

## IN BRIEF

**GENE REGULATION**

Orthologous transcription factors in bacteria have different functions and regulate different genes

Price, M. P., Dehal, P. S. & Arkin, A. P. *PLoS Comput. Biol.* **3**, e175 (2007)

The identification of orthologues with bidirectional best BLAST hits (BBH) is used to predict the functions of genes in bacteria. Price and colleagues found that using BBHs to assign functions to bacterial transcription factors was seriously flawed. Specifically, they examined a set of transcription-factor orthologues from *Escherichia coli* and *Bacillus subtilis* that were identified using BBHs. These transcription factors were rarely true orthologues and did not have conserved functions. Among the more closely related bacteria, orthologous transcription factors that were identified using BBHs were *bona fide* evolutionary orthologues, but an analysis of previously published transcriptome data revealed that these orthologues did not regulate the same set of genes or respond to the same signals. The authors conclude that bacterial gene-regulatory networks evolve incredibly quickly and recommend using more reliable phylogenetic trees to pinpoint the evolution of gene-regulatory pathways.

**HOST DEFENCE**

Rapidly evolving CRISPRs implicated in acquired resistance of microorganisms to viruses

Tyson, G. W. & Banfield, J. F. *Environ. Microbiol.* 26 Sep 2007 (10.1111/j.1462-2920.2007.01444.x)

The CRISPR (clustered regularly interspaced short palindromic repeats) system, which is present in bacteria and archaea, is proposed to function in a similar way to the eukaryotic RNA-interference system and to target and remove foreign DNA from phage and plasmid sources. Tyson and Banfield report that within a nearly clonal population of *Leptospirillum II* bacteria, which was identified by metagenomics in an acidophilic microbial biofilm, the evolution of the spacer collection in CRISPR regions is fast enough to promote cell individuality. They propose that CRISPR sequences diversify in response to phage predation. They also found an unusually large number of transposons in the CRISPR region, which might indicate a mechanism for transposon removal or CRISPR inactivation.

**METAGENOMICS**

A metagenomic survey of microbes in honeybee colony collapse disorder

Cox-Foster, D. L. *et al. Science* 6 Sep 2007 (10.1126/science.1146498)

A study published in *Science* used metagenomics to probe the aetiology of colony collapse disorder (CCD) in honeybees, which is a widespread economically relevant problem for beekeepers. A dramatic decrease in the number of adult bees occurs in a CCD hive. Four geographically distant hives with CCD were analysed together with a healthy bee hive and royal-jelly samples. Unbiased high-throughput pyrosequencing technology was used to produce an inventory of the microflora that was present in CCD and non-CCD hives. A strong correlation was found between the presence of the RNA virus Israeli acute paralysis virus (IAPV) and CCD. This study provides a basis for further investigation into the role of IAPV in CCD and might also establish a strategy for investigating epidemics of unexplained infectious disease.