CRISPR systems in microbiomes

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CRISPRs (Clustered Regularly Interspaced Short Palindromic Repeats) form a prokaryotic adaptive defense system that provides resistance against alien replicons such as viruses and plasmids [1]. Spacers in a CRISPR-cassette confer immunity against viruses and plasmids containing regions complementary to the spacers and hence they retain a footprint of interactions between prokaryotes and their viruses in individual strains and ecosystems. The human gut is a rich habitat populated by numerous microorganisms [2], but a large fraction of these are unculturable and little is known about them in general and their CRISPR-systems in particular. We used human gut metagenomic data from three publicly available projects in order to characterize the composition and dynamics of CRISPR-cassettes in the human-associated microbiota. Applying three available CRISPR-identification algorithms and a previously designed filtering procedure to the human gut metagenomic data, we reconstructed 388 full CRISPR-cassettes and identified their orientation. Their spacers tend to match sequences originating from the same metagenomic dataset, moreover, from the same individual. A considerable number of spacers did not match metagenomic sequences, nor any available bacterial or viral genomes. The spacers with matches in metagenomes are distributed unevenly across cassettes, demonstrating a preference to form clusters closer to the active end of a CRISPR-cassette, adjacent to the leader, and suggesting dynamical interactions between prokaryotes and viruses in the human gut. Hence, this study shows that CRISPR-cassettes are highly variable and a particular CRISPRome of an individual reflects its unique viriome diversity, abundance and dynamics.

References

1. R. Sorek, C.M. Lawrence, B. Wiedenheft (2013) CRISPR-Mediated Adaptive Immune

Systems in Bacteria and Archaea. Annu Rev Biochem., 82:237-66.

2. J. Lederberg (2000) Infectious history. *Science*, **288**: 287– 293.