EDITORIAL COMMENTARY

Bacterial Colonization: Can We Live With It?

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(See the article by O’Fallon et al. on pages 1375–81)

It is a time of change in America. Forces are aligning in ways not previously imagined to allow the possibility of substantial progress in preventing health care–associated infections. In January 2009, the US Department of Health and Human Services released a draft Action Plan to Prevent Healthcare-Associated Infections [1], confirming their commitment to bring together experts, policy makers, regulators, and funding organizations, to map out a strategic plan for significantly reducing the incidence of health care–associated infections. More evidence to inform this plan is needed.

In the context of this new world, O’Fallon et al. [2] offer the promise of data that will help in the “development of effective guidelines for the prevention of MDRGNB spread in the health care setting” [2, p. 1376]. In their article in this issue of Clinical Infectious Diseases, entitled “Colonization with Multidrug-Resistant Gram-Negative Bacteria: Prolonged Duration and Frequent Cocolonization” [2], O’Fallon and colleagues describe the natural history of multidrug-resistant gram-negative bacteria (MDRGNB) colonization in a small cohort of poorly functioning, elderly nursing home residents. Their major findings are well summarized in the title of their article: simultaneous colonization with more than one organism is common, and duration of colonization is prolonged.

Do O’Fallon and colleagues deliver on their promise? Do their findings inform efforts to prevent the spread of MDRGNB or, more importantly, to prevent health care–associated infection due to MDRGNB? To the extent that their findings confirm the natural history that we might have predicted and help to clarify what we should not do, the study could be considered a first step in the right direction.

The study’s finding that 20% of subjects were colonized by at least 1 MDRGNB strain is not a great surprise. This carriage rate is in line with recently reported rates of carriage of selected gram-negative bacteria among newly hospitalized patients (7%) [3], healthy vegetarians (14%) [3], and Saudi Arabian inpatients (26%) [4]. The persistence of these strains is also not unexpected, given published evidence regarding long-term persistence of strains of Escherichia coli [5–7]. The authors do not discuss the 80% of subjects who were not carrying MDRGNB, but one might surmise that the majority of them were colonized with other gram-negative bacteria, as are most humans, and that the natural history of their colonization might be similar. In short, it is likely that all residents of this nursing home (and, indeed, most individuals in the general population) are carrying gram-negative bacteria in their stool.

Once present in the feces, do MDRGNB cause harm to patients? O’Fallon and colleagues do not report data regarding clinical infections or evidence of cross-transmission of MDRGNB strains among subjects. The literature tells us that most patients who harbor MDRGNB in their intestines do not develop infection (although it is clear that intestinal colonization often precedes the onset of infection) [8]. Clinical gram-negative bacterial infections can cause substantial morbidity and mortality; moreover, multidrug-resistant organisms pose treatment challenges. Preventing these infections is a worthwhile endeavor.

How does the current study by O’Fallon et al. [2] guide our interventions? Given their finding of long-term persistence of MDRGNB colonization, O’Fallon and colleagues conclude that there is no role for surveillance cultures of stool in the management of fecal colonization. I would agree. Cultures of stool will always reveal the presence of bacteria that could cause a health care–associated infection. Interventions to keep stool from gaining access to sterile sites and to reduce fecal cross-contamination between patients should be universally practiced; neither their im-
plementation nor their discontinuation should be determined by the presence or absence of specific strains of fecal bacteria. But, beyond good infection prevention practices, is there a role for eradicating specific organisms that we find in the stool? If there is, is eradication even possible? And if it is possible, what are the unintended consequences of interventions aimed at individual organisms?

If we wish to consider strategies for interrupting the natural history of colonization with gram-negative bacteria, a deeper understanding of the fecal microenvironment and of the ways in which we knowingly and unknowingly influence it is helpful. This diverse community of literally billions of organisms is affected by an array of factors, ranging from simple dietary intake and medication exposure to complex genetic, ecological, and evolutionary factors [9–11]. O’Fallon and colleagues do not speculate on the source of the specific MDRGNB in their subjects’ feces and were not able to identify risk factors for their persistence in this fairly homogeneous population. Previous exposure to antibiotics was common. Fecal incontinence was almost universal, but data regarding urinary incontinence and the presence of urinary catheters are not reported, nor are data on the use of feeding tubes or the details of dietary intake. Factors such as these can affect the human intestinal tract in ways that might change its hospitality to colonizing or pathogenic bacteria (and perhaps explain the observation that colonization with Proteus species appeared to be particularly persistent in this study).

Specific changes associated with aging, which are potentially relevant to this study population, likely have profound effects on the ability of certain gram-negative bacteria to establish intestinal residence. A recent review article [12] outlined changes in taste, smell, chewing, and swallowing that can affect dietary intake, as well as changes in stomach acidity and intestinal motility that affect the chemical environment of the gut. In association with these physical and chemical changes, marked changes occur in the intestinal microbiota of even healthy elderly adults, including reductions in the number and diversity of beneficial anaerobes and increases in Clostridia species and facultative anaerobes [12]. It is certainly plausible that similar changes might occur in the guts of critically ill patients.

In response to MDRGNB colonization, a narrow focus on eliminating “bad bugs” might lead us to consider such interventions as selective digestive tract decontamination or selective oropharyngeal decontamination. Such strategies may eliminate harmful bacteria from the gut in the short term, and they may even prevent infection during limited periods of high risk, such as during colon surgery [13] or intensive care unit stay [14]. Yet even those antimicrobial agents with the narrowest spectrum affect many beneficial gut microorganisms, many of which are not even cultivable, but which perform a multitude of health-promoting actions [9]. Moreover, eradication of one organism is likely to pave the way for survival of another. As a long-term strategy, sequential eradication of ever-more-resistant organisms is likely to be futile at best and, at worst, potentially harmful to patients.

A more appealing approach may be to alter the intestinal environment in ways that prevent or reduce the duration of colonization with potentially pathogenic organisms. If disruptions in the normal balance of intestinal microflora that are brought about by diet, medication, aging, or other factors allow MDRGNB to establish residence in the human intestine, then interventions that restore the normal flora might result in their elimination. The use of probiotics, prebiotics, and synbiotics may be one way to achieve this restoration [12, 15]. Intriguing evidence has mounted about interventions ranging from “fecal bacteriotherapy” to successfully treat Clostridium difficile colitis [16] to the use of probiotics, such as Bifidobacterium longum and Lactobacillus acidophilus, in combination with prebiotics to inhibit the growth of enteropathogens in patients receiving antibiotics [17]. These interventions warrant further clinical study, because they appear to have fewer attendant unintended harmful consequences.

In the final analysis, however, our understanding of the fecal microenvironment is in its infancy. Although we certainly have the ability to influence the complex microbial community that inhabits the human intestine, our ability to control the effects that our interventions will have is limited, and the potential for inadvertent harm, especially over time, is significant. From the pragmatic standpoint of a hospital epidemiologist, the most important thing to know may be that, regardless of whether and how we choose to intervene, we will begin and end with a gut full of bacteria, many of which might become pathogens responsible for a health care–associated infection.

Collaboration with researchers working to explore the human intestinal microenvironment may ultimately reveal novel ways to preserve and protect the vibrant community within, to the benefit of both humans and the billions of organisms that live there. In the meantime, it may be time to reconsider the wisdom of labeling and targeting “bad bugs” (a nomenclature that itself implies a limited, human-centric perspective) and turn our attentions, instead, to containing them within their natural reservoirs, where they are less likely to do harm. Although we seek greater understanding and more-elegant tools, better adherence to such time-tested and universally applicable strategies as hand hygiene, barrier precautions during the care of incontinent patients, and appropriate use of antimicrobial therapy to minimize alteration of intestinal flora will serve us well.

Our world is changing; there is much good that can be done through collaborative and cooperative efforts. As we forge new alliances in our quest to eliminate preventable health care–associated infection, we might also consider a call to new...
and mutually beneficial ways of coexisting with the microbial flora of the world [18]. Bacteria in the gut may be a great place to start.

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References