

a given clinical problem? To what extent must the combinations be tailored to individuals, with their distinct genetic backgrounds, microbiomes, behaviors and medical histories<sup>8</sup>? And finally, what does it take to ensure the stability and resilience of the newly established 'healthy' microbial community, and what is the role of host factors, such as immune system functions, in this process (Fig. 1)?

The results of Lawley *et al.*<sup>1</sup> also have implications for currently available formulations of therapeutic bacteria. Probiotics contain live microorganisms that stimulate the growth of other microorganisms in a host<sup>9</sup>. Global sales of probiotics have reached \$25 billion<sup>10</sup>, and the size of this market is growing steadily. Most commercial probiotics are lactic acid-producing *Bifidobacterium* or *Lactobacillus* species and strains. Some contain combinations of strains or species, generally from two to eight. Despite claims of a wide variety of benefits, data that support the use of probiotics are available for only a few indications, including treatment of acute infectious diarrhea, prevention of antibiotic-associated diarrhea in adults and prevention of necrotizing enterocolitis in premature infants<sup>9</sup>. So far, the selection of probiotic species, strains and consortia for use in humans has not been based on broad assessments of the human microbial ecosystem<sup>6</sup>. But the probiotic market may soon be subjected to greater regulatory scrutiny, especially for products associated with claims about health benefits<sup>10</sup>. Despite the importance of synergy among members of complex communities and the emerging properties of community collectives, historical precedents suggest that regulators may approach probiotic cocktails as sets of individual strains, each requiring a separate risk-benefit assessment—even in the absence of relevant data on their individual behavior in the human host.

As we think more broadly about habitat restoration within the human microbial ecosystem, our goals should be promotion of native species, targeted removal of invasive species, and ecosystem management based on frequent monitoring. To achieve any of this, we will need to define the ecosystem services and service providers relevant to each aspect of human health<sup>2</sup>. In turn, we must create a wide variety of functional assays with which to measure these services. Although this will entail a great deal of work, the technologies and genomics resources needed to embark on this project are at hand.

#### COMPETING FINANCIAL INTERESTS

The author declares no competing financial interests.

1. Lawley, T.D. *et al.* *PLoS Pathog.* **8**, e1002995 (2012).

2. Costello, E.K., Stagaman, K., Dethlefsen, L., Bohannan, B.J. & Relman, D.A. *Science* **336**, 1255–1262 (2012).
3. Dethlefsen, L., McFall-Ngai, M. & Relman, D.A. *Nature* **449**, 811–818 (2007).
4. Holling, C.S. *Annu. Rev. Ecol. Syst.* **4**, 1–23 (1973).
5. Bohnhoff, M. & Miller, C.P. *J. Infect. Dis.* **111**, 117–127 (1962).
6. Lemon, K.P., Armitage, G.C., Relman, D.A. & Fischbach, M.A. *Sci. Transl. Med.* **4**, 137rv5 (2012).
7. Brandt, L.J. *et al.* *Am. J. Gastroenterol.* **107**, 1079–1087 (2012).
8. Goodman, A.L. *et al.* *Proc. Natl. Acad. Sci. USA* **108**, 6252–6257 (2011).
9. Guarner, F. *et al.* *J. Clin. Gastroenterol.* **46**, 468–481 (2012).
10. Food and Nutrition Board, Institute of Medicine. Consumer insights from the industry perspective. In *The Human Microbiome, Diet, and Health: Workshop Summary* (eds. Pray, L., Pillsbury, L. & Tomayko, E.) 99–119 (National Academies Press; 2012).

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