Prediction of Novel Genes for Heat-Adaptation

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Comparative genome analyses represent a powerful tool in discovery of novel genes responsible for adaptation to specific extreme environments. Methanogens stand out as the only group of organisms that have species capable of growth at 0°C (*M. frigidum* and *M. burtonii*) and 110°C (*M. kandleri*). A recent study of two psycrophilic methanogens (M. *frigidum* and *M. burtonii*) revealed 5 genes specific for only these two organisms, suggested to be involved in cold-adaptation (Saunders et al., 2003). Although not all the components of heat adaptation can be attributed to novel genes, the chaperones known as heat shock proteins stabilize the enzymes under elevated temperature. However, highly conserved chaperons found in bacteria and eucariots are not present in hyperthermophilic Archea, rather, they have a unique chaperone TF55. Our aim was to use software which we specifically developed for extremophile genome comparative analyses in order to search for additional novel genes involved in hyperthermophile adaptation. The following hyperthermophile genomes incorporated in this software were used for these studies: M jannaschii, M. kandleri, A. fulgidus and three species of Pyrococcus. Common genes were annotated and grouped according to their roles in cellular processes when such information was available and proteins not previously implicated in the heat-adaptation of hyperthermophiles were identified. Additional experimental data is needed in order to learn more about these proteins. To address a non-gene based components of thermal adaptation, all sequenced extremophiles were analyzed for their GC contents and aminoacid hydrophobicity and a prediction model of optimal growth temperature was developed.