BACTERIAL GENETICS

A CRISPR tool for *Yersinia* analysis?

A paper in the March issue of *Microbiology* has identified the origin of the spacer regions in a specific class of repetitive elements and indicates that these elements may be a useful addition to the tools used in *Yersinia* strain typing.

Clustered regularly interspaced short palindromic repeats (CRISPRs) are clusters of repeated sequences of 21–37 base pairs that are interspersed with spacers of a similar length. CRISPRs have been identified in a variety of Archaea and Bacteria and, although their biological function remains unknown, these elements are often associated with genes that are involved in DNA recombination and repair.

Three CRISPR loci with the same repetitive sequence were identified in the available complete genome sequences of *Yersinia pestis*. In this study, Pourcel *et al.* analysed these CRISPRs — designated YP1, YP2 and YP3 — in a large collection of *Y. pestis* isolates representing the three classical biovars Antiqua, Medievalis and Orientalis, the newly proposed biovar Microtus, and the atypical Pestoides, as well as some strains of *Yersinia pseudotuberculosis*. In total, 109 alleles were sequenced.

Analysis showed that the YP1 element was the most polymorphic of the CRISPRs present in *Y. pestis*, and more detailed work allowed the authors to construct a putative evolutionary scheme for this locus in the different biovars. In *Y. pseudotuberculosis*, the CRISPR elements were almost all larger than their *Y. pestis* counterparts, and many new spacer sequences were identified. Careful analysis of the new spacers from both species revealed the presence of homologues within an area of the genome that was identified as an inactive prophage, indicating that phages are the potential source of the spacer regions.

Pourcel *et al.* conclude by suggesting that analysis of the CRISPR loci in *Y. pestis* might be useful for strain typing of ancient *Y. pestis* DNA.

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References and links

ORIGINAL RESEARCH PAPER Pourcel, C. *et al.* CRISPR elements in *Yersinia pestis* acquire new repeats by preferential uptake of bacteriophage DNA, and provide additional tools for evolutionary study. *Microbiology* **151**, 653–663 (2005)