**Helicobacter pylori** tissue tropism: mouse-colonizing strains can target different gastric niches

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Studies with the mouse-adapted *Helicobacter pylori* strain SS1 had supported an idea that infections by this pathogen start in the gastric antrum and spread to the corpus after extensive mucosal damage. This paper shows that the unrelated strain X47 colonizes the corpus preferentially. Differences between strains in preferred gastric region were detected by co-inoculating mice with a mixture of SS1 and X47, and genotyping *H. pylori* recovered after 2–8 weeks of infection by vacA s allele PCR and RAPD fingerprinting. Mixed infections were found in each of 59 co-inoculated young C57BL/6J mice. On average, however, SS1 was fourfold more abundant than X47 in the antrum and X47 was threefold more abundant than SS1 in the corpus. Similar results were obtained in mice inoculated first with one strain and then the other strain 2 weeks later. SS1 was even more abundant in the antrum of elderly (>1 year old) mice (97% of isolates). Qualitatively similar SS1 and X47 tissue distributions were seen using unrelated mouse lines (AKR/J, AJ/J, DBA/2J, BALB/cJ, LG/J, SM/J), but with significantly different SS1 : X47 ratios in some cases. These results suggest the existence of at least two distinct gastric niches whose characteristics may be affected by host genotype and age (physiology), and indicate that strains differ in how effectively they colonize each niche. Differences among gastric regions and the mixed infections that these allow may contribute to *H. pylori* diversity and genome evolution.

**INTRODUCTION**

*Helicobacter pylori* chronically infects the gastric mucosa of more than half of all people worldwide, persists for years or decades once established, and constitutes a major cause of gastritis and peptic ulcer disease, and an early risk factor for gastric cancer (Cover et al., 2001; Sipponen et al., 1998). It is one of the most genetically diverse bacterial species: independent clinical isolates typically differ by some 2–5% in sequences of essential genes and by some 5% or more in gene content (Achtman et al., 1999; Alm et al., 1999; Israel et al., 2001; Salama et al., 2000). This diversity probably reflects a combination of factors including: (i) mutation (Bjorkholm et al., 2001; Wang & Taylor, 1999); (ii) recombination among divergent lineages (Achtman et al., 1999; Kersulyte et al., 1999; Suerbaum et al., 1998); (iii) gene transfer from unrelated species (Tomb et al., 1997); (iv) preferential transmission among family members, and thus little chance of selection for any one or few potentially optimal genotypes (Mukhopadhyay et al., 2003); and (v) diversity among hosts in traits that are important to individual strains, and selection for adaptive changes after transmission to new hosts (Dubois et al., 1999).

Certain differences among strains can impact on colonization or disease – among them: abilities to induce synthesis of cytokine IL-8 and thereby severe inflammatory responses (Censini et al., 1996), and to form vacuoles in host tissues (Atherton et al., 1995) (traits that depend on the cag pathogenicity island and s1-type alleles of the vacA toxin gene, respectively); adherence to carbohydrate Lewis B and other carbohydrate structures (Evans & Evans, 2000; Ilver et al., 1998; Mahdavi et al., 2002); survival after brief acid exposure, as in the gastric lumen (Karita & Blaser, 1998); and the genetically distinct ability to grow under mildly acidic conditions, as in the gastric mucin (pH ~5), where most *H. pylori* reside in vivo (Bijlsma et al., 2000; Schade et al., 1994).

The present study was begun to help examine inferences that human *H. pylori* infections start in the antrum (Fig. 1) and may spread later to the corpus (where acid-secreting parietal cells are located), if acid secretion is decreased by therapy or infection-induced mucosal damage (Dixon, 1994; Sipponen et al., 1998). The interplay between local gastric acidity and

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**Abbreviation:** RAPD, random amplified polymorphic DNA.

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Received 15 November 2002
Revised 7 March 2003
Accepted 21 March 2003

Microbiology (2003), 149, 1901–1909 DOI 10.1099/mic.0.26129-0
sites of \( H. \) \( \textit{pylori} \) infection that this implies has been modelled in mice using SS1, a strain that is sometimes proposed as the standard for experimental infection studies (Lee et al., 1997; Nolan et al., 2002). Given \( H. \) \( \textit{pylori} \)'s genetic diversity, it seemed that SS1 might not be fully representative of all \( H. \) \( \textit{pylori} \) strains; and that strains differ in tissue tropism, with some colonizing the corpus preferentially.

Also motivating our study were reports that infections by two or more strains are common in some societies (Berg et al., 1997; Brown et al., 2002; Morales-Espinosa et al., 1999), and interest in the dynamic bacterial–host interplay (Achtman et al., 1999), and interest in the dynamic bacterial–host interplay that may result. In particular, mixed infection should facilitate interstrain gene transfer, which in turn would speed adaptation to new or changing gastric mucosal environments (Achtman et al., 1999; Kersulyte et al., 1999; Suerbaum et al., 1998). In addition, infections that seemed to be mixed were reported to be associated with higher risk of overt disease (Morales-Espinosa et al., 1999). This might reflect: (i) a greater chance that at least one strain will be virulent; (ii) complementary ways of coping with host defences by different strains, and thereby more easily overwhelming these defences; or (iii) greater receptivity of the most disease-prone people to multiple strains. Finally, it seemed that experimental mixed infections could be used to gain new insights into \( H. \) \( \textit{pylori} \) tissue tropisms; and to improve diagnostic strategies to link particular bacterial genotypes to disease or the failure of therapy, or that distinguish new infection after therapy vs re-emergence of earlier infections.

\( H. \) \( \textit{pylori} \) tissue tropisms and the stability, underlying mechanisms, and possible disease and evolutionary consequences of mixed infections cannot be examined experimentally in human subjects for ethical reasons. Here we describe a mouse model for studying these phenomena, and report that co-inoculation of mice with strains SS1 and X47 generally results in persistent mixed infection; and that these two unrelated strains colonize different parts of the stomach preferentially.

**METHODS**

**\( H. \) \( \textit{pylori} \) strains and culture.** Two unrelated mouse-adapted \( H. \) \( \textit{pylori} \) strains were used: SS1 (Lee et al., 1997; Nolan et al., 2002) and X47 (also known as X47-2AL; Ermak et al., 1998). SS1 is much used as the standard mouse-adapted strain for experimental infection (‘The Sydney Strain’). It carries the \textit{cag} pathogenicity island, an \textit{s2} (putatively non-toxigenic) allele of the \textit{vacA} vacuolating cytotoxin gene (GenBank accession no. AY049006), and an \textit{On} allele of the \textit{oppA} gene (GenBank accession no. AF233683). X47 had been used primarily for studies of immune responses and for vaccine development (Ermak et al., 1998; Kleanthous et al., 2001; Londono-Arcila et al., 2002), but is becoming increasingly popular for mutational analyses (Jeong et al., 2001; O’Rourke et al., 2003), in part because it is easier than SS1 to transform with mutated DNAs. Strain X47 lacks the \textit{cag} pathogenicity island entirely, but contains an \textit{On} allele of \textit{vacA} (GenBank accession no. AY049007), and an \textit{Off} allele of \textit{oppA} (GenBank accession no. AF411912). Strains SS1 and X47 are easily distinguished by arbitrarily primed (RAPD) PCR or \textit{vacA} allele-specific PCR, as illustrated below.

\( H. \) \( \textit{pylori} \) was easily grown in a gas-controlled incubator under microaerobic conditions (5 % \( O_2 \), 10 % \( CO_2 \), 85 % \( N_2 \)) at 37 °C, usually on brain-heart infusion agar (Difco) supplemented with 7 % horse blood, 0-4 % Isovitalex and the antibiotics amphotericin B (8 \( \mu \)g ml\(^{-1}\)), trimethoprim (5 \( \mu \)g ml\(^{-1}\)) and vancomycin (6 \( \mu \)g ml\(^{-1}\)). Nalidixic acid (10 \( \mu \)g ml\(^{-1}\)), polymyxin B (10 \( \mu \)g ml\(^{-1}\)) and bacitracin (200 \( \mu \)g ml\(^{-1}\)) were added to this medium when culturing \( H. \) \( \textit{pylori} \) from mouse stomachs. \( H. \) \( \textit{pylori} \) was also sometimes grown on Brucella Agar (1-5 %) whose pH had been adjusted before autoclaving. Viability was scored quantitatively as the ability of single cells to form colonies after appropriate dilution, essentially as in Jeong et al. (2001).

**Acid resistance.** Acid-shock resistance was scored using cultures that had been grown overnight on BHI agar, suspended in 150 mM NaCl at a density of \( 2 \times 10^8 \) c.f.u. ml\(^{-1}\). Twenty-microlitre aliquots of bacterial suspension were then incubated with 180 µl pH-adjusted citrate buffer for 1 h, as recommended (Bijlsma et al., 2000; Clyne et al., 1995), diluted serially with phosphate-buffered saline, pH 7 (PBS), and spotted on BHI agar plates. Growth under mildly acidic conditions, which depends on different genetic factors (Bijlsma et al., 2000), was scored by spotting 10 µl aliquots of a series of dilutions of equivalent cell suspensions on Brucella Agar (1-5 %) whose pH had been adjusted before autoclaving. Viability was scored quantitatively, as the ability of single cells to form colonies after appropriate dilution, essentially as in Jeong et al. (2001).

**Mice.** All mice used here were from established inbred lines and were purchased from Jackson Laboratories; they were maintained in the Washington University Medical School Animal Quarters (Animal Welfare Assurance #A-3381-01) with water and standard mouse chow \textit{ad libitum}, and used in protocols approved by the Washington University Animal Studies Committee (approval #20010039). Those mice designated as ‘young adult’ in the text were 7–18 weeks old; ‘middle-aged’ were 25–48 weeks old, and were obtained as retired breeders; ‘elderly’ were 53–76 weeks old, and had been used in a mouse genetics breeding programme (Cheverud et al., 2001).

**Experimental infection.** Bacteria were grown overnight on BHI agar, and suspended in PBS at densities of approximately \( 2 \times 10^6 \) c.f.u. ml\(^{-1}\). Mice were then inoculated with 0.4 ml of suspension (SS1, X47, or a mixture of both strains). To score colonization, mice were killed by CO\(_2\) asphyxiation. Immediately after death, the mice were cut open with clean and sterile scissors; their stomachs were cut open and examined for the presence of \( H. \) \( \textit{pylori} \) colonies.
were removed and cut longitudinally along the lesser curvature (Fig. 1); and any food was removed with clean and sterile forceps. The forestomach (not a major site of *H. pylori* colonization) was identified as a rather thin structure, separated from the corpus by a white line, and was removed and discarded. The antrum and corpus from each longitudinal section were then separated at the transition between a thick brownish wall (corpus) and a thinner, paler and smoother wall (antrum), essentially as described by Lee et al. (1982).

Half of the antrum and half of the corpus were used for *H. pylori* culture, and the other half of each was used for DNA extraction for PCR. For quantitative culture, the corpus and antrum tissues were diced and homogenized in 200 μl PBS using a disposable Pellet Pestle (Kontes), and aliquots of each suspension were spread on BHI agar medium and incubated. *H. pylori* densities in the antrum and corpus were estimated by quantitative culture.

**RAPD typing.** To type *H. pylori* strains by arbitrarily primed PCR (RAPD) fingerprinting (Akopyanz et al., 1992), DNA was isolated from bacteria that had been grown from single colonies as 1 cm² confluent patches on BHI agar medium. Bacterial cells were suspended in 50 μl TE, and DNA was extracted by a standard phenol/chloroform method. One microlitre of DNA solution was used in 25 μl for RAPD fingerprinting with primer 1254 (Akopyanz et al., 1992; Kersulyte et al., 1999), with the following cycling conditions: 94°C, 1 min; 36°C, 1 min; 72°C, 2 min; 45 cycles. The PCR mixture also contained 1·75 units of Biolase (thermostable DNA polymerase; MidWest Scientific) and 4 mM MgCl₂. Samples (7 μl) were analysed by electrophoresis in 2% agarose/TAE gels.

**vacA allele typing.** To type strains by their *vacA* s alleles, PCR was carried out using DNA extracted by phenol/chloroform (above), or obtained by suspending cells from a fully-grown colony in 10 μl TE and heating to 99°C for 5 min. PCR was carried out with primers VA1-F and VA1-R (Atherton et al., 1995), 1 unit of Biolase, and 1 μl of DNA extract, to 10 or 20 μl final volume. PCR conditions were: 94°C, 50 s; 50°C, 80 s; 72°C, 50 s; 30 cycles.

**Statistical analyses.** *H. pylori* densities in the antrum and corpus in each group of mice were compared statistically using the paired *t*-test. The densities in mice of different age groups were compared using the unpaired *t*-test. The relative abundance of SS1 vs X47 in the antrum and corpus (paired samples) in various mouse groups had not been used for *H. pylori* culture, using the QIAamp DNA Mini Kit (Qiagen), as recommended by the manufacturer, except that tissue lysis was completed with overnight proteinase K digestion at 56°C, and DNA was eluted in the final step in 100 μl of the elution buffer provided by the manufacturer. PCR analyses of *vacA* alleles in DNA from infected stomach tissue were performed as above, except that 4 μl of the DNA solution was used with cycling conditions of 94°C, 40 s; 52°C, 40 s; 72°C, 40 s; 28–32 cycles.

**RESULTS**

**H. pylori** strains can differ in preferred sites of colonization

Initially C57BL/6J mice were inoculated with strain SS1 alone or strain X47 alone, and *H. pylori* densities in the antrum and corpus of the stomach (Fig. 1) were estimated by quantitative culture after several weeks of infection (Fig. 2). The number of c.f.u. was, on average, about four-fold higher in the antrum of SS1-infected than in X47-infected mice (1·0×10⁶ vs 2·4×10⁵, respectively; *P*<0·01), whereas the number of c.f.u. was about the same in the corpus of SS1- and X47-infected mice (1·0×10⁶ and 1·2×10⁵, respectively).

The antrum was about 0·41 as large as the corpus in these mice (31±4 μg vs 75±9 μg, respectively; *n*=27); the SS1 densities per μg were therefore estimated to be 2·5-fold higher in the antrum than in the corpus, in accord with an earlier report (Lee et al., 1997), and X47 densities were estimated to be 2·1-fold higher in the corpus than in the antrum.

The possibility that SS1 and X47 differ in their ability to colonize particular gastric regions was studied further by co-inoculating mice with 1:1 mixtures of these two strains, and characterizing the *H. pylori* recovered a few weeks later by RAPD and *vacA* s allele PCR typing. Initial tests showed that each of 70 isolates from seven co-inoculated mice was matched to either SS1 or X47 in RAPD pattern, and contained the expected *vacA* s1 and *vacA* s2 alleles, respectively (illustrated in Fig. 3). The two strain types were non-randomly distributed, however: of 35 antrum isolates typed, 27 were SS1 and eight were X47; whereas among 35 corpus isolates, only seven were SS1 but 28 were X47. Tests of *vacA* s allele types of another 370 isolates from 12 additional co-inoculated C57BL/6J mice again showed SS1 to be about...
threefold more abundant than X47 in the antrum but only one-fourth as abundant as X47 in the corpus (Table 1). Similar results were obtained with single colonies from mice after 9 weeks, rather than just 2–4 weeks, of infection.

**Changes in SS1 phenotype after long-term infection**

With six of nine mice that had been co-infected with SS1 and X47 for 9 weeks, minute barely visible colonies (~0·1–0·3 mm in diameter after 4–5 days of incubation) were formed by some 20–80 % of H. pylori from the antrum and 20–60 % of those from the corpus. In contrast, only normal-sized (~1 mm diameter) colonies were formed by H. pylori after just 2–4 weeks of infection. RAPD tests of minute-colony isolates using primer 1254 yielded profiles equivalent to those of SS1 in Fig. 3 in the cases of 45 of 46 randomly selected isolates from the antrum and 20 of 30 from the corpus. The minute-colony phenotype of each of 37 such SS1-like isolates persisted through two sequential restreakings, suggesting a genetic basis, whereas each of four X47-like isolates tested formed normal-sized colonies on restreaking. Further RAPD tests of 13 representative SS1-like minute colony isolates with three additional RAPD primers (1281, 1283, 1290) also yielded profiles that were indistinguishable from those of the parental SS1 strain (data not shown). Thus, the small-colony phenotype may reflect selection for SS1 derivatives that are better adapted to mice, and that might have arisen either by mutation or by DNA transfer from the co-infecting X47 strain.

**Strain distribution does not depend on order of inoculation**

Sets of mice were inoculated with either SS1 or X47, and then with the other strain 2 weeks later; the distribution of strain types recovered 2 or 7 weeks after the second inoculation was scored by PCR tests of single colonies. The results (Fig. 4A) showed that SS1 predominated in the antrum, and that X47 was generally as or more abundant than SS1 in the corpus, independent of the order of inoculation. Similar results were obtained by vacA PCR using DNAs from infected stomachs (Fig. 4B). Thus, the overall distribution of these two strains was not affected strongly by which strain became established first, nor by the duration of infection (Fig. 4A).

The differences among mice in SS1 : X47 ratios found by testing single colonies were larger than expected from sampling error alone. A few cases of significantly different SS1 : X47 ratios in different halves of the antrum or corpus of the same mouse were also seen when data from PCR tests of single-colony isolates and total gastric mucosal DNAs were compared [e.g. mouse 5, left panels in Fig. 4: SS1 predominated in antrum mucosal DNA (B), but not among single-colony isolates (A)]. Such differences may stem from use of different halves of the stomach in these two tests and the patchiness of many H. pylori infections (Bayerdorffer et al., 1989; Anonymous, 1986).

**Mouse age affects strain distribution**

To test for possible effects of age of host on receptivity to H. pylori, elderly (>1 year old) and middle-aged (34–38 weeks old) C57BL/6J mice were inoculated with 1 : 1 mixtures of strains SS1 and X47, and the H. pylori recovered 2–4 weeks later were analysed as above. No major differences in H. pylori densities in elderly vs middle-aged vs young adult mice were found (approx. 1–2 × 10^7 c.f.u. g⁻¹, on average, in antrum and 2·4 × 10^7 c.f.u. g⁻¹ in corpus in each age group). With elderly mice, however, 97·5 % (115 of 118) of antrum isolates were SS1, in contrast to 143 of 186 isolates (76·9 %) from young adult mice (P = 0·004; Mann–Whitney U test). An intermediate SS1 level (92·0 %, 218 of 237) was found in the antrum of middle-aged mice (Fig. 5). SS1 was also more abundant in the corpus of elderly than of young mice (50/116, 43·1 % vs 42/194, 21·6 %; P = 0·014), and again an intermediate value was seen in the corpus of middle-aged mice (97/234; 41·5 %).

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**Table 1. Strain distribution in young adult (7–18 week old) C57BL/6J mice inoculated with 1 : 1 mixtures of strains SS1 and X47**

Single colonies were typed by RAPD fingerprinting and/or vacA s allele PCR, as in Fig. 3. All isolates matched either SS1 or X47.

<table>
<thead>
<tr>
<th>Period (weeks)</th>
<th>No. of mice</th>
<th>Percentage SS1 (no. of SS1/total)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Antrum</td>
</tr>
<tr>
<td>2–4</td>
<td>19</td>
<td>77 (166/216)</td>
</tr>
<tr>
<td>9</td>
<td>9</td>
<td>73 (103/141)</td>
</tr>
</tbody>
</table>
Mouse genotype affects strain distribution

To test for possible effects of host genotype on tissue tropism, mice of six other inbred lineages (AKR/J, A/J, DBA/2J, BALB/cJ, SM/J and LG/J) were inoculated with mixtures of SS1 and X47, and bacterial densities and the distribution of strain types were estimated (Table 2). Co-colonization was observed in 130 of 142 infected mice. SS1 was more abundant in the antrum and X47 was more abundant in the corpus in all mouse lineages except AKR/J, where SS1 predominated in both gastric regions. More generally, the SS1:X47 ratios in antrum and corpus seemed to differ among lineages. These differences were statistically significant in several cases, as indicated by asterisks next to the values in Table 2 (e.g. medians of 17% vs 68% SS1 in corpus of young C57BL/6J vs young AKR/J mice, respectively). Some differences among lineages in overall bacterial densities were also evident in the quantitative culture data (Table 3). The SM mouse strain, in particular, harboured significantly fewer H. pylori than did C57BL/6J, especially in the antrum (Table 3).

Acid tolerance of strains SS1 and X47

The acid resistance of SS1 and X47 was compared because of differences in preferred sites of colonization by these two strains (see above), and because gastric acidity is higher in the corpus than in the antrum (Dixon, 1994). Two measures of acid resistance were used: (i) incubation in acidic buffer (Karita & Blaser, 1998); and (ii) formation of colonies on mildly acidic (pH ~5) culture medium (Bijlsma et al., 2000; Schade et al., 1994). The first test (Fig. 6A) showed that
strains SS1 and X47 each survived well during 1 h incubation in buffers ranging from pH 5–7 to 4–4, and that each strain was killed by incubation at pH 3–2 (survival ≤10^-3). At the critical threshold pH of 3–8, however, there was 120-fold more killing of SS1 than of X47 (S/SX = 0.0041 vs 0.50, respectively). SS1 is cag` + and X47 is cag` - . This difference in susceptibilities is in accord with studies of other strains that had indicated a relationship between cag pathogenicity island carriage and acid-shock susceptibility (Karita & Blaser, 1998). The second test (Fig. 6B), however, showed that SS1 formed colonies more efficiently than X47 on mildly acidic medium. This was most evident at pH 5–7, a condition in which SS1 formed colonies 67-fold more efficiently than did X47 (Fig. 6B). To test for genetic heterogeneity or acid adaptation in these populations, SS1 and X47 cells recovered after growth on pH 5–7 medium were cultured overnight on normal medium and then retested for ability to grow at pH 5–7 or pH 5–6. SS1 again

**Table 2.** Effect of host age and genotype on relative abundance of SS1 and X47 after mixed inoculation

Data from vacA s typing of 10–30 single-colony isolates per site per mouse were used. All isolates that were not SS1-like were X47-like in vacA s type. Bacterial densities in young adult mice were quantified (see Table 3).

<table>
<thead>
<tr>
<th>Mouse strain</th>
<th>Young adult (7–18 wk)</th>
<th>Middle-aged (25–48 wk)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>No. of mice</td>
<td>Percentage SS1 [Median (lower–upper quartiles)]</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Antrum‡</td>
</tr>
<tr>
<td>C57BL/6J</td>
<td>23</td>
<td>82 (63–93)</td>
</tr>
<tr>
<td>AKR/J</td>
<td>10</td>
<td>92 (84–92)</td>
</tr>
<tr>
<td>DBA/2J</td>
<td>16</td>
<td>49 (10–93)</td>
</tr>
<tr>
<td>BALB/cJ</td>
<td>15</td>
<td>77 (68–100)</td>
</tr>
<tr>
<td>A/J</td>
<td>11</td>
<td>70 (33–92)</td>
</tr>
<tr>
<td>SM/J</td>
<td>13</td>
<td>61 (9–94)</td>
</tr>
<tr>
<td>LG/J</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

†Percentage SS1 = (no. of SS1-like colonies/total no. of colonies typed) × 100.
‡Asterisks in these columns identify statistically significant differences (0.01 ≤ P < 0.05) in the same age group between C57BL6/J and other mouse strains, based on the Mann–Whitney U test.
§The results of Wilcoxon signed-rank test for antrum vs corpus (paired samples) in each mouse strain in each age group. Significant differences are shown as *** (P < 0.001), ** (0.001 < P < 0.01), * (0.01 < P < 0.05).

**Table 3.** Effect of host genotype on bacterial densities after inoculation with a mixture of strains SS1 and X47

All mice were young adults (7–18 weeks). Infections were allowed to proceed for 2–4 weeks before animals were killed, and bacterial densities (this table) and distribution of strain types (Table 2) were determined.

| Mouse strain | No. of mice | \( \log_{10}(\text{c.f.u. g}^{-1}) \text{, mean} \pm \text{SD (c.f.u. g}^{-1}, \text{mean)} | \( PT \|^\dagger | \text{Estimated c.f.u. g}^{-1} \text{ of SS1 and X47}^\dagger |
|--------------|-------------|-----------------|-----------------|-----------------|-----------------|
|               |             | Antrum\‡ | Corpus\‡ | PT\‡ | Antrum | Corpus |
| C57BL/6J  | 14  | 7.34 ± 0.33 (2.2–10^7) | 7.03 ± 0.33 (1.1–10^7) | ** | 1.8 × 10^6 | 4.0 × 10^6 |
| AKR/J  | 10  | 6.93 ± 0.45* (8.5–10^6) | 6.29 ± 0.24** (1.9–10^6) | *** | 7.8 × 10^6 | 6.8 × 10^6 |
| DBA/2J  | 16  | 7.25 ± 0.27 (1.8–10^7) | 6.88 ± 0.50 (7.6–10^6) | * | 8.8 × 10^6 | 9.2 × 10^6 |
| BALB/cJ  | 15  | 6.78 ± 1.05 (7.4–10^6) | 6.70 ± 0.65 (5.0–10^6) | | 5.7 × 10^6 | 1.7 × 10^6 |
| A/J  | 11  | 6.83 ± 0.33** (6.8–10^6) | 7.01 ± 0.38 (1.0–10^7) | | 4.8 × 10^6 | 2.0 × 10^6 |
| SM/J  | 13  | 5.45 ± 0.73*** (2.8–10^6) | 6.39 ± 0.38*** (2.5–10^6) | ** | 1.7 × 10^6 | 1.1 × 10^6 |

†The statistical significance of differences in \( \log_{10}(\text{c.f.u. g}^{-1}) \) in antrum or corpus between C57BL/6J and other strains was tested by the unpaired t-test. Significant differences are indicated as *** (P < 0.001), ** (0.001 < P < 0.01) and * (0.01 < P < 0.05).
‡The significance of differences in \( \log_{10}(\text{c.f.u. g}^{-1}) \) between antrum and corpus in each mouse strain was tested by the paired t-test and significant differences are identified as above.
§The colony number of each strain was estimated from the mean c.f.u. g^-1 in this table and mean percentage SS1 in Table 2.
formed colonies more efficiently than did X47 on mildly acidic medium (150-fold and 400-fold higher c.f.u. at pH 5.7 and pH 5.6, respectively) (data not shown).

**DISCUSSION**

We found that simultaneous or sequential inoculation of mice with the unrelated *H. pylori* strains SS1 and X47 resulted in persistent mixed infections. In general SS1 was more abundant than X47 in the gastric antrum, and conversely X47 was more abundant than SS1 in the corpus. These general patterns were seen in seven different inbred mouse lines, and in elderly as well as young adult mice. The SS1 : X47 ratio increased with age in C57BL/6J mice, one of the standard inbred mouse lines often used for experimental infection. However, the ratio also varied significantly among mouse lines. That is, preferential colonization of the antrum by SS1 and of the corpus by X47 seems to be host-adaptive, although whether the optimal affinity is high or low may depend on the particular glycan used as receptor (Evans & Evans, 2000; Ilver et al., 1994). Such results encourage consideration of other strain differences in traits that are important to individual strains, and consequently potentially new selection for adaptive changes with each infection of a new host (Dubois et al., 1999). To this list we would now add physiological differences between regions of a given host’s gastric mucosa. Each chance infection with a strain that previously had been best adapted for just one gastric niche (e.g. with X47, the corpus) would tend to select for derivatives that grew better in other available locations (with X47, the antrum, especially in elderly mice). Such changes would be selected, even if they also made these derivatives less suited for their originally preferred niche (the corpus, in the case of X47). The minute-colony SS1 variants that were found after 2 months, but not after 2 weeks, of mixed infection may have resulted from selection for improved growth in the host gastric mucosal milieu. As in any adaptation to complex environments (Lenski & Travisano, 1982), different early chance mutational events may lead a given strain to evolve along different trajectories in different individual hosts. Because established infections may persist for decades, even subtle selection pressures or differences in fitness could have dramatic effects on the distribution of genotypes that may ultimately emerge.

The nature of the niches to which SS1 and X47 are best adapted, e.g. whether discrete physical compartments, or positions in gradients of metabolites or macromolecules, is not known. A compartment model is suggested by occasional findings of intracellular *H. pylori* (Allen, 2000; Amiwa et al., 2002), if it is assumed that SS1 and X47 tend to occupy different cell types (one predominant in the gastric antrum, the other in the corpus). One attractive molecular gradient model was suggested by pH differences in the antrum vs corpus. However, although X47 was more resistant than SS1 to acid shock, it grew less well on mildly acidic medium, a condition thought to mimic *H. pylori*'s great genetic diversity has been ascribed variously to mutation (Bjorkholm et al., 2001; Wang & Taylor, 1999); recombination among divergent lineages and species (Achtman et al., 1999; Kersulyte et al., 1999; Suerbaum et al., 1998; Tomb et al., 1997); a highly fragmented genetic population structure, and consequently relatively few of the selective sweeps that might promote emergence of any one or few most-fit genotypes (Mukhopadhyay et al., 2003); and diversity among hosts in traits that are important to individual strains, and consequently potentially new selection for adaptive changes with each infection of a new host (Dubois et al., 1999).
implied by our present results might reflect distributions of molecules that SS1 and X47 can each use as receptors. Or, two niches might be created by the joint distributions of inhibitors of *H. pylori* growth (e.g. reactive oxygen metabolites, antibacterial peptides, macrophages, lymphocytes, etc.), and/or local concentrations of exudates that *H. pylori* uses for nutrition (Blaser, 1993; Blaser & Berg, 2001), if SS1 and X47 differ in resistance to host defences and/or effectiveness of nutrient scavenging. Finally, the two strains and X47 differ in chemotactic behaviour with respect to attractiveness of nutrient scavenging. Regardless of actual mechanism, these considerations emphasize the potential complexity of the gastric ecosystem, and how local differences within it may promote *H. pylori* genetic divergence during chronic infection – evolutionary changes that may affect the vigour or specificity of colonization of new hosts and the spectrum of diseases that can sometimes ensue.

**ACKNOWLEDGEMENTS**

We thank Ms Susan Pletscher for her skill in mouse breeding. K. O. was supported in part by a fellowship from the Sankyo Foundation of Science. The experiments described here were supported by grants from the NIH (ROI AI38166, RO3 AI49161, ROI DK53727 and P30 DK52574).

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