IN BRIEF

ENVIRONMENTAL MICROBIOLOGY

Conversion and conservation of light energy in a photosynthetic microbial mat ecosystem

Al-Najjar, M., de Beer, D., Jørgensen, B. B., Kühl, M. & Polerecky, L. *ISME J.* 12 Nov 2009 (doi:10.1038/ismej.2009.121)

Whereas photosynthesis in plants and algae is well studied, the energy efficiency of photosynthesis in microbial mats in benthic waters and in biofilms is only poorly understood. In this study, Al-Najjar and colleagues measured the light energy used in a cyanobacterial mat at submillimeter spatial resolution. They found that the efficiency of light energy conversion into chemical energy depends on the absorbed radiance, which correlates with the depth of the organisms in the water. At low light levels, 4.5% of the incident light was converted to chemical energy, with most of the light energy dissipating as heat, whereas at higher light levels the system became saturated and its efficiency decreased.

BACTERIAL PATHOGENESIS

Inclusion biogenesis and reactivation of persistent *Chlamydia trachomatis* requires host cell sphingolipids

Robertson, D. K., Gu, L., Rowe, R. K. & Beatty, W. L. *PLoS Pathog.* **5**, e1000664 (2009)

Chlamydia trachomatis is an intracellular bacterial pathogen that scavenges nutrients, including sphingolipids, from its host. Robertson and colleagues now show that these lipids are required for the formation of the membranous compartment, or inclusion, in which the bacteria reside. In host cells that are treated with an inhibitor of sphingolipid synthesis or that cannot make sphingolipids, the inclusions do not fuse, and they lyse after 30 hours compared with after 72 hours in untreated, wild-type cells. Although the released bacteria can reinfect host cells and their developmental cycle is accelerated, far fewer infectious progeny are formed in the presence of the inhibitor. In addition, the absence of sphingolipids leads to a decrease in reactivation from latency. These results show that the lipid environment of the inclusion is an important signal for the development of *Chlamydia* spp.

CELLULAR MICROBIOLOGY

The bacterial defensin resistance protein MprF consists of separable domains for lipid lysinylation and antimicrobial peptide repulsion

Ernst, C. M. *et al. PLoS Pathog.* **5**, e1000660 (2009)

The bacterial MprF protein provides protection against cationic antimicrobial peptides by decreasing the surface charge on the outer leaflet of the plasma membrane through the addition of specific amino acids to the membrane phosphatidylglycerol. The amino terminus of MprF consists of 14 transmembrane domains, and this new study shows that when the first 8 N-terminal transmembrane domains are removed, lysyl-phosphatidylglycerol (Lys-PG) is still synthesized but remains in the inner leaflet of the membrane. When these eight N-terminal transmembrane domains and the remainder of the protein are expressed separately, Lys-PG is synthesized and transferred to the outer leaflet of the membrane. Thus, MprF is a dual-domain protein, with an enzymatic domain and a 'flippase' domain that together allow the synthesis and proper localization of Lys-PG. Such a domain organization may be more prevalent among enzymes involved in the modification of the plasma membrane or the cell envelope.