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# The Role of Poly(A) Tail Modification of mRNA in the Embryogenesis

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## Abstract

Eukaryotic gene expression can be exquisite tuned at various levels, especially at the mRNA level. There are over 100 kinds of chemical modifications identified on mRNA. Poly(A) tail are high conserved and ubiquitous modifications, which regulated by poly(A) polymerases and deadenylases. Poly(A) tail affect the mRNA stability, translation efficacy, and abundance. As an essential stage of life – embryogenesis, poly(A) tail exerts a vast influence with dynamic length. In this review, we summarize the effect of poly(A) tail on early embryogenesis and provide the potential mechanism.

**Keywords:** Gene Expression; Poly(A) Tail; Deadenylases; Embryogenesis

**Abbreviations:** MZT: Maternal-To-Zygotic Transition; CPA: Cytoplasmic Polyadenylation; PABPC: Cytoplasmic Poly(A) Binding Protein; PABPN: Nuclear Poly(A) Binding Protein.

## Introduction

Eukaryotic gene expression can be regulated at many levels, poly(A) tail modification on mRNA are consistent and ubiquitous in eukaryotes [1]. Early embryogenesis is a unique and fine-tune stage. Emerging evidence suggest that poly(A) tail play a vital role in this stage. In this review, we post a potential link between poly(A) tail and embryogenesis and summarize the underlying mechanism.

## Effects of Poly(A) Tail on Early Embryogenesis and the Potential Mechanisms

Eukaryotic gene expression can be regulated at many levels, among which the regulation at the mRNA level is the most convenient way to adjust the efficiency of translation. In the mRNA level, it has been characterized by multi-level and diversified regulation. It includes transcription, translation, processing, transport out of the nucleus, cell location, storage, and degradation [2-4], among which post-transcription modifications is one of the key means of regulation of protein synthesis [5]. Over 100 types of chemical modifications have been identified in cellular RNAs, among which the 5′ cap modification and the poly(A) tail have been identified and characterized earlier [6].

Poly(A) tail are high conserved and ubiquitous in eukaryotes, ~ 250 nucleotides homopolymer adenosines at the 3′ end of RNA in mammalian cells added by polymerases, non-templated of RNA [7]. Poly(A) tail length correlates with mRNA stability and half-life, which balanced by polyadenylation (poly(A) polymerases) and deadenylation (deadenylases) [8]. The poly(A) tail at the 3′ end reflect their regulatory status and play important roles in the control of the fates of RNAs, such as nuclear export, translation efficiency, and recycling and promotes mRNA stability. There are various protein factors binding with poly(A) tail, such as cytoplasmic poly(A) binding protein (PABPC), nuclear poly(A) binding protein (PABPN), which contains potentially coordinated regulation [9,10]. As mounting evidence allude to, poly(A) tail plays a key role in mRNA decay. mRNA degradation is widely involved in pivotal biological processes, whose imbalance dynamic could induce the development of many major diseases, such as cancer, viral infections and neurodegeneration etc. [11,12]. Recent research by novel sequencing-based methods for checking the poly(A) tails length has revealed the dynamic nature of poly(A) tails in development.

In tradition view, a long poly(A) tail would protect the mRNA from decay and degradation. However, with the novel sequencing technology (TAIL-seq or Nanopore), it was a nuance that longer poly(A) tails hinted transcripts of lower abundance and poor translation [13-15]. And inadequate cleavage and polyadenylation may lead to human diseases, including cancer, Chronic lymphocytic leukaemia and neurological diseases [16]. However, limited on the sequencing technology, the mechanism would be difficult to elucidate. Recent researches focus on a specific cell context- the early embryogenesis. In this review, focusing on mRNA degradation, we discuss the role of poly(A) tails on embryogenesis.

During early embryogenesis in animals, after fertilization, the transcription is withdrawn for some time, and the deposited composition and utilization of the cellular transcriptome must be responsive to temporal cues, especially, a set of maternal mRNAs and proteins deposited in the egg [17]. Subsequently, at the key time point of maternal-to-zygotic transition (MZT), the significant events happen, including the occurrence of zygotic genome activation, the mass degradation of maternal mRNAs and major epigenetic reprogramming [9,18]. Cytoplasmic polyadenylation (CPA) is crucial for the translational regulation of maternal mRNAs, which exerts a vast influence on timely activation of maternal mRNAs at the period of both oocyte maturation and the early embryonic development. During the embryogenesis, the poly(A) tails of maternal RNAs remain short and gradually elongate in later stages, well-controlled by cytoplasmic polyadenylation (CPA). In these early embryonic stages, a twofold increase in the length of poly(A) tail corresponded to a large increase in translational efficiency [15]. Specifically, for GV-stage-arrested oocytes, a large number of maternal mRNAs contain with a short poly(A) tail (20 ~ 40 nt); upon meiotic maturation, maternal mRNAs contain with a long poly(A) tail (80 ~ 250 nt) [7]. Cytoplasmic polyadenylation may regulate the mid-blastula transition in at least two possible ways. First, it facilitates zygotic genome activation. Second, it is required for the clearance of maternal mRNAs [9]. Beyond polyadenylation, many factors involved in regulating mRNA decay, such as the MAPK cascade, CNOT6L, and BTG4 [19]. The relationship between the interaction factors regulated the mRNA tail remains unclear.

## Conclusion

In summary, in mRNA level, poly(A) tail modification can affect protein production during early embryogenesis through various mechanisms. Nonetheless, future studies into the mechanisms below the poly(A) in the embryogenesis will not only provide the answer to a specific cellular context but extend our understanding about fine-tuned gene regulation in mRNA level.

## Declaration of Competing Interest

There is no conflict of interest of all the authors declared.

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