

3. CONCLUSIONES

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Las principales conclusiones que se pueden extraer de los resultados obtenidos en el presente trabajo son las siguientes:

1. La virulencia de *S. typhimurium* no aumenta con el incremento de la tasa de mutagénesis espontánea producida por la inactivación del gen *mutS*.
2. La introducción en *S. typhimurium* de un plásmido portador de los genes *umuDC* de *E. coli*, responsables de la reparación tendente al error, no provoca un aumento de su virulencia.
3. El nivel de lesiones en el DNA que se produce a lo largo del proceso infeccioso en las células de *S. typhimurium* no es suficiente para activar completamente el sistema de reparación de emergencia o SOS.
4. Los mutantes *fur* poseen una menor concentración intracelular de cAMP que origina un descenso en la expresión de los genes controlados por dicho nucleótido.
5. La baja concentración intracelular de cAMP de los mutantes *fur* es atribuible a la presencia en éstos de una mayor cantidad de Fe^{2+} libre que incrementa la actividad de la enzima 3',5'-fosfodiesterasa codificada por el gen *cpdA*.
6. El promotor *flhDC*, además de estar regulado por el complejo CRP-cAMP, se encuentra bajo el control directo de la proteína Fur.
7. Los mutantes Fur^- de *S. typhimurium* presentan un descenso de un orden de magnitud en su virulencia cuando son inoculados intraperitonealmente. Esta disminución es atribuible a la menor expresión del gen *fliZ* y por sus bajos niveles de cAMP.

8. La expresión del gen *fljB*, que codifica una de las dos flagelinas alternativas de *S. typhimurium*, no está regulada por el complejo CRP-cAMP ni por la proteína Fur.
9. La inactivación del gen *zur*, cuyo producto regula los sistemas de transporte de zinc, solo origina un descenso de un orden de magnitud en la virulencia de *S. typhimurium* cuando se inocula intraperitonealmente.
10. La virulencia de *S. typhimurium* sufre una disminución de aproximadamente tres ordenes de magnitud cuando se mutageniza el gen *znuC*, responsable del transporte de alta afinidad de zinc.

4.BIBLIOGRAFÍA

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5. ANEXOS

ANEXO I

Virulence and mutation rates of *Salmonella typhimurium* strains with increased mutagenic strength in a mouse model

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Abstract

Two strains of *Salmonella typhimurium* presenting increased mutation rates, either spontaneous or mediated by DNA damage, have been constructed. One of the strains carries a null *mutS* mutation, while the other harbors plasmid pRW30, which contains the *Escherichia coli umuDC* operon. The virulence of these strains has been determined by inoculating BALB/c or Swiss mice. The 50% lethal dose of both strains is identical to that obtained for the wild-type. Likewise, the two strains and the wild-type contribute equally to animal death in mixed infections. The frequency of Nal^{R} mutants recovered from animals inoculated with either wild-type or MutS^- cells was not affected by the presence of pRW30. These results indicate that the DNA damage which *S. typhimurium* cells can suffer during the infectious process by host cell metabolites does not cause induction of the SOS response at levels able to trigger the error-prone DNA repair pathway. © 2000 Federation of European Microbiological Societies. Published by Elsevier Science B.V. All rights reserved.

Keywords: *Salmonella typhimurium*; *mutS* gene; Virulence; SOS mutagenesis

1. Introduction

Pathogenic bacteria rely on genetic variability to adapt to the changing environmental conditions found during infection, as well as to facilitate the evasion of host defenses. One source of genetic variation is mutation, either spontaneous or induced [1], and the importance of this factor has been shown in *Neisseria meningitidis* and *Haemophilus influenzae* [2]. In other pathogenic bacteria, data about the importance of mutagenic strength during infection remain inconclusive and based on indirect evidence. Thus, it has been reported that in isolates of commensal and pathogenic *Escherichia coli* and *Salmonella enterica* strains there is a higher percentage of mutator mutants than that found randomly in laboratory strain cultures [3,4]. These mutator strains present a higher spontaneous mutation rate because they are defective in either the *mutS* or the *mutL* genes belonging to the mismatch repair system which is responsible for removing misincorporations produced during DNA replication [5]. A role in the adap-

tational ability to environmental conditions and, as a consequence, a higher fitness in comparison with wild-type cells has been proposed for these mutator clones [1,3–5].

Another way to increase bacterial mutation rates is to activate the SOS repair system. When chromosomal replication is inhibited in bacterial cells as a consequence of DNA damage, a coordinated set of functions (known as the SOS response) is displayed to repair lesions and to increase cell survival. This system is positively regulated by the RecA protease and negatively controlled by the LexA repressor [6]. Among the genes belonging to the SOS network is the *umuDC* operon encoding the DNA polymerase V which, together with RecA and a modified form of the DNA polymerase III holoenzyme, is required for translesion synthesis to give rise to the SOS-dependent mutagenesis [7].

The presence of different *umuDC*-like genes in virulence plasmids has been reported in several pathogenic bacteria [8]. In some cases (*Shigella flexneri*) the DNA damage-mediated mutagenesis is due to these plasmid-encoded genes [8], whereas in others (*S. typhimurium*) it is *umuDC*-dependent [9]. Nevertheless, and unlike what happens in *E. coli*, *S. typhimurium* presents a very low level of both spontaneous and DNA damage-mediated mutagenesis because of several substitutions present in residues 26–

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59 of its UmuC protein [10]. However, a selective advantage for cells presenting a higher DNA damage-mediated mutagenesis as a consequence of the presence of either very active *umuDC* or related genes has been suggested [8].

Furthermore, little is known about the dynamics of spontaneous mutant appearance during the bacterial infectious process in vivo as well as the role which DNA repair genes play in this process. In this respect, *S. typhimurium* is an appropriate organism in which to study this aspect because of its decreased mutagenic ability, which may be easily increased by introducing *E. coli umuDC* genes.

For these reasons, we have studied the virulence and competitiveness of *S. typhimurium* in the murine model under two situations that increase mutagenic rates: inactivation of mismatch repair and introduction of *E. coli umuDC* genes. Likewise, the frequency of mutant recovery from infected animals in these conditions has also been determined.

2. Materials and methods

2.1. Bacterial strains and growth conditions

The bacterial strains, plasmids, phages and primers used in this study are listed in Table 1. *E. coli* and *S. typhimurium* strains were grown in LB broth [11]. Antibiotics were

added to the culture media at the concentrations previously reported [11].

2.2. Genetic and biochemical methods, and DNA techniques

Triparental matings using pRK2013 as the mobilizing plasmid were as previously reported [11]. *S. typhimurium* chromosome exchange markers, P22 HT-mediated transductions and plasmid electroporation were performed as described [11]. In all cases, absence of the P22 HT prophage in the transductants obtained was determined by streaking them in green plates. UV-mediated mutagenesis experiments were carried out as previously described [12]. All DNA methodology used was as published [11].

2.3. Animal studies

To determine the 50% lethal dose (LD₅₀), groups of four Swiss or BALB/c 6–8-week-old female mice were inoculated intraperitoneally with serial dilutions of the *S. typhimurium* desired strain. Mortality was recorded at 28 days post infection, and the LD₅₀ value was calculated by the method of Reed and Muench [13] without statistically significant differences in obtained values for each strain. For the competitive experiments, animals were inoculated with either 2×10^3 or 2×10^4 cfu depending on whether they were BALB/c or Swiss, respectively.

Table 1
Bacterial strains, plasmids and oligonucleotide primers used in this work

| | Relevant features | Source or reference |
|---|---|-----------------------|
| Organism | | |
| <i>E. coli</i> | | |
| DH5 α | <i>supE4</i> , Δ <i>lacU169</i> (ϕ 80 <i>lacZ</i> Δ M15), <i>hasdR17</i> , <i>recA1</i> , <i>endA1</i> , <i>gyrA 96</i> , <i>thi-1</i> , <i>relA1</i> | This laboratory |
| MC1061 (<i>λpir</i>) | <i>lacY1 hsdR</i> , lysogenized with <i>λpir</i> bacteriophage | This laboratory |
| <i>S. typhimurium</i> | | |
| ATCC 14028 | Wild-type strain | SLSA ^a |
| UA1770 | As ATCC 14028, but Rif ^R | This work |
| UA1771 | As UA1770, but <i>mutS</i> ::Gm | This work |
| UA1772 | As ATCC 14028, but carrying the pRW30 plasmid | This work |
| UA1773 | As ATCC 140128, but <i>mutS</i> ::Gm | This work |
| UA1774 | As UA1773, but carrying the pRW30 plasmid | This work |
| Plasmid | | |
| pRK2013 | Tra ⁺ of RK2, ColE1 replicon, Km ^R | D.R. Helinski |
| pGEM-T | Amp ^R | Stratagene |
| pGP704 | Amp ^R . Ori R6K Mob RP4 | [21] |
| pRW30 | pBR322 derivative containing the <i>E. coli umuDC</i> genes. Amp ^R | R. Woodgate |
| pUA873 | As pGEM-T, but carrying the <i>S. typhimurium</i> ATC 14028 <i>mutS</i> gene. Amp ^R | This work |
| pUA874 | As pUA873, but containing a 3.2-kb Gm-resistant cassette inserted into the internal <i>Sac</i> II point of the <i>S. typhimurium</i> ATC 14028 <i>mutS</i> gene. Amp ^R Gm ^R | This work |
| pUA875 | As pGP704, but carrying the <i>mutS</i> ::Gm construction | This work |
| Primer | | |
| | Sequence | Position ^b |
| MutS1 | 5'-GGATCCCTGTTACAGGAGCGTCAGG-3' | +374 |
| MutS2 | 5'-GGATCCGGAATAATGTAGCGTTCGGC-3' | +1509 |

^aSLSA, Servei de Laboratoris de Sanitat Agrària de la Generalitat de Catalunya.

^bPosition of the 5'-end of the oligonucleotide with respect to the translational starting point of the *S. typhimurium mutS* gene. Added restriction sites are shown in italics.

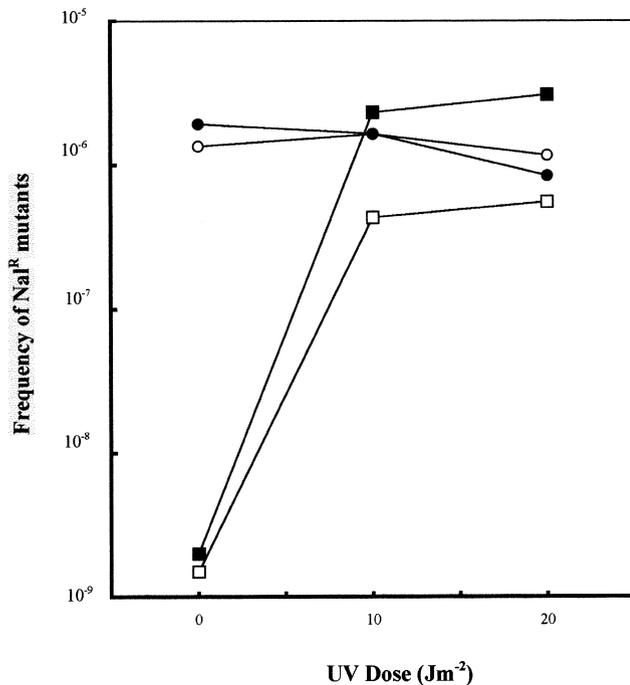


Fig. 1. UV-induced mutagenesis of *S. typhimurium* ATCC 14028 (□), *S. typhimurium* ATCC 14028 (pRW30) (■), *S. typhimurium* ATCC 14028 MutS⁻ (○) and *S. typhimurium* ATCC 14028 MutS⁻ (pRW30) (●) strains. For each dose of UV radiation the frequency of Nal^R mutants is the number of Nal^R clones divided by the number of survivors obtained. The values given are the mean of three independent experiments and they were reproducible to within an error of $\pm 10\%$. Three plates were used for each point.

Segregational stability of plasmids was monitored by replica plating of the cells recovered from each dead animal. For mixed infections, each strain was grown separately and mixed in an approximately 1:1 ratio before injection. The concentration of both strains was checked by plating serial dilutions of the bacterial suspensions onto LB medium before mixing. Samples of blood were recovered by heart puncture immediately after the death of the mouse (generally 7 days after inoculation), and the concentration of bacterial cells was determined by plating a dilution series in the appropriate medium. The number of Nal^R mutants in infected animals was determined by directly plating the blood sample recovered in LB medium supplemented with nalidixic acid ($50 \mu\text{g ml}^{-1}$). For each

strain, the frequency of mutagenesis was calculated by dividing the concentration of Nal^R clones by that of total cells recovered from each blood sample. In strains containing antibiotic resistance because of the presence of either the *mutS* mutation or the pRW30 plasmid, or both, the concentration of Nal^R and total cells was determined by plating in LB medium supplemented with the appropriate antibiotics. Mutagenesis experiments were only carried out in Swiss animals because of the low concentration of bacterial cells recovered from BALB/c [14], which is lower than the value of the mutation rate obtained for *S. typhimurium* ATCC 14028 wild-type strain under laboratory conditions.

3. Results and discussion

3.1. Construction of *S. typhimurium* ATCC 14028 derivatives with increased mutagenic rates

To construct a *mutS* null mutant of the ATCC 14028 virulent strain of *S. typhimurium*, an internal fragment of its *mutS* gene was amplified using oligonucleotide primers MutS1 and MutS2 (Table 1) corresponding to nucleotides 374–393 and 1509–1489 (with respect to its translational starting point) of the reported sequence of the *S. typhimurium* LT2 *mutS* gene. The 1.1-kb PCR fragment obtained with these primers was cloned in the pGEM-T vector, and to confirm that no mutation was introduced into the amplification reaction, its sequence was determined. Afterwards, a 3.2-kb gentamicin-resistant cassette was inserted into the internal *SacII* of the *S. typhimurium* ATCC 14028 *mutS* gene. This 4.3-kb fragment containing the *mutS*::Gm construction was then cloned in the pGP704 suicide vector and introduced by triparental mating in a Rif^R derivative of the *S. typhimurium* ATCC 14028 wild-type strain. Gentamicin-resistant transconjugants were screened for loss of vector-mediated ampicillin resistance to detect putative mutants which had exchanged their wild-type gene for the inactivated *mutS* as a consequence of a double cross-over event. For one of these strains (UA1771), this was unequivocally confirmed by PCR amplification of chromosomal DNA using MutS1 and MutS2 primers (data not shown).

It has been described that most rifampicin-resistant mu-

Table 2

LD₅₀ of *S. typhimurium* ATCC 14028, *S. typhimurium* ATCC 14028 (pRW30), *S. typhimurium* MutS⁻ and *S. typhimurium* MutS⁻ (pRW30) cells in BALB/c and Swiss mice^a

| Mouse strain | <i>S. typhimurium</i> strain | | | |
|--------------|------------------------------|--------------------|-------------------|---------------------------|
| | ATCC 14028 | ATCC 14028 (pRW30) | MutS ⁻ | MutS ⁻ (pRW30) |
| BALB/c | 9 | 13 | 21 | 16 |
| Swiss | 2×10^3 | 2.1×10^3 | 3.5×10^3 | 3.3×10^3 |

^aThe LD₅₀ was calculated as reported [12].

Table 3

Competition of *S. typhimurium* ATCC 14028 with either *S. typhimurium* ATCC 14028 (pRW30), *S. typhimurium* MutS⁻ or *S. typhimurium* MutS⁻ (pRW30) cells in BALB/c mice^a

| Strain inoculated | Percentage of strains recovered | | | | |
|--------------------------------------|---------------------------------|--------------------|-------------------|---------------------------|------|
| | ATCC 14028 | ATCC 14028 (pRW30) | MutS ⁻ | MutS ⁻ (pRW30) | |
| ATCC 14028+ATCC 14028 (pRW30) | 53 | 47 | – | – | 0.88 |
| ATCC 14028+MutS ⁻ | 54 | – | 46 | – | 0.85 |
| ATCC 14028+MutS ⁻ (pRW30) | 55 | – | – | 45 | 0.82 |

^aMice were inoculated intraperitoneally with a mixture of the indicated strains (1:1 proportion) and blood samples were taken as described in Section 2.

^bRatio of test strain to wild-type strain corrected for deviation observed in the corresponding inoculum ratio from a value of 1:1. Each competition experiment was performed on three separate occasions without statistically significant differences. Similar results were obtained when Swiss mice were used.

tants of *S. typhimurium* are avirulent in mice [15]. To prevent any putative interference of the Rif^R mutation in the behavior of our MutS⁻ mutant during the infectious process, the *mutS*::Gm region from the UA1771 strain was transferred by P22-mediated transduction to wild-type (Rif^S) cells of *S. typhimurium* ATCC 14028. The PCR profile of the chromosome of 10 Gm^R transductants, when amplified with MutS1 and MutS2 primers, revealed that all of them contained the desired *mutS*::Gm mutation. One of these transductants (UA1773) was kept out for further work.

In agreement with the PCR profiles, Fig. 1 shows how the *S. typhimurium* ATCC 14028 MutS⁻ mutant presents about a 1000-fold increase in the frequency of spontaneous Nal^R mutants over the wild-type strain. These values are in concordance with those obtained with transposon-induced MutS⁻ mutants of *S. typhimurium* [16].

After the *S. typhimurium* MutS⁻ mutant had been constructed, it was decided to further increase its mutagenic ability by transformation with plasmid pRW30, which encodes the *E. coli* wild-type *umuDC* operon. The presence of this plasmid does not increase the spontaneous mutation frequency in wild-type or in MutS⁻ cells (Fig. 1). As expected, the frequency of UV-mediated mutagenesis was about 10-fold higher in wild-type ATCC 14028 cells har-

boring pRW30. UV irradiation did not increase the mutation rates of MutS⁻ cells regardless of the presence of pRW30 (Fig. 1). This absence of UV mutagenesis in a MutS⁻ strain has recently been also reported for *E. coli* [17], but it is a novel observation in *S. typhimurium*. The reasons for this behavior are so far unknown.

3.2. Behavior of constructed *S. typhimurium* ATCC 14028 derivatives during animal infection

Table 2 presents the virulence of *S. typhimurium* wild-type, *S. typhimurium* (pRW30) and *S. typhimurium* MutS⁻ strains. Their LD₅₀ values are virtually identical, indicating that neither an increase of the spontaneous mutagenesis rate nor the DNA damage-mediated mutagenic ability significantly affects *S. typhimurium* virulence. It must be pointed out that pRW30 is stable in both MutS⁻ and wild-type cells during the infectious process, since more than 99% of colony-forming units recovered from dead animals were ampicillin-resistant. In agreement with these results, it has also been demonstrated that the virulence of *S. typhimurium* cells is not affected by the presence of a *mutL* mutation [18]. Likewise, it is known that *S. typhimurium mutS recD* double mutants show a general downshift in the purine metabolism interfering

Table 4

Mutation rate of *S. typhimurium* ATCC 14028, *S. typhimurium* ATCC 14028 (pRW30), *S. typhimurium* MutS⁻, and *S. typhimurium* MutS⁻ (pRW30) strains in Swiss mice^a

| Strain inoculated | Frequency of Nal ^R clones | Percentage of Nal ^R recovered, being | | | |
|--------------------------------------|--------------------------------------|---|-------------------|-------------------|---------------------------|
| | | Wild-type | Wild-type (pRW30) | MutS ⁻ | MutS ⁻ (pRW30) |
| ATCC 14028 | 1.4 × 10 ⁻⁹ | 100 | – | – | – |
| ATCC 14028 (pRW30) | 1.2 × 10 ⁻⁹ | – | 100 | – | – |
| MutS ⁻ | 5.3 × 10 ⁻⁶ | – | – | 100 | – |
| MutS ⁻ (pRW30) | 3 × 10 ⁻⁶ | – | – | – | 100 |
| ATCC 14028+ATCC 14028 (pRW30) | 1.1 × 10 ⁻⁹ | 51 | 49 | – | – |
| ATCC 14028+MutS ⁻ | 4.6 × 10 ⁻⁶ | 0.03 | – | 99.97 | – |
| ATCC 14028+MutS ⁻ (pRW30) | 2.6 × 10 ⁻⁶ | 0.05 | – | – | 99.95 |

^aSingle or mixed infections and evaluation of the frequency of Nal^R mutants were carried out as described in Section 2. The values given are the mean of three independent experiments. For each experiment the average of the results obtained with four animals was calculated. In all cases, data obtained were reproducible to within an error of ±10%. Three plates were always used to determine the number of Nal^R clones present in each blood sample.

with its infective process but without varying its LD₅₀ value [19].

To further analyze the behavior of these strains, competition assays upon mixed infection were carried out. Neither the *mutS* mutation nor the presence of the pRW30 plasmid affected the competitiveness of *S. typhimurium* cells (Table 3).

To investigate the impact of increased mutagenic activity upon the mutation rate beyond the infectious process, the frequencies of Nal^R mutants recovered from animals inoculated with either wild-type or MutS⁻ cells carrying or not the pRW30 plasmid in single or mixed infections were calculated. Data show that in all cases the obtained values in both single or mixed infections (Table 4) were practically the same as those found in the in vitro experiments (Fig. 1). So, from wild-type-inoculated animals, Nal^R clones were isolated at a frequency of about 10⁻⁹, regardless of the presence of the pRW30 plasmid. Likewise, the frequency of Nal^R mutants recovered from animals inoculated with either MutS⁻ or MutS⁻ (pRW30) cells was about 10⁻⁶. From these results, two points indicating that the putative damage produced in the bacterial DNA under these conditions is not enough to largely induce the *S. typhimurium* SOS response (and, consequently the error-prone DNA repair pathway) can be noted. The first point was the observation of similar rates of *S. typhimurium* wild-type Nal^R clones isolated from animals (Table 4) and in the in vitro experiments (Fig. 1). The second one, in contrast to the results obtained in the in vitro experiments (Fig. 1), was that the presence of the pRW30 plasmid in *S. typhimurium* cells did not increase the rate of their Nal^R derivatives recovered from animals (Table 4).

It has been proposed that intracellular pathogens like *S. typhimurium* are exposed to several putative mutagenic factors such as iron, hydrogen peroxide and alkylating agents, among others, during the infection process of an animal which directly or indirectly, through the SOS response, should be an important source of genetic variability in these environments [20]. Our data clearly indicate that other factors must be more determinant in the induction of this variability.

Furthermore, results reported in this work point out that cells of *S. typhimurium* with greater mutagenic strength are able to develop an infectious process normally and that they are neither excluded by nor dominant over the wild-type cells. Moreover, the non-exclusion of cells with a high mutagenic rate by the wild-type ones would enable the mixed population to attain a rapid adaptation to any possible new stimulus which may appear during animal infection.

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