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IN BRIEF

TECHNIQUES & APPLICATIONS

Genome transplantation in bacteria: changing one species to another

Lartigue, C. *et al. Science* 28 June 2007 (doi:10.1126/1144622)

As a first step towards creating a synthetic 'designer bacterium', Craig Venter, John Glass and colleagues have replaced the genome of one bacterial species with the genome from another, closely related species. The donor species involved was a *Mycoplasma mycoides* subspecies *mycoides* large colony (LC) strain expressing tetracycline resistance (*tetM*) and β-galactosidase (*lacZ*) genes. The recipient species was *Mycoplasma capricolum* subspecies *capricolum* strain California kid. Transformation with the naked DNA was achieved by using a polyethylene glycol (PEG)-mediated method, and transformants were selected using the *tetM* and *lacZ* genes. Successful transformants were subjected to genotypic and phenotypic analysis, and it was shown that the recipient *M. capricolum* cells were phenotypically identical to the donor *M. mycoides* LC cells and were free of detectable *M. capricolum* sequences. The mechanism responsible for this genome transplantation is unknown.

BACTERIAL VIRULENCE

Gram-positive three-component antimicrobial peptide-sensing system

Li, M. *et al. Proc. Natl Acad. Sci. USA* **104**, 9469–9474 (2007)

Michael Otto and colleagues have identified an antimicrobial peptide detection system in the Gram-positive organism *Staphylococcus epidermidis*. In a recent issue of the *Proceedings of the National Academy of Sciences USA*, Min Li, Yuping Lai and co-workers report on the response of *S. epidermidis* to human β defensin 3 (hBD3). Their microarray work led to the discovery of an unusual three-component sensor–regulator system termed the Aps system. It comprises a classical two-component sensor kinase and response regulator pair (ApsS and ApsR, respectively) and a third component of unknown function, ApsX. All three components were shown to be essential for *S. epidermidis* resistance to hBD3.

MICROBIAL ECOLOGY

Pyrosequencing enumerates and contrasts soil microbial diversity

Roesch, L. F. W. *et al. ISME J.* 05 July 2007 (doi:10.1038/ismej.2007.53)

Obtaining an accurate estimate of the number of bacterial and archaeal species present in 1 gram of soil has long been a goal of soil microbiologists. Different approaches have produced estimates that range from 2,000 to 10^7 species per gram. The main problem has been that the input data (number of sequences) for most calculations of diversity have been too small. Now, a team led by Eric Triplett have used pyrosequencing to address the question of microbial diversity in soil. They estimate microbial diversity as 1×10^5 to 5×10^5 species per gram and propose that approximately 700,000 input sequences are needed to identify 90% of the species in 1 gram of soil. Such a set of input sequences can be obtained in just one day with pyrosequencing. The maximum number of species per gram of soil was not likely to exceed 52,000 according to this report. They also showed that the diversity of phyla in forest soils vastly exceeded that present in agricultural soils, a finding that merits further investigation.