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Transcriptional Adaptation of *Shigella flexneri* during Infection of Macrophages and Epithelial Cells: Insights into the Strategies of a Cytosolic Bacterial Pathogen

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*Shigella flexneri*, the etiologic agent of bacillary dysentery, invades epithelial cells as well as macrophages and dendritic cells and escapes into the cytosol soon after invasion. Dissection of the global gene expression profile of the bacterium in its intracellular niche is essential to fully understand the biology of *Shigella* infection. We have determined the complete gene expression profiles for *S. flexneri* infecting human epithelial HeLa cells and human macrophage-like U937 cells. Approximately one quarter of the *S. flexneri* genes showed significant transcriptional adaptation during infection; 929 and 1,060 genes were up- or down-regulated within HeLa cells and U937 cells, respectively. The key *S. flexneri* virulence genes, *ipa-mxi-spa* and *icsA*, were drastically down-regulated during intracellular growth. This theme seems to be common in bacterial infection, because the Ipa-Mxi-Spa-like type III secretion systems were also down-regulated during mammalian cell infection by *Salmonella enterica* serovar Typhimurium and *Escherichia coli* O157. The bacteria experienced restricted levels of iron, magnesium, and phosphate in both host cell types, as shown by up-regulation of the *sitABCD* system, the *mgtA* gene, and genes of the *phoBR* regulon. Interestingly, *ydeO* and other acid-induced genes were up-regulated only in U937 cells and not in HeLa cells, suggesting that the cytosol of U937 cells is acidic. Comparison with the gene expression of intracellular *Salmonella* serovar Typhimurium, which resides within the *Salmonella*-containing vacuole, indicated that *S. flexneri* is exposed to oxidative stress in U937 cells. This work will facilitate functional studies of hundreds of novel intracellularly regulated genes that may be important for the survival and growth strategies of *Shigella* in the human host.
A number of genes required for plaque formation have been identified in S. flexneri (30); this has now allowed us to study Shigella-host interactions. The knowledge accumulated over past decades regarding Shigella-host interactions shows the value of taking a cellular microbiological approach to the study of bacterial disease. However, what has been lacking is an appreciation of all of the strategies used by Shigella to survive and to proliferate in the host cytosol. In 2002, Jin et al. published the first genome sequence for S. flexneri (30), and this has now allowed us to construct cDNA microarrays to identify all of the Shigella genes that show transcriptional adaptation during infection of epithelial cells and macrophages. We have used these data to compare the gene expression of S. flexneri with that of Salmonella enterica serovar Typhimurium, an enteric pathogen radically different from S. flexneri in terms of its intracellular survival strategy. These exciting data will strengthen the understanding of the biology of microbe-host interactions for both of these medically important pathogens.

**MATERIALS AND METHODS**

**Bacterial strains.** S. flexneri 2a strain 301 (Sf301) (30) was routinely grown at 37°C on tryptic soy agar supplemented with 0.01% Congo red. Prior to cell infection, liquid cultures were obtained by inoculation of red colonies into Luria broth (LB; Difco) and growth at 37°C with shaking (200 rpm) to early exponential phase (approximate optical density at 600 nm, 0.3). Growth conditions were chosen to ensure that the bacterial strains used in this study were different from S. flexneri.

**Construction of ShEcoli cDNA microarrays.** The microarrays used in this study are an enhanced version of the Escherichia coli K-12 cDNA microarrays used previously (2, 81). The ShEcoli microarrays have 4,262 open reading frames.
(ORFs) from *E. coli* K-12 strain MG1655 (6), 1,125 ORFs from enterohemorrhagic *E. coli* strain EDL933 (56), and 328 ORFs specific to *S. flexneri* SF301 (30). The criterion used to choose *E. coli* ORFs suitable for analysis of *S. flexneri* was that only those with more than 80% identity over at least 100 bp to the corresponding *S. flexneri* ORFs were selected. For ORFs shorter than 100 bp, more than 90% identity was required. We noted that for the *S. flexneri* SF301 genome, 613 ORFs, mostly insertion elements, have very closely related paralogs. These ORFs were all excluded from the microarrays. In summary, the extended *ShEcoli* 613 ORFs, mostly insertion elements, have very closely related paralogs. These

**RESULTS AND DISCUSSION**

DNA microarray, invasion models, and bacterial RNA isolation. We customized an *E. coli* DNA microarray that has already been successfully used for the transcriptional profiling of colicin-induced cell death in *E. coli* K-12 (81) and the phylogenomic analysis of pathogenic *E. coli* strains (2). This *ShEcoli* microarray allowed us to study the expression of 3,564 ORFs of *S. flexneri* SF301 (see Materials and Methods).

HEla epithelial and U937 macrophage-like human cells were chosen as model cells for infection because these two cell lines have been widely used for studying *Shigella* invasion and have produced consistent data in our experiments. The choice of U937 cells, rather than another widely used murine macrophage cell line, J774, reflects the fact that *S. flexneri* kills J774 cells very rapidly through apoptosis (90), preventing the recovery of sufficient intracellular bacteria for RNA isolation. In contrast, the development of apoptosis or oncosis following *Shigella* infection of U937 cells depends on the differentiation conditions (54). When treated with phorbol myristate acetate to induce differentiation, U937 cells become tolerant to *Shigella* infection; the onset of oncosis is delayed until many hours after infection, allowing the recovery of large numbers of intracellular bacteria (87). To obtain intracellular bacteria, HEla and U937 cells were infected with *S. flexneri* strain SF301 under the conditions described in Materials and Methods. At all time points, both cell lines were well attached to culture dishes, and no significant cell lysis was observed with a microscope.

The isolation of high-quality bacterial RNA that accurately reflected *S. flexneri* gene expression during infection was critical, and the important factors were recently discussed (27). We essentially followed the cold phenol–ethanol protocol,
which allows quick lysis of host cells and stabilization and preservation of bacterial RNA (18). The quality of RNA isolated from both cell lines at all time points was excellent, showing minimal degradation or host RNA contamination (Fig. 1). The amount of RNA isolated at each time point from both cell lines was at least 25 μg and was sufficient for hybridization to at least four microarrays with the labeling procedure outlined above.

**Global transcription profiles.** The gene expression profiles for intracellular *S. flexneri* bacteria were compared with the transcriptome of in vitro-grown bacteria (see Materials and Methods). In total, 597 *S. flexneri* genes were up-regulated and 332 genes were down-regulated more than threefold inside HeLa epithelial cells. The numbers of bacterial genes showing altered expression inside U937 cells were comparable, with 661 genes being up-regulated and 399 genes being down-regulated. Gene expression profiles for *S. flexneri* within HeLa and U937 cells were particularly similar toward the later stages of the infection, although epithelial cells and macrophages have radically different biological functions (Fig. 2). The relative changes in gene expression ranged from a 266-fold induction of the *yfdW* gene to a 63-fold down-regulation of the *treB* gene.

Examination of functional groups of intracellularly regulated bacterial genes confirmed the similarities of gene expression patterns in both cell lines (Fig. 3). In fact, no gene was found to be up-regulated in one cell line and down-regulated in the other, with the exception of *hdeA*, which was slightly down-regulated inside HeLa cells and up-regulated inside U937 cells. This gene is part of the YdeO regulon, which is discussed in more detail below. It appears that the adaptation of *S. flexneri* occurred more rapidly inside U937 cells; most of the changes occurred within 1 h of infection, whereas adaptation inside HeLa cells was a more gradual process (Fig. 4). These results may reflect the fact that differentiated phorbol myristate acetate-treated U937 cells possess macrophage characteristics (21) and therefore would be expected to have a greater effect on the gene expression of intracellular bacteria than HeLa cells.

It was important to ensure that this novel data set for *S. flexneri* in vivo-regulated genes was consistent with data from previous reports. Until now, the most comprehensive study relied on GFP-based technology to identify seven *S. flexneri* genes that were markedly up-regulated during infection of Henle epithelial cells (62). These genes included *uhpT* for hexose phosphate transport, *biaA* for biotin synthesis, *lysA* for lysine synthesis, *fluA* and *sitA* for iron transport, *pstS* for high-affinity phosphate transport, and *phaA*, encoding an alkaline phosphatase. It is striking that the gene expression profiles presented here showed similar levels of induction of these genes during HeLa and U937 cell infections compared to those of the original GFP-based measurements in Henle cells (Table 1). Since different cell lines and bacterial strains were used in these two independent studies, the agreement of the data for six of these seven genes indicates that data from our DNA microarray analyses are reliable and consistent with data from previous reports.

**Expression of essential invasion genes.** The expression of the plasmid-borne *ipa-mxi-spa* locus is known to be essential for *Shigella* entry into both epithelial cells and macrophages (see above). The expression of these genes was drastically down-regulated in both cell lines, although the reduction in the expression of these genes in HeLa cells was a gradual process (Fig. 5). The intracellular down-regulation of the *ipa-mxi-spa* genes in U937 cells was not unexpected, because bacteria would be free in the host cytosol by 1 h postinfection. Furthermore, there is no evidence that U937 cells form intermediate junctions, which are a prerequisite for the Ipa-dependent cell-to-cell spread of the bacteria (69). However, the down-regulation of the *ipa-mxi-spa* genes in HeLa cells is intriguing, as secreted Ipa proteins are required for intercellular bacterial spread within epithelial cell monolayers after entry (60, 72). We wanted to rule out the possibility that HeLa cells lost membrane integrity, exposing intracellular bacteria to gentamicin and altering the expression of particular genes.

To investigate this possibility, we repeated HeLa cell infection under the same conditions as those used above, monitored intracellular bacterial growth, and determined cytotoxicity by testing the levels of LDH released into the cell culture medium. Figure 6 shows that as the level of cytotoxicity increased gradually, the intracellular bacteria grew steadily over time. Hence, *Shigella* infection is only cytotoxic to a small proportion of HeLa cells, and most intracellular bacteria are well protected from gentamicin killing. Total bacterial RNA was also isolated from this independent infection experiment for use in an RT-PCR analysis; the resulting data verified the microarray results and confirmed that the expression of *icsA/virA* and *icsB/pgD* was significantly down-regulated during intracellular bacterial growth in HeLa cells (Fig. 7).

Headley and Payne reported that IpaBCD protein production was reduced significantly during the intracellular growth phase compared to that for bacteria grown in vitro and at the initial entry phase (23), and this report is consistent with our
transcriptome analysis. Thus, it is possible that the levels of ipa-mxi-spa expression and icsA expression remained sufficient to meet the need of intercellular bacterial spread, even though the level of gene expression was much lower than that for bacteria grown in vitro. Alternatively, we hypothesize that bacteria may split into two pools once they are inside HeLa cells; one pool becomes “dormant,” as in U937 cells, and the other pool maintains the “invasive” status, which is associated with the production of protrusions and infection of adjacent cells. In this scenario, the gradual decrease in virulence gene expression that we observed for the ipa-mxi-spa genes would then be a reflection of the reduction of the subpopulation that is still able to spread from cell to cell. This hypothesis needs to be tested experimentally.

The expression of the virulence phenotype of *S. flexneri* involves a complex regulatory mechanism (15). Two plasmid-borne genes, virF and virB, encode essential regulatory proteins. The VirF protein, an AraC-like transcription factor, activates virB and icsA/virG, and the VirB protein in turn binds to the promoters of the entry genes and activates them (65). The chromosomally encoded DNA-binding proteins Fis, IHF, and H-NS are involved in regulating virF and virB. Fis and IHF positively regulate virF. H-NS negatively regulates both virF and virG by binding to the promoters at temperatures below 32°C but not at 37°C, the permissive temperature for virulence gene transcription (18). The H-NS repression complex is sensitive to DNA supercoiling. The microarray data revealed that both fis and virF were moderately but reproducibly downregulated in both cell lines during the time course of the experiment. The expression of virB was decreased more mark-
edly (up to 12-fold) in the two cell lines (Fig. 5). These results suggest that the down-regulation of the *ipa-mxi-spa* and *icsA/virG* virulence genes was initiated through a dialog between the chromosome and the plasmid that was mediated by the *fis* and *virF* regulatory genes. The contributions of H-NS and DNA topology to the down-regulation of *virF* and *virB* are likely to be minor, as cell invasion was carried out at 37°C.

Previously, Eriksson et al. found that the expression of the *Salmonella SPI1* invasion genes is down-regulated inside macrophages but that SPI2, which is responsible for the survival of the bacteria in the *Salmonella*-containing vacuole (SCV), is up-regulated (18). Recently, it was reported that the expression of the locus of enterocyte effacement from enterohemorrhagic *E. coli* is also down-regulated after attachment of the bacteria to erythrocytes (11). *Salmonella SPI1* genes and the enteropathogenic *E. coli* locus of enterocyte effacement show more sequence homology to *Shigella mxi-spa-ipa* genes than to *Salmonella SPI2* genes (29). The consistency of these data

![Graph showing differential expression of *S. flexneri* genes divided into functional groups. Bars indicate percentages of genes in each group that showed significant changes in expression in HeLa (A) and U937 (B) cells. The white bars show the percentages of *S. flexneri* genes up-regulated and the black bars show the percentages of genes down-regulated during intracellular growth. Genes were divided into functional categories by using the Comprehensive Microbial Resource described by Peterson et al. (57). A.a., amino acid; int. metab., intermediary metabolism; hypoth. Prot., hypothetical protein; bind., prot., binding protein.]

FIG. 3. Differential expression of *S. flexneri* genes divided into functional groups. Bars indicate percentages of genes in each group that showed significant changes in expression in HeLa (A) and U937 (B) cells. The white bars show the percentages of *S. flexneri* genes up-regulated and the black bars show the percentages of genes down-regulated during intracellular growth. Genes were divided into functional categories by using the Comprehensive Microbial Resource described by Peterson et al. (57). A.a., amino acid; int. metab., intermediary metabolism; hypoth. Prot., hypothetical protein; bind., prot., binding protein.
suggests that the down-regulation of *ipa-mxi-spa*-like TTSS genes may be a conserved phenomenon that follows successful infection of mammalian cells by enteric pathogens.

Expression of the MxiE regulon. MxiE is a member of the AraC family of regulators which controls a set of late gene products that are secreted through the Mxi-Spa TTSS (12). The MxiE regulon has been reported to be transiently up-regulated after entry into epithelial cells (32); it includes *virA* (involved in the disruption of host microtubules and the formation of membrane ruffles that enhance bacterial entry) (85), *ipaH* (involved in the escape of *Shigella* into the host cytosol) (19), *ipaH* (the product of which is targeted to the host nucleus) (78), and the *osp* (outer *Shigella* protein) genes (whose functions are unknown) (8). MxiE works in concert with IpgC, the molecular chaperone for IpaBC, in *Shigella* and in *E. coli* (45). Activation by MxiE is mediated by binding to a 17-bp motif, coined the MxiE box, in the promoter region of the target genes (44). Strain Sf301 has 12 copies of *ipaH* genes—5 on the virulence plasmid and 7 on the chromosome. The MxiE box is present in each of the 12 *ipaH* promoter regions, although 3 of the chromosomal promoters have degenerate consensus sequences (30). Bioinformatic approaches
had suggested that all of the ipaH genes could be targets for activation by Mxi-IpgC. Previously, Kane et al. (32) used flow cytometry to show that the expression of GFP transcriptional fusions of virA, ipaH<sub>9.8</sub>, ospE2, ospB, ospC1, and ospF was increased at 90 min after entry into L2 mouse fibroblasts. In an independent study, Demers et al. (12) used lacZ fusions to show that during HeLa cell invasion, the expression of virA and the plasmid-borne multiple ipaH genes peaked at 60 min and then dropped close to the levels seen in the in vitro culture after 150 min. The findings of Kane et al. (32) and Demers et al. (12) suggest that MxiE-IpgC-activated genes would be up-regulated during the early stages of HeLa cell infection but that their expression levels would subsequently decrease.

The microarray data show that the members of the MxiE regulon can be split into two groups according to their expression profiles. The expression of virA, ospB, and ospE2 gradually

![Graph 1](image1)

**FIG. 6.** *S. flexneri* cytotoxicity for and growth inside epithelial cells. The bar graphs show the cytotoxic effect resulting from *S. flexneri* infection of HeLa cells (see Materials and Methods for details) (A) and the rate of *S. flexneri* replication inside HeLa cells (B). Values represent the means of measurements from three wells, and error bars indicate standard deviations.

![Graph 2](image2)

**FIG. 7.** Validation of microarray results by RT-PCR. The agarose gel analysis of the PCR fragments obtained after RT-PCR is shown along with the quantification of the corresponding bands (bar graphs). Numbers associated with the bars indicate fold differences relative to the data for the reference LB culture, which were established by densitometric analysis. Samples were isolated at 2, 4, 6, and 8 h after *Shigella* infection of HeLa cells, and data for these samples can be compared directly with data from the microarray experiment. The RNA used for RT-PCR was isolated from an infection independent from the infections used for gene expression profiling. One RNA sample was isolated from a mid-log LB culture and was used as a reference. Genes SF2715 and SF0115 were chosen as controls because they did not show any significant change in expression in the microarray experiment.
decreased from 2 h and continued to decline over time. In contrast, the expression of *ipaH*<sub>1.4</sub>, *ipaH*<sub>7.8</sub>, *ipaH*<sub>4.5</sub>, and *ospE*<sub>1</sub> was consistently and significantly up-regulated at all time points (Fig. 8). It is worth mentioning that our data also showed that the chromosomal *ipaH*<sub>6.5</sub> genes are induced intracellularly. However, various levels of potential cross-hybridization on our microarrays prevented us from making a definitive statement about the relative levels of expression of the seven *ipaH*<sub>6.5</sub> genes, which share much sequence identity. The down-regulation of *virA* and the up-regulation of *ipaH*<sub>1.4</sub> were independently confirmed by RT-PCR (Fig. 7). These data suggest that *virA*, *ospB*, and *ospE*<sub>2</sub> are solely regulated by the decreasing levels of MxiE during infection (see Table S1 in the supplemental material [http://www.ifr.ac.uk/safety/molmicro/pubs.html]). It is likely that unidentified regulators other than MxiE-IpgC are responsible for the up-regulation of *ipaH*<sub>1.4</sub>, *ipaH*<sub>4.5</sub>, *ipaH*<sub>7.8</sub>, and *ospE*<sub>1</sub> inside HeLa cells as well as inside U937 cells and that these may be important for the late stages of *Shigella* infection.

Expression of the 64 SIs. Strain Sf301 has 64 so-called *Shigella* islands (SIs) which have a size of >1 kb and which are thought to have been acquired by lateral gene transfer mediated by bacteriophages (30). Until now, it was unknown whether SI genes were up-regulated during infection. We found that a greater percentage of genes from SIs than from all other functional groups were up-regulated (30%) (Fig. 3), indicating that many of the SI genes are important following invasion. Apart from the *ipaH* genes mentioned above, a number of key SI genes are discussed below.

In SI-1, four genes (*sciA* and *sciCDE*) share homology with the *Salmonella* serovar Typhimurium virulence genes STM0266 and STM0268 to STM0270, respectively. The *sciC* and *sciE* genes were up-regulated by 10- and 4-fold, respectively, in both cell lines, and the *sciD* gene was unchanged. Interestingly, the orthologous *Salmonella* serovar Typhimurium genes show a similar pattern of expression during macrophage infection; STM0268 and STM0270 are induced, while STM0269 is unchanged. Because the functions of these genes are unknown (26), we cannot predict why the *sciCE* genes are expressed at a higher level in the cell cytosol. Nevertheless, they are good candidates for functional studies.

In SI-19 (*ipaH* island 2), there are four consecutive genes with homology to the *Salmonella* *sitABCD* genes and the *Yersinia yfe* operon (89). The *Salmonella* *sitABCD* genes are required for iron and manganese transport in the phagosome (33, 89) and are highly induced inside macrophages (Table S3). The *Shigella* *sitA* gene has already been reported to be up-regulated in the host cell cytosol (62), and *SitA* was recently demonstrated to transport iron for *Shigella* in vitro (63). We found up-regulation of *sitAB* by 10-fold and of *sitCD* by 3-fold in both cell lines throughout the infection (Table 1). SI-56 (also known as SHI-2) (80) harbors the *iucABCD* and *iutA* genes, which encode the *Shigella* aerobactin system (discussed below).

SI-3 harbor bacteriophage *ShI*, which mediates serotype conversion; the *gtrII* gene encodes a glucosyl transferase, and the *gtrB* gene encodes a bactoprenol glucosyl transferase (43). As both *gtrII* and *gtrB* were severely down-regulated in HeLa and U937 cells, type II antigen expression is probably not important for bacterial growth inside the cells. Consistent with this notion, the genes required for O-antigen synthesis, the *rfbGFEC* genes, were down-regulated in macrophages and epithelial cells. SI-49 is the previously identified pathogenicity island SHI-1, which harbors the *sipA* and *pic* genes, encoding the autoprotector proteases, and the *setAB* genes, encoding *Shigella* enterotoxin 1 (59). The expression of these genes was unchanged or was down-regulated, a finding which correlates with their role in causing extracellular tissue destruction. It is likely that this new data set for SI genes that are up-regulated during infection (see Table S1 in the supplemental material [http://www.ifr.ac.uk/safety/molmicro/pubs.html]) will identify new gene targets for determining novel aspects of the *Shigella* survival strategy in the cell cytosol.

Maintenance of virulence plasmid pCP301. Although it is known that the invasion plasmid is essential for *Shigella* virulence (68), very little is known about its maintenance during infection. The primary replication system of the virulence plasmid is that of plasmid R100, which belongs to the RepFIIA family of replicons (79). There are also multiple loci on

![FIG. 8. Expression of genes of the mxiE regulon in HeLa (A) and U937 (B) cells. The bar graphs show the levels of expression at all times relative to the data for the LB culture. The results for the *ipaH*<sub>1.4</sub> gene are from RT-PCR (Fig. 7).](image-url)
pCP301 which are homologous to sequences known to be involved in plasmid segregation and stable maintenance: parA and parB of the bacteriophage P1 partitioning system, stbB and stbA of plasmid R100, ccdA and ccdB of plasmid F, and mvpA and mvpT. Among these, mvpA and mvpT have been demonstrated to form an effective system to maintain stability in vitro: the mvpT product is toxic to plasmidless daughter cells, whereas the mvpA product is an antidote protecting plasmid-carrying bacteria from killing by MvpT (71). While all of the other maintenance genes were either unchanged or down-regulated, the transcription of mvpA was found to be consistently up-regulated by 10- and 8-fold in HeLa and U937 cells, respectively, throughout infection (Table 1). Unfortunately, mvpT was not present on the microarray; therefore, expression data are not available. Interestingly, both of the Salmonella serovar Typhimurium virulence plasmid-borne mvpA and mvpT orthologs (PSLT106 and PSLT107) were also found to be strongly up-regulated during macrophage infection (18). Our findings suggest that an increase in mvpA expression may ensure the stability of the virulence plasmid in the cell cytosol.

Two-component signal transduction systems, sigma factors, and stress responses. Two-component signal transduction systems play important roles in regulating virulence in S. flexneri. CpxR is able to bind to the virF promoter region when it is phosphorylated by CpxA (52, 53). The well-characterized PhoP-PhoQ system is crucial for persistent infection and resistance to killing by cationic polypeptides derived from polymorphonuclear leukocytes and other sources (50). We observed that the transcription of these and other two-component systems changed little during intracellular growth. A considerable change was observed for the ompR-envZ osmosensor system, which was down-regulated twofold. Accordingly, the expression of its target genes, ompC and ompF, was significantly decreased in both cell lines (Table 1). OmpC is required for virulence in vitro and in vivo, probably through its role in cell-to-cell spread (5). Coupled with the decreased ipa-mxi-spa expression, the decreased transcription of ompC is another indication that the bacteria reduce their capacity for intercellular dissemination.

The expression of the S. flexneri rpoS gene, the master regulator of general stress and stationary phase (24), and its regulon was not significantly altered during infection of macrophages or epithelial cells. Therefore, as for Salmonella (18), the gene expression pattern for intracellular bacteria did not reflect the stationary phase of bacteria grown in vitro. In fact, the expression of most of the genes encoding sigma factors did not change, except for a moderate up-regulation of rpoH and rpoE, which encode σ32 and σ5, respectively. However, the increase in the expression of rpoH was not accompanied by an induction of the known σ32-dependent genes, including dnaK and htpG (88). Similarly, the increase in the expression of rpoE had a limited impact on the expression of the σ5 regulon; only degP/lteA showed moderate up-regulation (by up to fivefold in both cell lines). The expression of other genes of the σ5 regulon, such as rpoA, surA, and imp, involved in envelope biogenesis, was unchanged. However, the spy gene (which encodes a periplasmic chaperone controlled by CpxRA), the esp gene (responsible for phage shock) (7), and the ibp/AB nonspecific heat shock genes (31) were strongly induced, indicating that intracellular S. flexneri bacteria probably experienced a degree of envelope stress. The significance and mechanisms of these stress responses for the Shigella intracellular survival strategy require further investigation.

Bacterial metabolism in the cell. Until now, there has been little information about the nature of S. flexneri metabolism during infection, and our intracellular gene expression data offer the first insight into this area. The intermediary metabolism and energy production systems were down-regulated during infection; genes encoding enzymes involved in glycolysis, the Krebs cycle, and oxidative phosphorylation were strongly decreased during intracellular growth in both cell lines. As both aceI and aceK are pseudogenes (29), S. flexneri is unable to utilize two-carbon compounds via the glyoxylate shunt. Taken together, these data suggest that intracellular S. flexneri exhibits reduced energy production, which accounts for the altered expression profiles of the genes encoding the aerobic respiratory chain. The bacteria appear to be rebalancing NAD+ regeneration, net electron efflux, and oxygen utilization to meet their new physiological needs. The ndh genes, encoding NADH dehydrogenase 1 (NDH-1), which can generate proton motive force, were strongly down-regulated, whereas ndh, encoding NADH dehydrogenase 2 (NDH-2), was strongly up-regulated. These data suggest that intracellular S. flexneri bacteria preferentially oxidizes NADH via the NDH-2 pathway, without the generation of proton motive force. The NDH-2 pathway would not primarily provide intracellular bacteria with energy but would recycle NADH into NAD+ to maintain the optimal redox balance. The strong up-regulation of the cysABCD genes suggests that the reducing equivalents generated by NADH oxidation were preferentially passed to oxygen via cytochrome bo, which has a lower affinity for oxygen than cytochrome bd, which is the alternative oxygen oxidase. Utilization of the NDH-2-cytochrome bo3 aerobic respiration pathway indicates that intracellular bacteria have low energy and oxygen requirements. None of the components of the anaerobic respiratory chain showed significant changes in expression, except for nitrate reductase A (narGH). The significance of this finding is not yet clear. In addition, we noted that the rplJL-rpoBC operon, encoding the β subunit of RNA polymerase, was moderately down-regulated (two- to fivefold) inside both HeLa and U937 cells. This finding is consistent with the down-regulation of the catabolic genes and the reduced rate of growth of S. flexneri within the cell cytosol (doubling time, about 40 min) compared with the rate of growth in LB (doubling time, about 30 min).

Interpretation of these changes during the adaptation of S. flexneri to the intracellular environment is challenging; regulation of the genes related to intermediary metabolism is complex, often involves many distinct pathways, and has not yet been studied in detail in S. flexneri. It will be important to determine whether the down-regulation of genes involved in glycolysis and other metabolic cycles that we observed is simply a consequence of growth in the intracellular milieu or is absolutely required for successful infection and whether the down-regulation is reflected at the level of enzyme activity.

Ionic composition of the cell cytosol. One important function of animal cells is to maintain ion gradients across the plasma membrane to regulate cell volume and drive the transport of nutrients inside the cell. Therefore, the ionic composition of the cytosol is tightly regulated. For example, the
Na\textsuperscript{+}-K\textsuperscript{+} pump ensures the formation of an electrochemical gradient that maintains high K\textsuperscript{+} and low Na\textsuperscript{+} intracellular concentrations (55). Furthermore, the levels of Mg\textsuperscript{2+}, Ca\textsuperscript{2+}, and HCO\textsubscript{3}\textsuperscript{-} are also tightly regulated (36). Therefore, *Shigella* bacteria will encounter during growth in vitro an ionic composition that is different from that in the cytosol; this property was expected to change the expression of certain genes after entry into host cells. Gene expression profiling is a powerful tool for reporting the type of environment being experienced by *Shigella* bacteria during infection; the bacteria effectively serve as environmental sensors. The observed up-regulation of the *proVWX* operon (by up to 57-fold in both cell lines) is likely to be a specific response to the cytosolic environment. Under high-osmolarity conditions, *ProVWX* actively transports a group of compounds termed neutral compatible solutes, including betaine and proline. These compatible solutes can substitute for other ions, such as K\textsuperscript{+} and glutamate, which inhibit enzyme function when present at high concentrations (37). However, the cytosolic osmolarity of mammalian cells does not differ greatly from that of in vitro LB. It is therefore possible that the induction of *proVWX* simply reflects differences in overall ionic compositions, such as high levels of K\textsuperscript{+}, rather than differences in osmolarity between LB and the intracellular environment.

We observed that the *phoRB* regulon, responsible for phosphate uptake, was significantly up-regulated, suggesting that the cytosol has restricted levels of available phosphate: *phoRB* expression was increased by nearly 10-fold, and the expression of many genes of the *phoBR* regulon also was increased significantly. These included the *phoA* gene, encoding periplasmic phosphatase, and the *pstS* and *phnC* genes, encoding ABC phosphate transporters.

The cytosolic Mg\textsuperscript{2+} concentration is about 0.8 mM (36). This concentration appeared to impose a degree of stress upon *S. flexneri*, because the transcription of *mgtA*, which encodes a P-type ATPase involved in the uptake of Mg\textsuperscript{2+} (74), was increased by three- and eightfold in HeLa and U937 cells, respectively. These data are consistent with a limited availability of magnesium to *S. flexneri* during mammalian cell infection.

The hypothesis that iron availability is restricted inside the cytosol was confirmed by the observed induction of the *sitABCD* genes, encoding a putative iron transport system, and the *iucABCD* and *iutA* genes, encoding the aerobactin, in *S. flexneri*. In contrast to the *sitABCD* system, which was induced equally in HeLa and U937 cells, the aerobactin system was induced only in the early stages of HeLa cell infection and was unchanged throughout the infection of U937 cells. These data suggest that the *Shigella* *sitABCD* system is the main iron transport system during intracellular infection. However, a recent study suggested that the presence of either *iuc* or *feoB* [encoding a membrane protein involved in Fe(II) uptake] (40) is sufficient to support plaque formation on Henle cell monolayers, despite the low level of expression of these genes compared to that of the *sitABCD* genes during infection (63). It is clear that the cytosolic ionic composition could limit the intracellular growth of *Shigella*, but the gene expression data describe an effective adaptation by the bacteria for obtaining essential factors through the up-regulation of at least four transport systems.

**Shigella genes differentially expressed between the two mammalian cell lines.** Epithelial cells and macrophages have radically different functions, with the latter possessing the ability to take up and kill microbes through the endocytic pathway. However, *Shigella* bacteria are thought to use a single strategy to escape into the cell cytosol in both cell types, and this notion is confirmed by the remarkably similar gene expression profiles reported here (see above). The most obvious difference between the two cell lines is the more gradual time-dependent change in expression during infection of HeLa cells than of U937 cells (Fig. 4 and 5). This finding is highlighted by considering the expression profiles for *S. flexneri* within HeLa and U937 cells at early and late time points. A comparison of the earliest time points between the two cell types reveals that 184 genes show a threefold difference in relative gene expression, while only 21 genes are differentially expressed at the final time points. Besides the *ipa-mxi-spa* virulence genes, the other genes that show a delayed response in HeLa cells encode proteins linked to energy production, such as NDH-1, cytochrome *bo*, and succinate dehydrogenase. These data suggest that the HeLa cell cytosol is a more favorable environment for bacterial growth than the macrophage cytosol at the early stages of infection.

Only 18 *S. flexneri* genes were differentially expressed between HeLa and U937 cells throughout the infection process (Table 2). Among these, *ydeP, yhiE, and ydeO* play a role in the acid resistance of *E. coli* (40), and these genes are activated by the response regulator EvgA. The overexpression of *YdeO* is known to induce the expression of additional genes implicated in acid resistance (41). Most members of the *YdeO* regulon are strongly induced in U937 cells (by 26-fold, on average, over all time points) but are not induced or are only slightly induced in HeLa cells. Further evidence to suggest that U937 cells have a more acidic cytosol than HeLa cells is that the expression of *asr* (part of the *phoB* regulon, encoding an acid shock protein) is up-regulated by more than 10-fold in U937 cells but is increased by only 2-fold in HeLa cells. Taken together, these data suggest that *Shigella* is exposed to a lower pH in the macrophage cytosol than in the epithelial cell cytosol.

**Comparison of Shigella and Salmonella transcriptional adaptations within macrophages.** *S. enterica* serovar Typhimurium is a pathogen radically different from *S. flexneri*, and this difference is reflected in the opposing strategies used during macrophage infection. In essence, both bacteria have effective tactics for avoiding contact with the toxic constituents of the lysosome, which are normally introduced into the phagosomal vacuole: *S. flexneri* escapes the vacuole, whereas *Salmonella* hijacks the cell by subverting the normal cellular trafficking processes, preventing lysosomal fusion, and creating the unique SCV (21, 46).

Eriksson et al. previously established the gene expression profile for *Salmonella* serovar Typhimurium during infection of murine macrophages (18), and we have used these data to compare the intramacrophage environments experienced by *S. flexneri* and *Salmonella* serovar Typhimurium. It should be remembered that this comparison involves bacterial growth in two distinct macrophage cell lines, one murine derived (*J774A.1*) and one human derived (*U937*). We compared the gene expression profile for each pathogen within macrophages with the gene expression profile observed for a mid-logarith-
mic-phase culture of each pathogen grown in LB in vitro. By normalizing the intramacrophage gene expression profile for each pathogen to the data obtained from the appropriate LB culture, we were able to perform direct comparisons. We identified which genes showed similar expression patterns and which ones showed differences between the two bacterial pathogens. These data are presented in Table S3 in the supplemental material (http://www.ifr.ac.uk/safety/molmicro/pubs.html). The relative levels of expression of some of the Shigella genes are distinct from the earlier data (18), because the LB medium used was as a comparator instead of an RPMI medium cell culture. A total of 1,422 of 4,408 Shigella genes are distinct from the earlier data (18), because the

<table>
<thead>
<tr>
<th>Gene name</th>
<th>Gene expression levels in the following cells at the indicated time (h), relative to those in LB medium:</th>
<th>Function or comments</th>
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<tr>
<td></td>
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</tr>
<tr>
<td></td>
<td>HeLa 2 4 6 8</td>
<td>U937 1 3 5</td>
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<td>20.3 17.5 17.8</td>
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<td>0.6 0.8 0.7 0.7</td>
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<tr>
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<td>0.5 0.9 0.6 0.6</td>
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<tr>
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<td>23.6 38.5 36.1</td>
</tr>
<tr>
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<td>SF2434 2.3 3.9 5.5 5.4</td>
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</tr>
<tr>
<td>godAα</td>
<td>SF3594 2.4 6.8 4.4 3.3</td>
<td>68.3 25.2 10.9</td>
</tr>
<tr>
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<td>ndI</td>
<td>SF2702 10.1 15.5 18.8 18.3</td>
<td>3.3 4.1 5.9</td>
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<tr>
<td>proU</td>
<td>SF1538 2.9 4.4 5.1 5.2</td>
<td>130.8 93.9 70.5</td>
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<tr>
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<tr>
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<td>30 25 24.9</td>
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<tr>
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<td>20.2 11.8 5.9</td>
</tr>
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<td>a</td>
<td>Member of the EvgA or YdeO regulon.</td>
<td></td>
</tr>
<tr>
<td>b</td>
<td>KAPA, 7-keto-8-aminopelargonic acid.</td>
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</table>
Conclusions. This is the first report to consider the gene expression profile for an intracellular bacterial pathogen within two fundamentally different human cell types. Obviously, U937 cells and HeLa epithelial cells are quite distinct at the cell biological level. Nevertheless, the broadly similar patterns of intracellular S. flexneri gene expression that we observed in HeLa and U937 cells suggest that these cells have comparable cytosolic environments. Notable exceptions were some acid-induced genes, including those of the EvgA and YdeO regulons, which are more highly induced in U937 cells than in HeLa cells. These data suggest that S. flexneri infection causes acidification of the macrophage cytosol; this notion remains to be verified experimentally. Most strikingly, S. flexneri bacteria show a drastically reduced expression of genes encoding the Ipa-Mxi-Spa and other virulence determinants in the cytosol, indicating that these are not crucial for the growth of bacteria once inside host cells.

Other exciting findings are that the bacteria have to compete for iron, magnesium, and phosphate and have to cope with the unique ionic composition of the cytosol. These goals are achieved by up-regulation of the sitABC, mgtA, phorB regulator, prot/WX, and other transport systems. In addition, we performed a novel comparison of the intracellular gene expression profiles for Salmonella serovar Typhimurium and S. flexneri and identified a surprising level of similarities in the ways in which these pathogens respond to the macrophage environment. These findings are a testament to the efficacy of the SPI2 and Spv-mediated systems in protecting Salmonella serovar Typhimurium from attack by the components of the phagosome, which Shigella manages to avoid by escaping the vacuole itself.

S. flexneri is exposed to numerous stresses within the cytosol of human cells, including starvation for essential minerals and oxidative damage. Nonetheless, S. flexneri is able to grow steadily in the cytosol, showing that it can readily adapt to intracellular life. The data that we have amassed are the first to describe this adaptation at the level of individual S. flexneri genes. The next challenge is to use these findings to develop an understanding of Shigella infection. Let us hope that this work lays the foundation for discovering the Achilles’ heel of one of the medically important bacterial pathogens.

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