

## MICROBIAL ECOLOGY

## Obeying the law

Large islands have more indigenous species than small islands — a reflection of the taxa-area relationship, an ecological law that applies to animals and plants.

Some scientists thought that the number of microbial species (both prokaryotes and eukaryotes) found in samples would be a random mix, since the dispersion of microorganisms is much less restricted than that of animals and plants. Essentially, this view held that species number would be independent of the size of the area sampled. Now, two papers published in *Nature* report that microbial diversity is area-dependent and that the taxa-area relationship is a universal law.

Using culture-independent sampling methods to document species diversity, two groups investigated whether the size of the area sampled has any relationship with microbial diversity. Green and co-workers sampled microbial *Ascomycota* fungi in the desert soil of a 62-square-mile Australian park, whilst Horner-Devine



and colleagues sampled bacteria in the sediment of half an acre of a salt marsh in New England, USA. Samples were analysed using molecular techniques such as ARISA (automated ribosomal RNA intergenic spacer analysis) — a community fingerprinting technique — for the fungal samples and 16S rDNA sequencing for the bacterial samples. Statistical analyses revealed that fungal and bacterial communities that were close together were more similar than communities that were separated by large distances. Community differences seem to result from the effect of local environmental factors rather than geographical separation.

Not only should microbiologists appreciate that the microbial world is incredibly diverse, uncultured and largely uncharacterized, we should now realize that microbial communities are not random mixtures but are structured communities that obey the universal taxa-area relationship. Since microorganisms participate in biogeochemical processes that are essential for life on Earth, understanding microbial diversity has important implications for all of us.

Susan Jones

### References and links

**ORIGINAL RESEARCH PAPERS** Green, J. L. *et al.* Spatial scaling of microbial eukaryote diversity. *Nature* **432**, 747–750 (2004) | Horner-Devine, M. C. *et al.* A taxa-area relationship for bacteria. *Nature* **432**, 750–753 (2004)

## 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 characterization 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)