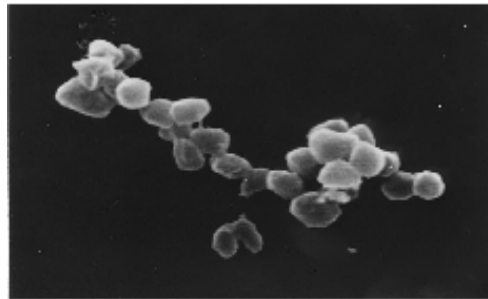


# Interspecies hybridisation and recombination in Archaea



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

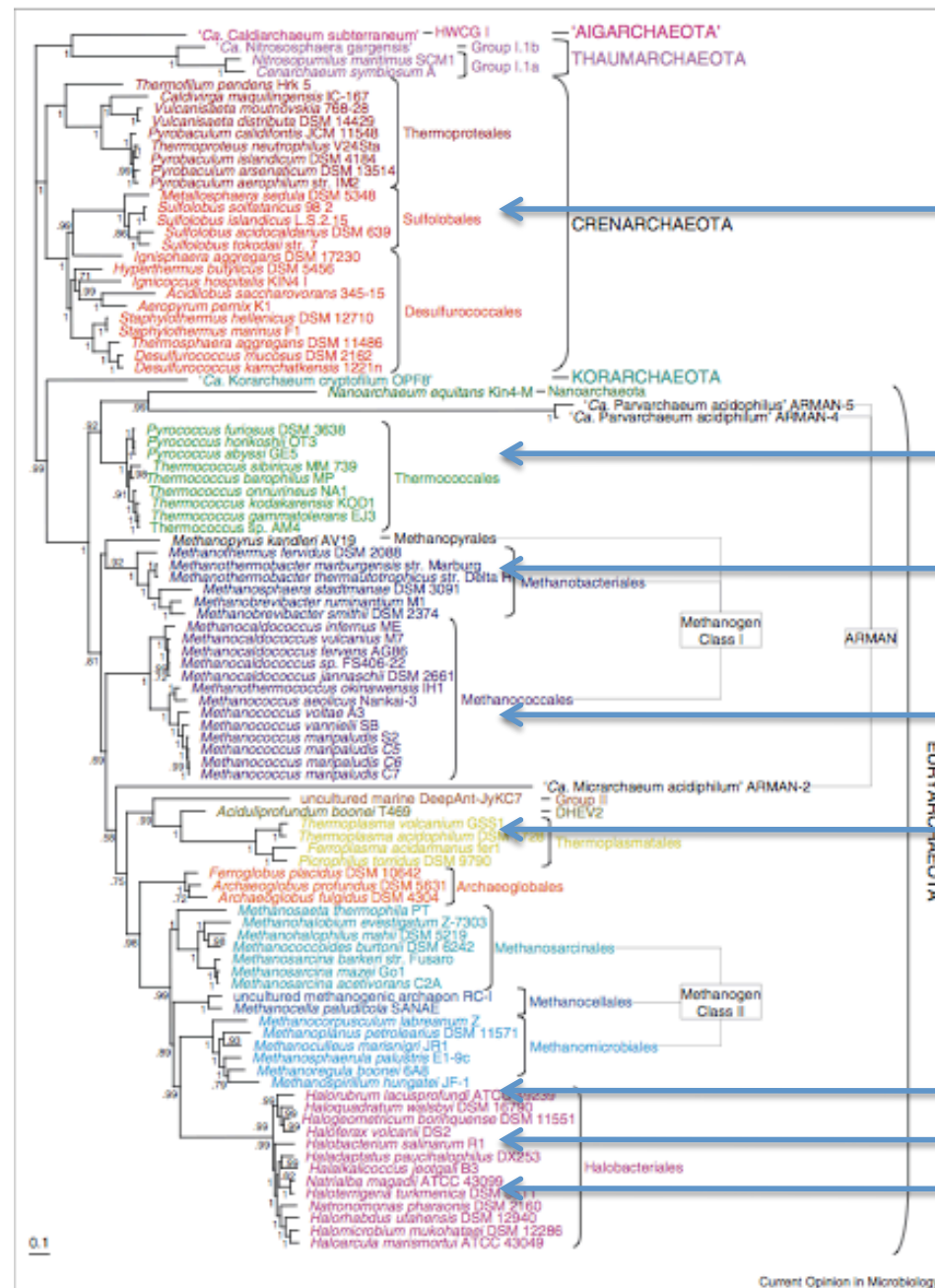
- Hybridisation as a term
- Transformation
- Transduction
- Conjugation
- Limitations and barriers

# Importance

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

# What do we know?

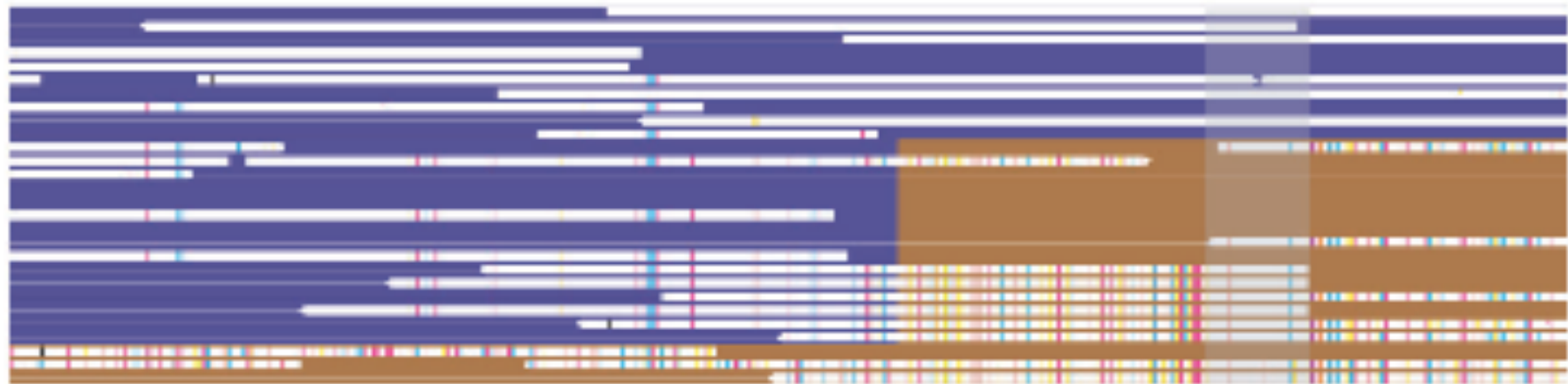
- *Ferroplasma* spp. (Eppley *et al.*, 2007)
- *Pyrococcus* spp. (Lecompte *et al.*, 2001)
- *Halorubrum* spp. (Papke *et al.*, 2004)
- *Methanothermobacter thermoautotrophicum* (Meile *et al.*, 1990)
- *Methanococcus voltae* (Bertani *et al.*, 1987)
- *Sulfolobus* spp. (Schleper *et al.*, 1995)
- Long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

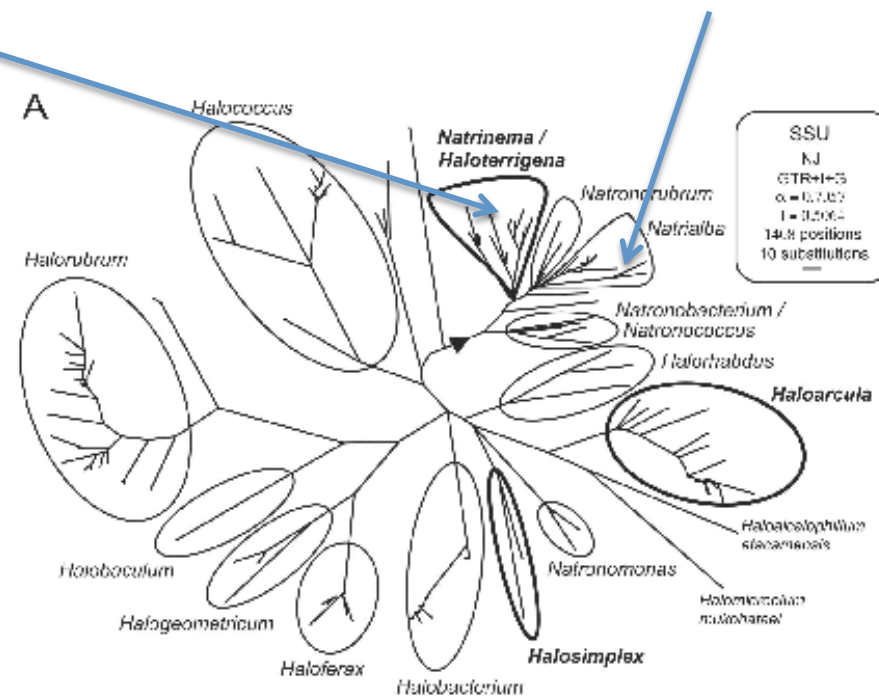


# *Halorubrum*

- 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*

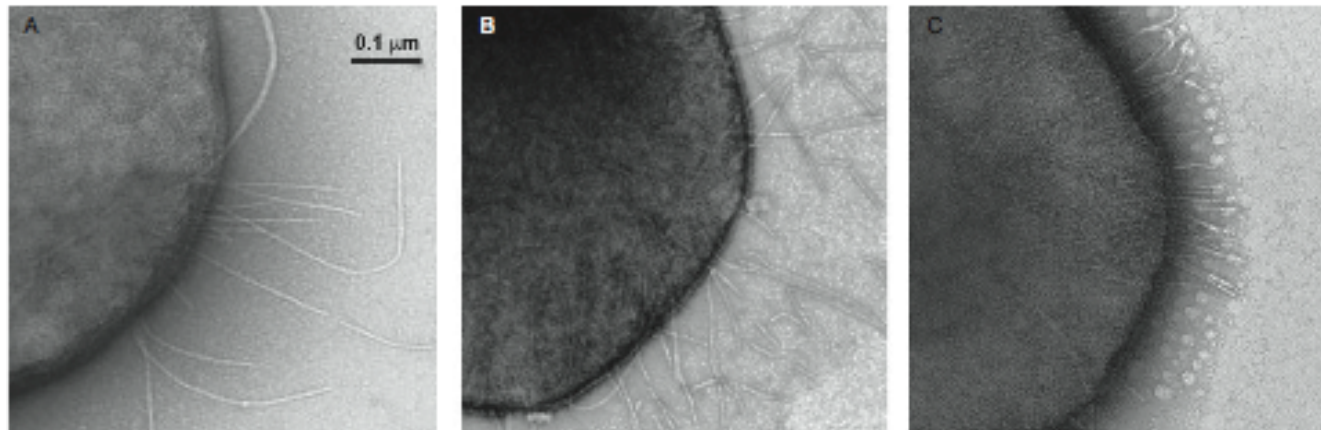
- Reversion of UV-induced mutations
- 2 to 100 transformants per  $\mu\text{g}$  of DNA
- Natural transformation
- Transduction
- *Voltae*-transfer agent (4.4kbp)
- Viral particle?

# *Methanothermobacter thermoautotrophicum*

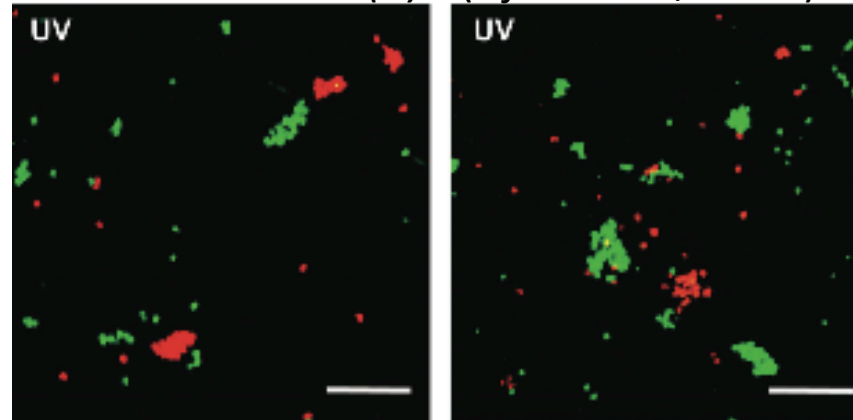
- Transduction
- Bacteriophage  $\psi$ M1
- Diversity of archaeal dsDNA viruses
- Lysogenic (non-lytic) lifestyle

# *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



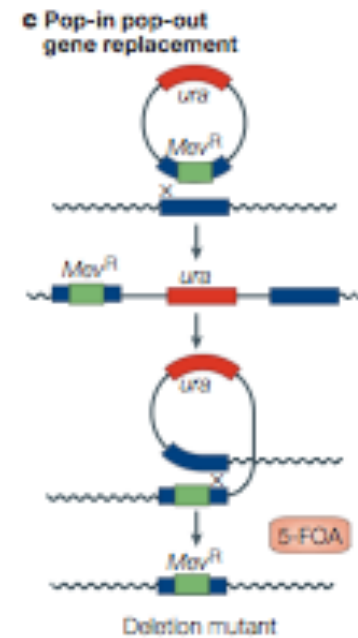
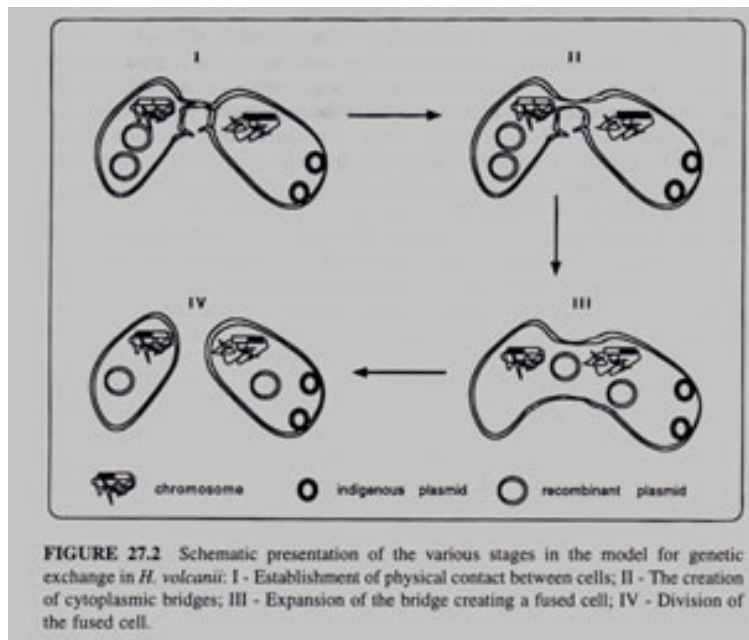
UV-inducible pili on electron micrographs of *S. solfataricus* (A), *S. tokodaii* (B) and *S. acidocaldarius* (C). (Ajon *et al.*, 2011)



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

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- 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