Short Communication

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Shifting Correlative Trends of G-C% Content and 3'UTR Length

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ABSTRACT

We report the moderate positive correlation (r=0.52), between low G-C% content and the length of the 3'UTRs, as well as moderate negative correlation (r=-0.57) between high G-C% content and the 3'UTR length. The results corroborate our previous data on the asymmetric distribution of microRNA target sites along the 3'UTR and point to the possible influence of nucleotide composition on the cis-acting regulatory elements within the 3'UTR.

Keywords: mRNA; 3'UTR; Nucleotide

Abbreviations: mRNA: messenger RNA; 3UTR: Untranslated Region

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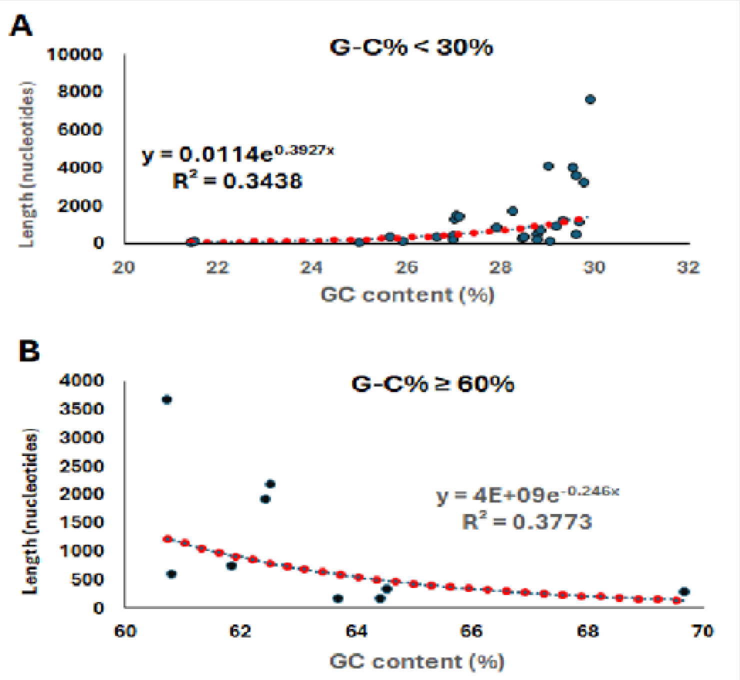
The growing number of reports indicate that codon usage bias and nucleotide content are among the important regulatory factors influencing gene expression at various levels. They may impact the nuclear mRNA concentration [1] and mRNA stability [2,3] and alter the expression of the heterologous genes in bacteria, plants, yeast, mammalian cells, and transgenic animals [4]. Previously we reported the moderate negative correlation between the 3'UTR length and the G-C% content in the 3'UTRs of 38 human mRNAs (in press). In this study we used the larger dataset of the prevailing transcripts of 824 human genes (RefSeq database [5]). We found the moderate positive correlation (r=0.52), between the low G-C% content (less than 30%) and the length of the 3'UTRs, as well as moderate negative correlation (r=-0.57) between the high G-C% content (more than 60%)

and the 3'UTR length (Figure 1). The results indicate some similarity with the previously obtained data on asymmetric distribution of microRNA-target sites along the 3'UTR and suggest a complex interplay between the nucleotide composition and the 3'UTR regulatory functions, which remain to be elucidated.



Note:

- A: Low G-C content (<3 0%), moderate positive correlation (r=0.52).
- B: High G-C content (≥ 60%), moderate negative correlation (r=-0.57).

Figure 1: Moderate correlation between the 3'UTR length (human mRNAs) and G-C% content.

References

1. Qian W, Zhang J (2021) Codon usage bias and nuclear mRNA concentration: Correlation vs. causation. Proc Natl Acad Sci 118.
2. Mishima Y, Tomari Y (2016) Codon Usage and 3' UTR Length Determine Maternal mRNA Stability in Zebrafish. Mol Cell 61: 874-885.
3. Hanson G, Coller J (2018) Codon optimality, bias and usage in translation and mRNA decay. Nat Rev Mol Cell Biol 19: 20-30.
4. Kofman Alexander, Marcus Graf, Alexandra Bojak, Ludwig Deml, Kurt Bieler, et al. (2003) HIV-1 gag expression is quantitatively dependent on the ratio of native and optimized codons. Tsitologiia 45: 86-93.
5. O Leary Nuala A, Mathew W Wright, J Rodney Brister, Stacy Ciufo, Diana Haddad, et al. (2016) Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Res 44: 733-745.

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