

IN BRIEF

FUNGAL PATHOGENESIS**Wheat stem rust effectors revealed**

Puccinia graminis f. sp. *tritici*, the causative agent of wheat stem rust, uses various effectors to infect its plant host. However, host recognition of effectors and the subsequent immune responses can provide resistance to infection and, in response, the fungal pathogen modifies its effectors. Two new studies now identify such effectors that are crucial targets of plant immune responses. Salcedo *et al.* compared whole-genome sequences of natural and mutagenized fungal strains to identify AvrSr35, which interacts with the Sr35 immune receptor. Insertion of a mobile element into and inactivation of the effector gene was associated with evasion of plant resistance. Chen *et al.* identified the AvrSr50 effector in a spontaneous virulent mutant that was able to overcome Sr50-dependent resistance. Identification of these two effectors will help with surveillance for the emergence of resistant wheat stem rust variants and the development of new strategies to provide plant resistance.

ORIGINAL ARTICLES Salcedo, A., Rutter W. *et al.* Variation in the AvrSr35 gene determines Sr35 resistance against wheat stem rust race Ug99. *Science* **358**, 1604–1606 (2017) | Chen, J., Upadhyaya N. M., Ortiz D. *et al.* Loss of AvrSr50 by somatic exchange in stem rust leads to virulence for Sr50 resistance in wheat. *Science* **358**, 1607–1610 (2017)

BACTERIAL PHYSIOLOGY**It's a wrap for *Burkholderia* flagella**

Flagella are central for bacterial motility and are involved in diverse bacterial behaviours, including host colonization and the establishment of symbiosis. Kinosita *et al.* used total internal reflection microscopy and fluorescent staining of flagellar filaments to characterize flagellum motion in the bean bug symbiont *Burkholderia* sp. RPE64. They showed that the flagellum wraps around the cell body like “a ribbon streamer in rhythmic gymnastics” and that this lets the bacteria reverse in a screw-like fashion. Interestingly, the authors were able to show the same type of motility in the squid symbiont *Aliivibrio fischerii*, leading them to suggest that flagellar wrapping is a strategy used by symbionts to ‘drill’ into and enter mucus-filled, crypt-like niches in their hosts, which cannot be entered by bacteria that use other modes of flagellated motility.

ORIGINAL ARTICLE Kinosita, Y. *et al.* Unforeseen swimming and gliding mode of an insect gut symbiont, *Burkholderia* sp. RPE64, with wrapping of the flagella around its cell body. *ISME J*. <http://dx.doi.org/10.1038/s41396-017-0010-z> (2017)

METAGENOMICS**Setting the bar for mycobiome analysis**

So far, surveys of the mycobiome have been hampered by the lack of fungal marker genes that are as universal as prokaryotic 16S rRNA genes. The internal transcribed spacer 1 (ITS1) region in the eukaryotic ribosomal cluster has been used as a marker gene, but the currently available primers have a limited potential to recover fungal diversity and are biased towards soil fungi. Usyk *et al.* have now developed a new set of ITS1 primers, which almost double the taxonomic coverage of a reference database and substantially increase the number of recovered sequences from fungal isolates compared with previously published primers. Notably, the coverage of the *Candida* genus, which includes important human pathogens, increased from ~60% to 100%. Increased taxonomic coverage and sequencing depth should facilitate future mycobiome studies.

ORIGINAL ARTICLE Usyk, M. *et al.* Novel ITS1 fungal primers for characterization of the mycobiome. *mSphere* **2**, e00488-17 (2017)