

MOLBİYOKON'18

5 - 8 September 2018

6th

International Congress of the
Molecular Biology Association
of Turkey

ABSTRACT BOOK

Izmir Biomedicine and
Genome Center

PT 020

Transcription Elongation in Connection to 3'UTR Ends*İbrahim Özgül,¹ Tolga Can,² A. Elif Erson Bengan,¹*

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Transcription machinery is a coordinated and complex process, where various proteins have dynamic interactions. We are interested in better understanding how transcription related processes determine the end of 3'UTRs. 3'UTRs harbor multiple polyadenylation signals that are selectively used by the polyadenylation machinery. While many factors may influence poly(A) signal selection, transcriptional initiation and/or elongation is expected to play a major role. To begin investigating this, we chose in silico approach to determine whether transcription elongation rates affect poly(A) signal selection by using an in-house algorithm called APADetect. APADetect reveals potential short and long 3'UTR isoforms, as an indication of differential poly(A) selection. Overall, while inhibition of transcription elongation is also linked to decreased mRNA levels, we detected several cases where target genes are upregulated with a shift in proximal/distal poly(A) site usage. We plan to further investigate whether these unexpected cases are due to indirect effects and/or mRNA stability issues.

Keywords: Alternative polyadenylation, Transcription, mRNA, 3'UTR