

Articles of Significant Interest Selected from This Issue by the Editors

Community Structure and Dynamics Determined by Microbial Warfare

Microbes live in complex communities. Like the formation of country borders as a result of military conflicts, microbial community structures are heavily influenced by antagonistic interactions. Using advanced imaging tools and bacterial species capable of mutual destruction as a model, Wong et al. (p. 6881–6888) provide direct visual evidence of how coexistence is achieved through the segregation of mixed populations into single-species clonal clusters that are driven by lethal interactions. The benefit of cluster formation is obvious: the threat of attack is eliminated for the cells inside, and it is greatly reduced for cells at the border.

Biofilm Formation by *Pseudomonas brassicacearum* Leads to *Caenorhabditis elegans* Starvation

In the soil, grazing predators like the nematode *Caenorhabditis elegans* represent a threat to bacterial persistence. Studies by Nandi et al. (p. 6889–6898) reveal that the biocontrol bacterium *Pseudomonas brassicacearum* strain DF41 is able to escape predation through two distinct mechanisms: the first involves exposing the nematode to toxic bacterial metabolites, and the second entails biofilm establishment on the nematode's head, which blocks feeding. Moreover, growth in the presence of nematodes leads to altered gene expression and metabolite production by DF41. This report clearly demonstrates the formation of biofilms on the surface of *C. elegans* by a pseudomonad.

Importance of Rare Taxa during Tree Mortality

With the rise in global temperatures and more frequent drought-like conditions, evergreen forests across the globe are experiencing large-scale mortality due to beetle infestation. In turn, terrestrial biogeochemical conditions are being altered. Mikkelsen et al. (p. 6912–6919) found that even though shifts in traditional ecological drivers such as pH or soil water content may be modest, the terrestrial microbial community is adapting to this large disturbance in the ecosystem. However, it is the metabolically active rare taxa that are playing a large and disproportionate role in this adaptation, indicating that the study of these microbes might provide a more sensitive indicator of disruption than edaphic parameter measurements.

Oxalobacter formigenes Reduces Intestinal Oxalate and Is Not Impacted by Normal Microbiota in Germfree Mice

A lack of colonization with the oxalate-degrading anaerobe *Oxalobacter formigenes* is a risk factor for recurrent calcium oxalate kidney stone disease, suggesting that the colonization of calcium oxalate kidney stone formers who lack this bacterium may be an effective way to minimize the risk of this disease. Li et al. (p. 6952–6960) show that *O. formigenes* colonizes germfree mice and retains efficient intestinal oxalate-degrading function following the addition of the altered Schaedler flora. This work supports the use of *O. formigenes* as a probiotic that has limited impact on the composition of normal microbiota but provides efficient oxalate-degrading function.

A New Source of Methane in Freshwater Environments

Methanogenesis occurs in anoxic environments, but high levels of methane are consistently observed in the surface waters of lakes, which are a significant source of atmospheric methane. Yao et al. (p. 6994–7003) demonstrate that phosphorus-limited freshwater bacteria can obtain phosphorus from methylphosphonate, releasing methane as a by-product, and that this process is modulated by phosphate availability. Freshwater metagenomic data show that the C-P lyase pathway that cleaves methylphosphonate is widespread, suggesting that methane emissions from fresh waters may be controlled not only by anoxia and carbon availability, which affect methanogenesis, but also by phosphorus availability.