

**P052** Genetic evidence for histone acetylation in the halophilic archaeon *Haloferax volcanii*

**Neta Altman-Price and Moshe Mevarech**

*Dept. Molecular Microbiology and Biotechnology, Tel-Aviv University, Tel-Aviv, Israel*

Protein acetylation and deacetylation reactions are involved in many regulatory processes in eukaryotes. Recently it was shown that similar reactions have regulatory roles also in bacteria and archaea. Sequence analysis of the haloarchaeon *Haloferax volcanii* genome enabled the identification of three putative protein acetyltransferases (*Pat1*, *Pat2* and *Elp3*) and two deacetylases; (*Sir2* and *Hdal*). Intriguingly, the gene that encodes for *Hdal* shares an operon with an archaeal histone homologue. We have used a gene knockout method to determine whether these putative genes are essential, and found that whereas *Sir2* knockout strain can grow normally, *Hdal* deletion is lethal. Moreover, the specific *Hdal* inhibitor Trichostatin A inhibits cell growth. We also showed that *Pat2* and *Elp3* are “synthetic lethals”. Genetic analysis of the histone gene has shown that it is essential for growth. Site directed mutagenesis of the two unique lysine residues of the histone established a link between the histone and the acetylation/deacetylation processes. Changing any of the lysine residues to glutamine made the cells more sensitive to Trichostatin A while mutagenesis of both residues to either lysine or arginine rendered the cells more resistant to that drug. We have also found that while *Hfx. volcanii w.t* strain loses viability after reaching the stationary growth phase, the double lysine mutant retains its viability. The same effect could also be achieved if the *w.t* strain was grown in the presence of TSA.