

Modularity of Zorya defense systems during phage inhibition

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Abstract

Bacteria have evolved an extraordinary range of defence systems to protect against bacteriophage infection, yet the molecular details of many of these systems remain unclear. The Zorya phage defence systems, in particular, have now been characterised in more detail. Structural analysis using cryo-EM has revealed that the core components of Zorya types I and II, ZorA and ZorB, form a 5:2 complex resembling ion-driven rotary motors found in systems such as flagellar rotation, type 9 secretion, gliding motility, and Ton-dependent nutrient uptake. This complex features a structured cytoplasmic tail formed by the bundled C-termini of ZorA subunits. Functional studies have shown that ion flow through the motor, peptidoglycan binding by ZorB's periplasmic domains, and the architecture of the ZorA tail are all essential for defence activity. In Zorya type II, the effector module ZorE, which acts as a nickase, plays a key role in mediating population-level immunity.

More recently, in the Mariano lab, we have discovered a fourth Zorya subtype. This novel subtype is phylogenetically distinct and encodes a different suite of effectors, pointing to an even greater diversity of mechanisms within the Zorya family.

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