

Abstract

Genetic code is defined as a set of rules, which encode aminoacid sequences in proteins, according to codon usage. It is widely known, that there are multiple codons for most aminoacids, thanks to the degeneracy of the genetic code. There was a hypothesis, that silent mutations, which result in a synonymous codon and not in incorporating of a different aminoacid into the peptide chain, don't affect the gene expression. Later however, it was found through more detailed research on molecular level, that codon usage bias is in fact one of the factors, that regulate translation effectivity and rate, mRNA stability or even protein folding and gene expression. There has been many studies published on these topics.

This bachelor thesis is a review of these studies. First, I summarize basic information on tRNA, its structure and modifications in anticodon loop. Next I write about base pairing between codon and anticodon, including the non-canonical wobble base pairing. Then I emphasize on codon bias, its causes, its relationship with genome GC content. I also include some author's conjectures about how to approach this phenomenon, which codons are optimal and what is the impact of codon usage bias on translation efficiency. I cite many studies on this topic, which was researched on many model organisms, including *Homo sapiens*.

Key words: tRNA expression, translation efficiency, codon usage bias, tRNA modifications, synonymous codons