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Respiration of *Escherichia coli* in the Mouse Intestine

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Mammals are aerobes that harbor an intestinal ecosystem dominated by large numbers of anaerobic microorganisms. However, the role of oxygen in the intestinal ecosystem is largely unexplored. We used systematic mutational analysis to determine the role of respiratory metabolism in the streptomycin-treated mouse model of intestinal colonization. Here we provide evidence that aerobic respiration is required for commensal and pathogenic *Escherichia coli* to colonize mice. Our results showed that mutants lacking ATP synthase, which is required for all respiratory energy-conserving metabolism, were eliminated by competition with respiratory-competent wild-type strains. Mutants lacking the high-affinity cytochrome bd oxidase, which is used when oxygen tensions are low, also failed to colonize. However, the low-affinity cytochrome bo oxidase, which is used when oxygen tension is high, was found not to be necessary for colonization. Mutants lacking either nitrate reductase or fumarate reductase also had major colonization defects. The results showed that the entire *E. coli* population was dependent on both microaerobic and anaerobic respiration, consistent with the hypothesis that the *E. coli* niche is alternately microaerobic and anaerobic, rather than static. The results indicate that success of the facultative anaerobes in the intestine depends on their respiratory flexibility. Despite competition for relatively scarce carbon sources, the energy efficiency provided by respiration may contribute to the widespread distribution (i.e., success) of *E. coli* strains as commensal inhabitants of the mammalian intestine.

The intestinal microflora is dominated by diverse anaerobes, providing both a health benefit to the host (15) and a barrier to infection (16, 21). Despite being present in substantially lower numbers, facultative anaerobes, primarily *Escherichia coli* and *Enterococcus faecalis*, are ubiquitous in mammalian intestines (40). While the intestine is commonly thought to be anaerobic (4), the tissues surrounding the lumen are oxygen rich and oxygen diffuses into the intestine at appreciable levels (20). Furthermore, oxygen from swallowed air is present in flatus (29). Oxygen in the intestine apparently has minimal impact on persistence of anaerobes, and it was recently shown that at least one predominant anaerobe, *Bacteroides fragilis*, respires oxygen at low concentrations (5). In contrast to obligate anaerobes, facultative anaerobes (e.g., *E. coli*) grow most rapidly when respiring oxygen and switch to anaerobic respiration in the absence of oxygen or to fermentation in the absence of alternative electron acceptors (17). However, the extent to which facultative anaerobes utilize oxygen to maximize their growth rate in the intestine is not known.

Nutrients consumed for growth of the microflora are thought primarily to be fermentable carbohydrates, the bulk of which are in the form of polysaccharides (37). *E. coli* colonizes the mouse intestine by growing within the polysaccharide-rich mucus layer covering the epithelium but is unable to degrade polysaccharides. Apparently, *E. coli* consumes the mono- and disaccharides released during degradation of mucosal polysaccharides and dietary fiber (8) by polysaccharide hydrolyase enzymes secreted by members of the anaerobic microflora (11) and, perhaps, host colonic epithelial cells (6). Recent studies from our laboratory demonstrate that seven mucus-derived sugars contribute to *E. coli* colonization of the mouse intestine, suggesting that biochemical flexibility is key to its competitiveness in vivo (8). *E. coli* is nearly equally flexible in its respiratory metabolism (17), but nothing is known about the role of bacterial respiration for coupling ATP generation to carbohydrate oxidation in vivo. Thus, it is important to test the hypothesis that respiration confers a competitive advantage to *E. coli* in the intestine.

Enterohemorrhagic *E. coli* (EHEC), has an infectious dose for humans as low as 10 microorganisms and, following ingestion, grows rapidly to a population approaching a billion bacteria per gram of feces (24). Since colonization is the first step in the infection process, it is crucial to understand how EHEC colonizes the intestine because low numbers can survive transport to consumers in foodstuffs such as leafy vegetables, which have caused recent outbreaks in the United States (36). It is not known how EHEC acquires nutrients and generates energy for growth in vivo. While respiration is not a virulence factor per se, our experiments seek to establish the fundamental importance of housekeeping functions, such as energy metabolism, for pathogenesis. Since most mucosal pathogens are facultative anaerobes, these studies of *E. coli* may be extended to include many diseases.

Here we report the results of a systematic mutational analysis designed to identify which respiratory pathways contribute to the ability of commensal and pathogenic *E. coli* to colonize...
the streptomycin-treated mouse intestine. Our findings lead us to conclude that respiration provides an enormous competitive advantage to *E. coli* in vivo. The results challenge the traditional view that the intestine is strictly anaerobic (4). Instead, we obtained evidence that *E. coli* colonization of the mouse intestine is maximized by the ability to respire oxygen.

### MATERIALS AND METHODS

**Bacterial strains and growth conditions.** The bacterial strains used in this study were derived from *E. coli* MG1655 Strr (streptomycin resistant), a K-12 strain (33), and *E. coli* EDL933 Strr, the prototypical O157:H7 strain (31). Cultures were grown at 37°C in Luria-Bertani (LB) medium with gyrotory shaking at 250 rpm. Null alleles were constructed by using the allelic replacement method of Datsenko and Wanner (14), as described previously (8), such that target genes were deleted and replaced with kanamycin or chloramphenicol resistance cassettes (used as selectable markers in mouse colonization assays, as described below). The null allele strains are identified in the text by the genes following the method of Datsenko and Wanner (14), as described previously (8), such as standard error of the mean of day 1 and day 9 data from 6 mice is shown. Differences of at least 1 order of magnitude (10-fold) are in boldface type; all values shown in bold are statistically significant (P < 0.005; Student’s t test).

**High-performance liquid chromatography analysis.** A Dionex DX-500 Microbore system was used with an IonPac AS11 column for anion analysis of mucus. Standards and blanks were analyzed, and standard curves were developed for a bore system was used with an IonPac AS11 column for anion analysis of mucus.

**Periplasmic nitrate reductase**

NarZ

**Nitrate reductases**

NarG, NarZ, Δ(narD-narA)

**Fumarate reductase**

ΔfdrA

**Table 1. Competitive colonization between respiratory mutants and wild-type *E. coli* strains**

<table>
<thead>
<tr>
<th>Respiratory enzyme</th>
<th>Mutant(s)</th>
<th>Day 1</th>
<th>Day 9</th>
<th>E. coli colonization (log_{10} CFU/g) by strain:</th>
</tr>
</thead>
<tbody>
<tr>
<td>ATP synthetase</td>
<td>Δ(apaA-apaG)</td>
<td>2.7 ± 0.1</td>
<td>5.6 ± 0.1</td>
<td>EDL933, 5.3 ± 0.5, MG1655, 5.9 ± 0.1</td>
</tr>
<tr>
<td>Regulator of aerobic genes</td>
<td>ΔnarA</td>
<td>4.7 ± 0.1</td>
<td>5.6 ± 0.2</td>
<td>EDL933, 3.0 ± 0.2, MG1655, 6.5 ± 0.3</td>
</tr>
<tr>
<td>Regulator of anaerobic genes</td>
<td>Δfur</td>
<td>1.4 ± 0.2</td>
<td>5.6 ± 0.2</td>
<td>EDL933, 1.3 ± 0.1, MG1655, 6.8 ± 0.1</td>
</tr>
<tr>
<td>Cytochrome bo oxidase</td>
<td>Δ(cyoA-cyoB)</td>
<td>0.1 ± 0.1</td>
<td>0.4 ± 0.3</td>
<td>EDL933, 0.4 ± 0.1, MG1655, 0.8 ± 0.1</td>
</tr>
<tr>
<td>Cytochrome bd oxidase</td>
<td>Δ(cyoD-cyoB)</td>
<td>2.8 ± 0.1</td>
<td>5.2 ± 0.1</td>
<td>EDL933, 3.8 ± 0.2, MG1655, 5.0 ± 0.1</td>
</tr>
<tr>
<td>Cytochrome bd oxidase (assembly)</td>
<td>Δ(cyoD-cyoC)</td>
<td>2.4 ± 0.1</td>
<td>5.0 ± 0.2</td>
<td>EDL933, 3.3 ± 0.1, MG1655, 6.0 ± 0.2</td>
</tr>
<tr>
<td>Nitrate reductase</td>
<td>ΔnarG</td>
<td>0.3 ± 0.1</td>
<td>2.0 ± 0.1</td>
<td>EDL933, 0.4 ± 0.2, MG1655, 2.2 ± 0.1</td>
</tr>
<tr>
<td>Nitrate reductase</td>
<td>ΔnarZ</td>
<td>0.6 ± 0.1</td>
<td>0.1 ± 0.1</td>
<td>EDL933, 0.3 ± 0.1, MG1655, 0.1 ± 0.2</td>
</tr>
<tr>
<td>Periplasmic nitrate reductase</td>
<td>Δ(narD-narA)</td>
<td>0.4 ± 0.1</td>
<td>0.1 ± 0.1</td>
<td>EDL933, 0.2 ± 0.1, MG1655, 0.6 ± 0.1</td>
</tr>
<tr>
<td>Nitrate reductases</td>
<td>ΔnarG, ΔnarZ</td>
<td>0.9 ± 0.1</td>
<td>2.3 ± 0.1</td>
<td>EDL933, 0.1 ± 0.1, MG1655, 2.9 ± 0.2</td>
</tr>
<tr>
<td>Nitrate reductases</td>
<td>ΔnarG, ΔnarZ, Δ(narD-narA)</td>
<td>1.3 ± 0.1</td>
<td>3.1 ± 0.1</td>
<td>EDL933, 0.9 ± 0.1, MG1655, 3.8 ± 0.1</td>
</tr>
<tr>
<td>Fumarate reductase</td>
<td>ΔfdrA</td>
<td>0.8 ± 0.1</td>
<td>3.1 ± 0.2</td>
<td>EDL933, 0.1 ± 0.1, MG1655, 2.8 ± 0.2</td>
</tr>
</tbody>
</table>

* Mice were fed 10⁷ CFU each of a mutant and its wild-type parent. Mice were transferred to fresh cages every day, and feces no older than 24 h were assayed every other day for 15 days. At each time point, the log_{10} CFU/gm of feces for the mutant was subtracted from the log_{10} CFU/gm of feces for the wild type. The average ± standard error of the mean of day 1 and day 9 data from 6 mice is shown. Differences of at least 1 order of magnitude (10-fold) are in boldface type; all values shown in bold are statistically significant (P < 0.005; Student’s t test).

**RESULTS**

**Colonization assays.** The preferred animal model for measuring the relative fitness of two bacterial strains for intestinal colonization is the streptomycin-treated mouse. Streptomycin treatment selectively removes facultative anaerobes while leaving the anaerobic microflora essentially intact; this opens a previously unavailable niche, which can then be colonized by newly introduced microorganisms such as *E. coli* (12, 27, 50). In this model, competing wild-type and mutant strains are fed together to mice and their populations are monitored in fecal plate counts. Previously we showed that colonization involves an initiation stage (5 h to 3 days postfeeding), in which nutrients are not limiting and the population increases from low to high numbers, and a maintenance stage (7 days post-feeding and beyond), in which nutrients are limiting and the population persists at a level correlated with the mutant strain’s relative fitness for colonization (8). For this reason, the colonization data shown in Table 1 are given for day 1 (initiation) and day 9 (maintenance) of the 15-day-long experiments.
compare the bioenergetics of a commensal strain to those of a pathogenic strain, each of the respiratory mutations described in this report was constructed in *E. coli* MG1655 (3), derived from the human isolate *E. coli* K-12, and *E. coli* EDL933 (34), the prototypical strain of *E. coli* O157:H7. Please note that the streptomycin-treated mouse serves as a colonization model for EHEC strains, which do not cause disease in CD-1 mice (49).

We found that each of the mutations tested in the commensal and pathogenic strains had a nearly identical impact on colonization. For this reason, colonization curves are shown for *E. coli* EDL933 experiments only.

**ATP synthase is necessary for colonization.** Since respiratory energy conservation, i.e., ATP generation, requires ATP synthase (32), we tested mutants that lack ATPase for their ability to compete with the wild type in the streptomycin-treated mouse colonization model. The ATPase mutant constructions deleted the *atpA* and *atpG* genes, which encode the F1 alpha and gamma subunits, respectively, resulting in strains capable only of fermentative energy metabolism (13). In competition with their respective wild-types, *E. coli* EDL933 Δ(*atpA*-*atpG*):cat and *E. coli* MG1655 Δ(*atpA*-*atpG*):cat mutants were eliminated from mice within 5 days (Table 1 and Fig. 1A). It is formally possible that mutations inadvertently introduced elsewhere on the genome caused the observed colonization phenotype. However, we would argue that this was not the case, for the following reasons. First, each of the allelic replacements described here and elsewhere (8, 28, 31, 33) was obtained with a frequency that varied less than 1 order of magnitude. Second, half of the mutants tested here and in similar studies (8) had no colonization defects. Third, the results were essentially identical in two different genetic backgrounds (EDL933 and MG1655). The failure of the Δ(*atpA*- *atpG*):cat mutants to initiate colonization could be due to a general inability to grow in the intestine rather than an inability to compete with the wild type. To distinguish these possibilities, the mutants were fed alone to mice and found to colonize at wild-type levels (Fig. 1B) (data not shown). The ability of the respiratory-defective mutants to colonize alone indicates that fermentation is sufficient for growth of *E. coli* in the mouse intestine, but oxidative phosphorylation is essential for competition with respiratory-competent strains. This finding led us to consider whether one or more modes of respiration are crucial to occupation of intestinal niches formed by electron acceptor availability.

**Respiration of oxygen is necessary for colonization.** Proof that aerobic respiration is essential for colonization by *E. coli* was obtained by competing mutants lacking the high-affinity cytochrome *bd* oxidase with their respective wild types. The Δ(*cydA-cydB*):cat mutant constructions deleted genes encoding both subunits (I and II) of cytochrome *bd* oxidase, as shown previously (19). The *E. coli* EDL933 Δ(*cydA-cydB*):cat and *E. coli* MG1655 Δ(*cydA-cydB*):cat strains were eliminated by day 11 during competition with their wild-type parents (Table 1 and Fig. 1C). The fitness defect observed for the Δ(*cydA-cydB*):cat strains was not merely a growth defect, since the mutants colonized when fed alone to mice (Fig. 1D) (data not shown). To...
confirm the requirement for high-affinity oxygen respiration, \( \Delta (\text{cydD-cydC}):\text{cat} \) mutants, which cannot assemble cytochrome bd oxidase in the membrane (39), were tested and found to have similar colonization defects (Table 1 and Fig. 2A). The \( \Delta (\text{cydD-cydC}):\text{cat} \) mutants were able to colonize when fed to mice alone (Fig. 2B) (data not shown). We note that in addition to CydDC being required for cytochrome bd oxidase assembly and activity (39), cydDC encodes a glutathione transport system (38), which if relevant might also be required for colonization. Since the \( \Delta (\text{cytA-cytB}):\text{cat} \) and \( \Delta (\text{cydD-cydC}):\text{cat} \) mutants failed to initiate colonization (i.e., 24 h), it was necessary to determine if they were also defective in the maintenance stage (beyond 7 days). Therefore, mice were precolonized (for 10 days) with \( E. coli \) EDL933 \( \Delta (\text{cydD-cydC}):\text{cat} \) and then challenged with the \( E. coli \) EDL933 wild type; the mutant was eliminated by the wild type in 7 days, confirming that functional cytochrome bd was important for maintenance of colonization (Fig. 2C).

We also examined the importance of the low-affinity cytochrome bo, oxidase for colonization. The construction of \( \Delta (\text{cyoA-cyoB}):\text{cat} \) mutants deleted the genes encoding subunits I and II of the cytochrome bo, oxidase, as shown previously (2). The results showed that \( E. coli \) EDL933 \( \Delta (\text{cyoA-cyoB}):\text{cat} \) and \( E. coli \) MG1655 \( \Delta (\text{cyoA-cyoB}):\text{cat} \) strains cocolonized with their respective wild-type parents, indicating that respiration of high oxygen levels was not necessary for colonization (Table 1). In summary, the colonization defects of the cytochrome bd oxidase mutants challenge the traditional view that the intestine is anaerobic (4). Instead, the results support the hypothesis that a microaerobic niche is critical for both establishing and maintaining \( E. coli \) in the intestine. Thus, a competitive advantage in vivo is conferred on strains that respire oxygen.

**Aerobic respiratory control is necessary for colonization.** \( E. coli \) governs respiratory flexibility via the global regulators ArcA and Fnr. ArcA is a two-component regulator of several hundred genes (30) that responds to the oxidation state of the quinone pool, which is sensed by ArcB (18). Under high oxygen tension, \( E. coli \) expresses the low-affinity oxidase cytochrome bo, (encoded by cyoABCDE) and the high-affinity oxidase cytochrome bd (encoded by cydAB) is repressed. Under microaerobic conditions, where oxygen scavenging may play an important role for growth and survival, ArcB phosphorylates ArcA, which represses the cyoABCDE operon and activates the cydAB and cydDC operons (1). Since the experiments described above indicated the importance of cytochrome bd, we reasoned that arcA mutants would have colonization defects. The construction of \( E. coli \) EDL933 \( \Delta \text{arcA}:\text{cat} \) and \( E. coli \) MG1655 \( \Delta \text{arcA}:\text{kan} \) deleted the gene encoding the response regulator of the ArcAB two-component system, as previously described (23). Although \( \Delta \text{arcA} \) mutants colonized when fed alone (Fig. 3B) (data not shown), they could not compete with their respective wild types and were eliminated from mice within 3 days (Table 1 and Fig. 3A). While it is tempting to speculate that the colonization defect of the \( \Delta \text{arcA} \) mutants resulted solely from failure to induce cydAB, the pleiotropic phenotype of the \( \Delta \text{arcA} \) strain makes a number of alternative explanations possible. What is clear from this experiment is that appropriate regulation of aerobic respiratory genes is necessary for \( E. coli \) to be competitive in vivo.
Anaerobic control is necessary for colonization. Induction of anaerobic processes in E. coli is controlled by Fnr, an oxygen-labile transcription factor, which activates transcription of hundreds of genes, including genes that encode respiratory pathways for nitrate and fumarate (25, 35). Since induction of anaerobic respiratory pathways requires Fnr, we constructed E. coli EDL933 fnr::kan mutants to test the contribution of this global regulator during colonization. The E. coli EDL933 fnr::kan and E. coli MG1655 fnr::kan mutants were fed together with their respective wild types and found to initiate colonization (although not as well as the wild type), and then they were eliminated by day 5 (Table 1 and Fig. 3C). The defect was not an inability to grow in the intestine, since the fnr::kan mutants colonized when fed alone to mice (Fig. 3D) (data not shown). Since the fnr::kan mutants exhibit colonization defects in competition with the wild type, this implies that E. coli experiences conditions in the intestine that are required for Fnr function (7): i.e., anaerobic or nearly anaerobic conditions. Thus, we conclude that Fnr-dependent genes contribute to colonization success. While these results indicate that appropriate regulation of anaerobic respiration is important for colonization, the specific roles of the alternative pathways were unclear.

Nitrate reductase is necessary for colonization. To determine which anaerobic respiratory pathways were used during colonization, we considered the in vivo role of nitrate reduction. Since E. coli has three systems for nitrate respiration, it was necessary to consider strains with mutations that eliminated each individually and in combination (17). Mutation of the primary nitrate reductase was accomplished by deleting narG (47) to create E. coli EDL933 ΔnarG::kan and E. coli MG1655 ΔnarG::kan. When ΔnarG::kan strains were fed together with their respective parent strains, they initiated colonization but then declined numerically (2.3 logs; \( P < 0.003 \)) (Table 1 and Fig. 4A). To test the involvement in colonization of the secondary nitrate reductase, mutants were constructed in which narZ was deleted, the phenotype of which was described previously (46). Likewise, the involvement of the periplasmic nitrate reductase was tested with a construction that deleted napD and napA, which encode the assembly protein and large subunit of the reductase, respectively (46). In colonization assays, E. coli EDL933 ΔnarZ::cat, E. coli MG1655 ΔnarZ::cat, E. coli EDL933 Δ(napD-napA)::cat, and E. coli MG1655 Δ(napD-napA)::cat cocolonized with their wild-type parents, indicating that strains with these individual mutations had no phenotype in the intestine (Table 1).

Although the individual ΔnarZ::cat and Δ(napD-napA)::cat mutants did not exhibit colonization defects, there is reason to believe these gene systems should be expressed in the wild types under the conditions present in the intestine. First, the intestine contains regions that are microaerobic and others that are anaerobic (20), yet apparently is sufficiently anaerobic overall for Fnr control to be a factor in success of the entire E. coli population (Fig. 3). Second, we measured a concentration of \( 2.62 \pm 0.21 \) mM nitrate in mouse cecal mucus (data not shown), a concentration which is physiologically relevant for controlling expression of the two nitrate-inducible systems (52). Third, E. coli cells isolated from the intestine show both
The absence of the primary nitrate reductase, we constructed the phenotypes of these nitrate reductase mutations in the intestine. To investigate reasonable to expect that both the periplasmic and secondary one-half of the maximal level at 2.5 mM (52). Thus, it is maximally induced at 1 mM nitrate and is expressed at AGHBC operon that encodes the periplasmic nitrate reductase is dependent and induced in stationary phase (9). The logarithmic and stationary-phase characteristics (26). The EDL933 in these experiments is statistically significant between the narG background, suggesting a synergy, rather than mere redundancy, between the primary nitrate reductase and the other two systems. Apparently, conditions in the intestine signal induction of the three nitrate reductase gene systems, which together confer a competitive advantage to E. coli.

**DISCUSSION**

Figure 5 shows a model of the respiratory pathways that are critical for successful colonization by both EHEC and commensal E. coli. The results indicate that the gut is not strictly anaerobic, because the high-affinity cytochrome bd oxidase is required to successfully compete with the wild-type for colonization (Fig. 1 and 2). Also, anaerobic respiration of nitrate and fumarate is essential for colonization.

**Fumarate reductase is necessary for colonization.** To test the importance of fumarate as an alternative electron acceptor in vivo, we constructed mutants with frdA, which are known to inactivate fumarate reductase (43). E. coli EDL933 ΔfrdA::kan and E. coli MG1655 ΔfrdA::kan mutants were fed together with their respective parent strains and found to initiate colonization but then declined by approximately 4 logs relative to the wild type (Table 1 and Fig. 4D). Thus, fumarate reductase mutants competed poorly, indicating that fumarate is used in the intestine as an alternative electron acceptor. Since fumarate was not detected in intestinal mucus (data not shown), it most likely was generated endogenously, giving rise to succinate as a fermentation product during anaerobiosis (41).
demands respiratory flexibility and use of the best available electron acceptor. The results allow us to deduce the intestinal environment as it is perceived by *E. coli*. Accordingly, the niches defined by mutational analysis of respiratory pathways should correspond with in vivo availability of exogenous electron acceptors (i.e., oxygen and nitrate) but not necessarily fumarate, which is generated endogenously by sugar degradation via central metabolism. These respiratory niches could be open to the entire population, wherein each bacterium simultaneously uses both oxygen and nitrate, or individual cells and microcolonies could each use different electron acceptors. If distinct microaerobic and anaerobic niches were to exist in the intestine, then mutants in the respective respiratory pathways would be maintained at populations corresponding to availability of the cogent electron acceptor when in competition with respiratory-competent wild types. However, since the loss of the high-affinity oxygen, nitrate, or fumarate respiratory pathways leads to the near or complete elimination of the entire population in competition with respiratory-competent wild types. However, since the loss of the high-affinity oxygen, nitrate, or fumarate respiratory pathways leads to the near or complete elimination of the entire population in competition with respiratory-competent wild types. However, since the loss of the high-affinity oxygen, nitrate, or fumarate respiratory pathways leads to the near or complete elimination of the entire population in competition with respiratory-competent wild types. However, since the loss of the high-affinity oxygen, nitrate, or fumarate respiratory pathways leads to the near or complete elimination of the entire population in competition with respiratory-competent wild types. 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consumed by bacterial respiration suggests the interesting possibility that facultative anaerobes may make the intestinal environment more microaerobic. Indeed, this conclusion is supported by previous studies of the effect of streptomycin treatment on the mouse anaerobic microflora, which selectively removes facultative anaerobes (i.e., E. coli, enterococci, streptococci, and lactobacilli). Following administration of streptomycin, populations of strict anaerobes (e.g., bifidobacteria and clostridia) decreased, while populations of so-called “anaerobes” were unchanged (22): e.g., Bacteroides fragilis, which respires oxygen when available in low concentrations (5). Thus, comparisons of the populations of anaerobes in mice with or without facultative anaerobes present support the hypothesis that oxygen-scavenging facultative anaerobes (e.g., E. coli) promote the stability of the predominantly anaerobic microflora, exemplifying how a minor member can have a large impact on an ecosystem.

Despite the apparent competitive advantage gained by oxygen respiration, the E. coli population is limited to between 10^6 and 10^9 CFU/g feces; i.e., E. coli represents between 1 in 1,000 and 1 in 10,000 bacteria in the intestine. The nutrient-niche hypothesis states that to be successful each species of the intestinal microflora must use at least one carbon source better than all other species (16). Corollary to this hypothesis, the population size of any member of the microflora is determined by the concentration of its preferred nutrient(s). The available concentrations of the seven sugars that contribute to colonization by E. coli MG1655 are quite low (12, 37). Since E. coli does not secrete polysaccharide-degrading enzymes, its preferred substrates are most likely provided by anaerobes, which degrade mucosal polysaccharides and dietary fiber and are thought to release the breakdown products for use by the host and other microbes (11). These facts lead to the conclusion that E. coli maximizes its growth yield by coupling oxidation of low nutrient concentrations to respiration in the intestine. This may be a general strategy of facultative anaerobes, which generally grow well on simple sugars but do not secrete polysaccharide-degrading enzymes. Thus, high-efficiency respiration may ensure the success of facultative anaerobes in the intestine, albeit always in lower numbers, by allowing them to maximize cell yield on scarce resources.

Since most mucosal pathogens are facultative anaerobes, our conclusions may extend to other mucosal pathogens. In support of this idea, Mycobacterium tuberculosis genes encoding cytochrome bd oxidase and the nitrate transporter were induced during mouse lung infection; a cytochrome bd oxidase mutant was attenuated during transition to chronic infection in mice (42). Likewise, Shigella flexneri cytochrome bd mutants showed decreased intracellular survival and attenuated virulence in mouse infections (53). These examples demonstrate the importance of respiration during infection by particular mucosal pathogens and support the idea that oxygen stimulates infectious disease by providing a competitive advantage for pathogens. Since there appears to be no distinction between enterohemorrhagic and commensal E. coli with respect to the respiratory pathways used in vivo, we suggest caution in targeting respiratory metabolism for combating EHEC infections because of potential collateral damage to commensal facultative anaerobes and the resulting instability of the intestinal microbiota (16).

In summary, we have shown that E. coli uses both aerobic and anaerobic respiratory pathways during colonization. The results presented in this study support the conclusion that the intestine is microaerobic and that aerobic bacterial respiration in the intestine is essential for competition and therefore successful colonization. Apparently, E. coli respires oxygen to optimize its reproduction in animals despite the low availability of its preferred carbon sources, which maximizes its colonization efficiency.

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REFERENCES


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