speculate that it may involve the resident microbes of the Kisameet clay, which includes Actinobacteria, a genus known to produce small bioactive molecules. This is the first step toward scientifically validating the medicinal properties of the clay, long used as a natural remedy by Heiltsuk First Nation people.

Behrooziad S, Svensson SI, Davies J. Kisameet clay exhibits potent antibacterial activity against the ESKAPE pathogens. mBio Published online 26 January 2016; doi:10.1128/mBio.01842-15

NEW FROM ASM
Selfish Drug-Resistance Mechanisms Require Less Drug

Bacteria exhibiting antimicrobial resistance utilize a number of mechanisms to do so. Some, such as drug export pumps, benefit only the resistant cell, while others, such as drug-modifying enzyme secretion, can benefit nearby cells regardless of their resistance profile. Data from the University of York in York, United Kingdom, now show that the sociality of the resistance mechanism influences the selective conditions for the related resistance plasmid. First author Michael Bottery and lead author Michael Brockhurst used Escherichia coli with the RK2 plasmid, which contains both a selfish drug-resistance mechanism (efflux pump) and a cooperative drug-resistance mechanism (modifying enzyme). In the absence of drug, plasmid-free bacteria had a clear growth advantage. Positive selection for plasmid-carrying bacteria required drug concentrations above the MIC of the plasmid-free strain for the selfish resistance mechanism, but just 1.3% of the MIC of the plasmid-free strain for the selfish resistance mechanism. These data suggest that selfish mechanisms such as efflux pumps play an important role for selective maintenance of multidrug-resistant plasmids.


NEW FROM ASM
Whole-Genome Sequencing Explains Hospital Outbreak

Whole-genome sequencing technologies have helped researchers understand the persistence of a years-long Swiss hospital outbreak. The University Hospital of Lausanne in Lausanne, Switzerland, experienced an outbreak of methicillin-resistant Staphylococcus aureus (MRSA) between 2008 and 2012. A collaboration between the University Hospital of Lausanne, John Radcliffe Hospital in Oxford, England, and the University of Bath, in Bath, England, was initiated by head scientist Dominique Blanc and first author Laurence Senn to investigate the outbreak. Patient screening revealed 70% of carriers had positive rectal swabs, which was surprising, because S. aureus is not normally considered part of the gastrointestinal microbiome. Sequencing results showed the outbreak was due to clonal spread of a specific strain expressing several genes that likely helped it to persist in the hospital, including genes conferring resistance both to mupirocin, commonly used to decolonize MRSA carriers, and to chlorhexidine, commonly used to disinfect hospitals. Combined with the unusual proclivity for enteric colonization, these traits likely facilitated adaptation specific for a health-care setting. The research team posited that intensified screening of hospital patients and increased disinfection of patient environments had the highest impact in quelling the outbreak.


NEW FROM ASM
Promising Microarray Tests Water Safety

Scientists are working on methods to detect hundreds of microbial species in a single assay, in order to streamline water safety testing. The research, performed as a collaboration between West Virginia University in Morgantown, W. Va. and University of South Florida in Tampa, Fla., became closer to reality as scientists at the two institutions validated methodology to screen pathogen genes via microarray. First author Xiang Li and lead scientist Jennifer Weidhaas took their method, which uses ultrafiltration concentration, nucleic acid extraction and amplification, and a unique microarray containing 411 distinct probes and controls, and tested it using both marine and fresh water. The array differentiated sources of fecal pathogens in surface water samples compared with samples spiked with sewage, a promising step forward, as human sewage contamination is strong predictor for human pathogens. The microarray did not compare favorably to qPCR in sensitivity tests, which the authors speculate may be due to uneven nucleic acid amplification. Future research will go toward refining sensitivity.