

# Infection of Mice by *Salmonella enterica* Serovar Enteritidis Involves Additional Genes That Are Absent in the Genome of Serovar Typhimurium

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***Salmonella enterica* serovar Enteritidis causes a systemic, typhoid-like infection in newly hatched poultry and mice. In the present study, a library of 54,000 transposon mutants of *S. Enteritidis* phage type 4 (PT4) strain P125109 was screened for mutants deficient in the *in vivo* colonization of the BALB/c mouse model using a microarray-based negative-selection screening. Mutants in genes known to contribute to systemic infection (e.g., *Salmonella* pathogenicity island 2 [SPI-2], *aro*, *rfa*, *rfb*, *phoP*, and *phoQ*) and enteric infection (e.g., SPI-1 and SPI-5) in this and other *Salmonella* serovars displayed colonization defects in our assay. In addition, a strong attenuation was observed for mutants in genes and genomic islands that are not present in *S. Typhimurium* or in most other *Salmonella* serovars. These genes include a type I restriction/modification system (*SEN4290* to *SEN4292*), the *peg* fimbrial operon (*SEN2144A* to *SEN2145B*), a putative pathogenicity island (*SEN1970* to *SEN1999*), and a type VI secretion system remnant *SEN1001*, encoding a hypothetical protein containing a lysin motif (LysM) domain associated with peptidoglycan binding. Proliferation defects for mutants in these individual genes and in exemplar genes for each of these clusters were confirmed in competitive infections with wild-type *S. Enteritidis*. A  $\Delta$ *SEN1001* mutant was defective for survival within RAW264.7 murine macrophages *in vitro*. Complementation assays directly linked the *SEN1001* gene to phenotypes observed *in vivo* and *in vitro*. The genes identified here may perform novel virulence functions not characterized in previous *Salmonella* models.**

*Salmonella* is a Gram-negative bacterium belonging to the family *Enterobacteriaceae*. The genus comprises two species, *S. bongori* and *S. enterica*, which include more than 2,500 serovars (17). *Salmonella enterica* serovar Enteritidis can infect a wide variety of hosts, including birds, rodents (mice), and humans (36). *S. Enteritidis* is a facultative intracellular pathogen that invades epithelial host cells and uses phagocytic cells to disseminate, causing a systemic, typhoid-like infection in mice and newly hatched poultry. In humans, *S. Enteritidis* causes a self-limited gastroenteritis characterized by diarrhea, fever, and abdominal cramps (45).

In recent years, *S. Enteritidis* has emerged as a primary cause of food-borne salmonellosis worldwide. Epidemiological studies suggest that *S. Enteritidis* filled the ecological niche vacated by the eradication of *S. Gallinarum* from commercial poultry flocks, increasing human infections progressively due to the consumption of contaminated eggs and egg products from apparently healthy hens (38, 63). Because the infection of adult hens by *S. Enteritidis* is asymptomatic, the contamination of eggs due to the colonization of the oviduct is hard to detect and prevent (38). To avoid poultry stock infection by this pathogen, some approaches have been addressed to design vaccines for laying hens using live, attenuated mutants (11, 16, 57) or bacteria killed by chemical agents or heat (6, 11, 21). None of these vaccines have been shown to significantly diminish the intestinal colonization or the shedding of the pathogen in the depositions. On the other hand, the emergence of strains resistant to the antibiotics commonly used to treat the disease encourages the identification of new targets for vaccine design.

The mechanisms involved in *S. Enteritidis* pathogenicity are

poorly understood. Most knowledge is based on research conducted on *S. Typhimurium*, which causes a similar disease in humans and a systemic disease in mice. Although these pathogens share virulence mechanisms central to epithelial cell invasion and survival within phagocytic cells, it is not yet clear how *S. Enteritidis* is able to cause infection, especially in one of its main reservoirs: mice. Nonetheless, because *S. Enteritidis* causes a systemic infection in newly hatched poultry and mice, an approach using the *in vivo* colonization of liver and spleen of BALB/c mice is a suitable model to study the major virulence factors involved in the acute phase of the infection.

Several studies using microarray-based genetic screening have been conducted to identify genes involved in *S. Typhimurium* pathogenesis in both *in vitro* and *in vivo* models (22, 24, 56, 72). However, these approaches have not been used to explore the basis of *S. Enteritidis* pathogenesis. In the present study, we performed a genome-wide search in order to identify genes and

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TABLE 1 Strains used in the present study

Strain	Genotype or relevant phenotype	Source or reference
<i>S. Enteritidis</i>		
P125109	<i>S. Enteritidis</i> PT4 wild type (NCTC13349)	Laboratory collection
WT/pNFB9	<i>attG1::pNFB9</i>	
$\Delta$ SEN1001	$\Delta$ SEN1001::FRT	This study
$\Delta$ SEN1001/pNFB9	$\Delta$ SEN1001::FRT <i>attG1::pNFB9</i>	This study
$\Delta$ SEN1001/pCSV1	$\Delta$ SEN1001::FRT <i>attG1::pCSV1</i>	This study
$\Delta$ SEN1976	$\Delta$ SEN1976::Cam	This study
$\Delta$ ROD21	$\Delta$ (SEN1976–SEN1999)::Cam	This study
$\Delta$ peg	$\Delta$ (SEN2144A–SEN2145B)::Kan	This study
$\Delta$ ROD40	$\Delta$ (SEN4290–SEN4292)::Kan	This study
<i>S. Typhimurium</i> SC203	14028 <i>zjg-8103::pir<sup>+</sup>/F' proAB lac<sup>f</sup> <math>\Delta</math>lacZM15 zzf8169::Tn10dKn</i>	Laboratory collection
<i>Escherichia coli</i> DH5 $\alpha$	K-12 F <sup>-</sup> $\phi$ 80lacZ $\Delta$ M15 $\Delta$ (lacZYA-argF)U169 <i>deoR recA1 endA1 hsdR17(r<sub>k</sub><sup>-</sup> m<sub>k</sub><sup>+</sup>) phoA supE44 thi-1 gyrA96 relA1 <math>\lambda</math><sup>-</sup></i>	Laboratory collection

genomic islands of *S. Enteritidis* that have a role in virulence during the infection of BALB/c mice. To accomplish this, we implemented a microarray-based negative-selection screen for mutants showing an impaired colonization of deep organs in mice. The phenotypes of selected insertion mutants that were less fit during infection in our screen were confirmed by competition assays with individual mutants of some of the genes or genomic islands identified in this study. Furthermore, the colonization defect presented by one of these mutants, the  $\Delta$ SEN1001 mutant, was directly linked to a defect in intracellular survival within macrophages.

## MATERIALS AND METHODS

**Bacterial strains, media, and growth conditions.** The bacterial strains used in the present study are listed in Table 1. All *S. Enteritidis* strains are derivatives of the sequenced phage type 4 (PT4) strain P125109 (77). Bacteria were routinely grown in Luria-Bertani (LB) medium (10 g/liter tryptone, 5 g/liter yeast extract, 5 g/liter NaCl) at 37°C with shaking or in E minimal medium (0.2 g/liter MgSO<sub>4</sub> · 7H<sub>2</sub>O, 2 g/liter citric acid · H<sub>2</sub>O, 13.1 g/liter K<sub>2</sub>HPO<sub>4</sub> · 3H<sub>2</sub>O, 3.3 g/liter NaNH<sub>4</sub>HPO<sub>4</sub> · 4H<sub>2</sub>O) with glucose (0.2%). When required, LB medium was supplemented with ampicillin (Amp) (100 mg/liter), chloramphenicol (Cam) (20 mg/liter), kanamycin (Kan) (50 mg/liter), or 5-bromo-4-chloro-3-indolyl- $\beta$ -D-galactopyranoside (X-gal) (50 mg/liter). Media were solidified by the addition of agar (15 g/liter).

**Standard DNA techniques.** Total genomic DNA was obtained by use of the GenElute bacterial genomic DNA kit (Sigma-Aldrich, St. Louis, MO). Plasmid DNA was obtained by use of the QIAprep Spin miniprep kit (Qiagen, Germantown, MD). Digestions using the restriction endonucleases EcoRI, BamHI, and BglII (Fermentas, St. Leon-Rot, Germany) and ligations using T4 DNA ligase (New England BioLabs, Beverly, MA) were conducted as recommended by the manufacturers. DNA samples were routinely analyzed by electrophoresis in 1% agarose gels (0.5× Tris-acetate-EDTA [TAE] buffer) and visualized under UV light after ethidium bromide staining.

Primers for PCR amplification were designed based on the reported sequence of *S. Enteritidis* PT4 strain P125109 (see Table S1 in the supplemental material), using Vector NTI Advance 9.0 software. PCR amplifications were performed by using GoTaq Flexi DNA polymerase (Promega, Madison, WI). Reaction mixes contained 1× buffer, 2 mM MgCl<sub>2</sub>, 200  $\mu$ M each deoxynucleoside triphosphate (dNTP), 200 nM each primer, 0.5  $\mu$ l of template DNA (50 to 100 ng), and 0.5 U of DNA polymerase. Standard conditions for amplification were as follows: 3 min at 94°C followed by 30 cycles of incubations at 94°C for 30 s, 55°C for 30 s,

and 72°C for 2 min, followed by a final extension step at 72°C for 5 min. PCR products were purified by using the QIAquick PCR purification kit (Qiagen, Germantown, MD).

**Construction of the transposon library.** *S. Enteritidis* PT4 strain P125109 was mutagenized with a mini-Tn5 derivative using the EZ-Tn5 <T7/KAN-2> promoter insertion kit (Epicentre Biotechnologies, Madison, WI). Briefly, transposome complexes were assembled *in vitro* by mixing 2  $\mu$ l of the EZ-Tn5 <T7/KAN-2> transposon (0.1 pmol/ $\mu$ l), 2  $\mu$ l of EZ-Tn5 transposase (1 U/ $\mu$ l), and 2  $\mu$ l of 100% glycerol. The mix was incubated for 30 to 45 min at room temperature. Immediately before mutagenesis, 3  $\mu$ l of transposome complexes was dialyzed against sterile water for 20 min at room temperature using filters with a 0.025- $\mu$ m pore size (Millipore). The dialyzed material was recovered, mixed with 1  $\mu$ l of Type One restriction inhibitor (Epicentre Biotechnologies, Madison, WI), and transformed into fresh electrocompetent P125109 cells. Transformants were allowed to recover in 2 ml of LB medium for 45 min at 37°C. Aliquots of 100  $\mu$ l from the transformation were plated onto LB supplemented with Kan (LB-Kan) agar plates and incubated overnight at 37°C. The mutagenesis procedure was repeated 4 times. A total of ~54,000 Kan<sup>r</sup> mutants generated were scraped from the plates, washed three times in sterile phosphate-buffered saline (PBS), and resuspended in LB medium to assemble the initial transposon library. Glycerol stocks of the library were aliquoted and stored frozen at -80°C.

To confirm transposon insertions, chromosomal DNA obtained from each of 15 randomly selected clones was used as a template for PCR amplification with primers designed to detect the KAN-2 gene (see Table S1 in the supplemental material). All 15 clones contained a transposon insertion (data not shown). The presence of single insertions at different chromosomal locations was confirmed by Southern blotting after DNA digestion with EcoRI and hybridization against a probe generated by the PCR amplification of the KAN-2 gene (data not shown). To select for auxotrophic mutants, 248 colonies were randomly selected and plated onto LB agar plates and onto E medium agar plates supplemented with glucose (0.2%). Of the 248 colonies, 5 were unable to grow in E medium compared to the rich medium. Thus, approximately 2% of auxotrophic mutants were obtained in the library.

**Animal studies in BALB/c mice.** A frozen glycerol aliquot of the library was used to inoculate 50 ml of LB-Kan. After overnight growth with agitation at 37°C, the bacteria were pelleted, washed three times, and diluted 1/100 in sterile PBS for inoculation. The exact titer of the inoculum was determined by serial dilution and plating onto LB-Kan agar. A group of 6 BALB/c mice (8- to 10-week-old females) was infected intraperitoneally (i.p.) with ~10<sup>6</sup> CFU of the library in 100  $\mu$ l of PBS. Samples of the inoculated material (input library) were kept frozen at -20°C until further use. Mice were euthanized at 48 h postinfection, and the spleen

and liver were removed aseptically and homogenized in 3 ml of ice-cold, sterile PBS. An aliquot of 100  $\mu$ l from each homogenate was used for serial dilution and determinations of titers on LB-Kan agar plates. The remaining homogenate was inoculated into 100 ml of LB-Kan. After overnight growth with agitation at 37°C, the bacteria (output libraries) were pelleted, washed 3 times in ice-cold sterile PBS, and stored frozen at -20°C until further use.

Individual mutants with an apparent phenotype in our microarray-based negative-selection screen were chosen for confirmation of mixed infections with wild-type *S. Enteritidis* PT4 strain P125109 to determine the competitive index (CI). Each mutant strain to be tested and the wild-type strain were grown overnight at 37°C with aeration, mixed at a 1:1 ratio, and diluted 1/100 in PBS for inoculation. The exact titer and ratio of strains in the inoculum were determined by serial dilution and plating onto LB agar (total CFU) and LB-Kan or LB-Cam agar (mutant CFU). Groups of 3 to 5 BALB/c mice (8- to 10-week-old females) were inoculated i.p. with  $\sim 10^6$  CFU of the mixture of the mutant and wild-type strains in 100  $\mu$ l of PBS. Mice were euthanized at 48 h postinfection, and the spleens and livers were removed and homogenized. Each homogenate was serially diluted, and aliquots of the dilutions were plated onto LB and LB-Kan or LB-Cam agar plates to determine the exact ratio of strains recovered. CI values were calculated as the mean ratio of mutant CFU to wild-type CFU, normalized to the input ratio and converted logarithmically. Statistical significance was determined by using a two-tailed Student *t* test.

**Labeling of DNA adjacent to transposon insertions and microarray analysis.** The DNA adjacent to transposon insertions in a mutant library was specifically amplified as described previously (5, 72), with modifications. Genomic DNA was prepared for the input and output libraries by using the GenElute bacterial genomic DNA kit (Sigma-Aldrich, St. Louis, MO). Four micrograms of genomic DNA from each library was then fragmented by sonication using a Branson Sonifier 150 instrument (Branson Ultrasonics). Poly(A) tails were added to the fragmented DNA using terminal transferase (TdT) as follows: 1.5  $\mu$ g of DNA fragments was incubated for 30 min at 37°C in a total reaction mixture volume of 50  $\mu$ l containing 40 U TdT (New England Biolabs, Beverly, MA), 1 $\times$  buffer, 0.25 mM CoCl<sub>2</sub>, and 0.4 mM dATP. Terminal transferase was subsequently inactivated at 70°C for 10 min, and the tailed product was purified by use of the QIAquick PCR purification kit (Qiagen, Germantown, MD).

A nested PCR strategy was used to amplify only the poly(A)-tailed DNA fragments containing the transposon end carrying P<sub>T7</sub> and the genomic DNA flanking the insertion. In the first amplification reaction, 50 ng of purified poly(A)-tailed DNA was used as a template for a PCR using primers DOPR2 and CCT<sub>24</sub>VN (see Table S1 in the supplemental material). The reaction mixture consisted of 1 $\times$  buffer, 200  $\mu$ M each dNTP, 1.5 mM MgCl<sub>2</sub>, 1.25 U *Taq* polymerase (Promega, Madison, WI), and 0.2  $\mu$ M each primer in a total reaction mixture volume of 25  $\mu$ l. The amplification was carried out under the following conditions: an initial denaturation step at 94°C for 1 min followed by 30 cycles with denaturation at 94°C for 10 s, annealing at 50°C for 10 s, and extension at 72°C for 5 s. The last cycle was followed by a final extension step for 3 min at 72°C. In the second amplification step, a nested PCR was performed by using 1  $\mu$ l of amplified product from the initial PCR as a template in a total volume of 50  $\mu$ l. Internal primer KAN2FP1-B and primer CCT<sub>24</sub>VN (see Table S1 in the supplemental material) were used under cycling conditions identical to those used during the initial PCR.

An aliquot of 5  $\mu$ l of the nested PCR mixture was used directly as a template for a 20- $\mu$ l *in vitro* transcription reaction mixture using the AmpliScribe T7 transcription kit (Epicentre Biotechnologies, Madison, WI) according to the manufacturer's protocol. The RNA was treated with RNase-free DNase (Epicentre Biotechnologies, Madison, WI), purified with the RNeasy minikit (Qiagen, Germantown, MD), and used as a template to synthesize labeled cDNA by the incorporation of Cy5-dCTP or Cy3-dCTP (Amersham Biosciences Piscataway, NJ) using SuperScript II reverse transcriptase (Invitrogen, Carlsbad, CA). The labeling protocol

was repeated with dyes reversed for input and output samples. Finally, the labeled cDNA was purified by using the QIAquick PCR purification kit (Qiagen, Germantown, MD) and hybridized in slides containing a *Salmonella* microarray based on *S. Typhimurium* LT2 genes and supplemented with genes specific to *S. Enteritidis* PT4 strain P125109 (65). The slides containing the microarray were printed in triplicate.

**Hybridization and data analysis.** Standard protocols for hybridizations in formamide buffer were applied for prehybridization, hybridization, and posthybridization wash processes ([http://catalog2.corning.com/Lifesciences/media/pdf/gaps\\_ii\\_manual\\_protocol\\_5\\_02\\_cls\\_gaps\\_005.pdf](http://catalog2.corning.com/Lifesciences/media/pdf/gaps_ii_manual_protocol_5_02_cls_gaps_005.pdf)). Immediately before hybridization, 2  $\mu$ g of labeled probes from the input sample was combined with 2  $\mu$ g of labeled probes from one of the output samples, and the volume was adjusted to 40  $\mu$ l with nuclease-free water. The mixture of probes was combined with 40  $\mu$ l of 2 $\times$  hybridization buffer (50% formamide, 10 $\times$  SSC [1 $\times$  SSC is 0.15 M NaCl plus 0.015 M sodium citrate], 0.2% SDS) and then denatured at >95°C for 5 min. The probes were hybridized to the *Salmonella* microarray at 42°C in a water bath. After incubation overnight, the slides were washed and scanned by using the ScanArray 5000 laser scanner (Packard BioChip Technologies, Billerica, MA) with ScanArray 2.1 software. Fluorescence signal intensities were quantified by using the QuantArray 2.0 software package (Packard BioChip Technologies, Billerica, MA). The data were normalized and analyzed by using Webarray (82) and WebarrayDB (<http://www.webarraydb.org>) (83), with quantile normalization.

**Mutant construction and analysis.** Mutant strains with specific deletions and concomitant insertions of a Kan or Cam resistance cassette were constructed by using the lambda Red recombination method (30), with modifications (72). PCR amplifications of an antibiotic resistance cassette flanked by the FRT (Flp recombinase target sequence) sites present in plasmid pCLF2 (Cam<sup>r</sup>) or pCLF4 (Kan<sup>r</sup>) were carried out under standard conditions using the primers described in Table S1 in the supplemental material. *S. Enteritidis* PT4 strain P125109 containing plasmid pKD46, which synthesizes the lambda Red recombination system, was grown to an optical density at 600 nm (OD<sub>600</sub>) of 0.5 at 30°C in LB medium containing Amp and L-arabinose (10 mM) and transformed with approximately 500 ng of each purified PCR product. Transformants were selected on LB agar plates containing Kan or Cam at 37°C. The presence of each mutation was confirmed by PCR amplification and transferred to the wild-type background by generalized transduction using the high-frequency transducing phage P22 HT105/1 *int*-201.

To generate nonpolar, in-frame deletions of selected genes of interest, the corresponding Kan<sup>r</sup> or Cam<sup>r</sup> derivatives were transformed with temperature-sensitive plasmid pCP20 that synthesizes the Flp recombinase (25, 30). Transformants were selected at 30°C on LB agar plates containing Amp. A few colonies were streaked two consecutive times at 37°C onto LB agar plates and tested for the loss of the antibiotic resistance cassettes and pCP20 by patching them onto LB agar plates containing Kan or Cam plus Amp. The presence of the mutant allele was confirmed by PCR amplification using primers flanking the sites of substitution.

**Cloning of the *SEN1001* gene for complementation assays.** Primers SEN1001\_out5\_BamHI and SEN1001\_out3\_BamHI (see Table S1 in the supplemental material), including restriction sites for BamHI endonuclease, were used to amplify a 1,181-bp fragment of the *S. Enteritidis* PT4 strain P125109 genome, including the *SEN1001* gene. The PCR product was purified and ligated into plasmid pGEM-T Easy (Promega, Madison, WI). The ligation mix was transformed by electroporation into competent *Escherichia coli* DH5 $\alpha$  cells, and transformants were selected on LB agar plates containing Amp and X-gal. Plasmid DNA was prepared from several independent transformants. The presence of the insert in each plasmid was confirmed by PCR amplification using primers T7 and SP6 (see Table S1 in the supplemental material), flanking the multiple-cloning site in pGEM-T Easy. Subsequently, the cloned fragment was subcloned into plasmid pNFB9, a *pir*-dependent plasmid carrying the *int* gene and the *attP* site of bacteriophage Gifsy-1 (49). To do this, a plasmid with *SEN1001* cloned in the same orientation as that of *P<sub>lac</sub>* into pGEM-T Easy



was digested with BamHI. The DNA fragment including *SEN1001* was purified and ligated into plasmid pNFB9 previously digested with BglII. The ligation mix was transformed by electroporation into *S. Typhimurium* strain SC203, and transformants were selected on LB agar plates containing Amp and X-gal. The presence of the insert in the recombinant plasmids was confirmed by PCR amplification using primers NFB9-MCS\_Out5 and NFB9-MCS\_Out3 (see Table S1 in the supplemental material). Plasmid pCSV1, carrying *SEN1001* cloned into pNFB9 in the same orientation as that of *P<sub>lac</sub>*, and plasmid pNFB9 were used to transform the *S. Enteritidis* P125109  $\Delta$ *SEN1001* mutant in complementation assays. The chromosomal insertion of pNFB9 derivatives was confirmed by PCR amplification using primers LepA\_F and LepA\_R (see Table S1 in the supplemental material), flanking the *attG1* site.

**Cell culture and intracellular survival assay *in vitro*.** RAW264.7 macrophages were grown in Dulbecco's modified Eagle medium (DMEM) supplemented with 10% fetal bovine serum (FBS). Monolayers for infection were prepared by seeding  $\sim 10^5$  cells into each well of a 48-well multiwell plate and incubating the cells for 20 h at 37°C in the presence of 5% CO<sub>2</sub>. Bacteria were grown overnight in LB medium at 37°C under static conditions, washed with PBS, suspended in DMEM-FBS (100  $\mu$ l), mixed, and added to RAW264.7 macrophages at a multiplicity of infection of  $\sim 50:1$ . After 45 min of incubation at 37°C, the macrophages were washed three times with PBS and incubated for 2 h or 20 h in DMEM-FBS containing gentamicin (50  $\mu$ g/ml) to kill extracellular bacteria. Cells were washed three times with PBS and lysed with 0.5% deoxycholate in PBS. Numbers of intracellular CFU were determined by serial dilution and plating. At each time point, the number of viable RAW264.7 cells was assessed by 0.4% trypan blue exclusion and counting. Each experiment was performed on two separate occasions, evaluating samples at least in duplicate. Statistical significance was determined by using the one-way analysis of variance (ANOVA) test and the Dunnett's posttest.

## RESULTS AND DISCUSSION

**Identification of genes with a role in *S. Enteritidis* pathogenesis in BALB/c mice by negative selection.** The aim of our study was to identify *S. Enteritidis* genes that are important for the establishment of a systemic infection in mice. The sequenced *S. Enteritidis* PT4 strain P125109 (77) colonizes the gastrointestinal tract of streptomycin-pretreated mice when administered orally (76). To evaluate whether this strain is able to colonize systemically during an acute infection of BALB/c mice when administered i.p., 3 mice were inoculated with  $\sim 4.4 \times 10^6$  CFU of *S. Enteritidis* P125109. The mice were euthanized 48 h after the inoculation, and the spleen and liver were aseptically removed. The infected organs looked normal in shape and color, but an enlargement of the infected spleens (splenomegaly) was evident, compared to the organs recovered from a control mouse inoculated with sterile PBS. A small but considerable enlargement of the infected livers was also observed. Bacteria colonizing the spleen and liver of each animal were counted. The number of CFU recovered from spleen ranged from  $3.8 \times 10^6$  to  $4.2 \times 10^6$ , while the number of CFU recovered from liver ranged from  $2.2 \times 10^6$  to  $6.9 \times 10^7$  (see Fig. S1A in the supplemental material).

Next, a library of transposon mutants was generated in *S. Enteritidis* P125109 using a mini-Tn5 derivative. Approximately 54,000 independent colonies were obtained, representing an average of more than 1 insertion per 100 bases. A group of 6 BALB/c mice was injected i.p. with  $\sim 4.2 \times 10^6$  CFU of the transposon library. After 48 h, bacteria were recovered from the spleens and livers of infected mice. The number of CFU recovered from spleen ranged from  $2.0 \times 10^6$  to  $6.6 \times 10^6$ , while the number of CFU recovered from liver ranged from  $2.2 \times 10^6$  to  $6.9 \times 10^7$  (see Fig. S1B in the supplemental material). Mutants carrying insertions in

genes contributing to fitness for the colonization of mice, underrepresented in the population recovered from infection, were identified by means of an array-based strategy similar to ABACUS (72), using a microarray designed for the study of several *Salmonella* serovars which includes *S. Enteritidis*-specific genes (65).

Data for all the genes on the arrays are presented in Table S2 in the supplemental material and are schematized in Fig. 1. Overall, there is an excellent correlation between data from spleen samples and data from liver samples (see Table S2 and Fig. S2 in the supplemental material), indicating that any genes differentially required for the colonization of liver or spleen by *S. Enteritidis* cannot be detected by this assay. The same observation was reported previously for *S. Typhimurium* (56). Of the 4,505 "spots" analyzed, representing 4,288 genes of *S. Enteritidis* (4,231 chromosomal genes and 57 genes carried on the virulence plasmid), 3,700 entries (3,521 genes) with a sufficient signal intensity to be detected were identified. As expected, mutants in genes considered essential for bacterial viability were not detected, since this class of genes does not tolerate insertion mutations. For example, mutants in all 26 genes of the essential ribosomal protein cluster, *SEN3244* to *SEN3269*, remained undetected in the control sample (see Table S2 in the supplemental material). Of the 3,521 genes detected, 306 had a statistically significant log<sub>2</sub>-fold attenuation score (*M*) in both organs (*M*  $\leq -0.75$  and *P*  $\leq 0.001$ ). The list includes 21 genes absent in the genome of *S. Typhimurium* (see Table S3 in the supplemental material). Thus, they were considered candidate genes for unique aspects of *S. Enteritidis* colonization of BALB/c mice by the intraperitoneal route.

**Identification of genes with a role in *S. Enteritidis* pathogenicity that are shared with other *Salmonella* serovars.** Analysis of the data in Table S2 in the supplemental material revealed that the most dramatic phenotypes were observed for mutations of genes carried on *Salmonella* pathogenicity island 2 (SPI-2). These results agree with those obtained previously by using *S. Typhimurium* in similar infection-based (22, 24, 56, 72) and *in vitro* (22) studies, consistent with the importance of SPI-2 for the growth within macrophages (26, 47), persistence (56), and pathogenicity (74) of *Salmonella*.

Mutants lacking the structural genes of the type III secretion system (T3SS) carried on SPI-1, its transcriptional regulators, and secreted effectors were underrepresented in our output libraries. This result agrees with earlier work with *S. Typhimurium* by Lawley et al. indicating that SPI-1 genes are needed for the colonization of the spleen and liver (56). Even though these results seem to challenge the original model that SPI-1 is needed for the gastrointestinal phase of salmonellosis but not the systemic phase (2, 36, 46, 81), it is conceivable that *Salmonella* may rapidly occupy additional niches in the mouse (such as the gut) after intraperitoneal infection, and bacteria in these niches may subsequently contribute to the population seen in internal organs. Therefore, mutants in genes that have a role in gastrointestinal infection may be underrepresented in the bacterial population harvested subsequently from spleen and liver (72).

Mutations of the magnesium transport-related genes *mgtB* and *mgtC* within SPI-3 were also negatively selected. The *mgtC* gene is required for growth in low Mg<sup>2+</sup> and for the survival in of *S. Typhi* in macrophages (69) as well as for the survival of *S. Typhi* in macrophages and pathogenicity in mice (12). In contrast, *mgtB* is dispensable for pathogenicity in BALB/c mice (12). *mgtB* is located downstream of *mgtC* in a single transcriptional unit, making

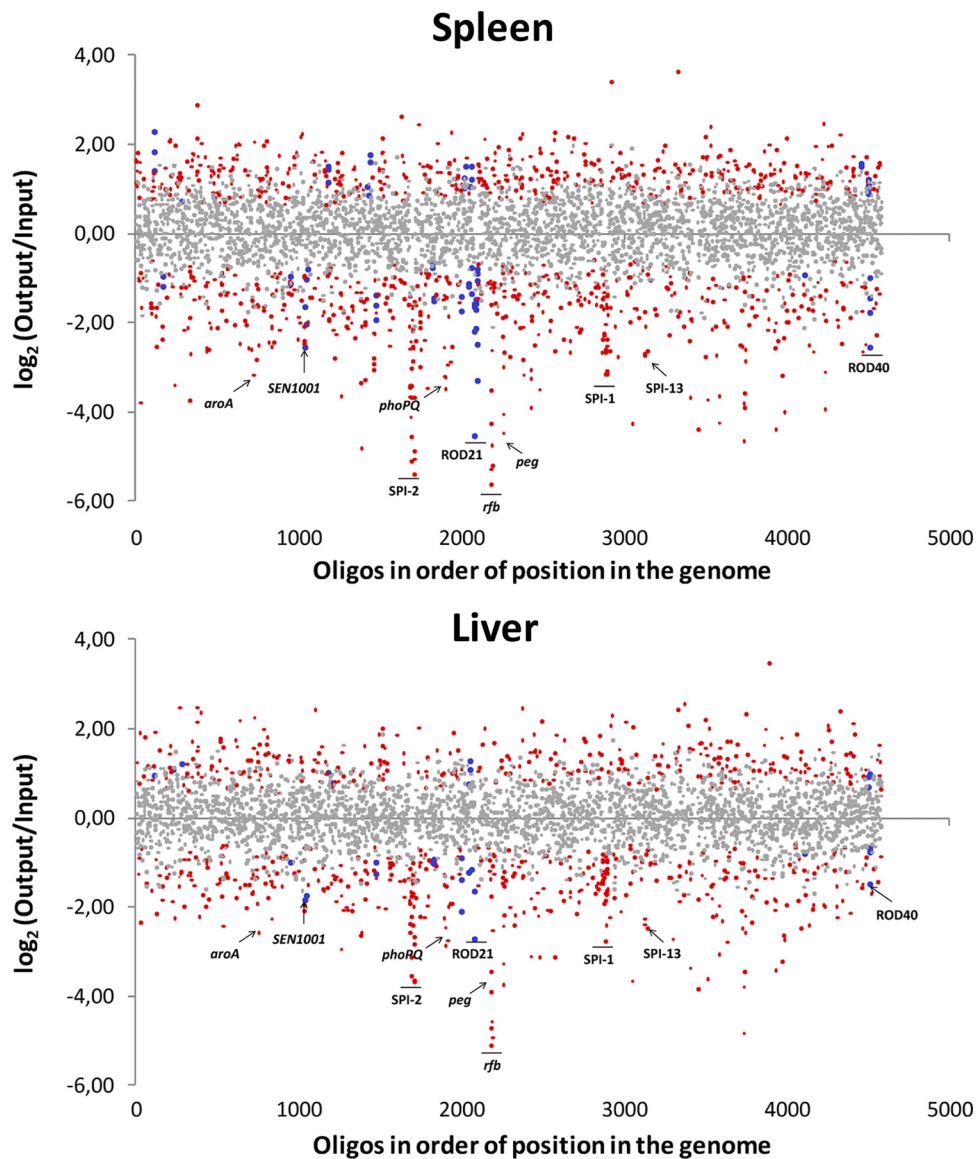


FIG 1 Loss of mutants after *in vivo* selection by i.p. injection into BALB/c mice and recovery from spleen and liver at 48 h postinfection. Six array hybridizations per organ were performed for a total of six mice. Data with  $P$  values of  $<0.001$  (see Materials and Methods) are depicted in red, and those with  $P$  values of  $>0.001$  are depicted in gray. Data from *S. Enteritidis*-specific genes with  $P$  values of  $<0.001$  are depicted in blue. The x axis plots the data for each of the probes in the array according to the position of the corresponding gene in the genome of *S. Enteritidis* strain P125109.

it likely that our transposon insertion in *mgtC* has a polar effect on *mgtB*.

Mutations of genes encoding a giant nonfimbrial adhesin and the cognate type I secretion system located on SPI-4 (37, 80) were underrepresented in our output libraries. Genes on SPI-4 are needed for the intestinal phase of disease (58) and were associated with the systemic infection of mice by *S. Typhimurium* and *S. Enteritidis* when bacteria were administered orally (54).

Three genes located on SPI-5, *pipB*, *pipC* and *sopB*, were also negatively selected in our screen. Genes of SPI-5 contribute to enteric but not to systemic infection by *S. Dublin* (81). However, this pathogenicity island was described previously to be coregulated with either SPI-1 or SPI-2 genes; thus, it may perform a dual function during infection (55). In fact, PipB is an effector protein translocated by the SPI-2 T3SS, whereas SopB is an effector pro-

tein translocated by the SPI-1 T3SS, and PipC is a putative chaperone assisting SopB secretion (55, 67, 81). Hence, it was not surprising to find these genes after negative selection.

Two recent studies evaluated the role of the five major SPIs in the pathogenicity of *S. Enteritidis* strain 147. One study indicated that bacterial pathogenicity in BALB/c mice was dependent exclusively on the presence of an intact SPI-2 (53), while the other study found that the colonization of chickens' liver and spleen was dependent on the presence of either SPI-1 or SPI-2. The absence of SPI-3, SPI-4, or SPI-5 individually did not influence the pathogenicity of *S. Enteritidis* for chicken, but the absence of the three islands collectively contributed to the colonization of the spleen (70). Our sensitive screen for the relative fitness of mutants in the presence of wild-type bacteria indicates that, in addition to genes in SPI-1 and SPI-2, some genes in SPI-3, SPI-4, and SPI-5 contrib-

ute to the systemic colonization of mice. Thus, infections in mice and chickens may be different with respect to the need for these three SPIs.

Mutations in groups of genes belonging to other pathogenicity islands were also detected in our screen. The *S. Enteritidis* genes *SEN2961* to *SEN2164* within SPI-13 and the genes *SEN0801* to *SEN0804* within SPI-14 were needed for full colonizing abilities. Phenotypes for mutations in genes within SPI-13 and SPI-14 during the systemic infection of mice by *S. Typhimurium* were also reported previously (22, 43, 72). In addition, both SPI-13 and SPI-14 were identified as being required for *S. Gallinarum* pathogenicity in a chicken infection model (73). Finally, the genes *SEN0535* and *SEN0536* within SPI-16 also were negatively selected during *S. Enteritidis* infection of mice. We have shown previously that the orthologous genes in *S. Typhimurium* are responsible for the “form variation” of the O12 antigen to generate the 12-2 variant that is critical for the persistence of this serovar in the murine intestine (15).

In addition to the genes belonging to highly conserved SPIs, other well-established pathogenicity-related genes that were negatively selected in our screen included (i) the aromatic amino acid biosynthesis genes *aroE*, *aroD*, *aroB*, and *aroP* and the purine biosynthesis genes *purF*, *purD*, *purB*, *purR*, and *purA*, which were previously identified by Chaudhuri et al. as being needed for the systemic infection of mice by *S. Typhimurium* (24), in accordance with previous reports showing that auxotrophic mutations of these genes lead to a reduced pathogenicity of *S. Typhi*, *S. Typhimurium*, and *S. Enteritidis* (11, 31, 62); (ii) the anaerobic metabolism genes *narH* and *narI* and the oxidative phosphorylation genes *cyoC*, *cyoE*, and *nuo*, which have been shown to contribute to the pathogenicity of *S. Typhimurium*, *S. Dublin*, and *S. Gallinarum* (78); (iii) the lipopolysaccharide (LPS) biosynthesis genes *rfaB*, *rfaG*, *rfaI*, *rfaJ*, *rfaL*, *rfaF*, *rfaH*, *rfaI*, *rfaK*, and *rfaC*, supporting data from previous reports that established an important role of LPS in the invasion of epithelial cells by *S. Typhi* and *S. Typhimurium* (50) and in the colonization of the intestine of mice by *S. Typhimurium* (29, 51, 60) and of chicken by *S. Enteritidis* (23) and a role for LPS in *S. Enteritidis* adherence to and survival in eggs (39, 40); and (iv) the membrane stability genes *tolA* and *tolB* and the transport system genes *sfbB* and *sfbC* (64), *SEN0715*, *SEN0716*, and *SEN1417* to *SEN1420*. TolC, a member of the AcrAB-TolC efflux system that was also negatively selected in our screening, was previously shown to be required for the infection of BALB/c mice by *S. Enteritidis* (75) and for the infection of poultry by *S. Typhimurium* (18).

Finally, mutants in genes involved in the regulation of responses to external stimuli, such as *phoP*, *phoQ*, *arcA*, *arcB*, *envZ*, *fimZ*, *rpoN*, *crp*, and *fur*, showed colonization deficiencies in our screen, consistent with their global importance in *Salmonella* pathogenicity (4, 34, 42, 56, 68, 79). In addition, we identified mutants in genes regulated by the PhoP/Q system (*pagO*, *pqaA*, and *pagD*). It is noteworthy that the *pagO* and *pagD* genes are dispensable for *S. Typhimurium* pathogenicity in mice (10, 41), and *pqaA* mutants of *S. Typhi* are fully virulent in the mouse mucin virulence assay (7), suggesting that transposon insertion mutants in these genes were identified in our screen due to polar effects on nearby virulence genes. Alternatively, *pagO*, *pqaA*, and *pagD* may play a specific role in *S. Enteritidis* pathogenicity in mice.

Some *S. Enteritidis*-specific regions were not sampled in our

study either because they were not represented in the array or because the corresponding probes produced weak hybridization signals. For example, the *yfg-env* locus was reported previously to be needed for chicken colonization by *S. Enteritidis* after oral inoculation, and a  $\Delta yfgL$  mutant was less motile than the wild type (3). More recently, it was shown that YfgL is necessary for the assembly and function of T3SSs, including flagella and those encoded in SPI-1 and SPI-2 (35). In addition, Chang et al. described a novel gene involved in the ability to survive or replicate inside the chicken host after subcutaneous delivery: *yhbC*. This gene encodes a hypothetical protein, and the  $\Delta yhbC$  mutant had a diminished ability to grow *in vitro* compared to the wild-type strain (23). We do not yet know the effect of mutations in these genes on mice.

**Identification of novel genes with a role in *S. Enteritidis* pathogenicity.** Thomson et al. described “regions of difference” (RODs) between the genomes of *Salmonella* serovars Enteritidis, Gallinarum, and Typhimurium (77). The regions reported as being specific to *Salmonella* serovar Enteritidis include ROD4 (*SEN0216*) and the prophages  $\phi$ SE14 (*SEN1378* to *SEN1398*) and  $\phi$ SE20 (*SEN1919A* to *SEN1966*).  $\phi$ SE14 includes the *S. Enteritidis*-specific locus *lyg*, identified previously by Agron and colleagues (1), and correspond to an unstable genetic element that is not required for the systemic colonization of BALB/c mice (71). However, in this study, we found that the genes *SEN1921* and *SEN1960* in  $\phi$ SE20 were needed for the colonization of BALB/c mice. These genes encode a putative tail fiber assembly protein and a conserved hypothetical protein called sb35, respectively.  $\phi$ SE20 carries fragments of the *sopE* and *orgA* genes previously implicated in *Salmonella* pathogenicity; however, these were not detected in our screening.

Mutations linked to other genes and genomic islands that have not been previously related to *S. Enteritidis* pathogenicity were identified as being negatively selected in this study (Table 2). These included *SEN1001* and *SEN1002*, carried on SPI-19 (13); a cluster of genes linked to tRNA-*asnT* in a putative pathogenicity island (*SEN1970* to *SEN1999*); the *peg* fimbrial operon (*SEN2144A* to *SEN2145B*); and components of a type I restriction-modification system (*SEN4290* to *SEN4292*).

*SEN1001* and *SEN1002* are remnant components of a type VI secretion system (T6SS) carried on SPI-19, a pathogenicity island recently described for *Salmonella* serovars Enteritidis, Gallinarum, Dublin, Agona, and Weltevreden (13). *SEN1002* encodes an Hcp-like protein that appears to be a structural and secreted component of these systems (59). *SEN1001* encodes a hypothetical protein of unknown function. The identification of these genes in our screening was unexpected, since *S. Enteritidis* does not encode all the components described as being essential for T6SS function. It is tempting to speculate that these genes have novel functions unlinked to the T6SS in *S. Enteritidis*. The T6SS of SPI-19 contributes to the colonization of the gastrointestinal tract and internal organs of chickens by *S. Gallinarum* (14).

The cluster of genes linked to tRNA-*asnT* (*SEN1970* to *SEN1999*), officially designated region of difference 21 (ROD21) (77), contains a putative integrase (*SEN1970*) and is flanked by direct repeats, properties common to genomic islands acquired by lateral gene transfer. This island includes *SEN1975*, encoding a Toll/interleukin-1 (IL-1) receptor (TIR) domain containing-protein called TlpA, described previously for *S. Enteritidis* strain LK5 (61). The secretion of proteins with TIR domains was shown previously to interfere with NF- $\kappa$ B induction, allowing the eva-



TABLE 2 New genes and genomic islands related to *S. Enteritidis* pathogenicity<sup>a</sup>

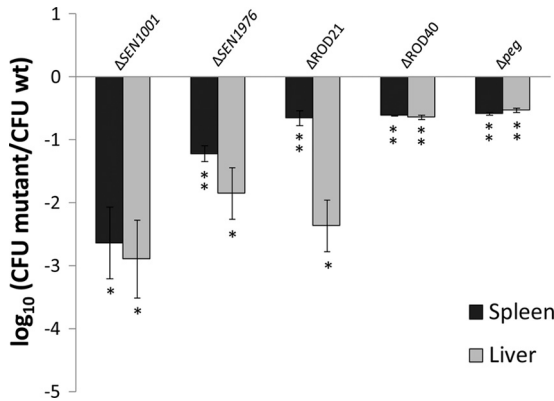
Locus tag	Gene	Island or gene cluster	Product	Spleen			Liver		
				<i>M</i>	<i>A</i>	<i>P</i>	<i>M</i>	<i>A</i>	<i>P</i>
<i>SEN1001</i>		SPI-19	Putative DNA-binding protein	-2.57	8.83	<b>3.18E-05</b>	-1.84	9.42	<b>2.75E-04</b>
<i>SEN1970</i>		ROD21	Phage integrase	0.68	11.83	1.29E-02	0.27	12.21	1.83E-01
<i>SEN1974</i>			Hypothetical protein	-0.07	7.62	8.72E-01	0.34	8.07	3.74E-01
<i>SEN1975</i>	<i>tlpA</i>		TIR-like protein A	-2.20	9.48	<b>2.49E-07</b>	-1.66	11.21	<b>4.11E-07</b>
<i>SEN1976</i>			Putative type IV prepilin protein (remnant)	-4.56	11.02	<b>1.05E-12</b>	-2.73	12.15	<b>7.14E-07</b>
<i>SEN1978</i>			Putative type IV pilin	-0.93	8.98	3.91E-02	-0.50	9.92	1.14E-01
				-1.26	8.72	4.05E-03	-0.72	9.83	1.10E-01
<i>SEN1980</i>			Possible conjugal transfer protein	-1.64	12.39	<b>5.53E-05</b>	-0.82	12.72	1.51E-02
				-1.60	11.20	<b>1.45E-04</b>	-0.74	11.46	2.08E-02
<i>SEN1981</i>			Hypothetical protein	-1.50	8.43	<b>9.55E-05</b>	-1.11	9.08	9.20E-03
<i>SEN1982</i>			Lipoprotein	-2.14	10.60	<b>5.60E-06</b>	-0.89	11.15	1.88E-02
				-1.50	10.41	<b>1.84E-05</b>	-0.22	10.85	5.55E-01
				-1.57	11.52	<b>3.07E-05</b>	-0.86	12.07	4.69E-03
<i>SEN1985</i>			Hypothetical protein	-0.68	7.45	1.68E-01	-0.66	7.63	7.44E-02
<i>SEN1986</i>			Conserved hypothetical protein	-1.72	12.42	<b>1.77E-06</b>	-0.25	13.29	3.27E-01
				-1.58	11.80	<b>1.15E-06</b>	-0.06	12.49	7.90E-01
<i>SEN1990</i>			Putative DNA-binding protein	-0.61	7.68	1.75E-01	-0.31	8.27	4.56E-01
<i>SEN1991</i>			Conserved hypothetical protein	-0.59	7.69	6.98E-02	-0.61	8.08	5.78E-02
<i>SEN1993</i>			Putative DNA-binding protein (histone-like protein Hlp-II)	-1.06	11.67	<b>6.37E-06</b>	-0.57	12.09	4.74E-03
				-0.92	12.24	<b>6.54E-05</b>	-0.27	12.88	1.69E-01
<i>SEN1994</i>			Putative membrane protein	-2.49	10.35	<b>1.15E-08</b>	-1.43	11.42	4.70E-03
<i>SEN1995</i>			Conserved hypothetical protein	-3.31	9.20	<b>2.06E-09</b>	0.28	10.59	6.39E-01
<i>SEN1999</i>			Conserved hypothetical protein	-0.81	12.77	<b>6.34E-04</b>	-0.30	12.57	2.46E-01
				-0.54	11.30	2.30E-02	-0.03	11.44	8.73E-01
<i>SEN2144A</i>	<i>pegD</i>	<i>peg</i> fimbrial operon	Putative exported protein	-1.91	12.93	<b>1.08E-08</b>	-1.34	13.01	<b>3.56E-06</b>
				-2.32	12.32	<b>1.40E-09</b>	-1.48	12.82	<b>2.19E-06</b>
<i>SEN2145</i>	<i>pegC</i>		Putative outer membrane usher protein	-0.90	13.93	<b>1.70E-05</b>	-0.12	14.28	6.27E-01
				-0.68	14.75	1.74E-02	-0.05	15.12	7.57E-01
				-0.72	13.83	<b>4.83E-04</b>	-0.12	14.13	4.30E-01
<i>SEN2145A</i>	<i>pegB</i>		Putative fimbrial chaperone protein	-4.48	10.47	<b>1.29E-10</b>	-3.75	11.22	<b>3.90E-10</b>
				-4.05	10.22	<b>9.07E-13</b>	-3.28	10.78	<b>1.08E-10</b>
				-3.00	9.64	<b>2.45E-08</b>	-2.43	10.31	<b>2.90E-09</b>
				-2.68	10.07	<b>1.37E-06</b>	-2.20	10.87	<b>5.93E-07</b>
<i>SEN2145B</i>	<i>pegA</i>		Putative fimbrial subunit protein	-1.03	10.16	6.25E-03	-0.95	10.63	8.07E-03
				-1.43	11.45	<b>7.79E-05</b>	-1.54	12.38	<b>4.70E-07</b>
				-1.29	11.50	<b>1.96E-05</b>	-1.22	11.86	<b>3.24E-07</b>
<i>SEN4290</i>		ROD40	Putative type I restriction-modification system methyltransferase	-2.57	10.63	<b>1.29E-08</b>	-1.50	11.86	<b>2.19E-06</b>
<i>SEN4291</i>			Putative type I restriction-modification system methyltransferase	-1.00	12.75	<b>2.61E-05</b>	-0.75	13.82	<b>1.73E-04</b>
<i>SEN4292</i>			Putative type I restriction enzyme	-1.48	14.77	<b>2.50E-06</b>	-0.67	15.62	<b>6.33E-04</b>
				-1.77	13.65	<b>5.01E-10</b>	-0.78	14.30	<b>4.46E-05</b>

<sup>a</sup> "M" corresponds to the log<sub>2</sub>-fold attenuation score ( $M = \log_2 \text{output} - \log_2 \text{input}$ ). *M* values of  $\leq -0.75$  are shaded. "A" corresponds to the average log<sub>2</sub>-fold signal intensity [ $A = (\log_2 \text{output} + \log_2 \text{input})/2$ ]. *A* values of  $\geq 9$  are in italic type. *P* values of  $\leq 0.001$  are highlighted in boldface type.

sion of immune defenses by the pathogen (27, 61). TlpA also induces caspase-1 activation, leading to IL-1 $\beta$  secretion and the induction of apoptosis in macrophages, and is needed for the systemic colonization of mice (61). Interestingly, ROD21 also harbors precursors and structural components of putative type IV pili (*SEN1976* to *SEN1978*), structures linked to motility, adherence, biofilm formation, and bacterial aggregation, and contributes to the invasion of the host cell (44). Our analysis identified these genes as being needed for the colonization of liver and spleen. Other regions of ROD21 identified in our screen include *SEN1980* to *SEN1982* and *SEN1993* to *SEN1995*, most encoding hypothetical proteins with an unknown function.

Fimbriae play a critical role in host cell adherence (33). According to our screen, two fimbrial operons, *peg* and *sef*, were needed for the full pathogenicity of *Salmonella* serovar Enteritidis in mice. It was previously demonstrated that SEF14 fimbriae are required to avoid uptake by macrophages after intraperitoneal infection of mice and are needed for *S. Enteritidis* survival in this model (32). Also, the importance of the *peg* fimbrial operon in the colonization of chicken ceca after oral administration was previously shown (28).

The genes *SEN4290* to *SEN4292* belong to the region annotated as ROD40 (77), which encodes a putative type I restriction-modification system, systems that protect bacteria from foreign



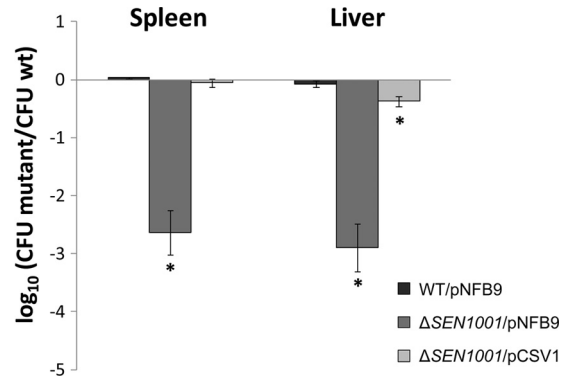
**FIG 2** Competition assays with individual mutants versus the wild-type (wt) strain and recovery from spleen and liver at 48 h postinfection. A total of  $10^6$  CFU of each selected mutant was administered at a 1:1 ratio with wild-type strain P125109 by the intraperitoneal route into 5 mice and recovered from spleen and liver at 2 days postinfection. CI values were calculated as a mean ratio of mutant to wild-type CFU, normalized to the input ratio and converted logarithmically. Error bars denote standard errors. Statistical significance was determined by using Student's 2-tailed *t* test, and asterisks indicate that normalized output ratios were significantly statistically different from the equivalent ratio in the inoculum (\*,  $P < 0.05$ ; \*\*,  $P < 0.001$ ).

DNA. The type I restriction-modification system consists of a protein complex with three different subunits responsible for the binding to, methylation of, and restriction of DNA (20, 66). Only one previous study conducted with *Yersinia pseudotuberculosis* linked a type I restriction-modification system with pathogenicity (66). However, the Dam system (type II restriction-modification system) was described previously to play an important role in *S. Typhimurium* pathogenicity through the epigenetic regulation of pathogenicity-related genes (48).

In conclusion, the microarray-based negative-selection screening developed in this study allowed the identification of novel *S. Enteritidis* genes playing an important role in the colonization of deep organs in a BALB/c mouse model. These genes have not been described for other serovars of the genus *Salmonella*.

**Validation of negatively selected mutants using competitive infection.** Targeted mutations in selected genes (*SEN1001* and *SEN1976*) and genomic islands (ROD21, ROD40, and the *peg* operon) of *S. Enteritidis* identified in our screen were constructed by the Red swap method (30, 72). Competition experiments using groups of BALB/c mice inoculated by the intraperitoneal route with a mixture of the wild-type strain and each mutant were performed. Forty-eight hours after infection, spleens and livers were obtained, and the numbers of wild-type and mutant bacteria were enumerated. Our results indicate that the  $\Delta$ *SEN1001*,  $\Delta$ *SEN1976*,  $\Delta$ ROD21,  $\Delta$ ROD40, and  $\Delta$ *peg* mutants were unable to colonize the internal organs of infected animals as efficiently as the wild-type organism (Fig. 2). These results confirm the predictions that we obtained from our microarray-based screen.

To test whether the colonization defect presented by the mutants was linked to an overall fitness defect in a nutrient-limited environment, bacterial growth in E minimal medium was assessed by using both individual cultures and *in vitro* competition assays with the wild-type strain. Growth curves of individual mutant strains were identical to that of the wild-type parental strain, with the only exception being the  $\Delta$ *SEN1001* mutant, which showed a slightly extended lag phase (data not shown). *In vitro* competition



**FIG 3** *SEN1001* is needed for successful *S. Enteritidis* colonization in mice. A complementation assay for a  $\Delta$ *SEN1001* mutant was performed. A total of  $10^6$  CFU of each strain was administered at a 1:1 ratio with wild-type strain P125109 by the intraperitoneal route into 5 mice and recovered from spleen and liver at 2 days postinfection. CI values were calculated as a mean ratio of mutant to wild-type CFU, normalized to the input ratio and converted logarithmically. Error bars denote standard errors. Statistical significance was determined by using Student's 2-tailed *t* test, and asterisks indicate normalized output ratios that were significantly statistically different from the equivalent ratio in the inoculum (\*,  $P < 0.05$ ).

experiments indicated that each mutant showed a slight but statistically significant defect compared to the parental strain when grown in minimal media (data not shown). However, this effect was tens to hundreds of times less than the defect observed *in vivo*. These results indicate that the observed large colonization defect presented by the mutants is not attributable to a strong defect in growth in a nutrient-limited environment.

***SEN1001* encodes a LysM domain-containing protein needed for systemic infection by *S. Enteritidis*.** *S. Enteritidis* harbors a truncated version of SPI-19 that includes an internal deletion compared with the same genomic region in *Salmonella* serovars Gallinarum, Dublin, Agona, and Weltevreden (13). *SEN1001* is one of the genes that remained in the *S. Enteritidis* chromosome after the deletion of most components of the T6SS.

To directly link the defect in systemic infection to the mutation in *SEN1001*, we complemented our  $\Delta$ *SEN1001* mutant and tested the colonization of the complemented strain during competitive systemic infections. An intact copy of *SEN1001* was cloned into pNFB9, and the resultant plasmid (pCSV1) was moved into  $\Delta$ *SEN1001*. Since pNFB9 derivatives can integrate at the Gifsy-1 attachment site (*attG1*) (49), a single copy of the complementing gene was restored in the *S. Enteritidis* chromosome. The complemented mutant ( $\Delta$ *SEN1001*/pCSV1) regained the ability to colonize systemic sites. In contrast, the mutant containing the empty vector ( $\Delta$ *SEN1001*/pNFB9) maintained a colonization defect during infection (Fig. 3). The wild-type strain and a derivative harboring an empty pNFB9 vector (WT/pNFB9) displayed similar levels of colonization during competitive systemic infections of mice (Fig. 3), indicating that the presence of the plasmid alone does not interfere with *S. Enteritidis* pathogenesis in our assay.

To test whether the defect of our  $\Delta$ *SEN1001* mutant in systemic colonization may be linked to a defect in the intracellular survival within macrophages of the host, the wild-type strain (WT/pNFB9) and the  $\Delta$ *SEN1001*/pNFB9 and  $\Delta$ *SEN1001*/pCSV1 derivatives were compared for internalization by and survival in RAW264.7 murine macrophages. In these assays, the  $\Delta$ *SEN1001*/



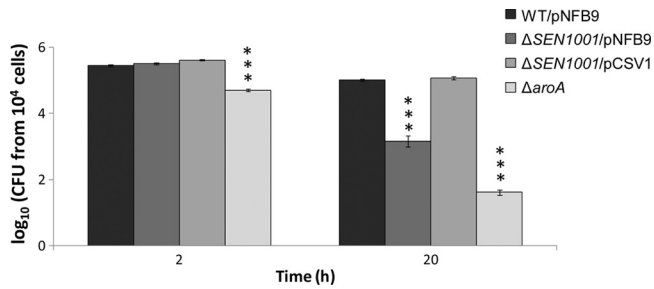


FIG 4 *SEN1001* is needed for intracellular survival of *S. Enteritidis* within macrophages of the host. Shown are data for intracellular CFU recovered from RAW264.7 macrophages. Each experiment was performed on two separate occasions, evaluating samples at least in duplicate. CFU values were normalized to  $10^4$  viable cells and converted logarithmically. Bars represent mean values, and error bars denote standard errors. The statistical significance of differences in the data was determined by using one-way ANOVA and the Dunnett's posttest. Asterisks indicate CFU values that are significantly different from that of the wild-type strain (\*\*\*,  $P < 0.0001$ ).

pNFB9 mutant was defective in intracellular survival after 20 h of infection compared to the wild-type strain. In contrast, the complemented  $\Delta SEN1001/pCSV1$  mutant survived as well as the wild-type strain within RAW264.7 macrophages (Fig. 4). As expected, a control  $\Delta aroA$  mutant included in our assays was impaired for intramacrophage survival from early time points (Fig. 4).

For a better understanding of the observed phenotypes, bioinformatic analyses were performed to identify conserved domains and similarities with other proteins present in related species. According to our analyses, *SEN1001* includes a lysin motif (LysM) domain (E value = 0.00032) that is thought to bind to peptidoglycan. The LysM domain is 40 to 44 residues long and is found in a variety of enzymes involved in bacterial cell wall degradation (52), similar to those in peptidoglycan hydrolases (19). However, our  $\Delta SEN1001$  mutant did not show growth deficiencies, impaired segregation, or membrane stress when cultured in LB medium under standard conditions or in the presence of SDS, EDTA, hydrogen peroxide, or deoxycholate (data not shown). Also, the LysM domain has been found in several proteins considered to be virulence factors, such as intimin from pathogenic *E. coli* (9) and Slt70 from *Shigella flexneri* (8), among others.

The LysM domain-containing protein *SEN1001* is required for *S. Enteritidis* pathogenicity in BALB/c mice, and its function enhances survival within macrophages. Thus, positive selection *in vivo* may explain why *SEN1001* was retained in the genome of *S. Enteritidis* during the degradation of SPI-19 in this serovar. Finally, *SEN1001* is a potential new target for the development of live-attenuated vaccines.

**Conclusions.** We performed a microarray-based negative-selection screen for *S. Enteritidis* mutants showing deficiencies in the colonization of spleen and liver in mice. *S. Enteritidis* PT4 strain P125109 was mutagenized using the mini-Tn5 derivative EZ-Tn5 <T7/KAN-2> to generate a transposon library of ~54,000 mutants to monitor changes in the library composition after selection during infection using microarrays.

Mutations in genes known to contribute to systemic (e.g., SPI-2, *aro*, *rfa*, *rfb*, *phoP*, and *phoQ*) and enteric (e.g., SPI-1 and SPI-5) infections were associated with colonization defects in our assay. The most dramatic phenotypes were observed for mutations in genes required for systemic infection. In addition, coloni-

zation defects were observed for mutations in genes and genomic islands restricted to *S. Enteritidis* or to a limited number of *Salmonella* serovars. These include genes encoding components of a putative type VI secretion system (*SEN1001*), a type I restriction-modification system (*SEN4290* to *SEN4292*), the *peg* fimbrial operon (*SEN2144A* to *SEN2145B*), and a cluster of genes linked to tRNA-*asnT*, forming a putative pathogenicity island (*SEN1970* to *SEN1999*). Conversely, one would also expect a similar or larger number of genes that are present in *S. Typhimurium* and absent in *S. Enteritidis* to have a known virulence phenotype in the better-studied *S. Typhimurium*. Surprisingly, there are few such genes, with possible candidates including *STM0274A*, *STM2599*, and *STM2231*. Thus, not only do these two serovars differ in the details of how they infect mice, but *S. Enteritidis* might also have a greater number of serovar-specific virulence genes.

Mutants with deletions of individual genes or entire regions presenting novel phenotypes in our screen were generated for confirmation in competition assays with wild-type strain P125109. Targeted mutants with deletions of the genes *SEN1001* and *SEN1976* and the gene clusters *SEN1976* to *SEN1999* (ROD21), *SEN2144A* to *SEN2145B* (*peg* operon), and *SEN4290* to *SEN4292* (ROD40) reiterated the phenotype observed in our microarray-based screening. Furthermore, a  $\Delta SEN1001$  mutant was impaired for intracellular survival within RAW264.7 murine macrophages *in vitro*. The phenotypes observed *in vivo* and *in vitro* for this particular mutant could be restored by the complementation of the gene using a plasmid that integrates into the chromosome of *S. Enteritidis*. With this, *SEN1001* is required for the full pathogenicity of *S. Enteritidis* in BALB/c mice and could be a new target for the development of vaccines. Further experiments to test its use as a live, attenuated vaccine are in progress in our laboratory.

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