DNA motif-based Discovery of Anti-defense Genes in Archaea viruses

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Abstract

In silico identification of novel anti-CRISPRs (Acrs) has relied completely on the guilt-by-association method with Acrs or anti-CRISPR associated proteins (Acas) as bait. Limited distribution of the characterized archaeal Acrs and Aca hinders our ability towards identifying new Acrs using the aforementioned method. In this paper, we leverage the possibility that all anti-defence genes ought to be expressed immediately post infection and hence must carry optimal and identical promoters, to identify anti-defense elements (ADE) within viruses without any prior knowledge of their protein functions. Using this consensus sequence based method, we have identified several potential anti-defense genes within archaeal viruses. Experimental screening identified the first subtype I-A inhibitor as well as the first virally encoded inhibitor of an archaeal abortive infection system within lytic and temperate viruses of archaea. Furthermore, we have also identified regulatory proteins potentially akin to Acas, which can lead to further identification of anti-defense genes in combination with the neighborhood method. These results demonstrate an approach for the extensive identification of ADEs among archaeal viruses with potential to be relevant among bacteriophages.

Keywords: phage antidefence mechanisms, AntiCRISPR

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