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.


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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 (icdlr,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-It 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 EcoRI 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. EcoRI 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.

Screening for antigens uniquely expressed in vivo in S.
Typhir 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 and
1 mM isopropyl-B-D-thiogalactopyranoside, and then the
membranes were placed on LB media containing kanamycin and
1 mM isopropyl-B-D-thiogalactopyranoside for 4 hours at 37°C to
induce transcription of insert DNA. Membranes were exposed to
chloroform-soaked blotting paper to lyse bacteria, blocked for 1 hr
using 5% milk in PBS with 0.25% Tween-20 (PBS/Tween),
was washed five times in PBS/Tween, and then incubated overnight
with adsorbed sera at 1:10,000 dilution. After membranes were
washed 3 times with PBS/Tween, immunoreactive clones were
detected using anti-human IgG conjugated to horseradish
peroxidase (MP Biomedicals/Cappel, Aurora, OH) at a 1:20,000
dilution, and immunoblots were developed with an enhanced
chemiluminescence (ECL) kit (Amersham, Piscataway, NJ).
Reactive clones were recovered from the master plates and saved
as frozen glycerol stocks.

To confirm immunoreactive clones, secondary screening was
performed comparing IgG immunoreactivity of the clones against
E. coli BL21DE3 with an empty pET30c vector. Inserts of
confirmed clones were sequenced to identify gene insert.
Constructs designed to express the full length native protein were
generated by amplifying the entire ORF of identified genes by
PCR, and cloning these amplicons into pET30c as NdeI and NotI
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://www.jcvi.org/cgi-scripts/CMR/CmrHomePage.cgi) and
Pam 26.0 (http://pfam.sanger.ac.uk/).

Purification of YncE
YncE (STY1479) was PCR-amplified from S. Typhi strain
CT18 and the product was cloned into Gateway vector
pDONR221 using BP reaction kit according to manufacturer's
instructions (Invitrogen). The full length sequence was verified
and transferred from pDONR221 into the Gateway expression vector
pDEST17 using LR reaction kit (Invitrogen) generating
pDEST17/His6-yncE. The reaction product was transformed first
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 HiPor 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 0.15 M NaCl, pH 8.0 using
dereducing concentrations of urea. Product purity was assessed by
polyacrylamide gel electrophoresis and Coomassie staining, and
product identity was assessed by Mass spectrometry analysis.
Protein concentration was determined via Coomassie (Bradford)
Protein Assay Kit (ThermoScientific, Rockford, IL).

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
carries undergoing elective cholecystectomy with negative bile
cultures, and 8 healthy Bangladeshis, 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 Laborato-
ries, Bar Harbor, ME) at a 1:1000 dilution, and peroxidase
activity was measured with the substrate 2,2-azinobis
(ethylbenzthiazolesulfonic 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
ing S. Typhi carriers confirmed by biliary culture), and then
Typhi antigens identified by IVIAT

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 S. 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>
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<tbody>
<tr>
<td>STY0712</td>
<td>corC</td>
<td>Hemolysin-related protein</td>
</tr>
<tr>
<td>STY1364</td>
<td>yncE</td>
<td>Possible ATP-binding protein</td>
</tr>
<tr>
<td>STY2248</td>
<td>sinA</td>
<td>Invasion response-regulator</td>
</tr>
<tr>
<td>STY2286</td>
<td>pduG</td>
<td>PduG protein</td>
</tr>
<tr>
<td>STY2386</td>
<td>yejE</td>
<td>Putative lipoprotein</td>
</tr>
<tr>
<td>STY2454</td>
<td>putH</td>
<td>Phosphoribosylaminomimidazolecarboxamidofomyltransferase and IMP cyclohydrolase (bifunctional enzyme)</td>
</tr>
<tr>
<td>STY2565</td>
<td>repE</td>
<td>Replication initiation protein</td>
</tr>
<tr>
<td>STY3709</td>
<td>repE</td>
<td>Replication initiation protein</td>
</tr>
<tr>
<td>HCM1.137</td>
<td>repE</td>
<td>Replication initiation protein</td>
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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 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 &gt;1250 U) and 50% (cutoff value &gt;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.
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 working 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-BarA [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]. PduG is a protein encoded within the pdu 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, STY2386 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 cytotoxin 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 (xapB 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 immunoprofiling and piloting confirmation of the carriage state that includes appropriate control groups. A second limitation is that IVIAT identifies non-protein antigens that are uniquely expressed in vitro compared to standard in vivo culturing, and that also induce an antibody response. Proteins that induce cellular responses and/or that are expressed both in vitro and in vivo 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 JHB RCL SBC JSG JBH RCL FQ SB ETR. Performed the experiments: RCC TS MMA YY YW MKB SMR LT JBH RCL DTL WAB SBC JSG JHB 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 JHB RCL DTL WAB TVTN SD BB SBC JF FK JSG FQ SB ETR.

References


