

A Prototype of Transcription Regulations, Which Have Highly Differentiated: Transcription Regulation by FFRPs

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The archaeon *Pyrococcus* sp. OT3 grows on amino acids. At a hydrothermal vent in the Okinawa Trough, where this archaeon was isolated, debris of marine organisms fell from the sea above. At the mid-growth phase, transcription of the gene coding an feast/famine regulatory protein (FFRP), FL11, is repressed by FL11 forming octamers in interaction with lysine. At the stationary phase in the absence of lysine, FL11 disassembles to dimers and the transcription repression is relaxed. Many FL11 dimers are expressed and repress transcription of ~20% of genes coded in the genome, thereby terminating synthesis of ATP upon degrading amino acids and other major metabolisms. This global regulation resembles another global regulation of the *E. coli* metabolism by an FFRP, the leucine-responsive regulatory protein (Lrp). FFRPs form a single group of transcription factors systematically distributed through archaea and eubacteria. The last common ancestor of extant organisms is believed to have differentiated to archaea and eubacteria first, with eukaryotes developing later. Characteristics common between the two global regulations suggest characteristics of a prototype transcription regulations once achieved in the common ancestor. Archaeal FFRPs are phosphorylated at Ser and Thr residues inside their DNA-binding domains, suggesting that the origin of eukaryotic modulation of transcription regulation can be traced back to archaea.