

Articles of Significant Interest Selected from This Issue by the Editors

Australian Dust Storm Associated with Potentially Pathogenic Marine Fungal “Bloom”

Dust from deserts not only deposits nutrients into the oceans, which can enhance primary production, but also spreads microbial communities. Using continuous plankton recorder technology, Hallegraeff et al. (p. 3315–3320) showed how an Australian dust storm triggered a massive coastal fungal “bloom” of *Aspergillus sydowii*, stretching over an area 25 times the size of England. While no impacts comparable to Caribbean coral disease were observed, Australian fungal cultures reduced *Symbiodinium* dinoflagellate coral symbiont motility, thus raising the possibility of future marine ecosystem impacts from dust storms harboring more-pathogenic strains. Dust storms are likely to increase in number with climate change as Australia becomes drier.

Novel Gene Replacement Procedure and Genome Expression

Lactic acid bacteria have shown significant potential as vaccine delivery vehicles, primarily through the use of plasmids that express bioactive compounds at mucosal surfaces, where they can stimulate appropriate immune responses. However, procedural problems have included antibiotic resistance and plasmid instability. In studies by Song et al. (p. 3321–3326), PP α T expression cassettes were inserted at the *upp* site of the *Lactobacillus casei* chromosome via site-specific recombination. The plasmid was subsequently deleted by increasing the temperature. However, the antigen gene may be replicated along with the bacterial chromosomal DNA, and antigen protein was demonstrated on the surface of bacterial cells.

Insights into Sustainable Biochemical Production by *Clostridium autoethanogenum*

Acetogenic bacteria, such as *Clostridium autoethanogenum*, use carbon monoxide (or carbon dioxide plus hydrogen gas) as their sole source of energy and carbon. They have attracted attention because of their potential for producing biofuels and chemicals while simultaneously lowering greenhouse gas emissions. Köpke and colleagues (p. 3394–3403) have identified and characterized the enzymes used by *C. autoethanogenum* to produce the valuable chemical intermediate 2,3-butanediol. Critically, this bacterium possesses a broad-specificity alcohol dehydrogenase for synthesizing 2,3-butanediol from acetoin. This enzyme is also highly active toward the nonphysiological substrate acetone, meaning that *C. autoethanogenum* is an effective whole-cell biocatalyst for converting acetone to isopropanol.

Spontaneously Inducible Prophages in *Lactobacillus gasseri*

Although numerous bacteriophages in probiotic microbes have been well characterized, the spontaneous induction, lytic host range, and range of transduction of temperate *Lactobacillus* phages have not been thoroughly investigated. Baugher et al. (p. 3508–3517) report that the common human commensal bacterium *Lactobacillus gasseri* ADH harbors two spontaneously inducible prophages: a previously characterized 43.8-kb *cos*-type *Siphoviridae* phage, ϕ adh, and a newly discovered, and possibly defective, 38.3-kb *pac*-type *Myoviridae* phage, jlb1. Each phage is capable of transducing plasmid DNA to other *L. gasseri* human isolate strains spontaneously in cocultivation experiments. Temperate phages of *L. gasseri*, a common resident of the human mouth, gastrointestinal tract, and vagina, likely serve as key vehicles for horizontal gene transfer among commensal lactobacilli.

Metabolic Potential of Microorganisms That Mediate Carbon and Nutrient Cycling in Peatlands

Northern peatlands store approximately one-third of Earth’s soil carbon, but the microbial communities that regulate carbon turnover in these wetlands remain understudied. Lin et al. (p. 3531–3540) linked peat decomposition and the fate of greenhouse gases with specific microbial groups and metabolic pathways. Metagenomic analysis revealed diverse genes and pathways associated with the depth-dependent microbial potential for sugar and phenolic compound metabolism, fermentation, methane dynamics, and nutrient acquisition, in agreement with peat decomposition as determined by the vertical distribution of plant-derived organic compounds. Moreover, the results obtained by closely coupling metagenomics with nuclear magnetic resonance spectroscopy in this study provide strong evidence for depth-dependent P limitation in the peat column.