ENVIRONMENTAL MICROBIOLOGY

Social drinking

Although microorganisms form mixed communities, the exchange of signals between fungal and bacterial species has not been extensively investigated. Now, the production of ethanol by *Saccharomyces cerevisiae* has been found to stimulate the growth of *Acinetobacter* species and enhance the virulence of this pathogen towards *Caenorhabditis elegans*, according to research published in *Molecular and Cellular Biology*.

In niches including soil and immunocompromised human hosts, it is likely that *S. cerevisiae*, the best-characterized fungal species, and *Acinetobacter* species could be found together and exchange signals. Smith *et al.* used co-culture to show that *S. cerevisiae* enhanced the growth of several *Acinetobacter* species. Contact between the yeast and bacterial cells was not required for growth enhancement, and the possibility that *S. cerevisiae* simply supplied a bacterial growth substrate was ruled out. Instead, a diffusible molecule produced during yeast growth was responsible.

Crude biochemical analyses revealed that ethanol satisfied the characteristics of the diffusible molecule and exogenous addition of ethanol was subsequently shown to enhance bacterial growth. Using gene knockouts the disruption of *S. cerevisiae* genes that encode alcohol dehydrogenases was correlated with a reduced ability of the mutant strains to produce ethanol and a concomitant reduction in their ability to promote bacterial growth.

Ethanol causes stress in bacterial cells and Smith *et al.* found that ethanol pre-treatment protected *Acinetobacter baumannii* against salt stress, but not heat or oxidative stress. Ethanol might trigger a signal-transduction cascade that results in the activation of both ethanol and salt tolerance genes. Because pathogens are subjected to stress during host infection, ethanol-treated *A. baumannii* was tested for virulence in *C. elegans*. *A. baumannii* is a food source for the worm, but ethanol pre-treatment rendered this species lethal to *C. elegans*. Elucidating the mechanism of worm killing — which might be due to increased bacterial virulence, or ethanol-mediated compromise of host immunity — is a key goal of further studies. The authors speculate that yeast signalling to *Acinetobacter* species could enhance bacterial virulence for worms — and ultimately worm death removes a predator of both yeast and bacterial species.

Humans often extol the benefits of consuming alcohol to enhance communication. Now it seems that ethanol signalling between yeast and bacterial species might benefit microbial communities too.

Susan Jones

References and links

ORIGINAL RESEARCH PAPER Smith, M. G. *et al*. Microbial synergy via an ethanol-triggered pathway. *Mol. Cell. Biol.* **24**, 3874–3884 (2004)

WEB SITE

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IN BRIEF

ENVIRONMENTAL MICROBIOLOGY

Characterization of *Bacillus* probiotics available for human use

Duc, L. H. *et al*. *Appl. Environ. Microbiol.* **70**, 2161–2171 (2004)

Commercially available probiotic products that contain *Bacillus* endospores have raised safety concerns as, although many were originally labelled as containing *Bacillus subtilis*, studies have shown that other *Bacillus* species can be present, including the gastrointestinal pathogen *Bacillus cereus*. In this work, researchers examined five commercially available probiotic products containing *B. cereus*, *Bacillus clausii* and *Bacillus pumilus*. Although there was evidence to support the claims that these microorganisms have a beneficial probiotic effect, it was also found that the *Bacillus cereus* strains produce enterotoxins, which raises significant safety concerns.

FUNGAL PATHOGENESIS

Inactivation of transcription factor gene *ACE2* in the fungal pathogen *Candida glabrata* results in hypervirulence

Kamran, M. *et al*. *Eukaryot. Cell* **3**, 546–552 (2004)

In bacterial pathogenicity, 'anti-virulence' genes are important in host–pathogen interactions for several bacterial species. Mutations in these loci enhance the ability of the microorganism to cause disease. In this study, Kamran *et al.* screened a signature-tagged mutagenesis library for putative anti-virulence genes in *Candida glabrata*, an important fungal pathogen that accounts for almost 20% of cases of systemic candidiasis. They identified a strain with an increased ability to persist in a murine model of candidiasis and went on to show that the anti-virulence gene, the first to be identified in a *Candida* species, encodes the *C. glabrata* homologue of the *Saccharomyces cerevisiae* transcription factor Ace2p.

MALARIA

Real-time, *in vivo* analysis of malaria ookinete locomotion and mosquito midgut invasion

Vlachou, D. *et al*. *Cell. Microbiol*. 31 March 2004 (doi:10.1111/j.1462-5822.2004.00394.x)

Imaging movement of malaria parasites during transmission by *Anopheles* mosquitoes

Frischknecht, F. *et al*. *Cell. Microbiol*. 31 March 2004 (doi:10.1111/j.1462-5822.2004.00395.x)

In the malaria transmission cycle, the molecular processes involved in the invasion of the mosquito midgut by ookinetes are unclear. Now, in *Cellular Microbiology*, Vlachou *et al.* present real-time, *in vivo* analysis of ookinete invasion of the mosquito midgut epithelia, using high-resolution confocal microscopy and transgenic parasites that express GFP under the control of an ookinete-specific promoter. The data obtained allowed this group to propose a detailed model for invasion of the midgut by *Plasmodium berghei* ookinetes that involves three different modes of motility. In a separate study, Frischknecht *et al.* used time-lapse microscopy of GFP-expressing parasites to obtain data on motility during the sporozoite stage of development and found evidence for gliding motility.