

IN BRIEF

 PRIONS**Not just an artefact**

Yeast prions have been proposed to act as epigenetic determinants, generating new phenotypic traits that may promote yeast survival. However, this was controversial, as prions had not been found in wild yeasts. Here, Lindquist and colleagues confirm that prions do exist in wild strains and can confer phenotypic changes. By testing 690 wild strains of *Saccharomyces* from diverse niches, they were able to identify [PSI⁺] and [MOT3⁺] in a small number of yeasts. Both prions could cause phenotypic changes, which could be beneficial or detrimental, depending on the circumstances. Interestingly, meiotic re-assortment of endogenous genetic variation led to fixation of one [PSI⁺]-dependent trait in some strains, making it prion independent. Moreover, wild strains harboured other prions that caused phenotypic changes and could be transferred to other strains via cytoplasmic transfer.

ORIGINAL RESEARCH PAPER Halfmann, R. et al. Prions are a common mechanism for phenotypic inheritance in wild yeasts. *Nature* **482**, 363–370 (2012)

 ENVIRONMENTAL MICROBIOLOGY**Tampering with cyanobacterial mats**

Changes in ambient temperature could alter the community composition of cyanobacterial mats, the dominant benthic primary producers in polar ecosystems. To examine this, the authors collected mat samples from the Arctic and the Antarctic and cultured them for 6 months. Small changes in temperature affected species composition, as mats cultured at 8 °C or 16 °C showed higher cyanobacterial species diversity than mats cultured at 4 °C or 23 °C. High species diversity was accompanied by higher levels of microcystins (which inhibit protein phosphatases). Cyanobacterial mats provide a habitat or nutrition to many organisms, so such moderate temperature increases may have broader effects on the polar ecosystem.

ORIGINAL RESEARCH PAPER Kleinteich, J. et al. Temperature-related changes in polar cyanobacterial mat diversity and toxin production. *Nature Clim. Chang.* 26 Feb 2012 (doi:10.1038/nclimate1418)

 BACTERIAL GENOMICS**A new source of antimicrobial targets**

Bacterial clone-based genome sequencing frequently results in gaps, which harbour hypothetical genes of unknown function. Sorek and colleagues show that these gaps contain a vast array of genes encoding proteins that are toxic to the sequencing host (*Escherichia coli*), including previously uncharacterized restriction enzymes, toxin–antitoxin systems and non-coding RNAs. They also identify motifs in the cloned DNA that were predicted to bind to DnaA and interfere with *E. coli* replication. The database of potential toxic genes and non-coding elements could be a useful tool for identifying antimicrobial targets.

ORIGINAL RESEARCH PAPER Kimelman, A. et al. A vast collection of microbial genes that are toxic to bacteria. *Genome Res.* 1 Feb 2012 (doi: 10.1101/gr.133850.111)