

ARCHAEA

Hot spots for *Sulfolobus*

The first functional characterization of the insertion sequences (ISs) present in the genome of a *Sulfolobus* species has recently been published in *Molecular Microbiology*.

The importance of mobile genetic elements in prokaryotic evolution has become increasingly clear as more and more complete bacterial genome sequences have become available. ISs are the smallest and most abundant class of these mobile elements. The complete genome sequence of *Sulfolobus solfataricus* strain P2 revealed that this hyperthermophilic archaeal species contains the most IS elements of all the prokaryotic genomes sequenced so far. However, given the evolutionary distance between Archaea and Bacteria, information on the functional diversity of ISs in bacterial genomes or their evolutionary significance for bacterial genomes cannot be extrapolated to archaeal species. Now, Blount and Grogan have identified, and carried out extensive functional characterization of, the ISs in a *Sulfolobus* genome.

The *Sulfolobus* strains examined were isolated from acidic geothermal springs in three different locations, and were shown to belong to the informal designated species *Sulfolobus islandicus*. A modified 'gene trap' strategy was used to recover the IS elements present, and a total of seven functional IS elements were obtained, ranging in length from 735 bp (the smallest IS element yet identified in *Sulfolobus* spp.) to 1,926 bp

(the largest yet identified). Six of the elements belonged to known IS families but had not previously been identified in *Sulfolobus* spp. and the final IS element did not belong to any known IS family. In addition to these IS elements, a type II miniature inverted-repeat transposable element (MITE), a short repetitive element present in abundance in eukaryotic genomes, was also recovered. Blount and Grogan then carried out a variety of detailed molecular characterization and quantitative genetic assays — including quantification of the transposition rates, determination of target-site selectivity and analysis of precise excision — for each of the recovered elements.

In general, the functional charac-

terization of IS elements in bacterial and archaeal genomes has failed to keep pace with the rate at which they are being identified. More specifically, it is unclear whether the functions of these small mobile elements are the same in Archaea as in Bacteria. With this comprehensive analysis, Blount and Grogan have made an excellent first step towards answering this question.

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References and links

ORIGINAL RESEARCH PAPER Blount, Z. D. & Grogan, D. W. New insertion sequences of *Sulfolobus* functional properties and implications for genome evolution in hyperthermophilic archaea. *Mol. Microbiol.* Dec 2004

(doi:10.1111/j.1365-2958.2004.04391.x)

FURTHER READING Chandler, M. & Mahillon, J. in *Mobile DNA II* (eds Craig, N. et al.) 305–366 (2002)

