Oxidative stress activates transcription of *Salmonella* pathogenicity island-2 genes in macrophages

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The type III secretion system encoded in the *Salmonella* pathogenicity island-2 (SPI-2) gene cluster facilitates intracellular growth of nontyphoidal *Salmonella* by interfering with the maturation of *Salmonella*-containing vacuoles along the degradative pathway. SPI-2 gene products also protect *Salmonella* against the antimicrobial activity of reactive oxygen species (ROS) synthesized by the phagocyte NADPH oxidase 2 (NOX2). However, a potential relationship between inflammatory ROS and the activation of transcription of SPI-2 genes by intracellular *Salmonella* is unclear. Here, we show that ROS engendered in the innate host response stimulate SPI-2 gene transcription. We found that the expression of SPI-2 genes in *Salmonella*-sustaining oxidative stress conditions involves DksA, a protein otherwise known to regulate the stringent response of bacteria to nutritional stress. We also demonstrate that the J and zinc-2-oxidoeductase domains of DnaJ as well as the ATPase activity of the DnaK chaperone facilitate loading of DksA onto RNA polymerase complexed with SPI-2 promoters. Furthermore, the DksA-driven transcription of SPI-2 genes in *Salmonella* experiencing oxidative stress is contingent on upstream OmpR, PhoP, and SsrB signaling events that participate in the removal of nucleoid proteins while simultaneously recruiting RNA polymerase to SPI-2 promoter regions. Taken together, our results suggest the activation of SPI-2 gene transcription in *Salmonella* subjected to ROS produced by the respiratory burst of macrophages protects this intracellular pathogen against NOX2-mediated killing. We propose that *Salmonella* have co-opted inflammatory ROS to induce SPI-2-mediated protective responses against NOX2 host defenses.

The facultative intracellular pathogen *Salmonella enterica* serovar Typhimurium causes countless cases of gastroenteritis around the world annually. Nontyphoidal serovars such as Typhimurium are also responsible for disseminated life-threatening systemic infections in people suffering from HIV or malarial comorbidities (1–5). The pathogenicity of nontyphoidal salmonellae is greatly reliant on the vacuolar remodeling attributes of the type III secretion system encoded within the *Salmonella* pathogenicity island-2 (SPI-2) gene cluster. Induction of SPI-2 genes primes the transition of this enteropathogen from an extracellular location in the gastrointestinal lumen to the intracellular niche of host cells (6, 7). Zoonotic nontyphoidal salmonellae exploit the SPI-2 type III secretion system to grow intracellularly in professional phagocytes and epithelial cells (8–10). SPI-2 transcription is induced in response to elevated proton concentrations and diminished Mg2+ levels, both of which are signatures of phagosomes and *Salmonella*-containing vacuoles (11, 12).

Expression of the 40 kb gene cluster encoding the *ssrAB* regulon, secretion apparatus, translocon, chaperones, and effectors, as well as substrate proteins encoded outside the SPI-2 pathogenicity island, imposes a considerable metabolic toll on *Salmonella*. Thus, *Salmonella* must tightly regulate transcription of this pathogenicity island. The combined actions of nucleoid proteins and transcriptional activators result in the timely expression of SPI-2 genes by *Salmonella*. Gene silencing, which is mediated through binding of homologous H-NS, YgdT, and Haa nucleoid proteins along extensive areas of noncoding and coding regions of the *ssrA* regulatory locus, is vital for the contextual expression of SPI-2 genes (13, 14). On the other hand, PhoP–PhoQ, OmpR–EnvZ, and PhoB–PhoR two-component systems responding to acidic pH, osmolarity, or shortages in Mg2+ or inorganic phosphorous activate SPI-2 gene transcription (15–17). As is the case for nucleoid proteins, the regulatory activities of PhoP, OmpR, SlyA, or PhoB converge into the *ssrAB* locus encoding a two-component system responsible for global expression of structural and effector SPI-2 gene products (18–21). The SsrB response regulator activates transcription by counteracting H-NS silencing, while simultaneously recruiting RNA polymerase to SPI-2 genes (22).

In addition to the hierarchical control emanating from interactions of traditional transcription factors to regulatory SPI-2 DNA regions, the SPI-2 locus is also operated at the level of transcription initiation. The combined actions of the nucleotide alarmone guanosine tetraphosphate (ppGpp) and the α-helical protein DksA on the kinetics of DNA–RNA polymerase open complexes favor SPI-2 gene transcription (23–25). Historically, DksA and ppGpp have been known for their participation in the stringent response, an adaptation to nutritional stress that is typified by the activation of amino acid biosynthetic genes and the repression of loci encoding...
translational machinery (26). Thus, placing SPI-2 transcription under the control of ppGpp and DksA may assist with the adaptation of Salmonella to transient nutritional scarcities within host cells.

In addition to responding to nutritional shortages, the stringent response is emerging as a key regulator of antioxidant defense in diverse bacterial pathogens (27–30). Transient amino acid auxotrophies resulting from the oxidative damage of biosynthetic pathways are sensed by the stringent response RelA protein (30, 31). Distorted uncharged tRNAs entering the A-site of the ribosome elicit the ppGpp synthetase activity of RelA (32). Simultaneously, ROS oxidize cysteine residues coordinating a zinc cation in the globular domain of DksA (33, 34). The resulting disulfide bonds unfold the globular domain, triggering interactions of DksA with the DnaJ cochaperone (33). DnaJ first reduces and then presents its unfolded DksA client to Dnak, which catalyzes the nucleation of DksA–RNA polymerase complexes onto DNA that encodes enzymes of amino acid biosynthesis (35). Binding of ppGpp to the resulting ternary DksA–RNA polymerase–DNA complex activates transcription of amino acid biosynthetic and transport genes in Salmonella that sustain oxidative stress (30, 33). Because SPI-2 gene transcription is activated by ppGpp and DksA (23–25) and because Salmonella utilize the SPI-2 type III secretion system to combat the phagocyte NADPH oxidase (NOX2) (36–41), herein we studied whether byproducts of the respiratory burst activate DksA-dependent transcription of horizontally acquired SPI-2 genes. Our investigations demonstrate that the DnaJ cochaperone enables the ROS-dependent formation of DksA–RNA polymerase–SPI-2-gene ternary complexes and thus fosters the expression of SPI-2 regulatory and effector genes in intracellular Salmonella exposed to NOX2 oxidative products.

**Results**

**Oxidative stress stimulates SPI-2 gene transcription**

We examined whether Salmonella modulate SPI-2 gene transcription after exposure to hydrogen peroxide (H₂O₂), an ROS synthesized by host phagocytes in response to this facultative intracellular pathogen (42). Salmonella activated expression of the SPI-2 sifA: lacZY reporter construct in response to increasing concentrations of H₂O₂ (Fig. 1A). Under the experimental conditions tested, H₂O₂ did not affect Salmonella growth (Fig. S1A). The concentration of molecular oxygen (O₂) in phagosomes has been estimated at 11 μM (43). Because of the enzymatic activity of both host NOX2 and Salmonella terminal cytochromes, it is possible that the cytoplasm of intracellular Salmonella is exposed to products of NOX2 under hypoxic or anaerobic conditions. Moreover, a sizable fraction of DksA is oxidized in Salmonella cultures grown aerobically in a shaker incubator (33). Taking into account the lines of reasoning, to examine in more detail whether exogenous H₂O₂ can induce DksA-dependent activation of SPI-2 gene transcription, we developed an anaerobic culture system. Anaerobic Salmonella failed to grow on N9 medium in the absence of an added terminal electron acceptor (Fig. S1B), likely because the growth of Enterobacteriaceae on casamino acids, the sole carbon source in the N9 minimum medium used in our experiments, relies on the electron transport chain (44). Accordingly, the addition of the terminal electron acceptor NO₃⁻ supported growth of anaerobic Salmonella in N9 medium (Fig. S1C). Therefore, the N9 medium used in all subsequent anaerobic experiments contained NO₃⁻. Compared with aerobic cultures (Figs. S1, D and E), the downshift of anaerobic Salmonella to 8 μM MgCl₂ N9 medium, pH 5.8, stimulated modest levels of transcription of both srrB and sifA SPI-2 genes (Fig. 1, B and C). The expression of srrB and sifA was stimulated upon treatment of anaerobic cultures grown in 8 μM MgCl₂ N9 medium with increasing concentrations of H₂O₂ (Fig. 1, B and C). The concentrations of H₂O₂ used in our assays are in keeping with the 1 to 17 μM H₂O₂ that are estimated to be synthesized in phagosomes (45, 46). Consistent with the transcriptional findings, H₂O₂ treatment of Salmonella in SPI-2-inducing N9 medium in an anaerobic chamber also resulted in the accumulation of SsrB protein (Fig. 1D). Collectively, these findings demonstrate that exogenous H₂O₂ triggers expression of SPI-2 genes.

**The DnaJ–DnaK chaperone couple facilitates DksA-dependent SPI-2 transcription following oxidative stress**

H₂O₂ did not trigger either srrB or sifA transcription in Salmonella grown anaerobically in 10 mM MgCl₂ N9 medium, pH 8.0 (Figs. 2A and S2A). In contrast, H₂O₂ activated significant SPI-2 transcription in anaerobic Salmonella grown under 8 μM MgCl₂+-inducing conditions (Figs. 2A and S2A). These findings suggest that H₂O₂ potentiates the transcription of SPI-2 genes induced in response to the downshift in the concentration of MgCl₂. Next, we determined the molecular mechanism underlying the H₂O₂-induced transcription of SPI-2 genes. Because DksA is a critical determinant in the expression of SPI-2 genes (23, 25) and ROS activate the stringent response (33, 35), we tested whether the H₂O₂-induced transcription of SPI-2 genes involves the DksA protein. According to the latter model, deletion of dksA prevented the H₂O₂-stimulated transcription of both srrB and sifA (Figs. 2B and S2B).

Oxidative stress precludes associations of DksA with RNA polymerase (34). The DnaJ–DnaK chaperone couple, nonetheless, can repair oxidized cysteine residues in the zinc finger domain of DksA (35), thereby fostering the formation of enzymatically active DksA–RNA polymerase complexes (33). As noted with amino acid biosynthetic genes (33, 35), ΔdnaJ and ΔdnaK mutant strains did not support srrB or sifA expression in anaerobic Salmonella grown in inducing N9 medium after H₂O₂ treatment (Figs. 2, C, D, S2, C and D). Plasmids expressing the dnaJ and/or dnaK genes complemented the srrB- and sifA-inducing capacity of ΔdnaJ and ΔdnaK Salmonella strains upon exposure to H₂O₂ (Figs. 2, E, F, S2, E and F). To test if the DksA-dependent activation of SPI-2 transcription stimulated by H₂O₂ depends on the oxidoreductase activity of DnaJ (33, 47, 48), we examined SPI-
2 gene transcription in a Salmonella strain expressing the DnaJ C186H mutant that disrupts thiol-disulfide exchange activity but preserves the zinc finger fold (Fig. S2G; (33)). A strain bearing the dnaJ C186H mutant allele was unable to stimulate SPI-2 gene transcription in anaerobic Salmonella exposed to H2O2 (Figs. 2G and S2H). Similar results were seen in a Salmonella strain bearing the dnaJ H33Q allele deficient in the J domain that enables the transferring of clients from DnaJ to DnaK (Figs. 2H and S2J). Moreover, studies using a Salmonella dnaK T199A strain showed that the DnaK-dependent

**Figure 1. Oxidative stress stimulates Salmonella SPI-2 gene expression.** A, induction of sifA gene expression by oxidative stress was determined by measuring β-galactosidase activity of sifA-lacZY-expressing Salmonella grown aerobically in a shaker incubator in N9 low Mg2+ minimal medium. H2O2 was added at the indicated concentrations for 30 min. The data are the mean ± SD (n = 4) from two independent experiments. ****p < 0.0001, as determined by one-way ANOVA. ns when compared with reaction treated with H2O2 and untreated. B and C, the sifA and ssrB transcripts were induced in wildtype Salmonella grown anaerobically in 10 μM Mg2+ N9 minimal medium, pH 5.8. Abundance of ssrB and sifA transcripts was measured by qRT-PCR, using the housekeeping gene rpoD as an internal control. ****, p < 0.0001, ns, nonsignificant, as determined by one-way ANOVA. D, SsrB protein was examined by Western blotting in specimens isolated from anaerobic Salmonella treated with or without 10 μM H2O2 for 1 h in 10 mM Mg2+ N9 media, pH 7.4, or 10 μM Mg2+ N9 media, pH 5.8. Density of proteins was measured with ImageJ, and fold change in density was calculated as density of SsrB/density of DnaK controls. The figure is representative of five independent experiments, and band density is shown as means ± SD (n = 5). *p < 0.05. H2O2, hydrogen peroxide; ns, nonsignificant; qRT–PCR, quantitative RT–PCR; SPI-2, Salmonella pathogenicity island-2.
The induction of SPI-2 gene transcription in anaerobic *Salmonella* treated with H$_2$O$_2$ is supported by the ATPase activity of this chaperone (Fig. 2I and S2J). Under the conditions used in our experiments, H$_2$O$_2$ did not visibly affect the growth of any of the mutants tested (Fig. S3, A and B). Collectively, this research suggests that the SPI-2 expression recorded in *Salmonella* exposed to H$_2$O$_2$ is dependent on DnaJ and DnaK.

**The DnaK–DnaJ chaperone couple activates ssrA in vitro transcription by oxidized DksA**

To directly test the involvement of DnaJ and DnaK on the activation of DksA-mediated SPI-2 transcription in *Salmonella* sustaining oxidative stress, we developed a reconstituted biochemical *ssrA in vitro* transcription system. Reduced DksA stimulated significantly ($p < 0.0001$) more *ssrA in vitro* transcription than oxidized DksA controls (Figs. 3A and S4A). The addition of neither recombinant DnaJ nor DnaK proteins to RNA polymerase–containing reactions activated *ssrA in vitro* transcription (Figs. 3A and S4A). Nonetheless, incubation of oxidized DksA with DnaJ and DnaK reconstituted *ssrA in vitro* transcription to levels supported by the reduced DksA protein (Fig. 3A). Incubation of reduced DksA with DnaJ and DnaK did not further potentiate the transcriptional activity induced by DksA alone. These findings demonstrate that the DnaJ–DnaK cochaperone system activates SPI-2 *in vitro* transcription by reactivating oxidized DksA.

The addition of DnaJ C186H or DnaJ H33Q recombinant proteins into the *in vitro* transcription system failed to activate *ssrA* expression by oxidized DksA and DnaK proteins (Figs. 3B and S4B), implicating oxidoreductase and J domains of DnaJ in this activity. The inability of DnaJ C186H or DnaJ H33Q variants to support DksA$_{oxi}$-dependent *ssrA in vitro* transcription cannot be explained by a failure of these variants to bind Zn$^{2+}$ (Fig. S2G). A DnaK T119A variant also failed to activate *ssrA* transcription by oxidized DksA and DnaJ proteins (Figs. 3B and S4B). Together, these investigations demonstrate that the ATPase activity of the DnaK chaperone synergizes with the oxidoreductase- and J-dependent functions of DnaJ to enable *ssrA* transcription by oxidized DksA.

**SPI-2 transcription in Salmonella sustaining oxidative stress requires upstream signaling**

The reconstituted *in vitro* transcription assay demonstrates that the activation of SPI-2 transcription can be achieved by DksA alone. In cells, however, recruitment of RNA polymerase to SPI-2 promoters is hindered by nucleoid proteins bound to

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**Figure 2. DnaK and DnaJ activate DksA-dependent *ssrB* gene transcription.** A–I, anaerobic *Salmonella* were grown in N9 high and low Mg$^{2+}$ minimal medium supplemented with 40 mM NaNO$_3$−. The abundance of *ssrB* transcripts was determined by qRT–PCR in RNA isolated from anaerobic *Salmonella* treated for 30 min with or without 10 μM H$_2$O$_2$. The expression of the housekeeping gene *rpoD* was used as internal control. Data are the means ± SD (n = 4–8) from two or three independent experiments. *p < 0.1, **p < 0.01, ****p < 0.0001, as calculated by one-way ANOVA. H$_2$O$_2$, hydrogen peroxide; ns, nonsignificant versus reactions treated with H$_2$O$_2$ and untreated; qRT–PCR, quantitative RT–PCR.
regulatory promoter regions (13, 22). PhoP, OmpR, or SsrB proteins help activate SPI-2 gene transcription by either countersilencing nucleoid proteins or recruiting RNA polymerase to the ssrAB locus (13). In the following investigations, we examined if the SPI-2-induced gene expression observed in Salmonella treated with H2O2 is dependent on upstream signaling steps. As reported previously, the downshift of Salmonella to 8 μM MgCl2 N9 medium, pH 5.8, activated modest expression of ssrB and sifA genes (Figs. 4A and S5A). Treatment of Salmonella with 10 μM H2O2 in N9-inducing medium activated the expression of ssrB and sifA (Figs. 4A and S5A). H2O2 treatment failed to activate transcription in control Salmonella strains deficient in dksA, ompR, phoP, or ssrB genes (Figs. 4, B–E and S5, B–E). The addition of H2O2 to anaerobic cultures of wildtype, ΔdksA, ΔompR, ΔphoP, or ΔssrB Salmonella did not affect bacterial growth (Fig. S5, F and G). Cumulatively, these findings suggest that the activation of DksA-dependent SPI-2 gene transcription in Salmonella undergoing oxidative stress is contingent on upstream PhoP, OmpR, and SsrB signaling.

**NOX-2-derived ROS activate intracellular SPI-2 gene transcription**

We next examined whether ROS produced enzymatically in the respiratory burst of macrophages activate SPI-2 transcription in intracellular Salmonella (Fig. 5, A and B). Salmonella expressed ssrA and sifA SPI-2 genes 9 h after infection of ROS-producing bone marrow–derived macrophages.
Compared with wildtype macrophages, the intracellular expression of ssrA and sifA genes was significantly (p < 0.0001) lower in Salmonella collected from macrophages derived from nox2−/− mice, a population of macrophages that cannot generate superoxide anion (Fig. S6) because of a mutation in the gp91phox subunit of the phagocyte NOX2 (Fig. 5, A and B). These data demonstrate that Salmonella activate SPI-2 transcription in response to ROS produced by NOX2 in the innate host response. The intracellular expression of ssrA and sifA was markedly reduced in ΔdksA and ΔdnaJ Salmonella (Fig. 5, A and B), demonstrating that the ROS-dependent intracellular expression of SPI-2 genes is under the positive control of DksA and DnaJ. Transcription of ssrA and sifA genes by ΔdksA and ΔdnaJ Salmonella was not recovered in BMDM from nox2−/− mice, demonstrating the necessity of DksA and DnaJ signaling for the expression of SPI-2 genes by Salmonella in macrophages.

Salmonella deficient in dksA or dnaJ were similarly hypersusceptible to bactericidal activity emanating from the respiratory burst of BMDM (Fig. 5, C and D). Although the ΔdksA Salmonella strain recovered some growth in nox2−/− BMDM, the burden of a ΔdksA mutant remained significantly (p < 0.0001) lower in nox2−/− BMDM compared with wildtype or ΔdnaJ Salmonella controls. We conclude that the DnaJ/DksA-driven expression of SPI-2 genes protects Salmonella against...
the respiratory burst of macrophages. This research also indicates that DksA and DnaJ play codependent roles at counteracting the antimicrobial activity of NOX2, although independent roles also appear to exist.

Discussion

Our investigations demonstrate that ROS produced in the innate response of macrophages are biologically relevant signals that activate SPI-2 transcription in intracellular Salmonella. Induction of SPI-2 genes in Salmonella undergoing oxidative stress helps this intracellular pathogen fight the antimicrobial activity of NOX2 flavohemoproteins. The activation of SPI-2 transcription in Salmonella exposed to ROS depends on the coordinated regulatory activities of DksA, DnaJ, and DnaK proteins. The oxidoreductase mapping to the zinc-2 domain of DnaJ is necessary for the DksA-dependent activation of SPI-2 transcription observed in Salmonella undergoing oxidative stress, possibly by reducing disulfide-bonded cysteine residues in the globular domain of DksA (33). In addition, DnaJ J domain contributes to oxidation-mediated activation of SPI-2 transcription by presenting DksA to the DnaK chaperone. Ultimately, the ATPase catalytic activity of DnaK enables the formation of DksA–RNA polymerase–DNA ternary complexes, thereby activating SPI-2 transcription in Salmonella sustaining oxidative stress.

Reduced DksA protein induces SPI-2 in vitro transcription as efficiently as the DnaK–DnaJ–DksA oxidation complex, and the DnaK and DnaJ proteins do not improve the transcriptional activity of reduced DksA. These findings suggest that the most important role the DnaJ–DnaK chaperone system plays in the expression of SPI-2 genes is to repair DksA molecules oxidized and unfolded in Salmonella undergoing oxidative stress. H2O2 arising from the univalent reduction of O2 in redox-active centers in the electron transport chain oxidizes a significant fraction of DksA molecules in aerobic Salmonella (33). DksA is also oxidized upon exposure of Salmonella to exogenous sources of ROS (34). As little as 1 μM H2O2 appears to be sufficient to oxidize DksA in Salmonella (33), a concentration of H2O2 well within the range achievable in phagosomes (46, 49). A significant fraction of DksA may be oxidized and incapable of activating SPI-2 gene transcription in macrophages supporting a respiratory burst. However, the DnaK–DnaJ chaperone system provides the redox buffering capacity that makes possible the DksA-dependent expression of SPI-2 genes during exposure of Salmonella to host-derived oxidants.

The addition of H2O2 to Salmonella grown under noninducing conditions fails to stimulate SPI-2 gene expression. In contrast, H2O2 induces the expression of sifA and srrB genes in anaerobic Salmonella grown in acidic and low Mg2+-inducing media. These findings suggest that the induction of SPI-2 gene expression by oxidized DksA protein is contingent on the prior recruitment of RNA polymerase by OmpR, PhoP, or SsrB. Accordingly, H2O2 failed to stimulate SPI-2 transcription in ΔompR, ΔphoP, or ΔsrrB Salmonella lacking key response regulators. SsrB and PhoP partially induce SPI-2 gene transcription by derepressing the actions of nucleoid proteins (22, 50). DksA-mediated activation of SPI-2 transcription must operate downstream of the PhoP- or SsrB-mediated derepression of nucleoid proteins and is probably unrelated to interactions of DksA with nucleoid proteins such as H-NS. This latter idea is supported by two independent lines of reasoning. First, the transcriptional factor DksA interacts with RNA polymerase through the secondary channel, rather than through binding to the promoter regions that are normally footprinted by nucleoid proteins. Second, recombinant DksA protein directly activates SPI-2 in vitro transcription, demonstrating direct effects of DksA on transcriptional open complexes.

Previous research linked SPI-2 gene transcription to signaling cascades traditionally associated with the adaptation of bacteria to oxidative stress. For example, RpoE, SoxS, and SlyA activate various SPI-2 genes by either activating srrA transcription or downregulating hns expression (13, 51–54). The regulatory proteins RpoE and SlyA increase fitness of Salmonella during periods of oxidative stress (55, 56), and the transcriptional activity of the [2Fe–2S] SoxR metalloprotein is stimulated by superoxide anion or redox species (57, 58). It remains unknown whether the activation of SPI-2 gene transcription supported by RpoE, SoxS, or SlyA reflects their responsiveness to ROS. Regardless of their mechanism, the absence of downstream DksA→DnaJ→DnaK signaling prevents the induction of SPI-2 gene transcription in Salmonella undergoing oxidative stress.

Aerobic respiration supports higher SPI-2 transcription than nitrate respiration. The differences in the levels of SPI-2 transcription between aerobic and anaerobic Salmonella may stem from higher energetic outputs supported by aerobic compared with nitrate respiration. Although not mutually exclusive, ROS produced adventitiously in aerobic metabolism may provide an additional signal for optimal SPI-2 induction. In support of this idea, H2O2 signals NO3– respiring Salmonella to upregulate the expression of SPI-2 genes. These observations could have important implications for SPI-2 expression in Salmonella residing in phagocytic cells. ROS synthesized by NOX2 may assume the function normally played by oxidative species produced endogenously in bacterial metabolism, the production of which must be precluded as the O2 is consumed during the respiratory burst of phagocytic cells.

Acidic pH and nutritional downshifts might be the primary mechanism for the activation of SPI-2 genes in vivo. Accordingly, Salmonella express SPI-2 genes in epithelial cells and some populations of macrophages unable to sustain the respiratory burst (10, 23). DksA, an effector of the stringent response in starving Gram-negative bacteria, may be a hub in which nutritional signals and oxidative stress are processed for the activation of SPI-2 transcription.

By ameliorating exposure to ROS generated by macrophages, the SPI-2 type III secretion system protects Salmonella against the antimicrobial activity of products of cell host NOX2 enzymatic complexes (37–39, 41, 59, 60). SPI-2 gene products decrease the genotoxicity endured by Salmonella from exposure to oxidants in macrophages (61). In addition to limiting the
contact of intracellular *Salmonella* to NOX2-derived oxidants, the suppressing apoptotic signals induced by the SPI-2 apparatus shields *Salmonella* from the respiratory burst of inflammatory neutrophils (40). Thus, induction of the SPI-2 type III secretion system by products of the respiratory burst provides a feedback loop to combat the antimicrobial actions of NOX2 enzymatic complexes.

**Experimental procedures**

**Bacterial strains, plasmids, and growth conditions**

Tables S1 and S2 list the derivatives of *S. enterica* serovar Typhimurium strain 14032s and *Escherichia coli*, as well as the plasmids used here. Deletion mutants were constructed using the λ-Red homologous recombination system (62). Bacteria were grown in LB broth, N9 high Mg2+ medium (100 mM Tris–HCl, 5 mM KCl, 7.5 mM (NH₄)SO₄, 1 mM KH₂PO₄, 38 mM glycerol, 0.1% casamino acids, and 10 mM MgCl₂; pH 8.0), or N9 low Mg2+ minimal medium (100 mM Tris–HCl, 5 mM KCl, 7.5 mM (NH₄)SO₄, 1 mM KH₂PO₄, 38 mM glycerol, 0.1% casamino acids, 8 μM MgCl₂; pH 5.8) at 37 °C as described (63). Penicillin, chloramphenicol, kanamycin, and tetracycline were added at final concentrations of 250, 40, 50, and 10 μg/ml, respectively.

**β-galactosidase activity**

SPI-2 gene expression was performed as previously described (64). Briefly, *Salmonella* expressing the sifA::lacZY::Km single-copy chromosomal fusion (64) grown in LB broth overnight were diluted 1:100 in N9 high Mg2+ minimal medium and cultured at 37 °C for approximately 4 h to absorbance of 0.5 at 600 nm. Cultures were collected, washed three times with N9 low Mg2+ minimal medium, and resuspended in N9 low Mg2+ minimal medium to an absorbance of 0.25. Cells were cultured at 37 °C for 2.5 h and then treated for 30 min with or without different concentrations of H2O2. β-galactosidase activity was determined in samples with o-nitrophenyl-β-D-galactoside substrate. Enzyme activity expressed as Miller Units was calculated as absorbance at 420 nm × 1000/(time [min] × absorbance at 600 nm × cell volume [ml]) (33). Growth was monitored by measuring absorbance at 600 nm after treatment with H2O2 for 30 min.

**Anaerobic culture and H2O2 treatment**

*Salmonella* grown overnight in LB broth at 37 °C in a BACTRON anaerobic chamber were harvested and resuspended in N9 high Mg2+ minimal medium supplemented with or without 40 mM NaNO3 (Sigma) to an absorbance of 0.1 at 600 nm. After incubation at 37 °C for about 6 h to an absorbance of 0.5 at 600 nm, cultures were harvested, washed with either N9 high Mg2+ or N9 low Mg2+ minimal medium two times, and resuspended in either N9 high Mg2+ or N9 low Mg2+ minimal medium supplemented with 40 mM NaNO3 to an absorbance of approximately 0.25 at 600 nm. Cells were cultured at 37 °C for 2.5 h and then treated with or without H2O2 for 30 min.

**Immunoblots**

Abundance of SsrB-FLAG protein in *Salmonella* cultures was detected by immunoblot assay. Cells grown anaerobically in either N9 high Mg2+ or N9 low Mg2+ minimal medium supplemented with 40 mM NaNO3 as described previously were collected after treated with 10 μM H2O2 for 1 h and disrupted by sonication in PBS. Protein concentrations of cell-free extracts were determined with Bicinchoninic Acid Protein Assay kit (Pierce), and then the samples were loaded onto 12% SDS-PAGE gels. The blots were treated with a 1:500 dilution of anti-FLAG monoclonal antibody (Sigma), followed by a 1:20,000 dilution of goat antimouse immunoglobulin conjugated with horseradish peroxidase (Pierce), and then visualized using the ECL prime Western blotting detection reagent (GE Healthcare Life Sciences) in the ChemiDoc XRS Imaging System (Bio-Rad). DNAK was used as internal control. Protein density was measured by the ImageJ program (National Institutes of Health).

**RNA isolation and quantitative RT–PCR**

The same culture method described previously was followed to isolate RNA from *Salmonella* cultured aerobically or anaerobically in either N9 high Mg2+ or N9 low Mg2+ minimal medium. Total RNA was isolated using the High Pure RNA Isolation Kit (Roche). The synthesis of complementary DNA (cDNA) was achieved using 1 μg of purified RNA, TaqMan Gene Expression Master Mix (Thermo Fisher Scientific), and N6 random primers (Thermo Fisher Scientific). Quantitative RT–PCR (qRT–PCR) was performed using specific primers and probes (Table S3) containing 5′ 6-carboxyfluorescein and 3′ black-hole quencher 1 modification in a CFX connect Real-Time System (Bio-Rad). PCR-amplified DNA fragments containing the gene of interest were used to generate standard curves. The abundance of transcripts within each sample was normalized to internal transcripts of the housekeeping gene rpoD.

**Overexpression and purification of proteins**

Protein expression and purification were performed as previously described (35). Briefly, *E. coli* BL21 (DE3) (Thermo Fisher Scientific) (Table S1) grown in LB broth at 37 °C to an absorbance of 0.5 to 0.8 at 600 nm were treated with 0.1 mM isopropyl-β-D-thiogalactopyranoside. After 3 h, the cells were harvested, disrupted by sonication, and centrifuged to obtain cell-free extracts. Glutathione-S-transferase (GST) and 6His-tagged fusion proteins were purified using Glutathione-Sepharose 4B (bioWORLD) and TALON metal-affinity chromatography (Clontech), respectively, according to manufacturer’s protocols. To purify the DksA proteins, the GST tags were removed from GST-DksA proteins bound to a Glutathione-Sepharose 4B resin. PreScission protease was added to recombinant GST-DksA proteins in PBS containing 10 mM DTT. After overnight incubation at 4 °C, untagged proteins were eluted with PBS. For further purification of DksA protein, size-exclusion chromatography on Superdex 75 (GE Healthcare Life Sciences) was used. Purified DksA
proteins were aliquoted inside a BACTRON anaerobic chamber (Shel Lab). The purity and mass of the recombinant proteins were assessed by SDS-PAGE.

**Determination of zinc content**

About 5 μM of DnaJ variants were treated with 150 (4-(2-pyridyl)do) resorcinol (Sigma) at 37 °C for 1 h in the presence of 8 M urea. The zinc−4-(2-pyridyl)do resorcinol chelate was quantified spectrophotometrically at an absorbance of 500 nm. Zinc concentrations were calculated from a standard curve with ZnCl$_2$ (65).

**In vitro transcription**

*In vitro* transcription reactions were quantified by qRT−PCR as previously described (33, 35). Briefly, oxidized or reduced DksA proteins were prepared by treatment with 1 mM H$_2$O$_2$ or 1 mM DTT in 40 mM Hepes, pH 7.4, at 37 °C for 1 h. Excess H$_2$O$_2$ or DTT was removed using an Amicon Ultra-10 centrifugal filter (Millipore Sigma). Transcription reactions were performed in reaction mixture containing 40 mM Hepes, pH 7.4, 2 mM MgCl$_2$, 60 mM potassium glutamate, 0.1% Nonidet P-40, 200 μM of each ATP, GTP, CTP, and UTP (Thermo Fisher Scientific), 8 U Ribolock RNase inhibitor (Thermo Fisher Scientific), 1 nM *livJ* DNA templates (Table S2), 5 nM *E. coli* holoenzyme RNA polymerase (New England Biolabs), and 2.5 μM of oxidized or reduced DksA proteins. Where indicated, the reactions contained 50 nM DnaJ variants in the presence and absence of 500 nM of DnaK variant proteins. Reactions were incubated at 37 °C for 10 min and then heat-inactivated at 70 °C for 10 min. After DNaseI treatment, template DNA was removed from the reactions with DNA-free DNA Removal Kit (Thermo Fisher Scientific), and the resulting RNA was used as template to generate cDNA using 100 U MMLV reverse transcriptase (Promega), 0.45 μM N6 random hexamer primers (Thermo Fisher Scientific), and 20 U RNase inhibitor (Promega). The amount of cDNA synthesized following 1 h of incubation at 42 °C was quantified by qRT−PCR using gene-specific primers and probes (Table S3). Specific transcripts were normalized to standard curves using known amounts of transcript concentrations.

**BMDMs**

Bone marrow cells were harvested in Dulbecco’s modified Eagle’s medium (DMEM) 10% medium (DMEM + 10% fetal bovine serum [FBS] + glutamate) from femurs of 8-week-old wildtype or *nox2*−/− C57BL/6 mice. Bone marrow-derived cells were centrifuged at 500g for 5 min and then resuspended 1 ml of ammonium−chloride−potassium lysis buffer for 1 min to lyse red blood cells and quenched after 1 min with 9 ml of DMEM 10% heat-inactivated FBS (Thermo Fisher Scientific). The cells were resuspended in L cell−conditioned DMEM (DMEM supplemented with 10% FBS, 5% horse serum, 1 mM sodium pyruvate, and 20% L cell−conditioned media) at a concentration of 4 × 10$^6$ cell/ml, and 25 ml of this suspension was seeded into 150-mm plates (Corning) and incubated at 37 °C with 5% CO$_2$ for 7 days. After 4 days, cell monolayers were rinsed once with prewarmed PBS and cultured in 25 ml of fresh L cell−conditioned DMEM. After 7 days, differentiated BMDMs were collected gently using a cell scraper and adjusted to a final concentration of 3.5 × 10$^6$ cells/ml in DMEM supplemented with 10% FBS and 100 U/ml penicillin/streptomycin (Thermo Fisher Scientific). Two milliliters was transferred into each well of a 6-well plate and incubated overnight. Cells in 6-well plates were washed once with RPMI* medium (Sigma) supplemented with heat-inactivated 10% FBS, 1 mM sodium pyruvate, 2 mM l-glutamine, and 20 mM Hepes (all reagents from Thermo Fisher Scientific). Collection of murine bone marrow cells was done following protocols approved by the University of Colorado Institutional Animal Care and Use Committee.

**Infection of BMDMs**

The BMDMs were infected with overnight cultures of *Salmonella* at a multiplicity of infection of 2 or 10 in RPMI* medium for killing assays or mRNA collection, respectively. The infected cells were centrifuged at 3000g for 1 min and incubated for 30 min at 37 °C in a 5% CO$_2$ incubator. Medium was replaced with fresh RPMI medium containing 10 μg/ml gentamicin. The cells were washed once with PBS after 8 h of infection, and the specimens were lysed with 0.1% Triton X-100. The specimens were vortexed for 20 s and centrifuged at 200g for 5 min at 4 °C. Intracellular bacteria were collected by centrifugation at 9300g for 3 min at 4 °C to be processed for RNA isolation.

**Survival of Salmonella in BMDM**

BMDMs infected with *Salmonella* at a multiplicity of infection of 2 were lysed with 0.1% Triton X-100 after 25 min of challenge (*i.e.*, *t* = 0). The medium was replaced with fresh RPMI medium containing 10 μg/ml gentamicin. Selected samples were lysed and plated onto LB agar at 2 or 19 h thereafter. The bacterial burden is expressed as colony-forming unit/well.

**Intracellular SPI-2 gene transcription**

DNA-free RNA was purified from BMDM 9 h after *Salmonella* challenge using a High Pure RNA isolation kit according to the manufacturer's instructions (Roche). cDNA was prepared from 1 μg RNA using a mixture containing 100 U MMLV reverse transcriptase, 0.45 μM N6 random hexamer primers (Thermo Fisher Scientific), and 20 U RNaseIn Plus RNase inhibitor (Promega). Reverse transcription was performed for 1 h at 42 °C. qRT−PCR was performed in a CFX connect Real-Time System (Bio-Rad). PCR-amplified DNA fragments containing the *ssrA*, *sifA*, or *rpoD* genes were used to generate standard curves. Reactions were prepared using Lunar Universal qPCR Master Mix (New England Biolabs) and incubated at 95 °C for 2 min, followed by 40 cycles of 95 °C for 15 s, and 58 °C for 1 min. Data are expressed as relative expression using the copy number of target gene over copy number of housekeeping gene *rpoD*. 

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Data availability

All data are contained within the article or supporting information.

Supporting information—This article contains supporting information (23, 33–35, 42, 64, 66–68).

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Abbreviations—The abbreviations used are: BMDM, bone marrow–derived macrophage; cDNA, complementary DNA; DMEM, Dulbecco’s modified Eagle’s medium; FBS, fetal bovine serum; GST, glutathione-S-transferase; H2O2, hydrogen peroxide; NOX, NADPH oxidase; O2, molecular oxygen; ppGpp, guanosine tetraphosphate; ROS, reactive oxygen species; SPI-2, Salmonella pathogenicity island-2.

References

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