

## IN BRIEF

## ANTI-INFECTIVES

Isolation and characterization of novel marine-derived actinomycete taxa rich in bioactive metabolites

Magarvey, N. A. *et al. Appl. Environ. Microbiol.* **70**, 7520–7529 (2004)

Nearly all actinomycetes cultured so far are saprophytic soil bacteria that produce a large array of secondary metabolites, many of which are potent anti-infectives. Following up on research which showed that uncultured marine actinomycete species were abundant in subtidal sediments, Magarvey and colleagues used a selective enrichment technique of cellulose filter paper on an agar-based medium to isolate more than 90 new strains of marine actinomycetes. These actinomycetes, which have been placed in two new genera, could prove to be a treasure trove of new bioactive molecules. Several of the secondary metabolites produced by these bacteria were shown to be active against Gram-positive pathogens, malignant cells and even vaccinia virus infection.

## VIROLOGY

Replicon system for Lassa virus

Hass, M. *et al. J. Virol.* **78**, 13793–13803 (2004)

Lassa virus, which causes an acute haemorrhagic fever, is endemic in several west African countries and is sometimes fatal, with ~5,000 deaths recorded annually worldwide. No vaccination or drug treatments are available but Hass and co-workers have advanced the search for therapeutics by developing a reverse genetics system for this pathogenic arenavirus. Minigenomic replicons were developed based on those already designed for another arenavirus, lymphocytic choriomeningitis virus (LCMV). The LCMV reverse genetics system requires vaccinia virus co-infection; however, the Lassa virus system does not, making it more convenient. Lassa virus is a biosafety level 4 pathogen, so this replicon system offers a safe alternative for those wishing to study replication or screen for antivirals.

## MICROBIAL ECOLOGY

Association of *Escherichia coli* O157:H7 with houseflies on a cattle farm

Alam, M. J. & Zurek, L. *Appl. Environ. Microbiol.* **70**, 7578–7580 (2004)

Outbreaks of *Escherichia coli* O157:H7, which causes a haemorrhagic colitis and a haemolytic uremic syndrome in humans, are often linked with visits to farmyards or consumption of contaminated undercooked beef. The main reservoir of infection is the intestinal tract of healthy cattle, with the pathogen shed in faeces, but what is the source of bacteria that colonize the cattle gut? Although this pathogen has been detected in sheep, dogs and birds, this question hasn't yet been answered. Flies might be the culprits, according to Alam and Zurek. Laboratory tests previously showed that this pathogen survived in fly larvae fed on contaminated faeces. Here, bacteria were cultured from individual flies caught on a cattle farm over a 4-month period. *E. coli* O157:H7-positive flies were found every week in the screening period. So, houseflies, which have a range of up to 2 miles, might contribute to the ecology and spread of this dangerous food-borne pathogen.