IN BRIEF

MICROBIAL ECOLOGY

Prokaryote–eukaryote interactions identified by using *Caenorhabditis elegans*

Peleg, A. Y. *et al. Proc. Natl Acad. Sci. USA* **105**, 14585–14590 (2008)

Interactions between different pathogenic microorganisms can often determine the potential virulence of either species to a host, but model systems to probe these interactions have been lacking. Peleg and colleagues have used the nematode worm *Caenorhabditis elegans* as a model to investigate the interaction between *Acinetobacter baumannii* and *Candida albicans*. *A. baumannii* was able to inhibit filamentation of *C. albicans in vivo*, resulting in decreased fungal virulence. *In vitro* assays were also used to show that *C. albicans* mounts a defence against *A. baumannii* that relies in part on the quorum-sensing molecule farnesol. *C. elegans* could therefore provide a useful system for investigating interactions during pathogen co-infection.

BIOREMEDIATION

Anaerobic degradation of naphthalene and 2-methylnaphthalene by strains of marine sulfate-reducing bacteria

Musat, F. *et al. Environ. Microbiol.* 22 Sep 2008 (doi:10.1111/j.1462-2920.2008.01756)

Biodegradation of the aromatic hydrocarbon naphthalene can occur under both aerobic and anaerobic environmental conditions. Compared with aerobic degradation, our understanding of anaerobic degradation is less developed. Musat and colleagues purified sulphate-reducing bacteria from Mediterranean sediment enriched with naphthalene. They identified two strains of Deltaproteobacteria (NaphS3 and NaphS6) that were closely related to another sulphate-reducing strain (NaphS2) that had previously been shown to degrade naphthalene. When exposed to 2-methylnaphthalene, they upregulated a 2-methylnaphthalene-activating enzyme during a long lag phase. Sulphate-reducing marine bacteria are therefore unlikely to use methylation as a first step in naphthalene degradation as previously proposed for a related terrestrial strain.

FUNGAL PATHOGENESIS

Quantitative expression of the *Candida albicans* secreted aspartyl proteinase gene family in human oral and vaginal candidiasis

Naglik, J. R. *et al. Microbiology* **154**, 3266–3280 (2008)

Secreted aspartic proteases are not required for invasion of reconstituted human epithelia by *Candida albicans*

Lerman, U. & Morschhauser, J. *Microbiology* **154**, 3281–3295 (2008)

The secreted aspartyl proteinase (*SAP*) gene family has long been thought to contribute to the pathogenesis of *Candida albicans* infection. However, two studies published in *Microbiology* reveal that *SAP1–6* do not seem to have an essential role during infection of reconstituted human epithelium. Lerman *et al.* and Naglik *et al.* generated mutants that lacked single or multiple *SAP1–6* genes, but none of the mutations affected fungal invasion. Although both studies question the role of Saps in this *in vitro* invasion model, the SC5314 parental strain used is known to be a poor colonizer and invader of mammalian epithelia. Further work is required to rule out an *in vivo* function for Saps.