

Comparative genomics reconstruction of transcriptional regulons for metal homeostasis and autotrophic pathways in Archaea

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One of the most intriguing features of Archaea is combination of eukaryotic-like basal transcription machinery with abundance of bacteria-like transcription factors. Though this observation was made more than ten years ago [1] there is not much information about regulation of archaeal gene expression. In current work we implemented comparative genomics knowledge-driven approach [2] that was previously used for bacterial regulons reconstruction on two archaeal systems.

Members of DtxR family proteins that are known as divalent ion-sensing transcription regulators in bacteria [3] are widely distributed in archaeal genomes. We applied the comparative genomics approach to reconstruct regulons controlled by the DtxR family of transcription factors in available archaeal genomes. The results suggest that the archaeal DtxR-family regulators control genes involved in iron and manganese homeostasis. The predicted ferric iron-responsive FetR regulons were classified into two groups based on the predicted regulon size. The small-size local FetR regulons control one or two iron transporter operons per genome (e.g. *feoAB*). The remaining FetR regulons has a larger number of predicted members due to massive duplications of iron transporter genes and subsequent regulon expansion.

Autotrophic carbon dioxide fixation pathways differ significantly between various lineages of Archaea [4]. Species from the Crenarchaeota phylum possess one of the two autotrophic pathways, either the hydroxypropionate–hydroxybutyrate cycle (in the Sulfolobales) or the

dicarboxylate–hydroxybutyrate cycle (in the Thermoproteales and Desulfurococcales). We identified novel DNA motifs associated with the autotrophic pathway genes in archaeal genomes from both lineages. Reconstruction of autotrophic regulons in the Crenarchaeota revealed several additional target genes involved in carbon metabolism that are potentially co-regulated with autotrophic pathway genes. The bioinformatically predicted regulons were assessed using the high-throughput expression data available for several model archaeal species.

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