

P038 CRISPR dynamics in *Sulfolobus islandicus* strains
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CRISPRs are widespread clusters of repeated sequences present in the majority of bacterial and archaeal genomes. They are organized as stretches of short identical repeats interspersed by spacers of unique sequences (about 30 - 40 bp) linked to specific *cas* genes. Many of the spacer sequences are identical (or very similar) to regions of viral or plasmid genomes. CRISPRs play a role similar to that of eukaryotic siRNA system but little is known about the CRISPR dynamics or the exact mechanism of “immunity” that they provide to the host. In this study we compared the sequences of CRISPRs A and B from the genome of the crenarchaeon *Sulfolobus islandicus* HVE 10/4 before and after infection by filamentous virus SIFV. After about 100 generations, CRISPR A was shown to have undergone rearrangements in SIFV resistant isolates. Furthermore, comparative genomic studies of closely related *S. islandicus* strains allowed us to identify: (1) the leader sequence for the CRISPRs A and B, and (2) the presence of the consensus sequences, upstream and downstream, of some proto-spacers identified by their copies in analysed CRISPRs. Finally, two *cas* genes were expressed, but both proteins were insoluble.