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IN BRIEF

BACTERIAL TRANSCRIPTION

The mechanism of bursting

Transcription of highly expressed bacterial genes occurs in stochastic bursts. Chong *et al*. now show that DNA gyrase regulates this transcriptional burst by decreasing positive DNA supercoiling. The authors designed an *in vitro* assay that enables transcription on individual chromosomal DNA loops to be monitored in real time and found that, during multiple rounds of transcription, supercoiling accumulated on the DNA template ahead of the RNA polymerase (known as positive supercoiling) and blocked transcription initiation and elongation. Notably, transcription initiation was restored following the addition of gyrase, which is the enzyme that resolves positive supercoiling. By using gyrase inhibitors or by overexpressing gyrase in *Escherichia coli*, the authors confirmed that this enzyme is the main regulator of transcriptional bursting. Future studies should clarify whether gyrase activity also regulates transcriptional bursting in eukaryotes.

ORIGINAL RESEARCH PAPER Chong, S. *et al*. Mechanism of transcriptional bursting in bacteria. *Cell* **158**, 314–326 (2014)

BACTERIAL TOXINS

New weapons for plant colonization

Agrobacterium tumefaciens is a soil bacterium that uses a type VI secretion system (T6SS) to enable plant colonization. Ma *et al*. now describe a new family of T6SS effectors that have DNase activity (the Tde family) and provide *A. tumefaciens* with a competitive advantage *in planta*. Tde1 and Tde2 were shown to degrade DNA when expressed in *Escherichia coli* but *A. tumefaciens* is protected against their toxic effects owing to the presence of the antitoxin proteins, Tdi1 and Tdi2, respectively. Importantly, mutant *A. tumefaciens* strains that lack each of the toxin–antitoxin pairs were less able to survive than wild-type *A. tumefaciens* strains or *Pseudomonas aeruginosa* — an opportunistic plant pathogen — following co-infiltration into plant leaves. These data show that *A. tumefaciens* uses Tde toxins to attack and outcompete both siblings and other species during plant colonization.

ORIGINAL RESEARCH PAPER Ma, L.-S. *et al*. *Agrobacterium tumefaciens* deploys a superfamily of type VI secretion DNase effectors as weapons for interbacterial competition *in planta*. *Cell Host Microbe* **16**, 94–104 (2014)

TECHNIQUES AND APPLICATIONS

Digging out bacterial hydrolases

Verastegui *et al*. combined stable-isotope probing (SIP) with functional metagenomics to identify new glycoside hydrolases produced by soil microorganisms, which have multiple biotechnological applications, owing to their ability to degrade complex carbohydrates. The authors added ^{13}C-labelled carbohydrates to different soil samples and enriched isotope-labelled (heavy) DNA by centrifugation. Sequencing of the heavy DNA revealed several taxa that could degrade the labelled complex carbohydrates, and annotation of the metagenomic data revealed several new potential glycoside hydrolase genes. The authors then constructed a cosmid library using the heavy DNA to carry out functional screens and identified several clones that can degrade cellulose and other complex plant polymers. These data show how SIP and metagenomics can be combined to identify novel functional genes from environmental samples.

ORIGINAL RESEARCH PAPER Verastegui, Y. *et al*. Multisubstrate isotope labeling and metagenomic analysis of active soil bacterial communities. *mBio* **5**, e01157-14 (2014)