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HOW THE TRANSCRIPTIONAL REGULATION MACHINERIES IN CYANOBACTERIA DIFFER FROM OTHER EUBACTERIA?

Akanksha Srivastava, SandhyaYadav, Subhankar Biswas, Yogesh Mishra*

Department of Botany, Center of Advanced Study in Botany, Institute of Science,
Banaras Hindu University, Varanasi 221005, India
***Corresponding author**: Yogesh Mishra Tel.: 0542-6701121
ymishra@bhu. ac.in; yogeshbhu@gmail.com

Abstract:

Cyanobacteria exhibit widest range of diversity in habitat among all photosynthetic organisms which suggests that they must have developed their genetic architecture in a way that allowed them to combat the stressful conditions over millions of years. Cyanobacterial ecological plasticity is remarkable, which makes these organisms as a model in order to understand the complex mechanism of gene expression and regulation under different habitats. Precise regulation of the transcription process ensures condition dependent differential gene expression. Transcription is first and foremost step of gene expressions which is performed by the RNA polymerase (RNAP) holoenzyme, embracing a core enzyme and a sigma (σ) factor. The transcriptional regulation machineries of cyanobacteria differ from eubacteria at level of (i) The unique structure of core RNAP, (ii) wide variety of σ-factors (and RNAP core subunits) and (iii) more than one type of promoter. These aforementioned differences during transcription regulation confer the great ecological plasticity to cyanobacteria. On the basis of studies reported previously, present review compares the cyanobacterial transcriptional processes and regulation with other eubacteria.

Introduction

Besides having the similarity in basic cellular features from other eubacteria, cyanobacteria possess some distinct and diagnostic characteristics. Cyanobacteria are only photosynthetic prokaryotes which perform oxygenic photosynthesis similar to higher plants (Picossi *et al*,. 2014). These distinct and unique characteristics make cyanobacteria stand at highest rank in bacteria domain. Ecological plasticity of cyanobacteria is very unusual. They can be spread out in almost any ecological niche e.g. fresh water, marine water, terrestrial and extreme environments including metal-defiled area (Lara *et al*., 2014). For adapting in different ecological region they must have evolved some mechanisms to tightly regulate the condition dependent differential genes expression.

Transcription is an important step in gene expression, in which a particular segment of DNA is copied into RNA by the enzyme RNA polymerase (RNAP) (Guo *et al*., 2014, Engel *et al*., 2018). Prior to research in molecular and cellular biology, understanding of transcriptional processes is very crucial. Transcription in prokaryotes is firmly regulated process and by precisely tuning this, transcriptional factors/regulators help the organisms to percept environmental stresses and subsequently assist in transduction of stress signals to acclimatize environmental insult

(Balleza *et al*,. 2009). Transcriptional regulation ensures that correct genes are expressed at the precise time in precise amounts.

In cyanobacteria, transcriptional processes and its regulation are somewhat similar to other eubacteria except slight differences.

2. Difference between transcriptional regulation machineries of cyanobacteria from other eubacteria:

The differences between the transcriptional regulation machineries of cyanobacteria from other eubacteria can be summaries in the following subheadings.

2.1. Differences at the level of core RNA polymerase structure

Transcription in prokaryotes is driven by a large, highly conserved multi-subunit enzyme, RNA polymerase (RNAP). Most of the work on prokaryotic RNAP has been done on the gram negative bacteria, *Escherichia coli*. Cyanobacterial core RNAP is quite similar to that of *E. coli* with one notable exception. In *E. coli* and other bacteria, RNAP holoenzymes consist of a core enzyme with subunits of $\sigma_2\beta\beta$' (Ishihama *et al,*. 2000) but in cyanobacteria, β' is usually split into two parts γ and β'. Thus, the composition of cyanobacteria core RNAP is $\sigma_2\beta\beta'\gamma$. This architecture is quite similar with almost all plant chloroplast RNAP ($\sigma_2\beta\beta'$ β'') (Imamura & Asayama,. 2009).

2.2. Difference at the level of σ-factor switching

Transcriptional regulation comes up from the interaction between trans-acting transcriptional regulators that bind to cis-regulatory elements. Cis-elements comprise all those DNA regions which are present in the vicinity of a gene such as the promoter, where the RNA polymerase initially binds and transcription factor-binding sites (TFBS), where transcription factors (TFs) bind to modulate the binding of the RNAP. Trans-acting transcriptional regulators cover all the diffusible cellular molecules that are able to bind to the DNA such as σ- factors and transcription factors (Browning & Busby, 2004). The coactivity of these molecular commodities composes the minimal transcriptional regulatory system in all living organisms. σ- Factors in complex with core RNAP provide determinants for promoter recognition and open complex formation; therefore they provide most fundamental level of control for gene expression. In bacteria, these σ-factors are divided into two main phylogenetic families: σ^{70} and σ^{54}. The σ^{70} family, which is a primary σ-factor, includes the housekeeping σ that is important for expression of genes under normal conditions and σ^{54}family covers those σ-factors which recognize promoters of nitrogen related genes. Though, cyanobacteria possess a system for nitrogen metabolism so they donot have any member of σ^{54} family (Imamura & Asayama,. 2009). Cyanobacterial genome codes for a number of σ-factor, on the basis of phylogenetic analysis they have been subdivided into three groups: Group 1, 2 and 3. Group 1 consist a principal σ-factor that is indispensible for cell viability. Group 2 is similar to group 1 in molecular structure, but it is not essential for cell viability. Group 3 σ-factors are an alternative type, they are structurally different from the group 1 and group 2 σ-factors and assist in the

transcription of regulons during adaptation in adverse environmental condition (Imamura *et al,*. 2003; Koskinen *et al*,.2015).

2.2.1. Group 1 σ-factors

Group 1 σ-factor (SigA) are indispensible for expression of housekeeping genes and it is very similar to σ^{70} of eubacteria. Under normal physiological condition these factors remain constant but some environmental condition such as heat-shock, darkness, nitrogen deprivation and salt stress, lead to a down-regulation of transcription of *sigA*. The reduction of group 1 σ-factor at protein level are related with σ-switching (Imamura & Asayama,. 2009).

2.2.2. Group 2 σ-factors

The group 2 σ-factors (SigB) basically consist of four distinct clusters, B, C, D and E (SigB, SigC, SigD and SigE, respectively). Protein level of SigB increases in response to nitrogen starvation, shift from continuous light to darkness, heat shock, and osmotic salt and osmotic stress. Therefore, SigB σ-factor is a multifunctional protein that assembles with core RNAP in environmental stress conditions. SigC is another group 2 type σ-factor, which is effective for cell viability in the stationary phase. SigD is effective in response to shift in light after adapting to darkness and SigE is induced in nitrogen deprived condition (Imamura *et al*, 2003).

2.2.3. Group 3 σ-factors

The group 3 σ-factors also consist of four distinct clusters F, G, H and I. SigF σ-factor is similar to sigma factors involved in general stress and in sporulation of other organism. It is also effective for photo-tactic movement by controlling gene which intend for pili formation. SigG and SigH-type after σ is essential for cell growth and they are similar to σ-factors involved in extra cytoplasmic function (Imamura *et al,*. *2*003; Koskinen *et al,*. *2*015). There is no information available regarding genes controlled by SigH-type and SigI-type σ-factors in cyanobacteria.

2.3. Difference at the level of recognizing promoter types

Transcription in cyanobacteria is carried out by core RNAP assembled with heterogeneous σ-factors which are assigned to groups 1, 2, and 3. Presence of many group 2 σ-factors is a unique character of cyanobacteria. The diversity of group 2 σ-factors impacts on promoter recognition which consequences in interference with group 1 σ-factors expression. Coordination among group 1 and 2 σ-factors results in sensing of stimulus produced by environmental changes and regulating transcription from type 1 or 2 promoters. However, a stringent control for promoter recognition has been reported for the type 3 promoter. There are three types of promoter have been reported in cyanobacteria which are mentioned below:

2.3.1. Promoter type 1

Type 1 promoter possess both -35 (TAGACA) and -10 (TATAAT) hexamers exactly similar to σ^{70}- dependent consensus sequence. Under normal physiological conditions type 1 promoter is mainly recognized by group 1 σ-factor, but at the time of stress add, some group 2 σ-factors may replace group 1 σ-factor in RNAP holoenzyme and drive the transcription more efficiently from type 1 promoter. There are several reason which is responsible for the replacement of group 1 with group 2 σ-factor : (1) under stress condition group 2 σ-factors are induced and increases, (2) under stress, co-activators and/or substances (e.g. ppGpp) are expressed which enhance binding of core RNAP to group 2 σ-factors by inhibiting group 1 σ-factors, (3) at post-transcriptional level, group 2 σ-factors are modified and resulting in its activation and (4) presence of anti-σ factors which activates group 2 σ-factors by inactivating group 1 σ-factors (Imamura *et al,. 2*003).

2.3.2. Promoter type 2

Type 2 promoters possess only the -10 hexamer or plus enhancer-motif sequences associated with transcriptional activator proteins which may compensate for lack of -35 function. Group 1 σ-factors can not bind with type 2 promoters because they lack -35 hexamer. Under environmental stress condition, group 2 σ-factors contribute to transcription by type 2 promoter even in presence of group 1 σ-factors (Imamura & Asayama,. 2009).

2.3.3. Promoter type 3

Nucleotide sequence of promoter type 3 is different than the promoter type 1 and 2 and transcription from promoter type 3 may be independent of group 1 and group 2 σ factors. Mainly group 3 σ factors contribute transcription from type 3 promoter (Imamura & Asayama,. 2009).

3. Conclusions

Transcription is a crucial step of gene expression which involves core RNA polymerase enzyme and various types of condition dependent σ-factors. Unique structure of core RNAP, coordination among various types of σ-factors and more than one type of promoter certifies the condition dependent gene expression in cyanobacteria. The uniqueness in the transcriptional regulation machineries may be another reason behind the wide adaptive capabilities of cyanobacteria in harsh environment.

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5. References

1. Balleza, E,; López-Bojorquez, L. N.; Martínez-Antonio, A.; Resendis-Antonio, O.; Lozada-Chávez, I.; Balderas-Martínez, Y. I.; Encarnacion S.; Collado-Vides, J. Regulation by transcription factors in bacteria: beyond description. *FEMS Microbiol.Rev.*2009, *33* (1), 133-151.
2. Browning, D. F.; Busby, S. J. The regulation of bacterial transcription initiation. *Nat. Rev. Microbiol.* 2004, *2*(1), 57-65.
3. Engel, C.; Neyer, S.; Cramer, P. Distinct Mechanisms of Transcription Initiation by RNA Polymerases I and II. *Annu. Rev. Biophys.* 2018, *47*, 425-446.
4. Imamura, S.; Asayama, M. Sigma factors for cyanobacterial transcription. *Gene Regul. Syst. Biol.* 2009, *3*, 65-87.
5. Imamura, S.; Yoshihara, S.; Nakano, S.; Shiozaki, N.; Yamada, A.; Tanaka, K.; Takahashi, H.; Asayama, M.; Shirai, M. Purification, characterization, and gene expression of all sigma factors of RNA polymerase in a cyanobacterium. *J. Mol .Biol.* 2003, *325* (5), 857-872.
6. Ishihama, A. Functional modulation of Escherichia coli RNA polymerase. *Annu. Rev. Microbiol.* 2000, *54* (1), 499-518.
7. Picossi, S.; Flores, E.; Herrero, A. ChIP analysis unravels an exceptionally wide distribution of DNA binding sites for the NtcA transcription factor in a heterocyst-forming cyanobacterium. *BMC Genomics.* 2014, *15* (1), 22.
8. Lara, Y.; Stelmach Pessi, I.; Durieu, B.; Lepoint, G.; Wilmotte, A.; Michel, L. In Search for Marine Antarctic Cyanobacteria. *In Book of Abstracts*. 2017; pp. 58.
9. Guo, J. Transcription: the epicenter of gene expression. *J. Zhejiang Uni. Science B.* 2014, *15*(5), 409–411.
10. Koskinen, S.; Hakkila, K.; Gunnelius, L., Kurkela, J.; Wada, H.; Tyystjärvi, T. In vivo recruitment analysis and a mutant strain without any group 2 σ factor reveal roles of different σ factors in cyanobacteria. *Mol. Microbiol.* 2016, *99* (1), 43-54.