Editorial Overview

RNA Polymerase Reaches 60: Transcription Initiation, Elongation, Termination, and Regulation in Prokaryotes

This year, 2019, marks the 60th anniversary ("diamond anniversary") of the discovery of RNA polymerase, the molecular engine of transcription ([1]; see also Refs. [2–4]). This year, 2019, also marks the 50th anniversary ("golden anniversary") of the discovery of σ, the first identified general transcription factor [5,6]. In honor of these major anniversaries, we have commissioned a comprehensive set of review articles on RNA polymerase, transcription initiation, transcription elongation, transcription termination, and transcriptional regulation in prokaryotes.

The review articles in this special issue summarize six decades of intensive analysis of transcription and transcriptional regulation in bacteria, archaea, and their viruses. The experimental approaches covered span the full range from genetics, to biochemistry, to structural biology and biophysics. The findings covered encompass early results identifying factors, processes, and pathways, as well as the recent explosion of structural information from crystallography and cryo-EM and the recent explosion of mechanistic insight from single-molecule biophysics.

The first nine review articles focus on transcription and transcriptional regulation in bacteria and their viruses. The review article by Mazumder and Kapanidis [7] summarizes transcription initiation by RNA polymerase holoenzyme containing the principal σ factor, σ^{70}/σ^{A}, and the article by Danson *et al*. [8] summarizes transcription initiation by RNA polymerase holoenzyme containing the structurally and mechanistically distinct alternative σ factor, $\text{sigma}^{54}/\sigma^{N}$. The review articles by Belogurov and Artsimovitch [9], Kang *et al*. [10], and Roberts [11] summarize transcription elongation and transcription pausing, and transcription termination, respectively. The review articles by Shen and Landick [12], Browning *et al*. [13], and Tabib-Salazar *et al*. [14] summarize the bacterial nucleoid ("bacterial chromatin"), bacterial activators and repressors, and bacteriophage activators and repressors, respectively. The review article by Strick and Portman [15] summarizes bacterial transcription-coupled DNA repair.

The next six review articles focus on the mechanisms of transcription and its regulation in archaea. Archaea, which constitute the second prokaryotic domain of life, are less understood than their bacterial brethren. Archaea first came to note due to their extreme environments in terms of temperature, pressure, acidity, and salinity [16]. More recent phylogenetic analyses demonstrate that archaea also inhabit more benign niches, including the sea, the soil, the human mouth, and the human gut [17], and the most recent phylogenetic analyses raise the possibility that eukaryotes are derived from a primordial archaeon related to extant archaea belonging to the Asgård phylum ([18]; see, however, Ref. [19]). Archaeal transcription exhibits a mosaic of bacteria-like features and eukaryote-like features [20,21]. Archaea, like bacteria, lack nuclei, have small genomes with genes organized in operons, and perform coupled transcription and translation [20]. At the same time, archaea have a eukaryote-like 12-subunit RNA polymerase, a eukaryote-like set of general transcription initiation and elongation factors, and, in most archaeal taxa, also have histones that form chromatin structures [21]. The review articles by Sanders *et al*. [22] and Kramm *et al*. [23] summarize the structure and regulatory role of archaeal chromatin, and the structure and function of archaeal RNA polymerase and general transcription factors, respectively. The review articles by Lemmens *et al*. [24] and Hackleya and Schmid [25] report on systems biology aspects of transcription regulation in response to oxidative stress. The review articles by Sauguet [26] and Blombach *et al*. [27] summarize inferred evolutionary relationships and critically evaluate the current understanding and challenges of transcription in archaea.

Taken together, the 15 review articles provide a firm foundation for understanding transcription and transcriptional regulation in bacteria, archaea, and their viruses, and provide an indispensable reference point for understanding the structurally conserved, but substantially more complex and substantially less characterized, processes of transcription and transcriptional regulation in eukaryotes.

With these contributions, we hope not only to inform the reader but also to encourage early career scientists at the cusp of independence to consider entering these areas of scientific enquiry. Even after six decades, there are fundamental questions to answer and much to do.

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