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DNA Damage and Reactive Nitrogen Species are Barriers to Vibrio cholerae Colonization of the Infant Mouse Intestine

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Abstract

Ingested Vibrio cholerae pass through the stomach and colonize the small intestines of its host. Here, we show that V. cholerae requires at least two types of DNA repair systems to efficiently compete for colonization of the infant mouse intestine. These results show that V. cholerae experiences increased DNA damage in the murine gastrointestinal tract. Agreeing with this, we show that passage through the murine gut increases the mutation frequency of V. cholerae compared to liquid culture passage. Our genetic analysis identifies known and novel defense enzymes required for detoxifying reactive nitrogen species (but not reactive oxygen species) that are also required for V. cholerae to efficiently colonize the infant mouse intestine, pointing to reactive nitrogen species as the potential cause of DNA damage. We demonstrate that potential reactive nitrogen species deleterious for V. cholerae are not generated by host inducible nitric oxide synthase (iNOS) activity and instead may be derived from acidified nitrite in the stomach. Agreeing with this hypothesis, we show that strains deficient in DNA repair or reactive nitrogen species defense that are defective in intestinal colonization have decreased growth or increased mutation frequency in acidified nitrite containing media. Moreover, we demonstrate that neutralizing stomach acid rescues the colonization defect of the DNA repair and reactive nitrogen species defense defective mutants suggesting a common defense pathway for these mutants.

Introduction

Maintaining genomic integrity during infection is important for several bacterial pathogens to colonize their hosts. DNA repair defects in Listeria monocytogenes, Salmonella typhimurium, Helicobacter pylori and others leads to decreased or even a complete attenuation of virulence [1–6]. While there are several types of DNA repair in bacteria [7], many of the studies showing a requirement for DNA repair in pathogenesis focus on three pathways: the SOS response, base excision repair, and mismatch repair [1–10].

The SOS response is a well studied and conserved stress response in bacteria that is elicited following DNA damage and replication fork arrest [for review [11]]. The SOS response is controlled by positive and negative regulators. RecA positively regulates the SOS response by binding to single-stranded DNA fragments generated by attempted replication past DNA lesions. The RecA/ssDNA nucleoprotein filament induces the autocleavage of the negative regulator LexA, a transcriptional repressor. Cleavage of LexA allows for expression of 57 genes in the E. coli SOS regulon including translesion DNA polymerases that are able to replicate DNA past noncoding base lesion, and proteins involved in the inhibition of cell division [for review [11]].

Base excision repair (BER) is the most common form of repair for single base damage [for review [7]]. In BER, a DNA N-glycosylase first excises the damaged base from the deoxyribose moiety in the DNA strand creating an abasic site. Class II apurinic/apyrimidinic (AP) endonuclease then hydrolyzes the phosphodiester bond immediately 5’ to the abasic site [for review (Kornberg and Baker 1992, Friedberg 2005)]. Subsequent actions process this site to prime and repair the abasic site ultimately by DNA synthesis with DNA polymerase I and ligation by DNA ligase.

Normal replication can also introduce errors in the form of mismatched DNA base-pairs. These mismatches can lead to permanent mutations after a subsequent round of DNA replication. Mismatch repair (MMR) specifically identifies and corrects these base pairing errors increasing the fidelity of the replication pathway nearly ~1000-fold [for review [7]].

While extensive work has shown the benefit of maintaining genomic integrity for an invading bacterium, there appear to be instances where lapses in genomic fidelity are beneficial for a pathogenic bacterium [12–14]. In order to colonize and thrive in a mammalian host, a bacterium must be able to adapt and respond to the conditions and stresses associated its new environment.
For example catalases/peroxidases decompose H₂O₂, superoxide and RNS. Each enzyme detoxifies a specific type of ROS or RNS. Interestingly bacteria have several defense mechanisms to detoxify ROS and oxygen species (ROS) and reactive nitrogen species (RNS) cause infection, defects in DNA repair may be detrimental or beneficial allowing rapid adaptation to the hostile host environment [14]. Thus individuals often has an increased mutation frequency, suggesting liability once adaptation had been reached [12]. Oliver et al. demonstrated that Pseudomonas aeruginosa from chronically infected individuals often has an increased mutation frequency, suggesting an increased mutation rate can be beneficial to P. aeruginosa to allow rapid adaptation to the hostile host environment [14]. Thus depending on the pathogen, the mode and duration of the infection, defects in DNA repair may be detrimental or beneficial to the infecting bacterium.

Several studies have indicated that host produced reactive oxygen species (ROS) and reactive nitrogen species (RNS) cause DNA damage to the invading bacterium [4,16,17]. Not surprisingly bacteria have several defense mechanisms to detoxify ROS and RNS. Each enzyme detoxifies a specific type of ROS or RNS. For example catalases/peroxidases decompose H₂O₂, superoxide dismutases dismutate superoxide and ferrisiderophore reductase removes nitric oxide [18,19]. As with certain DNA repair systems, loss of ROS and RNS defenses have been shown to attenuate bacterial pathogens [16,20].

Studies supporting the importance of ROS/RNS defenses and DNA repair pathways in bacterial pathogenesis often focus on intracellular pathogens [1,2,4]. To survive, intracellular pathogens engulfed by phagocytic cells are either able to escape the phagosome or have mechanisms to survive within it. Within the phagosome, captured bacteria may be exposed to host production of ROS and RNS in a host defense response called the oxidative burst. It is hypothesized that the oxidative burst is responsible for the DNA damage experienced by engulfed bacteria [4,16,17].

Vibrio cholerae is the causative agent of the severe human diarrheal disease cholera. V. cholerae is a non-invasive pathogen that colonizes the small intestine of its host [21,22]. As a non-invasive pathogen, V. cholerae is not expected to experience the same types of stresses as intracellular pathogens, such as an oxidative burst. However V. cholerae does pass through several hostile environments as the disease progresses. Immediately following ingestion, V. cholerae is exposed to the exceptionally antagonistic environment of the stomach where the pH of gastric acid can reach as low as 1 [23,24]. Furthermore, nitrite from both food sources and the salivary nitrite cycle can enter the stomach creating acidified nitrite [25,26,27]. Acidified nitrite has potent antimicrobial effects on gut pathogens [28,29,30,31]. These studies show that the viability of several pathogenic bacteria decreases rapidly under acidified nitrite conditions. Furthermore, nitrates, which can also be found in the stomach, have been shown to modify of gene expression reducing acid tolerance [32]. The antimicrobial effects of acidified nitrite are thought to be due to the generation of deleterious RNS [33]. However, with the exception of a few studies [34,35,36], the points of action of these RNS as well as the bacterial determinants required for protection against them have remained largely unexamined. After traversing the stomach V. cholerae faces several innate host defenses in the intestine including bile, lysozyme, small antimicrobial peptides and complement [37]. Thus, V. cholerae must overcome several barriers during infection that have the potential to cause DNA damage through a direct or indirect mechanism.

We report here that V. cholerae strain C6706 experiences increased DNA damage during passage through the murine gastrointestinal tract. We demonstrate that increased genomic stress is a potential barrier to host colonization by V. cholerae. We found that two important DNA repair pathways are necessary for V. cholerae to efficiently colonize the infant mouse intestine. Furthermore, we show that defense against RNS is also necessary for V. cholerae to colonize the infant mouse. In doing so we identify a novel protein required for defense against RNS in pathogenic bacteria. In vitro we show that all our colonization defective DNA repair and RNS defense mutants share a common sensitivity to acidified nitrite and we further show that neutralizing stomach acid rescues intestinal colonization defect of these mutants.

Results

Mismatch repair and base excision repair pathways are required for V. cholerae colonization of the infant mouse intestine

To determine if V. cholerae requires defenses against DNA damage during colonization, we tested a series of transposon mutants that contained insertions in different steps in three important DNA repair pathways for their ability to colonize the infant mouse intestine in competition with the wild type strain. These pathways were nucleotide excision repair (NER), base excision repair (BER) and mismatch repair (MMR) (Table 1). While the SOS response is an important contributor to genomic integrity we did not test a requirement for SOS since Quiones et al. previously showed that SOS activation is not required for intestinal cholera toxin production or colonization [38]. We used wxaC as a representative gene required for NER since wxaC is obligatory for NER. We found no difference in the ability of the wxaC::Tn containing strain to colonize the infant mouse relative to the parental strain suggesting that NER is dispensable for V. cholerae pathogenesis (Table 1). Apurinic/apyrimidinic (AP) endonucleases are critical in BER. BER has been most well studied in E. coli. E. coli encodes two class II AP endonucleases, Xih [endo II (endo VI)] and Nfo [endo IV]. In E. coli Xih is responsible for ~90% of the AP endonuclease activity in the cell [39,40]. Few phenotypes have been attributed solely to Nfo activity but Nfo is known to contribute to BER [41]. V. cholerae carries close homology of both Xih and Nfo (VC1860 and VC2360 respectively). Interestingly we found that the xih::Tn mutant was not
found this mutant also had a colonization defect. In order to repair such damage is detrimental for significant for this number of replicates tested (p < 0.05). Thus, these results suggest that BER is important for V. cholerae to colonize the infant mouse intestine when in competition. These results also show a critical function for Nfo in survival, which has not been apparent under laboratory conditions. Loss of mismatch repair function has been shown to be either beneficial or detrimental depending on the pathogen studied [12,13,14,15]. We found that a transposon mutant in mutS, which encodes the gene product that initially binds to a mismatch, resulted in a decrease in colonization efficiency (Table 1). We constructed a clean deletion of mutS (ΔmutS) to ensure the defect was not due to the transposon. We found that the clean deletion of mutS was also attenuated in its ability to colonize the intestine suggesting that mismatch repair or at least MutS is important for V. cholerae pathogenesis (Table 1). We also found that a second clean deletion of mutS showed a similar competitive index defect (CI = 0.10 ± 0.05) suggesting that the colonization defect was not due to mutations in the first mutS clean deletion strain. We noted that the mutS transposon mutant was more defective than its clean deletion counterpart (Table 1). This difference may be due to a polar effect of the transposon or mutations acquired by the mutS::Tn strain during outgrowth of the original isolate. We also tested the colonization proficiency of a Δnfo ΔmutS double mutant and found that the colonization defect of this double mutant appears slightly greater than either the Δnfo or ΔmutS mutant alone (Table 1) although this difference is not statistically significant for this number of replicates tested (p > 0.05).

The requirement of BER and MMR for V. cholerae to efficiently colonize the infant mouse intestine suggests that V. cholerae experiences DNA damage in the mouse, and that a reduced ability to repair such damage is detrimental for V. cholerae pathogenesis.

V. cholerae base excision repair and mismatch repair mutants show classic DNA repair defects

V. cholerae genes encoding Xth, Nfo and MutS were identified based on sequence similarity with their well-studied E. coli homologs. To ensure the V. cholerae homologs possessed their predicted functions we tested our mutant strains for the well characterized phenotypes described in other bacterial systems. Loss of mismatch repair causes an increase in mutation rate often referred to as a mutator phenotype [42]. We found that our ΔmutS mutant had a significantly increased mutation frequency compared with the wild type control (Figure 1A). The wild type phenotype could be restored by expression of mutS from a plasmid but not by the plasmid itself (Figure S1B). This result indicates that MutS in V. cholerae shares the same activity as its other well studied bacterial homologs in the repair of DNA replication errors.

Loss of Xth activity in E. coli renders the strain sensitive to hydrogen peroxide (H2O2) [43]. We found that our xth::Tn strain was also sensitive to H2O2 (Figure 1B). Loss of nfo activity alone does not greatly sensitize E. coli to H2O2 but loss of xth and nfo creates a strain with increased sensitivity to H2O2 [43]. We found a similar effect in V. cholerae where the xth::Tn Δnfo strain was much more sensitive to H2O2 than the xth::Tn mutant alone (Figure 1B). Furthermore, high level expression of nfo from a plasmid complemented the H2O2 sensitivity of the xth::Tn Δnfo mutant (Figure S1C). These results suggest that V. cholerae Nfo acts like its E. coli homolog.

Passage through the mouse increases the mutation frequency of V. cholerae

The requirement of BER and mismatch repair (MMR) systems for V. cholerae to efficiently colonize the mouse intestine suggests that V. cholerae experiences increased DNA damage while in the mouse. To address this possibility we measured the mutation frequency of V. cholerae following passage though the mouse as compared to passage in liquid culture. We inoculated five mice and five liquid cultures with the same size inoculums of V. cholerae. The following day we purified bacteria from the mouse intestine (see Materials and Methods). We plated both V. cholerae passed through the mouse and grown in liquid cultures followed by selection for resistance to two antibiotics we used as an indicator for measuring mutation frequency. The first was a gain of function mutation in rpoB conferring resistance to rifampicin; the second was a loss of function of thyA conferring resistance to trimethoprim. Mutations in rpoB and thyA are well characterized markers for increases in mutation frequency [44,45,46]. We found that following passage of V. cholerae through the mouse there was an ~2 fold increase in rifampicin resistance and ~2.5 fold increase in trimethoprim resistance compared to the liquid culture grown.

**Table 1.** Ability of V. cholerae mutants defective in DNA repair pathways to colonize the infant mouse intestine in competition with the parental strain (WT).

| Gene | Function | Repair Pathway | *Competitive Index: Tn Mutant/WT | *Competitive Index: Deletion Mutant/WT |
|------|----------|----------------|-------------------------------|-------------------------------------|
| uvrA | Excinuclease ABC | Nucleotide Excision Repair | 1.14±0.11 | 1.07±0.05 |
| xth  | Exonuclease III | Base Excision Repair | 0.15±0.01*** | 0.23±0.01*** |
| nfo  | Endonuclease IV | Base Excision Repair | 0.19±0.01*** | 0.22±0.01*** |
| xth/nfo | Double mutant | Base Excision Repair | N/A | 0.07±0.06** |
| mutS | Mismatch Recognition | Mismatch Repair | 0.01±0.01*** | 0.16±0.07*** |
| nfo/mutS | Double mutant | Base Excision and Mismatch Repair | 0.08±0.02* | |

*The competitive index is the ratio of mutant to parental (WT) cfu in the small intestine post infection divided by the input ratio of mutant to parental (WT) cfu. The average and standard error of 5–7 mouse experiments is shown for each mutant. The ΔmutS, Δnfo, xth::Tn Δnfo, ΔmutS, Δnfo mutant strains grew similarly to the wild type under free-living conditions (Figure S1A). The mean and standard error of 5–7 mouse experiments is shown for each mutant. Statistical significance of the competitive colonization defect of each mutant strain relative to the null hypothesis was determined as described in the materials and methods (*** p < 0.001). doi:10.1371/journal.ppat.1001295.0010
strains (Figure 2A, B). We sequenced 19 trimethoprim resistance isolates that were passed through the mouse and 20 isolates obtained following growth in liquid culture. We identified 39 unique mutations in \textit{thyA} (data not shown) suggesting that our results were not influenced by a mutation acquired early on in the procedure. We did not observe a bias in the types of mutation from the two conditions. These results suggest that passage through the mouse results in an increase in mutation rate for \textit{V. cholerae} suggestive of an increase in DNA damage and the need for repair mechanisms.

Defense against RNS is required for \textit{V. cholerae} to colonize the infant mouse

We have identified two DNA repair mechanisms required by \textit{V. cholerae} to efficiently colonize the infant mouse, and have shown that \textit{V. cholerae} passaged through a mouse has an increased mutation frequency. Thus, we sought to identify potential causes of DNA damage for \textit{V. cholerae} while in the mouse to understand the requirement for BER and MMR in the mouse. A major source of DNA damage for intracellular pathogens is from host produced...
ROS and RNS. While *V. cholerae* is a non-invasive pathogen we considered that it still may experience ROS and RNS at some point during infection. We used a genetic approach to determine if ROS/RNS affected *V. cholerae* colonization and if so what type(s) of ROS/RNS were most important during this encounter.

Bacteria have several enzymes to detoxify ROS/RNS. Each enzyme detoxifies a specific type of ROS or RNS [for review see [18,19]]. For example catalases/peroxidases decompose H$_2$O$_2$, superoxide dismutases remove superoxide and ferrisiderophore reductases remove nitric oxide. Bacteria can contain multiple proteins capable of dealing with one type of stress. *V. cholerae* possesses two catalases/peroxidases (KatB/PerA) and one alkyl hydroperoxide reductase (AhpC), three superoxide dismutases (SodA/B/C) but only one ferrisiderophore reductase (HmpA). We tested mutants defective for each of these different types of defense enzymes to identify the type(s) of radicals that may be damaging *V. cholerae* in the mouse (Table 2).

RNS, including nitric oxide, have been shown to be powerful antimicrobial agents. The most well studied RNS defense enzyme in bacteria is Hmp, a ferrisiderophore reductase that destroys nitric oxide [47]. *V. cholerae* carries an *hmp* homolog, *hmpA*. Both an *hmpA*::Tn mutant and a Δ*hmpA* deletion mutant showed a defect in colonizing the infant mouse intestine (Table 2). Deletion of *hmpA* delayed *V. cholerae* growth in the presence of a nitric oxide donor but not in the absence (Figure 3A) consistent with previous observations in other organisms [20,40]. This suggests that *V. cholerae* may encounter deleterious RNS during passage in the mouse. The growth defect of the Δ*hmpA* mutant in the presence of a nitric oxide donor could be complemented by ectopic expression of *hmpA* from the arabinose inducible plasmid pBAD18 (Figure S1E). In fact, expression of *hmpA* from pBAD18 allowed the Δ*hmpA* mutant to recover growth more rapidly than the parental strain in the presence of a nitric oxide donor.

After testing all previously predicted antioxidant enzymes we began to mine the *V. cholerae* genome for additional putative antioxidant enzymes. We began by searching for putative proteins that belonged to large antioxidant families. Enzymes, such as AhpC, belong to the Peroxiredoxin (PRX) family. Searching for peroxiredoxin family proteins yielded a putative defense enzyme we have called PrxA (NC2637). *PrxA*, classified as a peroxiredoxin-5 family protein, is found in several pathogenic bacteria and is a distant homolog of a macrophage peroxynitrite detoxification protein [49].

Deletion of *prxA* did not affect *V. cholerae* growth in LB alone but significantly delayed *V. cholerae* growth in the presence of a nitric oxide donor (Figure 3A). Furthermore, both the *prxA*::Tn mutant and the Δ*prxA* allele we constructed caused a decrease in the ability of *V. cholerae* to colonize the infant mouse in competition assays (Table 2). The growth defect of the Δ*prxA* mutant in the presence of a nitric oxide donor could be complemented by ectopic expression of *prxA* from the arabinose inducible plasmid pBAD18 (Figure S1E). The discovery of a new gene required for both defense against RNS and efficient colonization of the infant mouse further supports our findings that *V. cholerae* may be exposed to RNS during passage through the mouse.

We tested the sensitivity of a Δ*hmpA* Δ*hmpA* double mutant and found that the growth of the double mutant in the presence of a nitric oxide donor was even more delayed than either the Δ*hmpA* or Δ*hmpA* single mutant alone (Figure 3A). We also tested the colonization efficiency of a Δ*hmpA* Δ*prxA* (Table 2) and found that it was not significantly less than the Δ*hmpA* mutant alone (p>0.05). Thus *hmpA* and *prxA* are both important for colonization but the effects were not additive.

We asked if defects in ROS defense also affect *V. cholerae* colonization. Disruption of *ahpC*, *katB*, *perA*, *sodA* or *sodC* did not affect the ability of *V. cholerae* to colonize the infant mouse and these deficiencies did not affect the ability of *V. cholerae* to colonize the infant mouse in competition experiments (Table 2). We did not test the *sodB*::Tn mutant since both it and a *sodB* deletion strain we constructed had a decreased plating efficiency and grew very poorly compared to the parental strain (Figure S1F). Thus, while *SodB* appears to be important for growth of *V. cholerae* under laboratory conditions we did not pursue the *sodB* mutant in mouse experiments.

Interestingly, of *ahpC*, *katB* and *perA* only disruption of *perA* sensitized *V. cholerae* to H$_2$O$_2$ in vitro (Figure 3B). Furthermore, of strains disrupted individually for *sodA*, *sodB* and *sodC* only disruption of *sodB* sensitized *V. cholerae* to the superoxide generating compound plumbagin (Figure 3C). We also tested the Δ*prxA* mutant but found that it did not show increased sensitivity to either H$_2$O$_2$ or plumbagin (Figure S2A and data not shown). It is possible that some of these known ROS defense enzymes overlap

### Table 2. Ability of *V. cholerae* mutants defective in ROS or RNS detoxification to colonize the infant mouse intestine in competition with the parental strain (WT).

| Gene     | Function        | *Competitive Index: Tn Mutant/WT | *Competitive Index: Deletion Mutant/WT |
|----------|-----------------|---------------------------------|----------------------------------------|
| *ahpC*   | Peroxidase      | 1.41±0.02                       |                                        |
| *katB*   | Catalase        | 1.14±0.07                       |                                        |
| *perA*   | peroxidase      | 1.42±0.17                       |                                        |
| *sodA*   | Superoxide dismutase | 1.15±0.10                  |                                        |
| *sodB*   | Superoxide dismutase | N/A                          |                                        |
| *sodC*   | Superoxide dismutase | 1.25±0.06                  |                                        |
| *hmpA*   | Ferrisiderophore reductase | 0.13±0.02***                  | 0.16±0.01***                           |
| *prxA* (NC2637) | Peroxiredoxin putative | 0.14±0.02***                  | 0.09±0.01***                           |
| *prxA*/Δ*hmpA* | Double mutant     | 0.07±0.01**                     |                                        |
| Δ*hmpA*/Δ*prxA* | Double mutant     | 0.13±0.01***                    |                                        |

*The competitive index is the ratio of mutant to parental (WT) cfu in the small intestine post infection divided by the input ratio of mutant to parental (WT) cfu. The mean and standard error of 5–10 mouse experiments is shown for each mutant. Statistical significance of the competitive colonization defect of each mutant strain relative to the null hypothesis was determined as described in the materials and methods (*** p<0.001, ** p<0.01). doi:10.1371/journal.ppat.1001295.002*
in function masking the effects of a deficiency in any one gene in vitro or in vivo. For other bacterial pathogens and symbionts deletion of several or all catalases and superoxide dismutases has been required before a strong effect on virulence or symbiosis was observed [50,51,52]. Currently, the results from our analysis suggest RNS may pose a significant barrier to \( V. \) cholerae in colonizing the infant mouse. ROS may also play a role, however their effect is not immediately evident in our analysis.

XthA appears to be more important than Nfo in protecting \( V. \) cholerae against environmental stress in vitro (Figure 1B), yet Nfo appears to be more important for colonization of the small intestine (Table 1). The requirement for \( \Delta hmpA \) and \( \Delta prxA \) for efficient intestinal colonization lead us to ask if Nfo was required for defense against nitric oxide. We monitored the growth of the xth::Tn, \( \Delta nfo \) and xth::Tn \( \Delta nfo \) mutants in the presence of a nitric oxide donor. We found that, at least in vitro, xth::Tn was more...
important than Nfo for protection against nitric oxide (Figure 3D). We also found that the double mutant was again more sensitive to the stress than either single mutant alone (Figure 3D).

Colonization defective mutants have increased sensitivity to acidified nitrite

Our results led us to ask if our DNA repair and RNS defense defective V. cholerae mutants were sensitive to any host defenses. The intestine has several innate defenses [37]. We tested many of these defenses including lysozyme, phospholipase, antimicrobial peptides, complement, bile, changes in osmolarity and pH, however, we did not observe any difference in sensitivity between the parental and the mutant strains (data not shown). RNS have been shown to be generated by macrophages to kill phagocytosed bacteria [reviewed in [53]]. The RNS from macrophages is generated by an inducible nitric oxide synthase (iNOS). Inhibition of iNOS activity has been shown to rescue the virulence defects in hmp mutant strains of Salmonella enterica serovar typhimurium [20]. However, our hmp::Tn V. cholerae mutant showed no difference in its ability to colonize the intestine of a wild type or isogenic iNOS−/− infant mouse (Table S1).

Thus, our results suggest that the colonization defect of the DNA repair and RNS defense mutants may occur before V. cholerae is exposed to the host defenses found in the small intestine. In the stomach V. cholerae is exposed to low pH in combination with mM amounts of nitrite from ingested food and the salivary nitrite cycle [25,26,27]. Acidified nitrite produces a variety of toxic RNS. We quantified the amount of nitrite in the infant mouse stomach using the Griess reaction and found that it was 20.0±0.7 μM, which is similar to that of humans [26]. The pH range of human gastric juice is reported as 1–3 [23,24]. We determined the pH of the infant mouse stomach to be 4.5±0.1 using a fluorescent pH sensitive dye. This measurement is conservative and the pH of the infant mouse gastric juice may be even less (see Materials and Methods). Thus, the infant mouse stomach is sufficiently acidic to promote the formation of acidified nitrite.

At pH 3 in rich medium we found that V. cholerae had a greater than 99.9% decrease in survival in less than 1 minute (data not shown) agreeing with similar work examining V. cholerae acid tolerance [54]. We did not find a difference in survival between the parental and mutant strains at low pH (1−4) levels (data not shown). We gradually increased pH to identify the lowest level at which V. cholerae could grow. At pH 5.5 V. cholerae and the DNA repair and RNS defense mutants grew with identical kinetics (Figure 4A). We titrated nitrite into the growth medium and found that nearly all the mutant strains showed a growth defect compared to the wild type at pH 5.5 in the presence of 400 μM nitrite (Figure 4B). No differences in growth between wild type and mutant strains were observed at pH 7.0 with or without 400 μM nitrite (Figure S3A, B). Not only did low pH and nitrite slow the growth of our mutants but the ΔhmpA, ΔproA, Δnfo and ΔhmpA ΔproA Δnfo mutants began to show a decrease in optical density after longer exposure (Figure 4B) suggesting the cells were lysing.

Thus, MutS may be important to prevent acidified nitrite induced mutations that could impair the ability of V. cholerae to colonize the infant mouse. To further test this possibility we created a ΔhmpA ΔmutS double mutant and tested its colonization proficiency (Table 2). Interestingly, the colonization defect of the ΔhmpA ΔmutS double mutant was not significantly different than either of the single mutants alone (p>0.05). This result may suggest that HmpA and MutS may share a similar defense pathway in the infant mouse.

Additionally, E. coli MutS can recognize an O6-methyl-dG:dC base pair, a mutation which can occur by alkylation of G bases [55]. Therefore it is possible that MutS may also be important for protection against some type of alkylation that occurs in the mouse stomach.

Low pH and nitrite induce radical formation in V. cholerae

If acidified nitrite produces RNS that damaged V. cholerae DNA, we reasoned that we should be able to detect increased intracellular radical formation in V. cholerae following nitrite treatment. We grew V. cholerae at pH 5.5 with increasing amounts of nitrite and assayed for radical formation using 2′,7′-dichlorodihydrofluorescein diacetate (H2DCFDA). H2DCFDA is a cell permeable dye that fluoresces after reacting with RNS and ROS species. H2DCFDA reacts with several ROS and RNS including hydrogen peroxide, nitric oxide and peroxynitrite [56,57,58]. We found that H2DCFDA fluorescence correlated with increasing nitrite concentration at pH 5.5 indicating an increase in intracellular radicals (Figure 4D). For comparison, we found that H2DCFDA fluorescence did not increase over the concentrations of nitrate examined at pH 7.0. These results further support the requirement for low pH to induce radical formation from nitrite sources (Figure 4D).

A colonization defect is observed for the DNA repair and RNS defense mutants early after inoculation

Our results suggested that V. cholerae may experience DNA damage as it passes through the stomach. If so, we were curious if a colonization defect could be observed at an early time point after inoculation. We repeated the competitive colonization assays testing the ΔmutS, Δnfo, ΔproA and ΔhmpA mutants. We found that at 3 hours post inoculation each mutant strain already showed a 50–60% colonization defect when co-inoculated with the wild type (Table S2) though this defect was not as great as the ~50–20% defects reported in Table 1. This suggests that a defect of the mutant strains is detrimental for colonization early after inoculation. Angelichio et al. [59] reported that V. cholerae populations in the small intestine do not show a significant increase in number until between 10–24 h post inoculations. These results suggest that the effects of the DNA damage are ~50% detrimental at the earliest stages of infection and become more apparent as the bacteria replicate to high numbers in the intestine. Such a conclusion is consistent with the concept of damage occurring primarily in the stomach.

The colonization defect of the DNA repair and RNS defense mutants is rescued by neutralizing stomach acid

Our results support a relationship between acidified nitrite sensitivity and colonization defects in our RNS and DNA repair. We reasoned that if acidified nitrite in the stomach was responsible for the colonization defects of our mutants then neutralizing stomach acid in the mouse should relieve, at least in part, the observed colonization defects. We used sodium bicarbonate to neutralize the mouse stomach acid. When we inoculated infant mice with our DNA repair and RNS defense defective mutants in
the presence of sodium bicarbonate all four mutant strains (Δ
\textit{inf0}, Δ
\textit{mutS}, Δ
\textit{prxA} and Δ
\textit{hmpA}) showed significant improvement in their ability to colonize the intestine in competition with the parental strain (Table 3). In fact the colonization defect of the Δ
\textit{mutS} and Δ
\textit{inf0} mutant was completely rescued. The colonization defect of the Δ
\textit{prxA} was restored to near wild type levels. The colonization defect of the Δ
\textit{hmpA} mutant was partially rescued although this difference is not statistically significant for the number of replicates tested (p>0.05).

The nitrite concentration of the infant mouse stomach after sodium bicarbonate treatment remained nearly unchanged at 20.3±0.8 μM.

**Discussion**

We have shown that \textit{V. cholerae} must defend against DNA damage to efficiently colonize the infant mouse intestine and that such damage likely occurs early during infection as \textit{V. cholerae}...
Table 3. Effect of NaHCO3 on mutant V. cholerae ability to colonize the infant mouse intestine in competition with the parental strain (wild type).

| Gene       | *Compeitive Index: Deletion Mutant/WT | NaHCO3 Treatment* Competitive Index: Deletion Mutant/WT |
|------------|----------------------------------------|--------------------------------------------------------|
| nfo        | 0.23±0.01                               | 1.10±0.03**                                           |
| mutS       | 0.16±0.07                               | 0.92±0.05†                                            |
| prxA (VC2637) | 0.09±0.01                              | 0.74±0.06†                                            |
| hmpA       | 0.16±0.01                               | 0.45±0.01                                             |

*The competitive index is the ratio of mutant to parental (WT) cfu in the small intestine post infection divided by the input ratio of mutant to parental (WT) cfu. The average and SEM of 4-7 mouse experiments is shown for each mutant. The NaHCO3 treatments that causes significant rescue of the mutant colonization defect are indicated († p<0.05, ** p<0.01, *** p<0.001). NaHCO3 treatment did not cause significant rescue of the HmpA mutant (p>0.05). doi:10.1371/journal.ppat.1001295.t003

enters the stomach. We have demonstrated that V. cholerae specifically requires BER and MMR pathways to efficiently colonize the infant mouse intestine. Furthermore, we have identified one previously known and one novel RNS defense protein that facilitates intestinal colonization of the infant mouse. These DNA repair and RNS defense proteins were also required for V. cholerae to grow or maintain genomic fidelity in the presence of acidified nitrite. Furthermore the colonization defects of each mutant could be partially or fully complemented by neutralizing stomach acid suggesting that RNS defense and DNA repair share a common defensive role in the mouse.

V. cholerae has been shown to be very sensitive to low pH [54]. For this reason, human volunteers have their stomach contents acidified nitrite. We propose that the defect in colonization of the parental strain (wild type).

DNA damage induced by acidified nitrite radicals occurs, or that DNA damage induced by acidified nitrite radicals occurs, or continues to occur, in the upper intestinal tract. As gastric juice exits the stomach it is neutralized by bile salt, etc. and can reach a pH close to 8 [24]. Since the stability of at least some RNS, such as peroxyrinitre, increases with increasing pH [63] the upper intestinal tract may provide a more favorable environment for RNS to reach V. cholerae and induce DNA damage.

Bicarbonate has been shown to induce V. cholerae virulence genes in a ToxT dependent fashion [64]. Abuaita and Wisby show that significant upregulation of both cholera toxin and tcpA gene expression are observed 3-4 h after addition of bicarbonate [64]. While our inoculation of V. cholerae occurs on a much shorter time scale (~5–15 min after exposure of bicarbonate) and the majority of V. cholerae has passed into the small intestine before 3 h, it is possible that some bicarbonate induced gene regulation may also aid in the bicarbonate rescue of the colonization defect of our DNA repair mutants.

While the debate over the benefits and detriments of increased mutation frequency for pathogenesis continues, we have shown that increased mutation frequency is detrimental to V. cholerae pathogenesis, at least for the short-term colonization of the infant mouse intestine. However, we cannot exclude the possibility that increased mutation frequency affects long-term survival of V. cholerae in the host. After the initial decrease in competitiveness it is possible that increased mutation frequency in V. cholerae could make it more competitive in later stages of colonization or during release into the environment. It would be interesting to test multiple clinical isolates for a mutator phenotype to address this question.

The Xth and Nfo homologs of V. cholerae have strong sequence similarity to their E. coli counterparts. We have shown that V. cholerae and E. coli deletion mutants of xth and nfo also share a similar pattern of sensitivity to hydrogen peroxide. Nfo and Xth have been most extensively studied in E. coli. In E. coli Xth is responsible for greater than ~90% of all AP endonuclease activity in the cell [39,40]. In E. coli, an xth mutant is very sensitive to a variety of DNA damaging agents whereas nfo mutants generally show milder effects [41]. Interestingly, we have shown that in V. cholerae Nfo is more important for colonization of the infant mouse than Xth. Our nfo xth double mutant suggests that Xth may play a role in colonization when Nfo is absent. However, for whatever damage is occurring, Nfo appears to play a more important role in the mouse.
It is possible that Nfo and Xth are also used differentially for repair of specific types of lesions. Preferences for specific types of damaged bases between Nfo and Xth from E. coli have been previously reported [63]. If RNS are responsible for DNA damage in the mouse we suggest that Nfo may have enhanced ability to aid in the repair of nitrosylative base damage. Additionally, there may be differential expression of xth and nfo or their preferential glycosylase partners in the host.

In our efforts to identify ROS and RNS defense enzymes required for intestinal colonization, we identified a new protein we have called PrxA that was required for RNS defense. Until now Hmp has been the only bacterial protein identified to detoxify RNS, specifically nitric oxide. We have shown that HmpA, PrxA protects V. choleræ against the nitric oxide donor spermine NONOate. Similarly, HmpA and PrxA both protect V. choleræ against acidified nitrite. This agrees with previous work showing that HmpA protects Salmonella against nitric oxide and acidified nitrite [34]. While the species(s) produced by acidified nitrite that HmpA and PrxA defend against is not clear, we presume that it is a RNS. PrxA homologs are not as prevalent in bacteria as HmpA homologs, but they are found in several pathogens including Yersinia pestis, Haemophilus influenzae and Neisseria gonorrhoeae. It will be interesting to determine if PrxA homologs share a similar RNS defense role in other bacteria.

Our observation that HmpA and PrxA are required for colonization lead us to suggest that V. choleræ encounters RNS stress during infection. When studying ROS defense genes we found that deletion of SodB was detrimental for normal V. choleræ growth. This indicated that normal growth of V. choleræ must generate a significant amount of superoxide managed by SodB. The growth defect of the ΔsodB mutant prevented us from analyzing it by competition in the mouse model. While we did not identify any other single ROS defense enzyme that affected intestinal colonization it is possible that construction of various double mutants may show that V. choleræ must also deal with ROS during disease progression. In bacterial pathogens where SODs have been shown to be necessary for virulence, it is generally the periplasmic SOD that is required as this SOD encounters superoxide entering the cells from the environment [16,66]. However, the V. choleræ periplasmic SOD, SodC, was not required for intestinal colonization suggesting V. choleræ does not experience superoxide stress from the host.

Materials and Methods

Ethics statement

The animal experiments were performed with protocols approved by Harvard Medical School Office for Research Protection Standing Committee on Animals. The Harvard Medical School animal management program is accredited by the Association for the Assessment and Accreditation of Laboratory Animal Care, International (AAALAC), and meets National Institutes of Health standards as set forth in the Guide for the Care and Use of Laboratory Animals (DHHS Publication No. (NIH) 85-23 Revised 1996). The institution also accepts as mandatory the PHS Policy on Humane Care and Use of Laboratory Animals by Awardee Institutions and NIH Principles for the Utilization and Care of Vertebrate Animals Used in Testing, Research, and Training. There is on file with the Office of Laboratory Animal Welfare (OLAW) an approved Assurance of Compliance (A3431-01).

Bacterial strains

Strains and plasmids are listed in Supporting Table S3. V. choleræ El Tor biotype strain C6706 and a spontaneous lacZ− derivative of C6706, were used as parental (wild type - WT) strains. E. coli DH5α pir and Sm100 pir were used for cloning and conjugation, respectively. Antibiotic concentrations used were streptomycin (Sm: 100 μg/ml or 500 μg/ml), kanamycin (Kan: 50 μg/ml), carbenicillin (Carb: 75 μg/ml) and chloramphenicol (Cm: 2.5 μg/ml for C6706 and 10 μg/ml for E. coli DH5α pir). LB was used for all growth conditions [10 g/liter of tryptone (Bacto), 5 g/liter of yeast extract (Bacto), and 5 g/liter of NaCl], and was supplemented with 16 g/liter of agar (Bacto) for growth on plates. Arabinoose was used at 0.1% for complementation assays. All ID numbers/ Accession numbers for genes highlighted in this study are shown in Table S5.

DNA manipulations

The genomic sequence of C6706 has not been completed. We used the sequence of the close relative, N16961, for clone construction. For in-frame gene deletions of nfo, mutS, hmpA and prxA, genomic DNA surrounding the respective gene was amplified by crossover PCR and cloned into pWM91 for subsequent sodB-mediated allelic exchange in V. choleræ, as described [67,68]. For complementation constructs, the respective gene was amplified from chromosomal DNA and cloned into plasmid pBAD18 after digestion with KpnI and Sall. The respective gene was induced by adding arabinose to the growth medium. All cloning products were sequence-verified, and the nucleotide sequence of all primers used is listed in Table S4.

Infant mouse colonization competition assays

A modified version of the protocol of Baselski and Parker [69] was performed for infection and recovery of C6706 derived strains. C6706 or C6706 lac− and mutant strains were grown on LB-agar plates with Sm overnight at 37°C. Wild type and mutant strains were mixed together in LB. 50 μl of this competition mixture (~50 0000 bacteria) was inoculated into a 5-day-old CD1 mouse pup (Charles River Company). Serial dilutions of the competition mixture were plated in LB+Sm100 and enumerated to determine the input ratio of wild type and mutant strain. After incubation at 30°C for 3 h or 18 h the mouse pups were sacrificed and small intestines were removed and homogenized in 10 ml of LB. Serial dilutions were plated in LB+Sm100 and enumerated to determine the output ratio of wild type and mutant strain. The competitive index for each mutant is defined as the input ratio of mutant/wild type strain divided by the output ratio of mutant/wild type strain. A minimum of four mice were assayed for each mutant strain. The in vivo experiments for the transposon and clean deletion strains were the accumulation of results performed on different days. For ease of communication we reported the average competitive index.

For NaHCO3 recue experiments, mice pups were first inoculated with 50 μl of 2.5 g/100 mL NaHCO3. After 3 h the pups were inoculated with 50 μl of the competition mixture in 2.5g/100 mL NaHCO3, iNOS−/− (##002609) and control C57BL/6J (#000664) mice were purchased from The Jackson Laboratory.

Mutation frequency assays

Rifampicin resistance assays. i) For ΔmutS mutation frequency and complementation assays cultures were grown to saturation at 37°C in LB Sm100 or Sm100, 500 μl of culture was plated on LB agar+50 μg/mL rifampicin. After overnight growth at 37°C rifampicin resistant colonies were scored. ii) For mouse passaged assays, 5 day old mouse pups were inoculated with 50, 000 cells of wild type V. choleræ. After incubation at 30°C for 18 h the mouse pups were sacrificed and their small intestines removed.
and homogenized in 10 ml of LB+Sm500. The 10 ml of homogenized intestine was passed through cheese cloth and a 3.1µm filter. This filtering retained >90% of V. cholerae and removed the majority of eukaryotic materials as determined by western blot against mouse actin (data not shown). We recovered ∼250 000–500 000 V. cholerae cfu per small intestine. The filtrate was grown to saturation. For the control experiment 50 000 wild type V. cholerae were inoculated into 10 mL of LB+Sm500 and grown to saturation. We then plated an equal number of cfu from both mouse passaged and control cultures on LB agar+50 µg/mL rifampicin and scored resistant colonies. Control mouse samples in which no V. cholerae had been inoculated did not grow in LB+Sm500. Primers used for sequencing tpeB are shown in Supporting Table S3.

Trimethoprim resistance assays. A modified version of the Belfort and Pedersen-Lane protocol [44] was used for identified trimethoprim resistant colonies. For mouse passaged trimethoprim assays, 5 day old mouse pups were inoculated with 50 000 cells of wild type V. cholerae. After incubation at 30°C for 18 h the mouse pups were sacrificed and their small intestines removed and homogenized in 10 ml of LB Sm500+50 µg/mL thymine. The 10 ml of homogenized intestine was passed through cheese cloth and a 3.1µm filter. This filtering retained >90% of V. cholerae and removed the majority of eukaryotic materials as determined by western blot against mouse actin (data not shown). We recovered ∼250 000–500 000 wild type V. cholerae cfu per small intestine. The filtrate was grown to saturation. For the control experiment 50 000 wild type V. cholerae were inoculated into 10 mL of LB Sm500+50 µg/mL thymine and grown to saturation. We then plated an equal number of cfu from both mouse passaged and control cultures on M9 agar+0.1% CAS, 0.2% glucose, 50 µg/mL thymine and 20 µg/mL trimethoprim. After overnight growth at 37°C trimethoprim resistant colonies were scored. Control mouse samples in which no V. cholerae had been inoculated did not grow in LB+Sm500. The nucleotide sequences of the primers used for sequencing thyA are shown in Supporting Table S4.

To calculate the relative mutation frequency we plated equal numbers of cfu for both mouse and passaged and control samples. We calculated the average and standard error for the mutation rate for the control samples. Next we normalized the individual mutation frequencies from our 5 mice passaged samples and 5 control samples to the average control sample mutation frequency. This normalized the average control sample mutation frequency to 1 and showed the relative mutation frequency increase in mouse passaged samples.

Stomach pH and nitrite concentration determination

We have developed a fluorescence based assay to determine the pH of the infant mouse stomach. We first determined a standard curve using the fluorescent pH indicator Yellow/Blue DND-160 (Invitrogen) over a range from pH 3–8. We then extracted the gastric juice from 5 individual mice, diluted the sample 1:2 with ddH2O (pH 7), added Yellow/Blue DND-160 and determined the fluorescence of the solution. Comparing these fluorescent values to our standard curve we determined the pH of the infant mouse stomach to be 4.5±0.1. We also note that this is a conservative measurement. In order to obtain enough liquid we diluted the gastric sample ~1:2 with ddH2O that was at ~pH 7. Thus while water is not a buffer, the dilution of the gastric juice likely raised the final pH of our measurements.

Nitric oxide sensitivity growth curves

Strains were grown to exponential phase in LB with Cm when required. Strains were serial diluted and spotted on LB plates containing increasing concentrations of hydrogen peroxide and incubated at 37°C overnight. For complementation Cm and arabinose were added while strains were growing in liquid, as well as in the LB agar plates.

Growth in acidified nitrite

Overnight cultures were diluted into LB and grown to log phase at 37°C with aeration. Cultures were diluted to OD600 0.05 in 25 mM MES buffered LB of pH 7.0 or 5.5 with or without the addition of 400 µM sodium nitrite (Sigma-Aldrich). The LB media and MES were adjusted to a pH of 7.0 and 5.5 (Corning pH meter 240) with additions of HCl, and filter sterilized (0.22 µm, Corning) prior to use. The growth of strains under various treatments were determined by OD600 measurement using a 96 well format spectrophotometer (SpectraMax Plus 384, Molecular Devices). Environmental parameters were set to 37°C with shaking and readings were taken every 15 minutes for 16 hours. Studies were conducted in triplicate.

Fluorescein assay

Overnight cultures were diluted into 100 mL LB with Sm100 and grown to OD600−0.8 (37°C, aeration). 10 mL of culture was dispensed into 15 mL conical and centrifugated at 5,000 RPM for 5 minutes. The supernatant discarded and cells resuspended in an equal volume of 25 mM MES buffered LB of pH 7.0 or 5.5 with or without the addition of sodium nitrite (500 µM, 1 mM, 5mM, or 10 mM). Cells were treated for 1.5 hours at 37°C with aeration then centrifugated at 5,000 RPM for 5 minutes at 4°C. The cells were incubated at room temperature for 30 minutes then centrifugated and washed three times to remove all free, extracellular dye. The cells were lysed in 225 µL of lysis buffer (MilliQ water with 0.1M EDTA) via sonication. Cell lysates were centrifugated at 15,000 RPM for 5 minutes, supernatant transferred to another 1.5 mL eppendorf tube. The cells were centrifugated and washed an additional two times in 1x PBS before being resuspended in 1 mL PBS (LONZA), and transferred to a 1.5 mL eppendorf tube. The cells were centrifugated and washed an additional two times in 1x PBS before being resuspended in 1 mL PBS with 10 µM 2′,7′-dichlorodihydrofluorescein diacetate (Molecular Probes, Invitrogen). The cells were incubated at room temperature for 30 minutes then centrifugated and washed three times to remove all free, extracellular dye. The cells were lysed in 225 µL of lysis buffer (MilliQ water with 0.1M EDTA) via sonication. Cell lysates were centrifugated at 15,000 RPM for 5 minutes, supernatant transferred to another 1.5 mL eppendorf tube and centrifugated again. Fluorescence was measured at 490 nm / 519 nm (excitation/emission) (SpectraMax Gemini XS). Fluorescence was normalized against protein concentrations, as determined by Bradford assay. Studies were conducted in triplicate.

Statistical methods

Statistical significance was assessed for mouse colonization assays and ΔmutS mutation frequency assays using a one-way analysis of variance (ANOVA) using a Bonferroni post test to determine significant differences in competitive index between all pairs of V. cholerae mutants used in our study. Statistical significance of acidified nitrite, nitric oxide and H2O2 sensitivities was assessed using a mixed model, repeated measures two-way analysis of variance (ANOVA); generating a p value for each pair wise curves
over the concentration range of H$_2$O$_2$ to determine the significance of our results. Statistical significance of rifampicin and trimethoprim resistant mutants from LB vs. mouse passed samples were assessed using a paired t-test. Differences were considered significant at p<0.05. All calculations were performed using Graphpad Prisim version 5.

Supporting Information

**Figure S1** A. Growth of wild type (black square), ΔmutS (red triangle), ΔhmpA (blue circle) and ΔhmpAΔhmpC (green inverted triangle) in LB at pH 7.0. Growth was measured by changes in the cultures OD$_{600}$ readings. The averages of 3 experiments are shown for each strain. B. Complementation of the mutator phenotype of the ΔmutS mutant. The number of wild type+pBAD18 colonies was normalized to 1. The averages of 3 experiments are shown (*** p<0.001). C. Complementation of H$_2$O$_2$ sensitivity of the ΔhmpA xth::Tn mutant by overexpression of Nfo. Wild type+pBAD18 (■), ΔhmpA xth::Tn mutant+pBAD18 (▲) and ΔhmpA xth::Tn mutant+pΔhmpA (▲). The averages of 3 experiments are shown. D. Complementation of ΔhmpA mutant nitric oxide sensitivity. Exponentially growing cultures of wild type+pBAD18 (black squares), ΔhmpA mutant+pBAD18 (blue circles) and ΔhmpA mutant+pΔhmpA (green triangles) were grown with 1 mM spermine NONOate as a nitric oxide donor. The recovery and growth of each strain was monitored over time. The averages of 3 experiments are shown for each strain. E. Complementation of ΔprxA mutant nitric oxide sensitivity. Exponentially growing cultures of wild type+pBAD18 (black squares), ΔprxA mutant+pBAD18 (blue circles) and ΔprxA mutant+pΔprxA (green triangles) were grown with 1 mM spermine NONOate as a nitric oxide donor. The recovery and growth of each strain was monitored over time. The averages of 3 experiments are shown for each strain. F. Growth of wild type (●) and the Δadk2 (▲) mutant in LB at pH 7.0. Growth was measured by changes in the cultures OD$_{600}$ readings. The averages of 3 experiments are shown for each strain.

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**Figure S2** A. Hydrogen peroxide sensitivity. Wild type (●) and ΔprxA mutant (▲) were plated on agar containing increasing concentration of the hydrogen peroxide (H$_2$O$_2$). CFU were determined after overnight growth. The average of 3 experiments is shown.

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**Figure S3** Exponentially growing cultures of wild type and ΔmutS, ΔhmpA, ΔprxA, ΔhmpAΔhmpC and ΔhmpAΔxth::Tn mutants were grown in LB buffered at pH 7.0 in the absence (A) or presence (B) of 400 μM sodium nitrite. Growth was measured by changes in the cultures OD$_{600}$ readings. The average of three experiments is shown for each strain. Wild type (black squares), ΔmutS (blue triangles), ΔhmpA (orange circles), ΔprxA (green inverted triangle), ΔhmpAΔxth::Tn (red diamond) and ΔhmpAΔhmpC (yellow open square).

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**Table S1** Colonization of C57B and isogenic iNOS−/− infant mice by the hmp::Tn mutant.

Found at: doi:10.1371/journal.ppat.1001295.s004 (0.02 MB DOC)

**Table S2** Ability of V. cholerae mutants defective in DNA repair pathways to colonize the infant mouse intestine in competition with the parental strain (WT) 3 h post inoculation.

Found at: doi:10.1371/journal.ppat.1001295.s005 (0.03 MB DOC)

**Table S3** Bacterial strains and plasmids used in this study.

Found at: doi:10.1371/journal.ppat.1001295.s006 (0.06 MB DOC)

**Table S4** Primers used in this study.

Found at: doi:10.1371/journal.ppat.1001295.s007 (0.03 MB DOC)

**Table S5** ID numbers/ Accession numbers for genes used in this study.

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Author Contributions

Conceived and designed the experiments: BWD RWB LAS JJM. Performed the experiments: BWD RWB NMD TAIG. Analyzed the data: BWD RWB NMD TAIG LAS JJM. Contributed reagents/materials/analysis tools: BWD RWB LAS JJM. Wrote the paper: BWD RWB NMD TAIG LAS JJM.
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