

NEWS BRIEFS

Superbugs hide in hospital wastewater, genomic tests reveal

A dangerous brew percolating beneath the National Institutes of Health (NIH) Clinical Center in Bethesda, MD, may hold a key to tracking the spread of antibiotic-resistant organisms in hospitals, according to a new study that sought to track infections among hospital patients. Comparing genomic samples from patients



with environmental samples collected around the hospital, NIH researchers tracked down the extrachromosomal elements known to harbor resistance genes. They found plasmids flourishing in the drainpipes and wastewater

systems under the hospital. The study's findings, published in February 2018 in *mBIO*, an open-access journal of the American Society for Microbiology, could lead to better surveillance techniques and countermeasures to combat resistant organisms in hospitals. Particularly dismaying in this case, the investigators found plasmids harboring genes conferring resistance to carbapenems, a class of antibiotics considered a last resort against multidrug-resistant organisms. The microbiologists who led the study suggested that use of these antibiotics in hospitals is contributing to the buildup of these resistance genes in wastewater systems, where they can be passed among various bacterial species, even if the organisms themselves are never directly exposed to the antibiotics. The 5-year study was conducted in response to a 2011 outbreak of carbapenem-resistant *Klebsiella pneumoniae* among NIH hospital patients. While the organisms in the sewers did not pose an immediate threat to patients, investigators suggested that whole-genome analysis methods could help prevent future outbreaks. —Karyn Hede, *News Editor*

British project to sequence 100,000 genomes lagging behind schedule

Apparently, with the flatworm *Planaria* less is more. The master of body-part regeneration is missing genes previously thought to be essential for life, yet it not only survives but thrives when cut into tiny pieces. The recently completed flatworm genome is leaving biologists slack-jawed by its unique structure and missing genes. Scientists at the Max Planck Institute of Molecular Cell Biology and Genetics and collaborators reported in a January 2018 issue of *Nature* that *Schmidtea mediterranea* contains giant repeated elements, has new genes unique to the organism, and, crucially, is missing key genes previously thought vital to existence. Previous attempts to sequence the *Planaria* genome resulted in leftover short genomic crumbs that scientists could not place. To solve the problem, geneticists used newer sequencing technology capable of reading very long stretches of contiguous sequence, up to 40,000 base pairs in length. Once completed, the genome was revealed to be unlike any other. For instance, the organism lacks the genes *MAD1* and *MAD2*, which had been thought essential to maintaining chromosome integrity. Investigators now plan to use the information to inform studies of evolution, stem cell biology, and regenerative medicine.

—Karyn Hede, *News Editor*



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