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T7-like promoter function: DNA physics implication

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Motivation and Aim: RNA polymerase – promoter interactions has been the subject to extensive studies for decades. However, there are still certain relevant mechanistic details to be established. Recent advances in the field was enabled to more attention paid to DNA physicochemical properties in addition nucleotide sequence analysis. This biomolecules properties are primarily responsible for their interaction, particularly at initial stages of RNA-polymerase--promoter interaction. T7 bacteriophage and related genomes can serve as suitable study objects in the field due to their small genomes being transcribed by two different RNA-polymerase including host-specific and native one encoded by phage DNA. The latter enzyme is characterized by small size, high processivity, and capability of discriminating promoters that have very similar primary structure but differ in biochemical and physical properties as well as activation time during lifecycle [1]. The DNA physicochemical properties of the promoter are likely to affect their differential recognition as well as implication in replication, etc. [2].
Methods and Algorithms: The extent to which the T7-DNA promoter are susceptible to melt under superhelicity stress was assessed using Stress-Induced Duplex Destabilization (SIDD) model [3]. Molecular dynamics (MD) simulations were used to determine contribution of various promoter DNA and T7-RNA-polymerase to root mean squared deviation of the molecules in the structurally resolved complex as well as in free form.
Results: Native promoters representing class III are substantially more destabilized as compared to class II ones according to their SIDD profiles. Promoters serving as secondary replication origin demonstrates higher SIDD maxima. MD experiments have yielded RMSD dynamics for a highly destabilized strong T7-promoter (class III consensus sequence) and weaker class II promoter sequence.
Conclusions: Highly similar or identical in their nucleotide sequences promoters of T7 bacteriophage were shown to differ in their physicochemical properties. This both directly or by modulating promoter strength may affect their specific recognition by native RNA-polymerase and genes expression regulation.

References

1. Kamzolova S.G., Beskaravainy R.M., Osypov A.A. et al. Electrostatic map of T7 DNA: Comparative analysis of functional and electrostatic properties of T7 RNA polymerase-specific promoters. *Journal Biomolecular Structure Dynamics*. 2014;32:1184-1192.
2. Orlov M.A., Ryasik A.A., Sorokin A.A. Destabilization of the DNA Duplex of Actively Replicating Promoters of T7-Like Bacteriophages. *Mol. Biol*. 2018;52(5):686-692.
3. Wang H., Benham C.J. Promoter prediction and annotation of microbial genomes based on DNA sequence and structural responses to superhelical stress. *BMC Bioinformatics*. 2006;7:248.