Transcriptional Regulation in Archaeabacteria

As is often the case, epoch-making ideas carry with them implicit, unanalyzed assumptions that ultimately impede scientific progress until they are recognized for what they are. So it is with the prokaryote-eukaryote distinction. Our failure to understand its true nature set the stage for the sudden shattering of the concept when a "third form of life was discovered in the late 1970s, a discovery that actually left many biologists incredulous. Archaeabacteria, as a third form has come to be known, have revolutionized our notion of the prokaryote, have altered and refined the way in which we think about the relationship between prokaryotes and eukaryotes... and will influence strongly the view we develop of the ancestor that gave rise to all extant life.

- C. Woese and R. S. Wolfe (1985)

Archaea: life at the extremes

Methanogens are responsible for the production of methane.

Volta’s experiment in 1776 showing “combustible air” produced at the bottom of lakes.

Universal Phylogentic Tree

Archaeal Transcription

Archaearaphiles at the University of Florida

Department of Microbiology & Cell Science

Dr. Julie Maupin-Furtow
Specialist in biological and biochemical regulation of cells by proteolytic enzymes, development of enzymes, and metalloprotein structure and function. With a specialization in the biochemistry of the rumen methanogen, she is engaged in studies of protease inhibitors in rumen microbes.

Dr. Madeline Raschke
Investigates the physiology and molecular mechanisms of the halophilic archaeon, Halobacterium, which is a model system for studying the effects of high salinity on cellular processes and gene expression.

Dr. Thomas Bobik
Collaborating with Dr. Raschke studying the biochemistry of methane production in methanogens. Other studies are related to encasement of vitamin B12-dependent enzymes within polyhedral organelles in Salmonella.

Photo of Thiobacillus kindly provided by Dr. Henry Aldrich
Archaeal factors

1) TATA binding protein (TBP): 30 kDa
2) TFB (homolog to TFIIB)

TBP

View from +1 back upstream at TBP bound at TATAAA

Archaeal Transcription

Red = Pyrococcal
green = yeast

TBPs in Archaeabacteria are nearly identical to those in eucaryotes. Many Archaea have multiple TBP's.

Tsai et al. In: Cold Spring Harbor Symposia vol. LXIII, pp. 53-61

Fig. 5

Archaeal Transcription

Yeast TBP or Pyrococcal TBP

The peptide repeats of TBP are more symmetrical in their contact with TATAAA. Only 60/40% preference for TATAAA over TTTATA.

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Archaeal Transcription

Typical eucaryotic promoter:

BRE spacing important

Upstream elements

TATAAA or TTTATA

BRE = 5’-G/C-G/C-G/A-CGCC-3’ (metazoa)

Inr = Py-Py-A, N-T/A-Py-Py (mammals)

DPE = A/G-A/T-CGTG (Drosophila)

Note: only TATAAA is known in plants

Polarity of transcription is determined by

1) TATAAA
2) BRE
3) Inr (initiation region or initiator)
4) DPE (downstream promoter element)

Archaeal Transcription

Typical Archaeal promoter:

-110

BRE -30 +1

Upstream elements

TATAAA or TTTATA

BRE = 5’-c-A/G-n-a-A-n-T-T-T/A-t-r-3’

Polarity of transcription is determined by

1) TATAAA
2) BRE
3) Inr; weakly conserved; Py-Pu,

Basal factors

TFIIB/TBP/DNA complex

TFIIB

conserved core domain has two repeat structures (R1 & R2).