IN BRIEF

ANTIMICROBIALS

Fitness benefits for resistant *S.* Typhi

Although the vast majority of antibiotic resistance mutations confer a fitness cost in the absence of antibiotic selective pressure, a study by Baker *et al.* now challenges this dogma. *Salmonella enterica* subsp. *enterica* serovar Typhi strains that have fluoroquinolone resistance mutations in the DNA gyrase gene *gyrA*, the topoisomerase gene *parC* or in both genes were competitively grown with an isogenic fluoroquinolone-sensitive wild-type strain in the absence of antibiotics. Most of the resistant mutants out-competed the wild-type strain, and interestingly, strains that had two mutations showed higher fitness than single mutants, which suggests that resistance mutations epistatically interact to increase fitness. These findings imply that resistant *S.* Typhi mutants would persist even after drug withdrawal and that antibiotic exposure is not the only factor that contributes to the maintenance of resistant strains.

ORIGINAL RESEARCH PAPER Baker, S. *et al.* Fitness benefits in fluoroquinolone-resistant *Salmonella* Typhi in the absence of antimicrobial pressure. *eLife* **2**, e01229 (2013)

PARASITE BIOLOGY

ART resistance marker discovered

Resistance of *Plasmodium falciparum* to artemisinin (ART) combination therapies is increasing in Southeast Asia, but the mechanisms of resistance have been unclear. Now, using a combination of *in vitro*, *in vivo*, genomic and epidemiological approaches, Ariey *et al.* show that mutations in the 'propeller domains' of the kelch protein K13 are a key determinant of resistance. These proteins contain multiple repetitive amino acid sequences and are thought to be involved in several protein–protein interactions. K13-propeller mutations were prevalent in clinical parasite isolates from regions where ART resistance is widespread but were rare or absent in regions where resistance is uncommon. Clinical ART resistance is defined by prolonged parasite clearance rates, and the K13-propeller mutations were also found to strongly correlate with the presence of slow-clearing parasites. The identification of these mutations is a crucial advance for efforts that aim to monitor and contain the spread of ART resistance.

ORIGINAL RESEARCH PAPER Ariey, F. *et al.* A molecular marker of artemisinin-resistant *Plasmodium falciparum* malaria. *Nature* http://dx.doi.org/10.1038/nature12876 (2013)

INDUSTRIAL MICROBIOLOGY

Bacterial enzyme fuels CO_2 hydrogenation

Difficulties with the storage and transport of hydrogen have limited its use as an energy substrate for biofuel production, and, although formate is a more desirable storage material for hydrogen, its production by chemical hydrogenation of CO_2 is technically challenging. However, a study now reports the discovery of a bacterial hydrogen-dependent carbon dioxide reductase (HDCR) from the acetogenic bacterium *Acetobacterium woodii* that is capable of directly and reversibly catalysing the hydrogenation of CO_2. The enzyme is advantageous for industrial use as it does not need external cofactors and the directionality of the reaction is easily controlled. Furthermore, in addition to CO_2 and hydrogen, syngas (synthesis gas) could be used as a 'greener' substrate for formate production by whole-cell catalysis. Thus, the isolated HDCR enzyme or an *A. woodii* whole-cell system could be exploited for the storage and production of hydrogen.

ORIGINAL RESEARCH PAPER Schuchmann, K. & Müller, V. Direct and reversible hydrogenation of CO_2 to formate by a bacterial carbon dioxide reductase. *Science* **342**, 1382–1385 (2013)