On Negative Selection Against ATG Triplets Near Start Codons in Archaebacterial Genomes

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1 Introduction

Translation initiation mechanisms in eubacteria and eukaryotes are quite different. In eubacteria, ribosome binds directly to the Shine-Dalgarno sequence located several bases upstream of the start codon. In eukaryotes, on the other hand, ribosome binds to the CAP structure located at the 5' end of mRNA, and scans the mRNA until it finds the start codon. However, the translation initiation mechanism of archaebacteria is not at present clearly understood. We have previously shown that extra ATG triplets near start codons can confuse the translation initiation process and thereby be negatively selected in both eubacterial and eukaryotic genomes [3]. However, decreasing patterns of frequencies of ATG triplets in eubacteria are symmetrical around start codons (Fig. 1(a)), whereas those of eukaryotes are asymmetrical (Fig. 1(b)), presumably due to some difference in the translation initiation mechanisms.

In this work, computer analyses of the frequency of ATG triplets around predicted start codons in four completely sequenced archaebacterial genomes were conducted in order to infer how ribosomes recognize translation initiation sites.

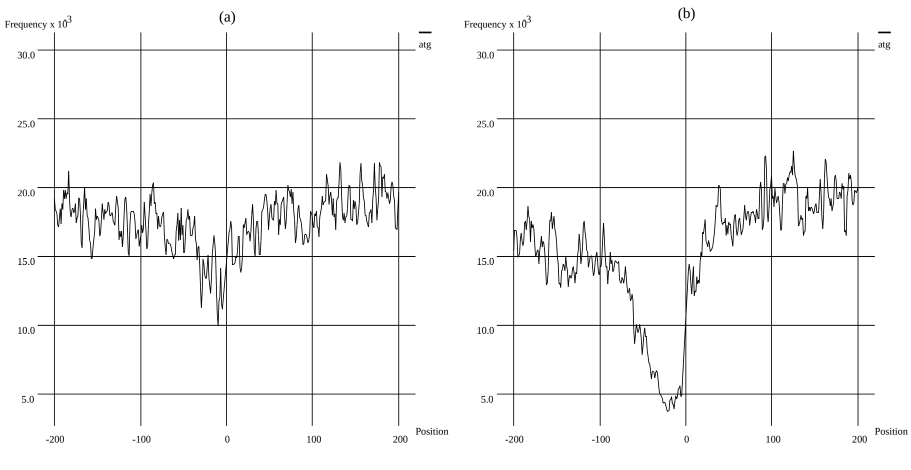

Figure 1: Frequency of ATG triplets around start codons in (a) *E. coli* (eubacteria) and (b) *S. cerevisiae* (eukaryotes).

2 Results and Discussion

Among the species investigated, *P.horikoshii* and *M.jannaschii* showed asymmetric patterns with stronger ATG depletion before start codons (Fig. 2(a)-(b)), which are similar to the eukaryotic pattern. This observation implies that these species employ scanning of the mRNA from the 5' to the 3' direction in the process of translation initiation. On the other hand, we have found that these archaea have SD-like sequences, which are complementary to the 3' end sequence of 16S rRNA [2]. These two results, given simultaneous consideration, lead us to conclude that these archaea probably use a hybrid mechanism [4]; their ribosome scans the mRNAs from the 5' to the 3' direction, then the 16S rRNA binds to the SD-like sequence of the 5' UTR.

In *A. fulgidus* and *M. thermoautotrophicum*, there appears to be no significant ATG triplet depletion (data not shown). One possible explanation for this finding is that these species have short 5'UTRs, as in the case in some other archaebacteria [1]. Thus, in these species, ATG triplets before start codons are not often transcribed and have not been the subject of negative selection.

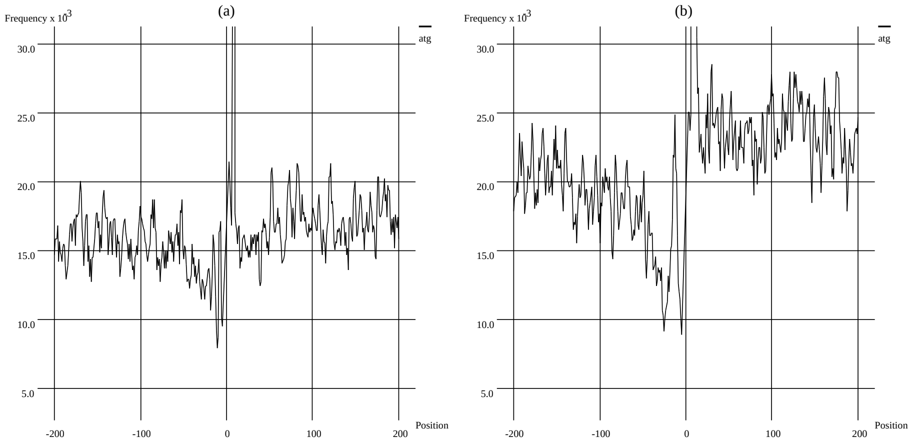

Figure 2: Frequency of ATG triplets around start codons in (a) *P. horikoshii* and (b) *M. jannaschii.*

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References

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