

Moderate Negative Correlation Between The 3'UTR Length And G-C% Content

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ABSTRACT

The presence of cis-acting regulatory elements may depend on the nucleotide content of the gene fragment. We report the moderate negative correlation between the 3'UTR length (500-2000 nucleotides) and the G-C% content.

Keywords: mRNA; 3'UTR; Nucleotide

Abbreviations: mRNA: messenger RNA; UTR: Untranslated Region

Introduction

Codon usage varies among the biological species and even the genes of the same organisms [1]. Correlations between the codon usage and intron length, the codon pattern (G-C% content at the third codon position) and the cellular and chromosomal location of the genes [2] as well as the reported possible effects of codon usage on mRNA stability [3,4] prompted us to explore the 3'UTR nucleotide

content of human genes. We observed the lower G-C% content within 3'UTR as compared to the whole mRNA sequence, which could be explained by the presence of the poly(A) tail. We also found the moderate negative correlation ($r=-0.44$) between the 3'UTR length (500-2000 nucleotides) and the G-C% content (Figure 1). We conclude that the asymmetric distribution of microRNA target sites within human mRNA 3'UTR [5] may be related to the nucleotide content variations.

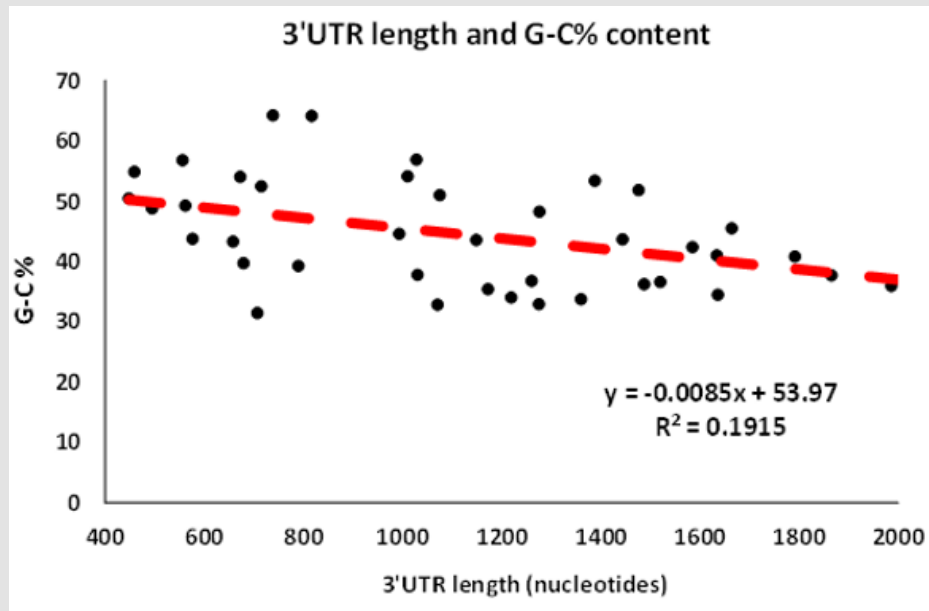


Figure 1: Moderate negative correlation ($r=-0.44$) between the 3'UTR length (human mRNAs) and the G-C% content.

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