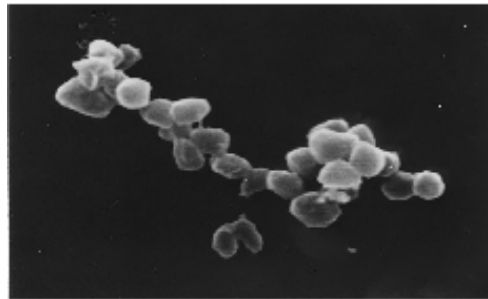


Interspecies hybridisation and recombination in Archaea



Scanning electron micrograph of donor strain NOB8H2 and 1:1 mating mixtures of NOB8H2 x *S. solfataricus*, showing cellular appendages of the donor strain and cell aggregates and intercellular bridges in the mating mixture. (Schleper et al, 1995)

What I will discuss

- What is hybridisation and recombination?
- Why it is important to understand in archaea?
- What do we know and how do we know it?
- Relevance of the Gophna paper

Hybridisation and recombination

- Hybridisation as a term
- Transformation
- Transduction
- Conjugation
- Limitations and barriers

Importance

- Systematics and the species problem
- Origin of eukaryotic sex
- Source of diversity
- Disease
- Archaeal symbionts

What do we know?

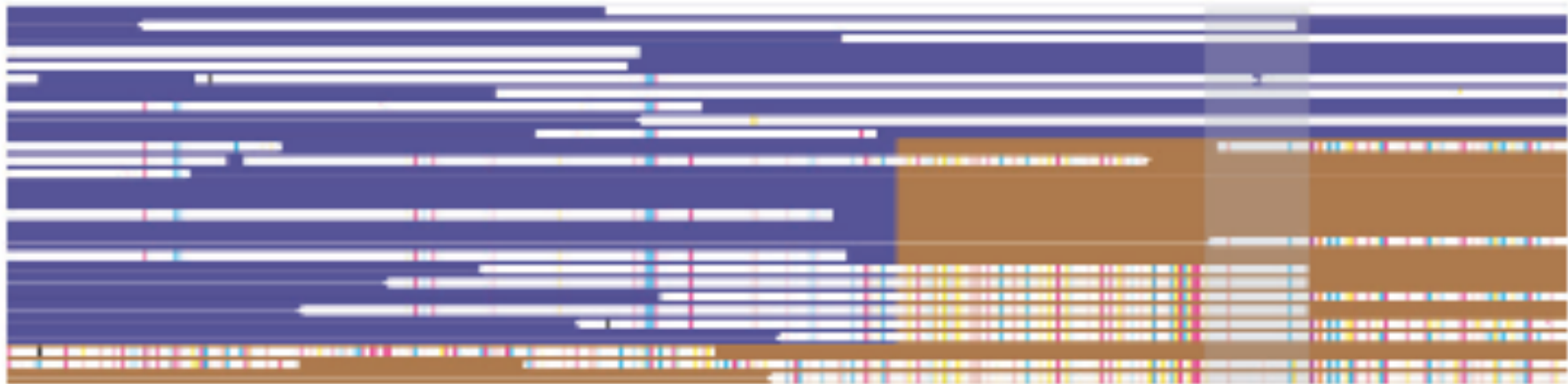
- *Ferroplasma* spp. (Eppley *et al.*, 2007)
- *Pyrococcus* spp. (Lecompte *et al.*, 2001)
- *Halorubrum* spp. (Papke *et al.*, 2004)
- *Methanothermobacter thermoautotrophicum* (Meile *et al.*, 1990)
- *Methanococcus voltae* (Bertani *et al.*, 1987)
- *Sulfolobus* spp. (Schleper *et al.*, 1995)
- Long distance haloarchael events (Boucher *et al.*, 2004)
- *Haloferax* spp. (Rosenshine *et al.*, 1989)



Unrooted Bayesian tree of the archaeal domain based on a concatenation of 57 ribosomal proteins present in at least 89 of 99 genomes (5838 unambiguously aligned amino acid positions) showing locations of observed recombination in the archaea (adapted from Brochier-Armanet *et al.*, 2011)

Ferroplasma

- Metagenomic study
- Uncharacterised mechanism
- 87% sequence similarity
- 77% of recombination around origin of replication



Ferroplasma type II composite genome as the reference for comparing genomes with type I, ticks as SNPs and the grey box highlights area of high similarity (from Eppley, *et al.*, 2007)

Pyrococcus

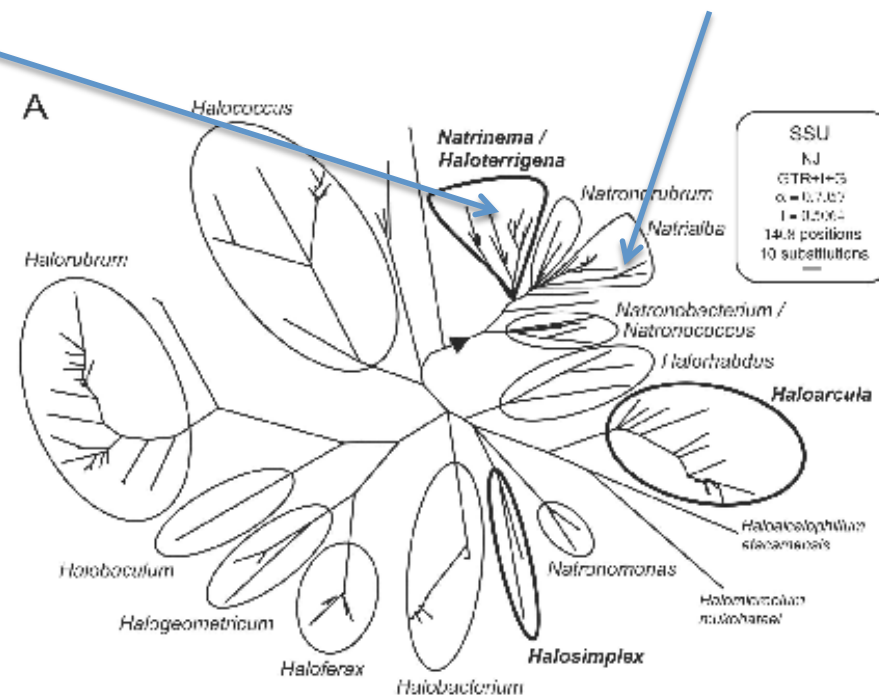
- Genome comparison study
- DNA traffic between:
 - *Pyrococcus abyssi*
 - *Pyrococcus horikoshii*
 - *Pyrococcus furiosus*
- Intergenomic disruption synteny
- Long clusters of tandem repeats (LCTRs)
- tRNAs

Halorubrum

- Population genetics
- Multiple locus sequence typing approach
- Near linkage equilibrium
- Allopatry
- Undetermined mechanism
- Up to 7% sequence difference

Long distance haloarchael events

- *Natrinema* sp. strain XA3-1 and *Natrialba magadii*
- LSU genes
- Largest recorded phylogenetic distance



Best maximum-likelihood distance tree for the SSU gene for the archaeal order Halobacteriales (from Boucher *et al.*, 2004)

Methanococcus voltae

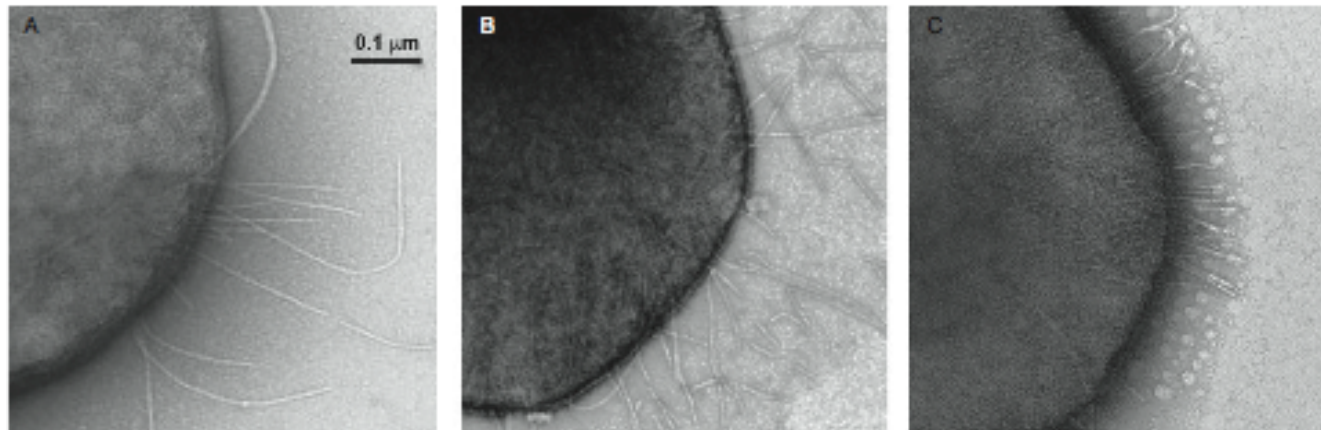
- Reversion of UV-induced mutations
- 2 to 100 transformants per μg of DNA
- Natural transformation
- Transduction
- *Voltae*-transfer agent (4.4kbp)
- Viral particle?

Methanothermobacter thermoautotrophicum

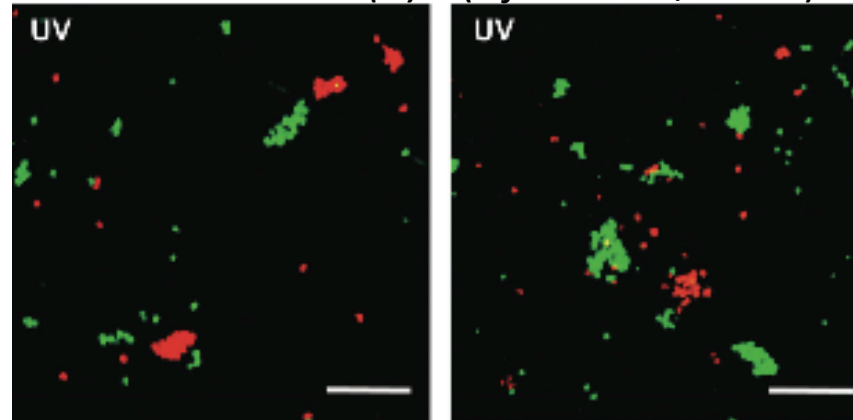
- Transduction
- Bacteriophage ψ M1
- Diversity of archaeal dsDNA viruses
- Lysogenic (non-lytic) lifestyle

Sulfolobus

- Biochemical/Genetic studies
- Multicopy plasmid transfer
 - *Sulfolobus solfataricus*
 - *Sulfolobus acidocaldarius*
 - *Sulfolobus tokodaii*
- Short regularly spaces repeats (SRRPs) and
- Clustered regularly interspaced short palindromic repeats (CRISPRs)
- *SuaI* restriction system
- tRNAs and the SSV1 virus



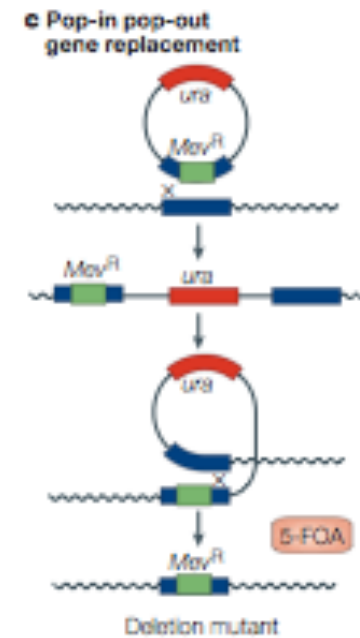
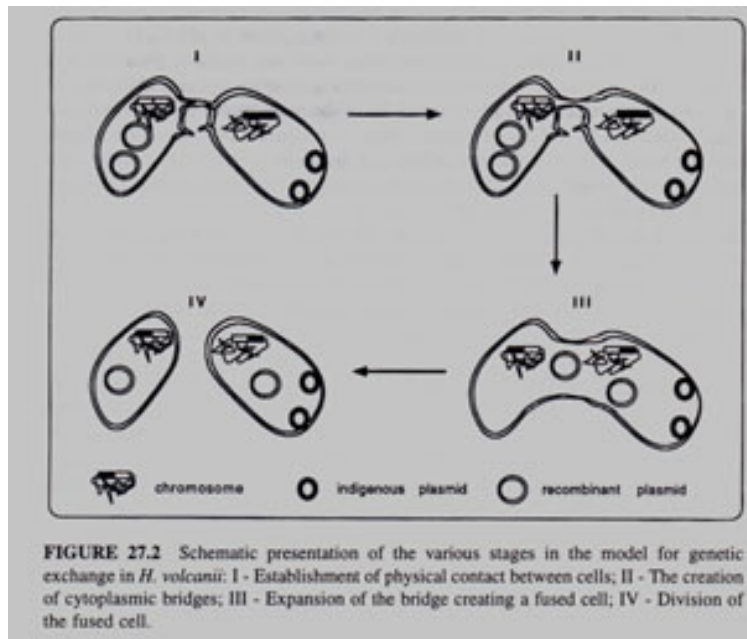
UV-inducible pili on electron micrographs of *S. solfataricus* (A), *S. tokodaii* (B) and *S. acidocaldarius* (C). (Ajon *et al.*, 2011)



Fluorescent *in situ* hybridization (FISH) with species-specific probes. UV-irradiated mixture of cells. *S. solfataricus* (green) with *S. tokodaii* (left) (A) and *S. acidocaldarius* (green) with *S. tokodaii* (red) (right) (Ajon *et al.*, 2011)

Haloferax

- *Haloferax volcanii* (and *H. mediterranei*)
- Bidirectional
- Cytoplasmic bridge
- Rescue phenotypes
- DNAase treatment
- Recombinant plasmids travel within genus



From (Allers *et al.*, 2005)

Gophna Paper

- “Efficient Inter-species Recombination in Halophilic Archaea and the Formation of a Recombinant Hybrid”
- *Haloferax volcanii* and *Haloferax mediterranei*
- 300kb fragments at 86% similarity
- Less than haloarchael intergenomic rRNA recombination

Conclusions

- Transformation
- Conjugation
- Putative Transduction
- Sequence similarity and repetitive sequences
- Same barriers as bacteria
- Potential importance of Gophna paper

References

- Cohan (what are bacterial species?)
- Prangishvili, D., Garrett, R. A. & Koonin, E. V. Evolutionary genomics of archaeal viruses: Unique viral genomes in the third domain of life. *Virus Res.* 117, 52–67 (2006)
- Li et al (2009) Prevalence and molecular diversity of Archaea in subgingival pockets of periodontitis patients
- Bergerat et al (1997) An atypical topoisomerase II from archaea with implications for meiotic recombination
- Brochier-Armanet et al., 2011 (Phylogeny and evolution of the Archaea: one hundred genomes later)
- T.R. Papke, A critique of prokaryotic species concept, *Methods Mol. Biol.* 532 (2009) 379–395.
- **Lecompte et al 2001 Genome Evolution at the Genus Level: Comparison of Three Complete Genomes of Hyperthermophilic ArchaeaP**
- **Papke et al., Searching for species in haloarchaea 2007**
- Eppley et al., Exchange in ferroplasma 2007
- Boucher et al., 2004 Intragenomic Heterogeneity and Intergenomic Recombination among Haloarchaeal rRNA Genes
- Mongodin et al. 2005 The genome of *Salinibacter ruber*: Convergence and gene exchange among hyperhalophilic bacteria and archaea
- Schleper et al, 1995 TRANSFER OF MULTICOPY PLASMID OF *SULFOLOBUS* STRAINS