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IN BRIEF

BACTERIAL GENETICS

An ancient mycobacterial proofreader

In *Escherichia coli*, DNA proofreading is performed by the *dnaQ*-encoded 3′–5′ exonuclease; however, a new study now shows that the *dnaQ* homologue in *Mycobacterium tuberculosis* does not have a role in replication fidelity. Instead, the polymerase and histidinol phosphatase (PHP) domain of the *M. tuberculosis* replicative polymerase DnaE1 has intrinsic 3′–5′ exonuclease activity and is capable of correcting mismatches. Mutant strains in which the PHP domain of DnaE1 was inactivated exhibited growth defects and mutation rates that were increased by ~3000-fold. Furthermore, the authors report that most bacterial replicative polymerases contain an active PHP exonuclease, which suggests that the PHP domain is the most common replicative exonuclease in the bacterial kingdom and might be an ancestral prokaryotic proofreader. Finally, inactivation of the PHP domain renders mycobacteria sensitive to nucleoside analogues, possibly providing a new strategy for the treatment of drug-resistant *M. tuberculosis*.

ORIGINAL RESEARCH PAPER Rock, J. M. *et al.* DNA replication fidelity in *Mycobacterium tuberculosis* is mediated by an ancestral prokaryotic proofreader. *Nature Genet.* http://dx.doi.org/10.1038/ng.3269 (2015)

BACTERIAL PHYSIOLOGY

Migration is a group effort

To survive in the environment, the soil-dwelling bacterium *Bacillus subtilis* must overcome several challenges, including flagellum-independent migration over solid surfaces. Kolter and colleagues show that *B. subtilis* forms multicellular structures that facilitate collective cell migration. The authors found that during colony expansion, cells at the leading edge are organized into bundles (termed van Gogh bundles) that consist of tightly aligned cell chains that form filamentous loops. Colony migration depended on the synergistic interaction between two specific cell types: surfactin-producing cells reduce the friction between cells and their substrate, enabling matrix-producing cells to form van Gogh bundles at the colony edge. Time-course microscopy studies revealed that van Gogh bundles push themselves away from the colony centre as the filamentous loops grow, thus driving migration.

ORIGINAL RESEARCH PAPER van Gestel, J., Vlamakis, H. & Kolter, R. From cell differentiation to cell collectives: *Bacillus subtilis* uses division of labor to migrate. *PLoS Biol.* **13**, e1002141 (2015)

TECHNIQUES & APPLICATIONS

Expanding the toolbox to study *Chlamydia*

Routine genetic manipulation approaches are currently limited in *Chlamydia*. Here, Kokes *et al.* generated a collection of chemically mutagenized *Chlamydia trachomatis* strains and identified the induced single-nucleotide variants (SNVs) using whole-genome sequencing. The authors describe the use of this library in a microscopy-based forward genetic screen for mutants impaired in filamentous actin assembly at chlamydial inclusions, and they identified a role for the bacterial inclusion membrane protein InaC in proper actin localization at these sites. The authors also found that *C. trachomatis* tolerates nonsense mutations in distinct genes of the tricarboxylic acid cycle and the DNA damage response. Thus, this method could be a useful tool for reverse and forward genetic applications that can be applied to microorganisms that are not amenable to classic genetic manipulations.

ORIGINAL RESEARCH PAPER Kokes, M. *et al.* Integrating chemical mutagenesis and whole-genome sequencing as a platform for forward and reverse genetic analysis of *Chlamydia*. *Cell Host Microbe* http://dx.doi.org/10.1016/j.chom.2015.03.014 (2015)