Identification of Immunogenic *Salmonella enterica* Serotype Typhi Antigens Expressed in Chronic Biliary Carriers of S. Typhi in Kathmandu, Nepal

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Abstract

**Background:** *Salmonella enterica* serotype Typhi can colonize and persist in the biliary tract of infected individuals, resulting in a state of asymptomatic chronic carriage. Chronic carriers may act as persistent reservoirs of infection within a community and may introduce infection to susceptible individuals and new communities. Little is known about the interaction between the host and pathogen in the biliary tract of chronic carriers, and there is currently no reliable diagnostic assay to identify asymptomatic *S. Typhi* carriage.

**Methodology/Principal Findings:** To study host-pathogen interactions in the biliary tract during *S. Typhi* carriage, we applied an immunoscreening technique called *in vivo*-induced antigen technology (IVIAT), to identify potential biomarkers unique to carriers. IVIAT identifies humorally immunogenic bacterial antigens expressed uniquely in the *in vivo* environment, and we hypothesized that *S. Typhi* surviving in the biliary tract of humans may express a distinct antigenic profile. Thirteen *S. Typhi* antigens that were immunoreactive in carriers, but not in healthy individuals from a typhoid endemic area, were identified. The identified antigens included a number of putative membrane proteins, lipoproteins, and hemolysin-related proteins. YncE (STY1479), an uncharacterized protein with an ATP-binding motif, gave prominent responses in our screen. The response to YncE in patients whose biliary tract contained *S. Typhi* was compared to responses in patients whose biliary tract did not contain *S. Typhi*, patients with acute typhoid fever, and healthy controls residing in a typhoid endemic area. Seven of 10 (70%) chronic carriers, 0 of 8 bile culture-negative controls (0%), 0 of 8 healthy Bangladeshis (0%), and 1 of 8 (12.5%) Bangladeshis with acute typhoid fever had detectable anti-YncE IgG in blood. IgA responses were also present.

**Conclusions/Significance:** Further evaluation of YncE and other antigens identified by IVIAT could lead to the development of improved diagnostic assays to identify asymptomatic *S. Typhi* carriers.


Editor: Joseph M. Vinetz, University of California San Diego School of Medicine, United States of America

Received March 6, 2013; Accepted June 12, 2013; Published August 1, 2013

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**Funding:** This work was supported by the ICDDR,B and grants from the Wellcome Trust of the United Kingdom (TVTN, SD, BB, JF, SB) and the National Institutes of Health, including the National Institute of Allergy and Infectious Diseases (AI100023 and AI077883 [ETR, FQ], AI058935 [SB, ETR and FQ], Training Grant in Vaccine Development and Public Health (D43 TW005572 [MMK, FK, TS, ETR, FQ]), Career Development Awards (K01 TW07409 [JHG]; K01 TW07144 [RCL]; K08 AI089721 [RCC]; K08 AI100923 [DTL]); an American Recovery and Reinvestment Act (ARRA) Post-doctoral Fellowship in Global Infectious Diseases (TW005572 [DTL, RCC]), a Clinical Research Scholars Award (R24 TW07988 [SBCC] from the Fogarty International Center, a Physician Scientist Early Career Award from the Howard Hughes Medical Institute (RCL), a Massachusetts General Hospital Physician Scientist Development Award from Massachusetts General Hospital (RCC), a Burroughs Wellcome Fund/American Society of Tropical Medicine and Hygiene Postdoctoral Fellowship in Tropical Infectious Diseases (DTL), and an iSURF Award from the Harvard Global Health Institute (LLT). The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

**Competing Interests:** The authors have declared that no competing interests exist.

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**Author Summary**

*Salmonella enterica* serotype Typhi is the cause of typhoid fever and infects over 21 million individuals and causes 200,000 deaths each year. With adequate treatment, most patients recover from their acute stage of illness and clear infection. However, a small percentage of *S. Typhi* infected individuals develop a chronic but asymptomatic infection in the biliary tract that can persist for decades. Since *S. Typhi* is a human-restricted pathogen, chronic carriers may act as reservoirs of infection. Correctly identifying and treating asymptomatic chronic carriers could be critical for ultimate control of typhoid fever. Using an immunoscreening technique called *in vivo*-induced antigen technology (IVIAT), we have identified potential biomarkers unique to *S. Typhi* chronic carriers. Further evaluation of these antigens could lead to the development of improved diagnostic assays to detect asymptomatic *S. Typhi* carriers in typhoid endemic zones, and to an improved understanding of the pathogenesis of *S. Typhi* in the chronic carrier state.

**Introduction**

*Salmonella enterica* serovars Typhi (*S. Typhi*) and Paratyphi A (*S. Paratyphi A*) are human-specific pathogens, and the predominant cause of enteric (typhoid) fever globally. Enteric fever affects over 21 million people each year, resulting in 200,000 deaths [1]. Infection with *S. Typhi* and *S. Paratyphi A* usually begins with ingestion of contaminated water or food. The pathogens invade the gastrointestinal mucosa, translocate to the lymphoid follicles where they survive and replicate within macrophages, and then disseminate via the bloodstream to the liver, spleen, intestinal lymph nodes, bone marrow, and gallbladder [2]. With adequate treatment, most patients recover from their acute stage of illness and clear infection. However, a small percentage of *S. Typhi* (and *S. Paratyphi A*) infected individuals develop a chronic, but apparently asymptomatic, infection in the biliary tract that can persist for decades [3–6]. The likelihood of this is not known, but it is estimated that chronic carriage can complicate perhaps 1–3% of acute infections [7].

Since *S. Typhi* and *S. Paratyphi A* are human-restricted pathogens, chronic carriers may act as reservoirs of infection within a community. They contribute to the transmission cycle through the intermittent shedding of bacteria in feces (especially in areas of low transmission [8]) and may act as vehicles for introducing *S. Typhi* and *S. Paratyphi A* into previously uninfected communities. Therefore, correctly identifying and treating asymptomatic chronic carriers is critical for the long-term control of enteric fever. Currently, there is no reliable diagnostic assay to identify asymptomatic *S. Typhi* and *S. Paratyphi A* carriage. Bacterial stool culture has been used, yet is challenging due to the expense and logistics of obtaining multiple samples from patients, since shedding is typically low level and intermittent [5]. Measurement of antibody responses to the *S. Typhi* capsular Vi antigen has been previously described as a potential method to detect chronic *S. Typhi* carriers [7]. In laboratory settings, IgG to the Vi antigen has been shown to have a sensitivity of 75% and specificity of >95% and has proven to complement other strategies in outbreak investigations [7,9–11]. However, its role in detecting asymptomatic carriers in a general endemic-zone population is unclear. In Chile, anti-Vi antibody responses had a sensitivity of 75% and specificity of 92%–97% for *S. Typhi* carriage; however, due to a low prevalence rate of carriage in the general population, its positive predictive value was only 8–17% [12]. In Vietnam, a large community-based survey for anti-Vi antibodies demonstrated a 3% positivity rate in the population; however, *S. Typhi* was never detected in the stool of individuals identified by such anti-Vi screening [13].

Understanding the mechanisms involved in development and persistence of the carrier state may facilitate development of improved diagnostic assays and therapeutic approaches for *S. Typhi* carriage. Currently, little is known about host-pathogen interactions in the biliary tract of chronic human carriers. Much of what is known about biliary carriage has been extrapolated from *in vitro* and murine studies with *S. Typhimurium*, which causes an enteric fever-like illness in mice [5]. From these animal studies and a complimentary study in humans, we know that gallstones facilitate *S. Typhi* carriage [5]. In the presence of bile, the bacterium regulates the expression of genes that allow it to colonize and persist in the gallbladder through formation of biofilms that mediate resistance against host defenses [14,15]. There are likely other niches of persistent infection outside of the gallbladder, including the biliary tree, liver, and mesenteric lymph nodes. This is suggested by the observation that although cholecystectomy increases cure rates, it does not always result in clearance of the pathogen in humans [16]. In a murine model of *Salmonella* chronic infection, *S. Typhimurium* infection in Slc11a1 (Nramp1) wild-type mice demonstrated that the most common site of persistent infection was in hemophagocytic macrophages within mesenteric lymph nodes [2,17,18].

To advance our understanding of *Salmonella* pathogenesis of the chronic carrier state, and identify potential biomarkers unique to *S. Typhi* chronic carriers, we applied an immunoscreening technique called *in vivo*-induced antigen technology (IVIAT) [19–21]. IVIAT identifies humorally immunogenic bacterial antigens expressed *in vivo* and not in bacteria grown in standard laboratory conditions. We hypothesized that *S. Typhi* surviving in the biliary tract of humans may express a proteomic profile distinct from that expressed in bacteria grown using standard *in vitro* conditions or during acute infection.

**Methods**

**Ethics statement**

This study was approved by the human studies committees of the involved research institutions: Massachusetts General Hospital, International Centre of Diarrheal Disease Research, Bangladesh (icddr,b), Patan Hospital, The Nepal Health Research Council, and the Oxford Tropical Research Ethics Committee. The study was conducted according to the principles expressed in the Declaration of Helsinki/Belmont Report, and informed written consent was obtained from adult participants and from guardians of children prior to study participation.

**Bacterial strains, plasmids, and media**

*Salmonella enterica* serotype Typhi strain CT18 [22] was obtained from the *Salmonella* Genetic Stock Centre (Calgary, Alberta, Canada). Genomic DNA from this strain was used to construct a genomic inducible expression library in host strain *Escherichia coli* strain BL21(DE3). Bacterial strains were grown in Luria-Bertani (LB) media (with 50 μg/ml kanamycin for clones containing pET30 constructs) and maintained at −80°C in LB broth containing 15% glycerol.

**Patient and control sera**

Individuals undergoing elective cholecystectomy in Kathmandu, Nepal were enrolled. At the time of cholecystectomy, a venous blood sample was stored and a bile sample was taken for...
microbiologic analysis as previously described [6]. Patients were categorized as (1) S. Typhi carriers if their bile culture was positive for S. Typhi; (2) S. Paratyphi A carriers if their bile culture was positive for S. Paratyphi A, or (3) cholecystectomy controls if their bile cultures were negative for any organism. Sera samples were also obtained from the following groups: (1) healthy Bangladeshi residents of Dhaka (a typhoid endemic area) enrolled at the International Centre for Diarrhoeal Disease Research, Bangladesh (icddr,b); and (2) acute (day 0–3) and convalescent sera (day 14–28) of Bangladeshi patients who presented to icddr,b with S. Typhi bacteremia [23–25].

Construction of genomic inducible expression library

Genomic DNA was purified from S. Typhi strain CT18 using a Genomic DNA Isolation kit (Qiagen, Valencia, CA), sheared using a Covaris sonicator (Woburn, Ma) optimized to generate 0.5–1.5 kb DNA fragments, and resulting fragments were gel purified using the Qiagen Qiaquick Gel Extraction kit. After terminal overhangs were removed using End-Hi DNA end-repair kit (Epicenter Biotechnologies, Madison, WI), the blunt-ends products were ligated into pET-30c vectors (Novagen, San Diego, CA) that had been digested with EcoilRV and treated with calf intestinal alkaline phosphatase. The library was electroporated into E. coli DH5α and bacteria were plated onto selective LB media containing kanamycin. After overnight incubation at 37°C, the plates were scraped and the plasmid DNA from collected colonies was recovered using Qiagen Miniprep kit. EcolRI and KpnI digestion was performed on a random sample of plasmids, and an insertion frequency greater than 80% and insert size between 500 to 1500 bp was verified. The plasmid DNA mixture was electroporated into E. coli DH5α and then the recovered plasmid was transformed into the expression strain BL21AI. To overproduce His6-YncE, E. coli BL21AI (pDEST17/His6-yncE) was grown in 250 mL LB broth containing ampicillin at 37°C until OD600 0.6, and then expression of His6-yncE was induced by the addition of L(+)-arabinose (0.2%). After 4 hours, the pellet was harvested by centrifugation, and the cells were lysed by sonication after resuspension in 15 mL lysis buffer (50 mM Tris HCl, 5% glycerol, 0.1 M NaCl pH 8) containing 100 µg/ml lysozyme. Following centrifugation, the pellet was washed in lysis buffer with and without 1% Triton X-100, and the pellet was resuspended in 10 mL of 8 M urea, 50 mM NaH2PO4 and 300 mM NaCl (pH 7.4). His6-YncE was purified by HisPur Cobalt Resin (ThermoScientific, Rockford, IL) under denaturing conditions per the manufacturer’s instructions. His6-YncE was then refolded by dialysis into 25 mM Tris HCl pH 8.0 under denaturing conditions with urea and product identity was assessed by Mass spectrometry analysis. Protein concentration was determined via Coomassie (Bradford) Protein Assay Kit (ThermoScientific, Rockford, IL).

Screening for antigens uniquely expressed in vivo in S. Typhi carriers

Convalescent sera of 5 patients with bile cultures positive for S. Typhi were pooled, and adsorbed with in vitro grown S. Typhi strain CT18 and E. coli BL21 [DE3] [19]. Immunoblot techniques were used as previously described [19]. Briefly, the genomic library was plated on LB plates containing kanamycin to obtain a colony density of approximately 500 to 1000 clones per plate. After overnight incubation at 37°C, the resultant colonies were lifted off the plate using nitrocellulose membranes, and then the membranes were placed on LB media containing kanamycin. After overnight incubation at 37°C, the plates were scraped and the plasmid DNA from collected colonies was recovered using Qiagen Miniprep kit. EcolRI and KpnI digestion was performed on a random sample of plasmids, and an insertion frequency greater than 80% and insert size between 500 to 1500 bp was verified. The plasmid DNA mixture was electroporated into E. coli BL21 (DE3), and collected colonies were stored in LB broth containing 15% glycerol.

Evaluation of serum IgG and IgA responses to YncE and S. Typhi capsular VI antigen

To further characterize immunoreactivity of the antigen with the most prominent immunoreactivity in our initial screening, anti-YncE (STY1479) IgG and IgA responses were measured in the sera of 10 S. Typhi carriers, 3 S. Paratyphi A carriers, 8 patients at acute (day 0–3) and convalescent phase (day 14–28) of typhoid fever with confirmed S. Typhi bacteremia, 8 Nepalese controls undergoing elective cholecystectomy with negative bile cultures, and 8 healthy Bangladeshi, in duplicate. Plates were coated with 100 ng/well of YncE and then sera were added at a 1:200 dilution. Bound antibody was detected with anti-human IgG or IgA conjugated with horseradish peroxidase (Jackson Laboratories, Bar Harbor, ME) at a 1:1000 dilution, and peroxidase activity was measured with the substrate 2,2-azinobis (ethyl- benzthiazolinesulfonic acid). To compare across plates, kinetic readings (mAb/sec) of samples were averaged, divided by kinetic readings (mAb/sec) of an in-house pooled standard (pooled sera of five S. Typhi carriers confirmed by biliary culture), and then inserts. Immunoreactivity of these full ORF clones was compared to E. coli BL21DE3 with an empty pET30c vector. To assess immunoreactivity of identified antigens among the pertinent general population, immunoreactive clones were also screened using pooled sera of individuals living in a typhoid endemic area (Bangladesh). These sera were pre-adsorbed against in vitro grown E. coli BL21DE3, as described above, to reduce background reactivity against the host strain.

Functional classifications of identified proteins were assigned using published articles and available protein information resources, including J. Craig Venter Institute annotations (http://cmr.jcvi.org/tigr-scripts/CMR/CmrHomePage.cgi) and Pfam 26.0 (http://pfam.sanger.ac.uk/).
Typhi antigens identified by IVIAT

Results

S. Typhi antigens identified by IVIAT

In the primary screen of over 120,000 clones, 565 clones were identified as immunogenic; 210 were confirmed by secondary screening. Sequence analysis of these inserts (many of which carried multiple potentially expressible ORFs) revealed 268 genes of interest with over 20% of genes identified multiple times, supporting validity of their identification and saturation of library screening. We subsequently sub-cloned the full coding sequences of 235 genes into individual expression plasmids, and identified 56 proteins with prominent IgG immunoreactivity using S. Typhi carrier sera, comparing immunoreactivity of expression clones to a clone containing an empty vector (Supplementary Table S1). Forty-eight of the identified genes are encoded on the chromosome of S. Typhi, 5 are encoded on the drug resistance plasmid pHCM1, and 3 on cryptic plasmid pHCM2. The most highly represented functional groups included proteins of unknown function and those involved in transport and binding, synthesis or salvage of ribonucleotides, and energy metabolism.

To assess the degree of immunoreactivity of antigens identified by IVIAT within the pertinent endemic-zone population, we screened the 56 immunoreactive clones against pooled sera of individuals living in a S. Typhi endemic area (Bangladeshi residents of Dhaka) [26]. Of these 56 proteins, 13 proteins had more prominent immunoreactivity when screened with sera of S. Typhi carriers compared to sera of healthy Bangladeshis. These 13 proteins included a number of putative membrane proteins, lipoproteins, and hemolysin-related proteins (Table 1). YncE, a possible ATP-binding protein, had the overall highest differential immunoreactivity compared to healthy endemic-zone control sera in our immunoblot assay.

Anti-YncE serum responses as a diagnostic biomarker for asymptomatic S. Typhi carriage

To further characterize whether the immunoreactivity to YncE in S. Typhi carriers was specific, we also evaluated the immunoreactivity to YncE using sera of 3 groups of individuals: (1) S. Typhi carriers, (2) patients at the acute and convalescent phase of typhoid fever, (3) S. Paratyphi A carriers, (4) individuals who underwent cholecystectomy in Nepal whose bile cultures were negative for any pathogen, and (5) healthy controls from a typhoid endemic area (Dhaka, Bangladesh). We found significantly higher IgG immunoreactivity to YncE in S. Typhi carriers compared to bile culture-negative patients (p = 0.0205), healthy Bangladeshis (p = 0.0005), and patients at the acute and convalescent phases of typhoid infection (p = 0.0044 and p = 0.0266, respectively); there was a trend toward statistical significance when compared to S. Paratyphi A carriers (p = 0.21) (Figure 1A). Of the 10 S. Typhi carriers, 7 (70%) had an anti-YncE IgG response (Units >100). None of 8 bile culture negative controls (0%), 0 of 8 healthy Bangladeshis (0%), 0 of 3 Paratyphi A carriers (0%) and 1 of 8 (12.5%) Bangladeshis at the acute and convalescent phase of S. Typhi had an anti-YncE IgG response. Thus, in our small subset of patients, using a cut-off value of >100 Units (U), anti-YncE IgG had a sensitivity of 70%, and specificity of 100% when using endemic zone healthy individuals and cholecystectomy patients without detectable S. Typhi as controls. The specificity decreased to 95% if we included patients with acute typhoid fever.

Although, the values did not reach statistical significance, S. Typhi carriers also had a higher IgA immunoreactivity to YncE compared to our two control groups: bile culture-negative patients (p = 0.2370) and healthy Bangladeshis (p = 0.2031) (Figure 1B). There was no significant difference between the IgA immunoreactivity to YncE in S. Typhi carriers in comparison to patients

Table 1. Proteins identified by IVIAT with higher IgG immunoreactivity in S. Typhi carriers compared to healthy typhoid-endemic zone controls.

<table>
<thead>
<tr>
<th>Locus</th>
<th>Gene</th>
<th>Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>STY0712</td>
<td>corC</td>
<td>Hemolysin-related protein</td>
</tr>
<tr>
<td>STY1364</td>
<td></td>
<td>Hypothetical periplasmic protein</td>
</tr>
<tr>
<td>STY1479</td>
<td>yncE</td>
<td>Possible ATP-binding protein</td>
</tr>
<tr>
<td>STY2155</td>
<td>sinA</td>
<td>Invasion response-regulator</td>
</tr>
<tr>
<td>STY2248</td>
<td>pduG</td>
<td>PduG protein</td>
</tr>
<tr>
<td>STY2386</td>
<td></td>
<td>Putative lipoprotein</td>
</tr>
<tr>
<td>STY2454</td>
<td>yejE</td>
<td>Putative binding-protein-dependent transporter</td>
</tr>
<tr>
<td>STY2657</td>
<td>xapB</td>
<td>Xanthosine permease</td>
</tr>
<tr>
<td>STY3709</td>
<td>purH</td>
<td>Phosphoribosylaminomimidazolecarboxamideformyltransferase and IMP cyclohydroxylase (bifunctional enzyme)</td>
</tr>
<tr>
<td>HCM1.137</td>
<td>repE</td>
<td>Replication initiation protein</td>
</tr>
<tr>
<td>HCM1.213c</td>
<td></td>
<td>Putative transposase</td>
</tr>
<tr>
<td>HCM2.0043</td>
<td></td>
<td>Hypothetical protein</td>
</tr>
<tr>
<td>HCM2.0069c</td>
<td></td>
<td>Hypothetical protein</td>
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doi:10.1371/journal.pntd.0002335.t001
convalescing from acute typhoid infection or S. Paratyphi A carriers.

Comparison with anti-Vi serum responses

Since immune responses to S. Typhi Vi antigen have been the best characterized diagnostic method for identifying S. Typhi carriers to date, we also assessed the anti-Vi IgG and IgA responses in the same cohort of patients. We found significantly higher IgG immunoreactivity to Vi antigen in S. Typhi carriers compared to PTA carriers (p = 0.0070), bile culture negative controls (p = 0.0343), healthy Bangladeshis (p = 0.0021), and patients at the acute phase of typhoid infection (p = 0.0155). (Figure 2A). There was a trend toward statistical significance when the immunoreactivity of S. Typhi carriers to Vi antigen was compared to patients at the convalescent phase of typhoid infection (p = 0.0830) (Figure 2A). In our evaluation of IgA anti-Vi responses, we did not find a significant difference in the immunoreactivity of S. Typhi carriers compared to healthy Bangladeshis (p = 0.0155), and patients convalescing from acute typhoid infection (p = 0.0266) (Figure 2B). There was no significant difference in immune responses between S. Typhi carriers and bile-culture negative patients, S. Paratyphi A carriers, or patients at the acute phase of typhoid infection. The sensitivity for anti-Vi IgG and IgA was 40% (cutoff value >1250 U) and 50% (cutoff value >1250 U), respectively. The specificity was 100% for IgG irrespective of controls. For IgA, the specificity was 97% when using endemic zone healthy individuals and cholecystectomy patients without detectable S. Typhi as controls. The specificity was 94% if patients with acute typhoid fever were included in the analysis.

Figure 1. Characterization of anti- YncE immune responses. Anti-YncE IgG (A) and IgA (B) responses in S. Typhi carriers (Typhi carrier), S. Paratyphi A carriers (PTA carrier), Nepalese controls undergoing elective cholecystectomy with negative bile cultures (GB control), Healthy Bangladeshi controls (HB control), and patients at the day 0–3 acute (Typhi acute) and day 14–28 convalescent phase (Typhi conv) of typhoid fever with confirmed S. Typhi bacteremia.
doi:10.1371/journal.pntd.0002335.g001

Figure 2. Characterization of anti- Vi immune responses. Anti- Vi antigen IgG (A) and IgA (B) responses were evaluated in S. Typhi carriers (Typhi carrier), S. Paratyphi A carriers (PTA carrier), Nepalese controls undergoing elective cholecystectomy with negative bile cultures (GB control), healthy Bangladeshi controls (HB control), and patients at the day 0–3 acute (Typhi acute) and day 14–28 convalescent phase (Typhi conv) of typhoid fever with confirmed S. Typhi bacteremia.
doi:10.1371/journal.pntd.0002335.g002
Combined YncE and Vi antibody measurements for the detection of S. Typhi carriers

In our analysis, using a cut-off value of >100 U of anti-YncE IgG and/or >1250 U anti-Vi IgA, we could identify 8 out of 10 S. Typhi carriers. There was no added benefit seen when pairing anti-YncE responses with anti-Vi IgG.

Discussion

In our immunoscreen using IVIAT, we were able to identify 56 immunogenic S. Typhi proteins using the sera of S. Typhi carriers. Of these, 13 had higher immunoreactivity when screened with S. Typhi carrier sera compared to sera of endemic zone residents. These proteins represent a tracking list of candidate diagnostic biomarkers of asymptomatic S. Typhi carriage and their analysis may further our understanding of survival adaptations of S. Typhi in chronic carriers.

Human epidemiologic studies as well as murine models of S. Typhi carriage suggest that gallstones facilitate the development of the chronic carrier state [5]. In support of this, we identified SirA in our IVIAT screen, which is part of the two-component response regulator SirA-BacA [27]. In S. Typhimurium, this regulator plays a role in the down-regulation of genes involved in invasion (i.e. Salmonella Pathogenicity Island-1) when the bacterium is in the presence of bile [28], and mutations in sirA result in decreased biofilm formation on plastic surfaces [28]. The role SirA may play in human or murine Salmonella carriage, or why a cytoplasmic regulatory protein generated a humoral response, has yet to be characterized. Other proteins identified in the IVIAT screen may also affect carriage in the presence of gallstones.

Although S. Typhi may persist in the gallbladder in association with gallstones [3], S. Typhi likely has other niches of infection, including the gallbladder epithelium, biliary tree, and in macrophages of mesenteric lymph nodes [2,3,5,16–18]. Proteins identified in our screen may play a role in persistence of S. Typhi within host cells or the stringent environment of bile. For instance, YejE is a putative permease that is thought to be a component of a putative ABC transporter system. YejE plays a role in survival within epithelial cells and in antimicrobial peptide resistance [29]. In both S. Typhi and S. Typhimurium, yejE expression is upregulated inside host macrophages [30,31]. PheG is a protein encoded within the phe operon that is part of the coenzyme B12-dependent 1,2-propanediol utilization pathway [32]. This operon is upregulated during acute S. Typhi and S. Paratyphi A infection in humans [24,33], and may be associated with use of alternative carbon sources in the nutrient-limited environment of the Salmonella-containing vacuole within host cells [32]. We also identified PurH and XapB, which are proteins involved in purine biosynthesis and acquisition, respectively, by functional classification. In S. Typhimurium, PurH is associated with virulence [34], and we have previously shown that genes involved in purine synthesis are upregulated during acute typhoid infection in humans [24]. CorC is a hemolysin-related protein involved in magnesium and cobalt efflux, and is part of the CorA transporter system containing CorA-D [35]. CorA, with associated proteins, is required for efflux of Mg²⁺ [35]. CorA is required for S. Typhimurium virulence [36], and corA is expressed by S. Typhi during acute human infection [24]. However, while some information is known regarding the above mentioned Salmonella carrier-specific antigens, their potential role in carriage is presently unclear.

The majority of the genes identified by IVIAT encode for proteins with putative or unknown function. For example, STY2396 is an uncharacterized lipoprotein found uniquely in Salmonella. STY1364 is a hypothetical periplasmic protein in S. Typhi and S. Paratyphi A, and is rarely found in other Salmonella spp. STY1364 belongs to the structural classification of bacterial enterotoxins and is a subtilase cytoxtoxin subunit B-like protein. We previously identified STY1364 in S. Typhi infected patients using a separate immunoscreening technology (immunoaffinity proteomic-based technology, IPT) [23].

In our screening, YncE (STY1479) was the most immunoreactive antigen identified, and we thus focused our more detailed analysis of immunoreactivity on this antigen. YncE has a putative N-terminal signal sequence suggestive of export, with ATP and DNA-binding domains. yncE is present in a number of Salmonella spp., and has orthologs in a number of other Gram-negative enteric organisms, including Escherichia coli, Citrobacter spp., and Shigella spp. In E. coli, YncE is secreted into the periplasm via the Sec-dependent pathway [37], and its expression is induced under iron-restricted conditions when repression by the Fur protein is relieved [38]. Its role in the pathogenesis of Salmonella infection has yet to be characterized. However, our results suggest that it may be involved in long-term persistence of the bacterium in chronic carriers.

In our analysis, we show that S. Typhi carriers have an IgG response to YncE that is not present in bile culture-negative controls in Nepal or healthy controls in Bangladesh. Although we did not reach statistical significance in this small pilot study, a similar trend was seen for IgA as well. One patient convalescing from acute typhoid infection had a detectable IgG anti-YncE response, and another had an IgA response. This may suggest that anti-YncE responses occur during acute disease; however, it should be noted that we do not know the current or future carrier status of the acute typhoid patients, and an elevated level of YncE during an episode of typhoid fever may represent an acute on chronic infection, or may be a marker of future progression to the chronic carrier state.

All of the identified genes except three (sapB and the two genes encoded on the cryptic plasmid pHCM2) are present in the genome of S. Paratyphi A sequenced strains ATCC 9150 and AKU 12601 based on <60% nucleotide identity. It is interesting then, that we did not see an IgG or IgA immune response to YncE in S. Paratyphi A carriers. This finding may suggest that S. Typhi and S. Paratyphi A use different strategies to persist in chronic carriers, that expression of YncE may be distinct in these two organisms, or that our study did not have sufficient power to examine this, as it included only three S. Paratyphi A carriers.

Despite this, in our small cohort of patients, measurement of anti-YncE IgG responses did appear to be both relatively sensitive and specific for identifying asymptomatic chronic S. Typhi carriers. Further studies will be needed to evaluate the diagnostic capabilities of anti-YncE responses in a larger and different cohort of patients. Of note, if such studies demonstrate higher anti-YncE IgA levels in S. Typhi carriers than in control groups, that information could support consideration of a salivary diagnostic to facilitate community-based screening for carriage.

The other antigens identified in our IVIAT analysis may also be useful diagnostic biomarkers of S. Typhi carriage, and the sensitivity of carrier detection may be improved when responses against these or anti-Vi responses are paired with responses to YncE. For example, in our analysis, using a cut-off value of >100 U of anti YncE IgG and/or >1250 U anti-Vi IgA, we could identify 8 out of 10 S. Typhi carriers. There was no added benefit seen when pairing anti-YncE responses with anti-Vi IgG. Another potential pairing could include a marker of biliary tract inflammation such as elevated bilirubin values, since S. Typhi carriage is often associated with chronic inflammation of the gallbladder [5]. We did not assess this parameter in this study.
Our study has a number of limitations. First, the number of patients involved in our study is small, although it should be noted that our analysis is the largest study involving immunoproteomic screening and pilot confirmation of the carriage state that includes appropriate control groups. A second limitation is that IVIAT identifies proteins that are uniquely expressed in vivo compared to standard in vitro culturing, and that also induce an antibody response. Proteins that induce cellular responses and/or that are expressed both in vivo and in vitro may also play a role in the pathogenesis of chronic carriage and serve as useful biomarkers for asymptomatic carriage. In addition, altering in vitro culturing conditions may also change the expression profile of S. Typhi, thereby changing the comparison groups. In addition, IVIAT does not identify non-protein antigens that may also be useful in diagnostic assays. However, despite these limitations, we have used IVIAT to identify a subset of immunoreactive antigens in S. Typhi carriers, including YncE. Further evaluation of YncE and other identified antigens could lead to the development of improved diagnostic assays to detect asymptomatic S. Typhi carriers in typhoid endemic zones, and analysis of YncE, along with other identified antigens, could lead to an improved understanding of host-pathogen interactions during chronic carriage of S. Typhi in humans.

Supporting Information
Table S1 Proteins identified by IVIAT with higher IgG immunoreactivity in S. Typhi carriers compared to immunoreactivity to empty vector. (XLS)

Author Contributions
Conceived and designed the experiments: RCC JBH RCL SBC JF FK JSG FQ SB ETR. Performed the experiments: RCC TS MMA YY YW MKB SMR LT TVTN SD BB FK. Analyzed the data: RCC TS YY YW DTL WAB SBC JSG JBH RCL FQ SB ETR. Contributed reagents/materials/analysis tools: SBC ETR FQ FK WAB SB JF BB SD TVTN. Wrote the paper: RCC TS MMA YY YW MKB SMR LT JH BCL DTL WAB TVTN SD BB SBC JF FK JSG FQ SB ETR.

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