Journal of Clinical Epigenetics
ISSN: 2472-1158

Open access Commentary

Skeletal Muscle Development in Gene Expression through RNA Polymerase

Allen Appel*

Department of Clinical Epigenetics, University of Kean, USA

DESCRIPTION

In eukaryotic cells, the process of gene expression is confined to the nucleus and enabled by multi subunit RNA polymerases (RNAPs). Many viruses use the host cell's gene expression machinery during infection, thus transferring their genomes to the host nucleus, at least temporarily. However, the smallpox virus has developed a different strategy for spreading. Their double-stranded DNA genomes are transcribed into the host cytoplasm by virally encoded RNAPs (vRNAPs) that are evolutionarily related to eukaryotic RNA polymerase. This review highlights recent high-resolution structures of the smallpox virus transcription apparatus during various stages of action. These structures, together with biochemical data, now allow the definition of a comprehensive model of poxvirus gene expression and its regulation. Skeletal muscle development and regeneration is controlled by the combined actions of Myf5, MyoD, Mrf4, and MyoG, also known as myogenic regulatory factors (MRFs). These transcription factors are expressed in a highly spatiotemporally restricted manner, ensuring the significant functional and metabolic diversity observed across different muscle groups. This review describes the elaborate expression patterns of MRFs in particular, and the multiple levels of regulation that help control myogenic genes in general. We highlight all the major regulatory processes involved in myogenesis processes that regulate chromatin state and transcriptional competence, including modifications such as alternative splicing, polyadenylation and other mRNA modifications, or post-translational protein modifications. All of these processes are exquisitely and closely coordinated to ensure proper activation, maintenance, and termination of myogenic processes.

Translation of mRNA is a critical step in the expression of protein-coding genes. As the mechanisms that govern the post-transcriptional regulation of gene expression are increasingly revealed, it is becoming clear that the transcriptional program is not fully reflected in the proteome. Here, we highlight a previously underappreciated post-transcriptional mode of regulation of gene expression called translational buffering. In principle, translational buffering counteracts the effects of changes in mRNA levels on the proteome. It also describes three types of translation buffering. Between species or individuals; the equilibrium that maintains the stoichiometry of the paths. The offset acts as a reversible mechanism that keeps the levels of selected protein subsets constant despite genetic and/or stress-induced changes in the corresponding mRNA levels. Although the mechanisms underlying compensation and equilibrium have been reviewed elsewhere, the main focus of this review is the less understood mechanism of translational equalization. Finally, we discuss possible roles of translational damping in homeostasis and disease.

CONCLUSION

Nuclear speckles are dynamic membrane less body located in the cell nucleus. They harbour RNAs and proteins, many of which are splicing factors, that together exhibit complex biophysical properties that determine nuclear speckle formation and maintenance. Although these nuclei were discovered decades ago, it is only recently that thorough genomic analysis has begun to reveal their critical role in regulating gene activity. Significant advances in genomic mapping techniques combined with microscopic approaches have revealed the role nuclear staining plays in enhancing gene expression and how gene placement at specific nuclear landmarks can regulate gene expression and RNA processing insight was obtained. Several studies have linked nuclear spots to disease.

ACKNOWLEDGEMENT

None.

CONFLICTS OF INTERESTS

The authors declare that they have no conflict of interest.

Received:	30-August-2022	**Manuscript No:**	IPJCE-22-14769
Editor assigned:	01-September-2022	**PreQC No:**	IPJCE-22-14769 (PQ)
Reviewed:	15-September-2022	**QC No:**	IPJCE-22-14769
Revised:	20-September-2022	**Manuscript No:**	IPJCE-22-14769 (R)
Published:	27-September-2022	**DOI:**	10.21767/2472-1158-22.8.41

Corresponding author Allen Appel, Department of Clinical Epigenetics, University of Kean, USA, E-mail: allenappel732@gmail.com

Citation Appel A (2022) Skeletal Muscle Development in Gene Expression through RNA Polymerase. J Clin Epigen. 8:41.