Overprescription of antibiotics is selecting for antibiotic resistance, contributing to one of the great medical problems of our time. Diagnosis of bacterial infections, and determination of antibiotic susceptibility profiles are slow and tedious, and consequently, patients may frequently receive antibiotics to which their particular infection is resistant. Now Mats Nilsson and Dan I. Andersson of Uppsala University in Sweden and collaborators have developed a general method to rapidly identify culprit bacteria species and determine their antibiotic susceptibility profiles. An initial, short cultivation step to be conducted both in the absence, and in the presence of different antibiotics is combined with a sensitive species-specific padlock probe detection of the bacterial target DNA, to determine whether the bacteria are growing or not, to indicate resistance versus susceptibility. In a proof-of-concept for urinary tract infections, they applied the method to determine the susceptibility profile of Escherichia coli for two drugs. Accuracy was 100%; duration, just 3.5 hours. That, the investigators write, would minimize the need for prescribing broad-spectrum antibiotics due to unknown resistance profiles of the treated infection.


Malaria afflicts around 200 million people annually, killing more than 600,000, mostly in Africa, according to the Centers for Disease Control and Prevention. Now Nicholas A. Malmquist of the Pasteur Institute, Paris, France, et al. show that compounds derived from inhibitors of the histone-modifying methyltransferase enzymes kill malaria parasites in culture, as rapidly as the fastest-killing antimalarials available. They show further that these compounds are highly effective against multidrug resistant field isolates from Cambodia, and clinical isolates of the two most prevalent species of human malaria, Plasmodium falciparum and P. vivax. Furthermore, the compounds kill the malaria parasites specifically, that is, while remaining harmless to animal models and to their microbiomes. Additionally, they kill the parasites in both the form they takes in mosquitos, and in that in which they inhabit mammalian hosts.

“All this suggests that this compound series can be developed into new antimalarials effective at both killing and reducing transmission of the relevant parasites currently threatening people in endemic regions,” says Malmquist.


Some Flu Viruses Potentially More Dangerous Than Others

Certain subtypes of avian influenza viruses have the potential to cause more severe disease in humans than do others. Jeffery K. Taubenberger of the National Institute of Allergy and Infectious Disease et al. show that viruses expressing the avian H1, H6, H7, H10, or H15 hemagglutinins led to rapid weight loss and fatal pneumonia infections in mice and caused more cell damage in normal human lung cells than did avian influenza viruses with other hemagglutinin subtypes. Conversely, mice infected with H2, H3, H5, H9, H11, H13, H14, and H16-expressing viruses suffered only mild weight loss, with no significant disease. The team showed similar results using hemagglutinins from two 2013 H7N9 flu viruses from outbreaks in China. These results suggest that hemagglutinins may not require immune cells to trigger cell damage, but instead may cause apoptosis or other molecular processes that could lead to fatalities, says Taubenberger.


Restrooms: Not as Unhealthy as You Might Think

Microbial succession in a sterilized restroom begins with bacteria from the gut and the vagina, and is followed shortly by skin microbes. “We