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IN BRIEF

STRUCTURAL BIOLOGY

Type III CRISPR–Cas complexes in the spotlight

CRISPR–Cas (clustered, regularly interspaced short palindromic repeats–CRISPR-associated proteins) loci of bacteria and archaea encode small CRISPR RNAs (crRNAs) and Cas proteins that assemble into effector complexes to target and destroy invading nucleic acid in a sequence-specific manner. CRISPR–Cas systems are classified into three types (I, II and III), and several subtypes, according to the set of Cas proteins that they contain; type II systems function with a single Cas9 protein, whereas types I and III contain several different Cas proteins. Previous work has mainly focused on the characterization of type I systems, which form a complex known as Cascade. Now, three studies report the structural characterization of type III CRISPR–Cas complexes from *Sulfolobus solfataricus*, *Pyrococcus furiosus* and *Thermus thermophilus*. Electron microscopy shows that, despite having divergent Cas proteins and crRNAs, the complexes from all three organisms have a similar overall shape, which consists of a crRNA-binding helical backbone that resembles the seahorse shape of Cascade. This striking architectural similarity between type I and type III systems reveals that distantly related CRISPR–Cas complexes share a common functional design, which suggests that they evolved from a common ancestor. Furthermore, functional insights into the nucleolytic activity of type III systems were also uncovered. Rouillon *et al.* show that the type III-A complex from *S. solfataricus* can bind but cannot cleave target double-stranded DNA, which suggests that a nuclease must be recruited to the complex. This is also reminiscent of Cascade, which functions as a surveillance complex and recruits a distinct nuclease for target degradation. By contrast, Staals *et al.* find that the type III-B complex of *T. thermophilus* has nucleolytic activity, although the exact component of the complex responsible for target degradation is unclear. Collectively, these studies provide unparalleled insight into the composition and function of type III CRISPR–Cas complexes, which can now be exploited for further biochemical characterization of CRISPR-mediated interference.

ORIGINAL RESEARCH PAPERS Rouillon, C. *et al.* Structure of the CRISPR interference complex CSM reveals key similarities with cascade. *Mol. Cell* **52**, 124–134 (2013) | Spilman, M. *et al.* Structure of an RNA silencing complex of the CRISPR-Cas immune system. *Mol. Cell* **52**, 146–152 (2013) | Staals, R. H. J. *et al.* Structure and activity of the RNA-targeting Type III-B CRISPR-Cas complex of *Thermus thermophilus*. *Mol. Cell* **52**, 135–145 (2013)

VIROLOGY

SARS-CoV ancestor found in Chinese bats

A new study reports the isolation of a novel coronavirus (CoV) from Chinese horseshoe bats, which is more closely related to severe acute respiratory syndrome coronavirus (SARS-CoV) than any previously identified bat CoV, providing strong evidence that SARS-CoV might have originated in bats. Whole-genome sequencing of the novel CoV revealed that it shares 95% sequence identity with human SARS-CoV, with the receptor-binding domain (RBD) in the spike protein from both viruses showing an identical amino acid sequence. The RBD of human SARS-CoV uses the cellular receptor angiotensin-converting enzyme 2 (ACE2) for cell entry, and infectivity assays confirmed that the novel CoV also uses human ACE2 for cell entry, suggesting that it might be capable of directly infecting humans. Furthermore, preliminary *in vitro* data suggest that the new virus has broad species tropism.

ORIGINAL RESEARCH PAPER Ge, X.-Y. *et al.* Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor. *Nature* http://dx.doi.org/10.1038/nature12711 (2013)