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Perspective

Role of Transcription Factors (TFs) for Gene Regulation in Various Stages of its Development

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DESCRIPTION

Genetic material encoded in DNA is transformed into mRNA during the transcription process by RNA polymerase enzymes. Whereas eukaryotes have three RNA polymerases to transcribe the variety of eukaryotic genes, bacteria only have one RNA polymerase to transcribe all of their genes. In order to create the transcript, RNA polymerase also needs additional components or proteins. These elements, which are collectively known as Transcription Factors (TFs), either directly interact with RNA polymerase or contribute to the construction of the transcription machinery.

Our cells most frequently employ TFs to regulate gene expression. The parasite *Plasmodium falciparum* is in charge of transmitting the most dangerous type of malaria to people. The majority of its traits are those that are typical of eukaryotic transcription; however, it is thought that *P. falciparum's* transcriptional regulatory mechanisms are somewhat unique from those of other eukaryotes.

In transcription, a number of enzymes work together to create an RNA molecule that is complementary to the DNA template. Both prokaryotic and eukaryotic transcription have three sequential events: initiation, elongation, and termination. The most crucial stage is initiation, which involves RNA polymerase attaching to double-stranded DNA. The covalent addition of nucleotides to the polynucleotide chain's 3' end is known as elongation, and the identification of the transcription termination sequence and the release of RNA polymerase are known as termination. The first checkpoint in the expression of a gene is transcription. A "transcription unit" is a segment of DNA that is translated into an RNA molecule and typically encodes at least one gene. Eukaryotic cells' transcription is significantly more complicated than that of bacterial cells. In bacteria, a single RNA polymerase is responsible for the transcription of every gene, but in eukaryotic cells, there are numerous RNA polymerases that each transcribes a particular class of gene. The intricate regulation of gene expression required to control the various cell types in multicellular animals is most likely made easier by the increased complexity of eukaryotic transcription. Several kinds of genes are transcribed by three separate nuclear RNA polymerases in eukaryotic cells. The protein-coding genes are transcribed by RNA polymerases I and III, and the Ribosomal RNAs (rRNAs) and Transfer RNAs (tRNAs) are transcribed by RNA polymerases I and III to produce mRNAs.

RNA polymerase needs additional proteins, referred to as Transcription Factors (TFs), in order to create the transcript in an efficient manner. A protein known as a TF, or sequence-specific DNA-binding factor, attaches precisely to DNA sequences and regulates the flow of genetic information from DNA to mRNA. RNA polymerase is recruited to particular genes by TFs and other proteins in a complex, which promote (activator) or block (repressor) the recruitment of RNA polymerase. The primary roles of TFs include binding to RNA polymerase, other TFs, and cis-acting DNA sequences. TFs typically function in groups or complexes, generating a variety of interactions that provide varied degrees of control over transcription rate.

Genes in eukaryotes are typically in an "off" state; hence, TFs primarily function to "turn on" gene expression. While in bacteria, a TF must turn a gene's expression "off" for it to continue. The majority of eukaryotic genes have a promoter region upstream of the gene as well as an enhancer region upstream or downstream of the gene, both of which often include certain motifs that particular TFs may identify. The fact that TFs include DNA-Binding Domains (DBDs) that enable them to bind to particular promoter or enhancer regions is one of their distinguishing characteristics. Initiating the transcription process, TF binding causes the other TFs to bind, forming a complex that ultimately makes it easier for RNA polymerase to attach. The core promoter of a protein-coding gene, which is typically located around 50 bases upstream of the transcription

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initiation site, is where the basal transcription complex and RNA polymerase II join.

The most dangerous and pervasive parasitic disease affecting humans is malaria, which is brought on by the parasite *Plasmodium falciparum*, which is carried by mosquitoes. Posttranscriptional regulation may be important in the regulation of gene expression in *P. falciparum* because it has been proposed that posttranscriptional mechanisms regulate protein levels throughout the life cycle of the malaria parasite. Seven significant developmental phases of the *P. falciparum* life cycle were compared in terms of mRNA and protein levels. Even though each stage's transcriptome and proteome showed comparatively good correlations, a sizeable portion of the genes showed a delay between the peak abundance of mRNA and protein.

Given the failure of efforts to eradicate malaria worldwide, it is crucial to understand the biology of *Plasmodium*, particularly the processes of gene regulation that control its growth cycle, in order to suggest new malaria-fighting tactics. There aren't many TFs from *P. falciparum* that are well described. They include High Mobility Group Box (HMGB) proteins, the Myb1 protein, and the Apetala2 (AP2) domain-containing proteins. Several of these significant TFs have also been identified in protozoan parasites from other species. For instance, an HMGB member was discovered in *Entamoeba histolytica*, while certain Myb family members were characterized from *Trichomonas vaginalis*.