

CRISPRome: Exploring Adaptive Immunity in Extremophiles

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CRISPR systems, with their associated Cas proteins, have revolutionized our understanding of microbial immunity and hold immense promise for genome editing applications. However, the vast diversity of CRISPR systems in natural environments remains largely unexplored. It is known that 80% of microbes in extremophiles contain CRISPR-cas systems compared to 50% in mesophiles making hot springs an attractive place to expand our understanding on CRISPR-cas systems in nature. Here, whole metagenome samples from various non-volcanic hot spring environments were analyzed using a powerful suite of bioinformatic tools like MINCED, CRISPRCasFinder, and CRISPRtracrRNA. This comprehensive analysis successfully identified and classified a plethora of CRISPR arrays, spacer sequences, and cas genes. A significant portion of the identified CRISPR arrays originated from unknown organisms, hinting at the presence of potentially novel CRISPR systems thriving within hot springs. The cas gene analysis revealed a compelling assortment, encompassing well-characterized subtypes alongside less explored ones. Furthermore, the identification of putative novel cas proteins within these uncharacterized CRISPR arrays intensifies the intrigue, beckoning future studies to unravel their roles in these unique systems.

KEYWORDS: CRISPR-Cas system, hot spring, phage, whole metagenome sample

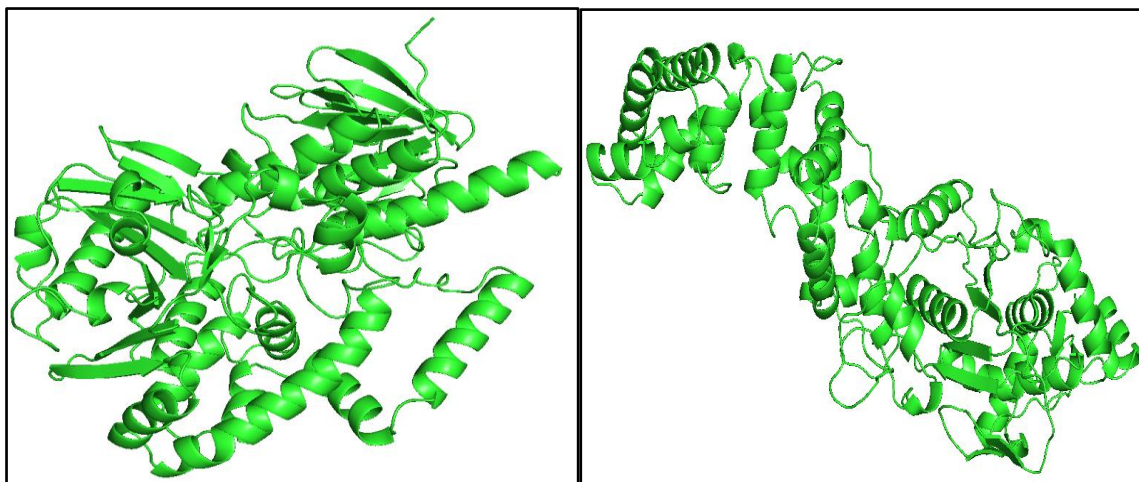
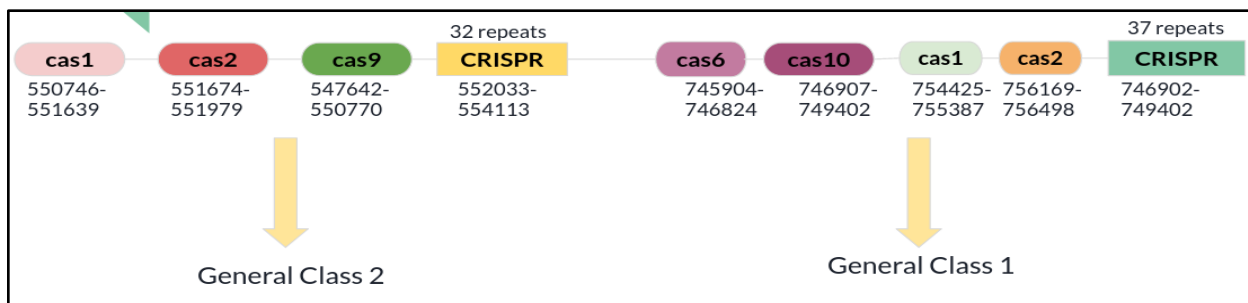


Figure: The first figure represents a unique architecture found in few of the sequences. The second and third figure represents predicted structures of potential effector proteins missing in the operon based on homology.