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IN BRIEF

STRUCTURAL BIOLOGY

MshEN: possible for c-di-GMP binding

Several important bacterial processes are regulated by cyclic di-GMP (c-di-GMP) signalling. Wang *et al.* report a novel mode of c-di-GMP binding by the MshE amino-terminal (MshEN) domain, which has recently been shown to specifically and potently bind to c-di-GMP. A 1.37 Å-resolution structure of a *Vibrio cholerae* MshEN domain showed that c-di-GMP binds to two motifs of 24 conserved residues that do not share homology with canonical c-di-GMP-binding motifs; the functional importance of conserved residues was confirmed by mutant phenotypes that were defective in pilin production and biofilm formation. Furthermore, kinetic experiments demonstrated a binding affinity for c-di-GMP that was ten-fold stronger than the PilZ c-di-GMP-binding domain. Finally, the authors found that MshEN is widely distributed in bacteria, which suggests that it is an ancient regulator and may explain the basis for c-di-GMP signalling in bacteria that lack known c-di-GMP receptors.

ORIGINAL ARTICLE Wang, Y.-C. *et al.* Nucleotide binding by the widespread high-affinity cyclic di-GMP receptor MshEN domain. *Nat. Commun.* **7**, 12481 (2016)

ARCHAEAL GENOMICS

3′ UTRs: a paradigm for archaeal gene regulation?

Dar *et al.* investigated transcription termination in archaea by sequencing the 3′ ends of the transcriptomes of the euryarchaeon *Methanosarcina mazei* and the crenarchaeon *Sulfolobus acidocaldarius*. A comparison with *Bacillus subtilis* revealed two interesting differences between archaea and bacteria. First, the lengths of 3′ UTRs were significantly longer in archaea than in *B. subtilis*. Second, 25–40% of genes in archaea had secondary transcription termination sites in addition to the primary site, whereas no such sites were detected in *B. subtilis*. These features of archaeal transcripts are reminiscent of transcript architectures that are commonly found in eukaryotic genes, in which alternative extended 3′ UTRs have a regulatory function by varying the provision of microRNA binding sites. Interestingly, 20 of 23 previously validated *M. mazei* non-coding RNAs had sequences with a potential for complementary binding with 14% of *M. mazei* 3′ UTRs, which may reflect a eukaryotic-like mechanism of gene regulation in archaea.

ORIGINAL ARTICLE Dar, D. *et al.* Widespread formation of alternative 3′ UTR isoforms via transcription termination in archaea. *Nat. Microbiol.* **7**, 12481 (2016)

VIRAL INFECTION

A gateway protein for norovirus

The host factors that noroviruses rely on for invasion, replication and pathogenesis, and that consequently determine the species tropism of the virus, are largely unidentified. Virgin and colleagues used CRISPR–Cas9 to perform a genome-wide screen for host factors that are required for the infection of mouse cells by murine norovirus (MNoV). Four loss-of-function mutations in a single gene (*Cd300lf*) were identified that enabled mouse cells to survive infection by MNoV. Additional experiments in cell lines, primary cells and *in vivo* confirmed that Cd300lf is specifically required for the binding and replication of MNoV, and that Cd300lf is the primary receptor for MNoV infection. Expressing murine Cd300lf in HeLa cells made these human cells permissive for infection by MNoV, thus removing the species tropism barrier of MNoV infection. Finally, structural analysis of Cd300lf, which is a cell-surface immunoglobulin domain-containing protein, revealed a putative ligand binding site in its ectodomain.

ORIGINAL ARTICLE Orchard, R. C. *et al.* Discovery of a proteinaceous cellular receptor for a norovirus. *Science* **353**, 933–936 (2016)