

The instability of the genome of *Halo-bacterium halobium* and of closely related halophiles received special attention. Recent studies of its chromosomal organization and of various extra-chromosomal elements (W. Goebel, University of Würzburg and F. Pfeifer, University of California, San Francisco) shed some light on the structural basis of the instability. The main chromosomal fraction, FI DNA, is 68% G+C-rich and can be readily separated from the more A+T-rich FII DNA fraction. The latter is complex and contains a heterogeneous collection of covalently closed circular DNAs, including a large plasmid carrying many insertion elements, as well as various minor components. Also present in the FII DNA are non-circular 70 kilobase (kb) 'islands' that probably associate with the chromosomal FI DNA; these also contain inser-

tion elements and participate in the genetic variation. A phage, ϕ H, isolated from the halophiles, also exhibits a high degree of genetic variability. No conclusive explanation was offered for the functional significance of the lability of the *H. halobium* genome, although some genomic changes seem to be reversibly inducible by changes in external salt concentration.

Exciting developments were reported in the characterization of virus-host systems (W. Zillig, Max-Planck-Institut für Biochemie, Martinsried) that will prove valuable in future for investigating the molecular genetics of the archaeobacteria. They included the nucleotide sequence of the virus-like SSV1 from *Sulfolobus solfataricus* that has a 16-kb genome, and the identification of four viruses from *Thermoproteus tenax*, that partially resemble eukaryotic viruses in their structural orga-

nization. The ϕ H phage and the plasmid pSL10 from *S. ambivalens* are especially suited to vector development; other potentially important phage and plasmid vector systems were described for the methanogens.

The regulation of gene expression also figured prominently, with emphasis on the more readily isolated rRNA and tRNA genes and the bacterio-opsin gene of *H. halobium*. The observation of multiple transcriptional starts for the single rRNA operon of *H. cutirubrum*, occurring at regularly repeated sequences that include the motif 5'-A-A-G-T-A-A-3', was unexpected (P. Dennis, University of British Columbia, Vancouver). Another putative promoter sequence 5'-G-A-A-N-T-T-T-C-A-3' was deduced from sequencing the *purE*, *proC*, *hisA* and *argG* genes of various methanogens expressed in *Escherichia coli* (J. Reeve, Ohio State University, Columbus). Termination sites are less easily found; although some potential signals resemble those of eubacteria, others do not — it was suggested that five consecutive thymidines might be sufficient for ending the methyl-CoM-reductase gene of *Methanococcus voltae* (A. Klein, Phillips University, Marburg).

The detection of introns among the extreme halophiles and in a thermoproteale was a surprise. A 105-bp intron has been found in the tRNA^{Trp} gene of *H. volcanii* and other halophiles, with a fairly well-conserved sequence (C. Daniels and W. Doolittle, Dalhousie University, Halifax). Moreover, a 622-bp intron containing an open reading frame has been located in the 23S rRNA gene of *Desulfurococcus mobilis* (J. Kjems and R. Garrett *Nature*, in the press) in a similar position to that of an intron in the corresponding gene of the lower eukaryote *Physarum polycephalum*. Although no introns have been reported for protein messenger RNAs, the new results, together with an earlier report of putative small introns in the tRNAs of the sulfolobales, suggest that the presence of introns within ribosomal and tRNAs constitutes another fundamental difference between archaeobacteria and eubacteria.

Various disputes arose concerning archaeobacterial origins and centred on the order in which the extreme halophiles, methanogens and the extreme thermophiles separated from one another and from eubacteria and eukaryotes. The proposal by J. Lake (University of California, Los Angeles) that the sulphur-dependent thermoproteales and sulfolobales should be considered a separate kingdom because a few of their biochemical properties differ markedly from those of the extreme halophiles and methanogens received an extremely negative reaction, as did his contention (Lake, J. *et al. Proc. natn. Acad. Sci. U.S.A.* **82**, 3716; 1985) that the extreme halophiles should be grouped with eubacteria because their ribosome shapes are compara-

The loess region of China

DELEGATES from ten overseas countries recently attended the international symposium on loess research held in Xi'an, in the People's Republic of China (5–13 October, 1985), the first such meeting to be held in the classic Chinese loess region.

A 5-day field excursion before the meeting traversed several loess regions, distinguished by their geomorphological features, between Xi'an and Ansai, 400 km to the north. Our route crossed the broad Wei River flood plain which is mantled by loess and dissected by a few small gullies. Northwards, the hill country is dominated by long, loess-covered ridges termed liang. Limestone quarries along the road gave a unique opportunity to observe how the liangs are related to the underlying bedrock. Smaller, loess-covered hills, known as mao, separate this area from the flat-topped loess plateau, termed yuan. Here the loess is about 100–200 m thick and is extensively cultivated with wheat and maize, a little cotton and tobacco.

The most spectacular features of these yuans are the deep erosional gullies that dissect the plateau. In particular, near Luochuan, the gully is some 130-m deep and in the near-vertical cliffs a sequence of more than 15 palaeosols can be seen overlying the basal red clay. One site has been studied for about 30 years and the chronological sequence has been established primarily by palaeomagnetic measurements of a core nearby. These results imply that the 130-m deep section spans the last two magnetic epochs, the Brunhes and the Matuyama. Detailed magnetic stratigraphies reaching back into the Gauss normal epoch (Heller, F. & Liu, T-s *Nature* **300**, 431; 1982), indicate that loess deposition may have started as early as 2.66 Myr ago. This is similar to the 2.9 Myr date reported by G.J. Kukla (Lament-Doherty, Geological Observatory) for the beginning of

non-biogenic silica incorporation in a marine core off the Japanese coast. Similar and more continuous records are expected from the Qaidam Basin, closer to the source area of the loess, and it is tempting to correlate the palaeosols with the interglacial periods revealed by the deep-sea oxygen-isotope record.

Another feature of the symposium was the integration of geotechnical and chronological studies of loess. A large number of physical properties, such as the bulk dry-density and liquid limit, have been measured and related to the probability of landslides and collapse of loess when it is waterlogged. These properties are of interest as the area is bounded by major active faults and records document many major earthquakes in the past two thousand years.

A highlight of the field trip was a visit to an experimental conservation area, in Ansai County, Shaanxi Province, set up in 1980 by the Northwest Institute of Soil and Water Conservation of Academia Sinica. Erosion of the loess and subsequent landslides are major problems for agriculture, road maintenance and the safety of villages. Experiments designed to measure water run-off and removal of loess have been set up on the top of a hill overlooking the field station, and different types of shrubs and trees have been planted to try to stabilize the surface. We are also privileged to be the first foreigners to visit a village where the results of this research have been applied. Higher crop yields and more terracing have enabled the villagers to cover the upper slopes with trees and leguminous plants, which protect their livelihood.

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