FITC conjugated anti-C3 antibody
268 and surface-bound C3 measured with flow cytometry. Non-glucosylated strains (STy-Basal
269 and STy-Acetyl) exhibited significantly more surface-bound fluorescence than glucosylated
270 strains (STy-Gluc and STy-FM) (Fig. 3B). Acetyl modification did not significantly alter C3-
271 binding (comparison between STy-Basal to STy-Acetyl and STy-Gluc to STy-FM).

272

273 **Recognition of *S. Typhi* O-antigen from a murine immunization model**

274 We assessed whether O-antigen modification affected the specificity of antibodies generated
275 in a murine immunization model. Mice were immunized with either STy-Basal (no O-
276 antigen modification) or STy-FM (acetylated and glycosylated O-antigen) and serum was
277 collected. LPS from the four strains with defined *gtr* expression was used in a Western blot
278 assay and probed with serum from individual mice (Fig. 4). This approach allowed
279 identification of the O-antigen moieties recognized by antibody, and discrimination from
280 antibody directed to the shared lipid A and core.

281

282 Irrespective of the immunizing strain, there was variation between the responses of individual
283 mice (Fig. 4A & B). Immunization with non-modified O-antigen uniformly resulted in
284 recognition of lipid A + core (Fig. 4A). Some animals (3/9, i.e. panel 10) failed to show any
285 additional recognition of the O-antigen structures. When an O-antigen response was evident,
286 the composition of O-antigen from the immunizing strain was most frequently recognized

287 (5/9), and in some cases the only O-antigen that was recognized (3/9; i.e. panel 3) Notably,
288 only one serum recognized all four forms of *S. Typhi* O-antigen (e.g. panel 2).

289

290 In contrast, in mice immunized with the STy-FM strain expressing a fully modified O-
291 antigen, the unmodified form of O-antigen was only recognized in 1/7 mice (e.g. panel 7),
292 suggesting a general immunodominance of the *gtr*-dependent modifications (Fig. 4B).

293 In only 3/7, e.g. panel 4, all three modified O-antigen forms were recognized. The remaining
294 mice produced antibodies specific for either the glucosylated or the acetylated form despite
295 having been immunized with a strain expressing both modifications. These data predict that
296 *gtr*-mediated modifications mostly are immunodominant over the unmodified form (Sty-
297 Basal), but that neither acylation nor glucosylation is preferentially recognized after
298 immunization with a strain expressing O-antigen with both modifications.

299

300 **DISCUSSION**

301 The occurrence of strain and serovar-dependent O-antigen modification in the *Salmonellae*
302 has long been recognized (33), but only recently has the potential for *gtr*-mediated
303 modification been described in this genus (15). Here, we investigated two *gtr* operons in the
304 human host-restricted pathogen *S. Typhi*. Our data show that the family 3 *gtr* operon
305 catalyses a α 1->4 glucosylation of the galactose, as has been previously described for a
306 family 3 *gtr* operon for the serovar *S. Typhimurium* (20). Additionally, we demonstrate that
307 the family 2 *gtr* is required for acetylation of the rhamnose, as was suggested previously (21).
308 Thus, family 2 GtrC is not a glycosyltransferase but an acyltransferase, and the *gtr* acronym
309 thus only reflects proximity to (remnant) *gtrAB* genes (15). The galactose glucosylation in
310 the *S. Typhi* O-antigen was previously reported (33), but this is, to our knowledge, the first

311 report of rhamnose acetylation in *S. Typhi*. Acetylation of the family 3-dependent glucose
312 modification also may occur but the genes encoding this process remain to be identified (33,
313 34).

314

315 Acetylation of the rhamnose moiety will be heterogeneous in a bacterial population due to
316 phase variation of expression of family 2 *gtr*. This is consistent with a role in, and a
317 mechanism of, immune evasion (19). In contrast, the STy family 3 *gtr* regulatory region
318 deviates from the known phase variation signature sequence in one GATC sequence, which
319 caused abrogation of phase variation. Thus, glucosylation should be uniformly expressed
320 among cells in a population, likely contributing to the high degree of glucosylation observed
321 in *S. Typhi* O-antigen compared with other *Salmonella* serovars (34, 35). The sequence
322 variation associated with this lack of phase variation is present in both CT18 and Ty2 *S.*
323 *Typhi* genomes.

324

325 O-antigen glucosylation has implications for virulence in non-typhoidal serovars. In *S.*
326 *Typhimurium*, family 3-dependent glucosylation is associated with increased persistence in
327 the mouse intestine (20), and glucosylation of the *S. Enteritidis* O-antigen is associated with
328 an increase in virulence in a chicken-to-egg transmission model (35). The role we identified
329 for family 3-dependent glucosylation in serum resistance adds to the evidence that O-antigen
330 glucosylation can affect *Salmonella*–host interactions (14, 36). This one finding does not
331 exclude further benefits of this modification for *S. Typhi*.

332

333 Antibody recognition of a pathogen is an important feature for the clearance of infection. In
334 *S. Typhi*, the Vi capsular polysaccharide contributes to immune evasion (37) and antigen O9

335 antibodies can affect antibody mediated serum resistance. This role of O9 antibodies may be
336 relevant for antibody-mediated killing when there is reduced Vi capsule expression during
337 the infection cycle (38, 39). Our data highlight that both *gtr* mediated O-antigen
338 modifications can influence antibody recognition of the O-antigen. The trend from the
339 murine model was that immunization with a strain with modified O-antigen generated
340 antibodies that predominantly recognized the modified version of *Salmonella* O-antigen and
341 did not recognize the basal, unmodified O-antigen. These modifications thus could impact on
342 antibody-dependent killing mechanisms during *S. Typhi* infection.

343

344 In other *Salmonella* serovars, dominant epitopes induced by O-antigen modification have
345 been shown to be relevant for eliciting a protective immune response. For example, OafA-
346 dependent acetyl-modification of the abequose is required for protective antibodies against *S.*
347 *Typhimurium* (40, 41). A protective *S. Paratyphi A* glycoconjugate LPS vaccine required
348 acetylation, which is likely dependant on the described rhamnose acetylation modification
349 (42, 43). Based on the data presented here linking rhamnose acetylation to family 2 *gtr*, this
350 can now be attributed to the family 2 *gtr* encoded in the *S. Paratyphi A* genome (15).
351 Rhamnose acetylation was also implicated in the strain-specific dominant epitope of the
352 invasive *S. Typhimurium* D23580 isolate (41), which also can be attributed to the phage
353 encoded family 2 *gtr* that is expressed in this specific strain (21). However, detailed
354 analyses in context of the host, disease and serovars are needed to further clarify the impact
355 of O-antigen acetylation and glucosylation (44) (45).

356

357 Our results expand the body of evidence demonstrating that O-antigen composition in
358 *Salmonella* impacts upon host-pathogen interactions during infection. Strains within a

359 specific serovar may have a different repertoire of O-antigen modifying genes, and
360 expression may fluctuate by phase variation. Consequently, antibody generated by primary
361 infection or immunization may not wholly recognize subsequent infections by the same
362 serovar. Indeed, disease associated *S. Typhi* strains are not clonal and the genetic repertoire
363 of O-antigen modifying genes may vary (15, 46, 47). Furthermore, the response to the
364 Ty21a oral vaccine elicits a strong O-antigen antibody response, and thus any factors that
365 modify this response may impact serovar and strain cross-reactivity. In conclusion, we
366 suggest that O-antigen modification repertoires may need to be considered in vaccine design
367 to enhance efficacy against a broad range of *S. Typhi* isolates and phenotypes.

368

369

370 **Acknowledgements**

371 We thank Peter Roggentin for providing the O12₂ serum, Rob Kingsley for the BRD948 *S.*
372 *Typhi* strain, and Jane Dalton for assistance with the murine immunization experiments.

373

374 **Funding Statement**

375 This work was supported by the Wellcome Trust of the United Kingdom, through the project
376 grant WT094333MA awarded to MvdW. SB is a Sir Henry Dale Fellow, jointly funded by
377 the Wellcome Trust and the Royal Society (100087/Z/12/Z). Work carried out at the CCRC
378 was supported by U.S. Department of Energy grant (DE-SC0015662) to PA. The funders had
379 no role in study design, data collection and interpretation.

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514

515 **Table 1.** Methylation analysis of the three LPS samples.

No.	Glycosyl Linkage	Mole per cent		
		BRD948	STy-Gluc	STy-FM
a	t-Tyv	0.2	2.3	3.0
b	4-Rha	13.2	15.4	17.2
c	t-Glc	17.6	15.2	19.4
d	2-Man or 3-Man	1.8	3.0	3.2
e	3-Gal	6.8	3.6	3.3
f	4-Glc	24.7	20.4	19.7
g	2,3-Man	15.6	16.2	15.9
h	3,4-Gal	11.3	16.8	15.6
i	4,6-Glc	1.5	1.6	0.8
DG ^a		62.3	82.4	82.5

516 ^aDG (degree of glucosylation)=(h/(h+e)*100)

517

518

519 **Table 2.** Expression of *S. Typhi* *gtr* operons

Strain	Lac phenotype	Miller Units ^a	ON to OFF	OFF to ON
			switch frequency	switch frequency
LT2 ^{F2reg-lacZ}	Lac+/Lac-	1116 (42)	3.0 x 10 ⁻³	3.3 x 10 ⁻³
LT2 ^{F3reg-lacZ}	Lac+	763 (28)	n/a	n/a

520 a. Standard deviations are shown in parenthesis. Miller units were calculated for 100%

521 ON cells for phase varying isolates.

522

523 **Figure Legends**

524 **Figure 1. Effect of *gtr* modifications on *S. Typhi* O-antigen.**

525 (A) Expression of family 3 *gtr* leads to recognition by O12₂ sera. LPS was prepared as
526 described in the methods and run on TSDS-PAGE. Blots were probed with commercial OMA
527 sera (top panel) and O12₂ sera (bottom panel). B = STy-Basal; WT = parent strain BRD948
528 (“wild-type”) *S. Typhi*; Ac = STy-acetyl; G = STy-gluc; FM = STy-FM.

529 (B) Summary of results from the chemical analysis of *S. Typhi* BRD948 O-antigen.

530 (C) Schematic of the O-antigen of engineered strains used in these studies. See Figure S1 for
531 additional silver stain analysis of the *S. Typhi* O-antigen.

532

533

534 **Figure 2. Alignment of *S. Typhi gtr* regulatory regions to the phase varying regulatory**
535 **region of the *S. Typhimurium* family 3 *gtr* operon.**

536 The GATC sites are underlined and the OxyR binding sites are outlined in light gray boxes.
537 The -35/-10 sigma sites and the +1 transcriptional start site are indicated. Alignment was
538 performed in TCOFFEE.

539

540 **Figure 3. Serum sensitivity of *S. Typhi* strains with different *gtr* modifications.**

541 (A) Results from the serum survival assay for strains grown to stationary phase and
542 incubated in 50% serum. Different symbols represent the data obtained from individual
543 experiments. One-way ANOVA and Tukey post-analysis were performed in GraphPad Prism
544 (version 5.0d). * $p < 0.05$. (B) Binding of C3 complement protein to *S. Typhi* strains with
545 different O-antigen composition. Strains were incubated in human serum followed by anti-C3
546 FITC-conjugated antibody and surface-bound fluorescence measured with flow cytometry.

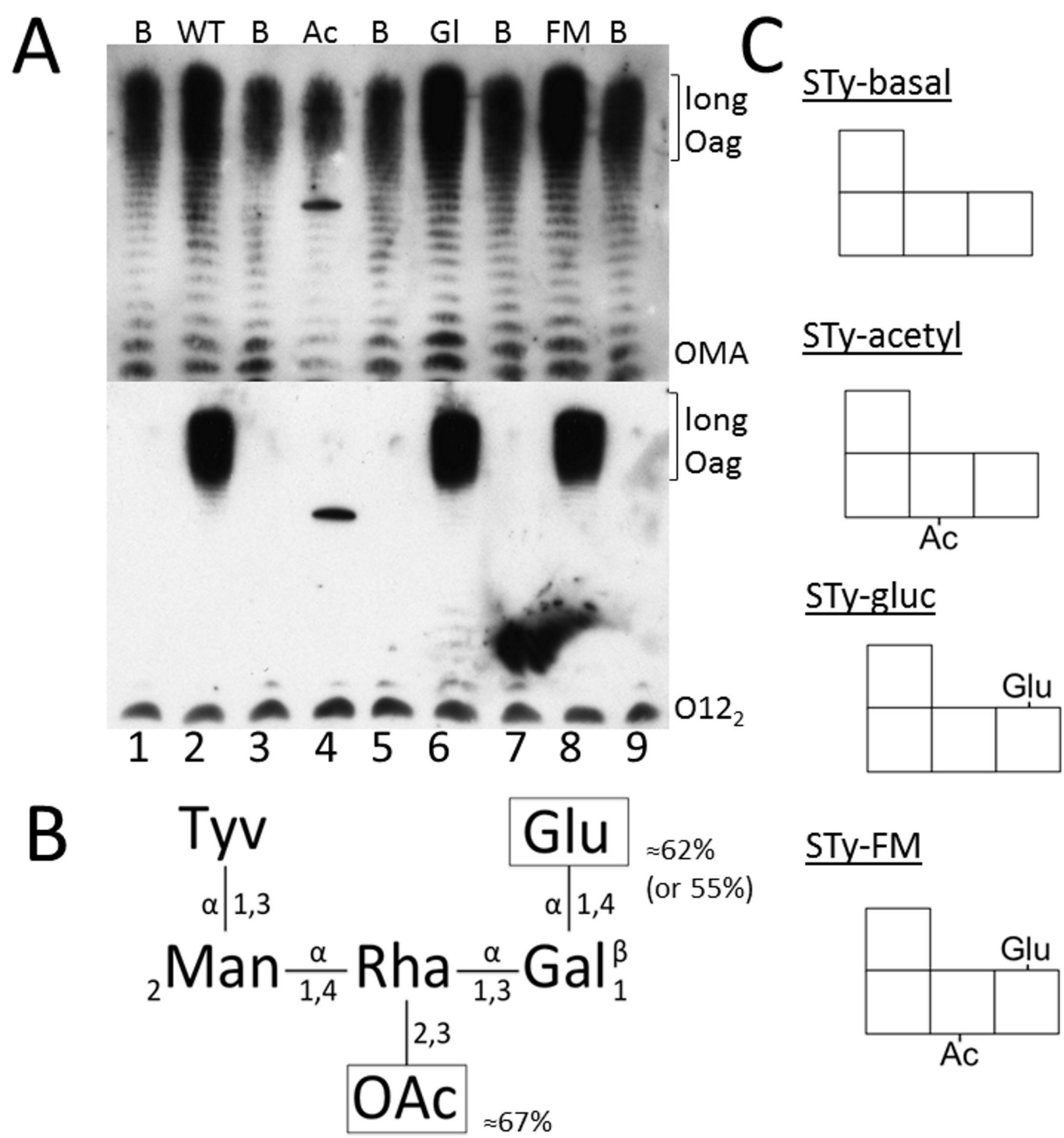
547 Data is combined from four experiments. MESF = molecules of equivalent soluble
548 fluorochrome. One-way ANOVA and Tukey post-analysis were performed in GraphPad
549 Prism (version 5.0d). * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Error bars indicate mean \pm SEM.

550

551 **Figure 4. Recognition of *S. Typhi* O-antigen by serum in a murine immunization model**
552 **depends on the O-antigen composition of the immunizing strain.**

553 In a LPS Western blot, LPS from different strains was probed with serum from mice
554 immunized either with Sty-Basal (A) or STy-FM (B). In (A), panel #1 (numbered in lower
555 left hand corner) shows reactivity of pooled serum from the PBS-immunized control group,
556 and each following panel (2-10) represents the serum from an individual mouse. In (B) panel
557 #1 shows reactivity of OMA commercial serum, which recognizes several *Salmonella*
558 serovars; each following panel represents the serum from an individual mouse. Lanes 1-4 in
559 each panel have LPS from the following strains: as follows 1) STy-Basal; 2) STy-Acetyl; 3)
560 STy-Gluc 4) STy-FM.

561



STm-F3 GATCGGTAACAACGATCAATTAATAAGATAACAATAACTTTAAACTATTGAATAC
STy-F2 GATCGATAACATCGATCAATATATTTAAACTCAATAGCTTAAACTATTAAAAAT
STy-F3 GATCGGTAACAACGATCAATTAATAAGACAACAATAAGTTCAAGCTATCAATAT
 ***** ***** ***** ** * * ***** ** ** ***** ** *

STm-F3 CACATTATTGATCGTTTATATCGATCAAAGCAATTTGTAGTGCTACACTCCAGAC⁻³⁵ ⁻¹⁰ ⁺¹
STy-F2 ACAATTATTGATCGCTTATATCGATCAAACCAATTTGTAGTGCTACACTCCAGAC
STy-F3 AACATTATTGATCGTTTATATCGAAAAAGCAATTTGTAGTACTATACTCCAGAC
 ***** ***** *** ***** *****

