

Title: Relative synonymous codon usage and codon pair analysis of depression associated genes

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Abstract: Depression negatively impacts mood, behavior, and mental and physical health. It is the third leading cause of suicides worldwide and leads to decreased quality of life. We examined 18 genes available at the genetic testing registry (GTR) from the National Center for Biotechnological Information to investigate molecular patterns present in depression-associated genes. Different genotypes and differential expression of the genes are responsible for ensuing depression. The present study, investigated codon pattern analysis, which might play imperative roles in modulating gene expression of depression-associated genes. Of the 18 genes, seven and two genes tended to up- and down-regulate, respectively, and, for the remaining genes, different genotypes, an outcome of SNPs were responsible alone or in combination with differential expression for different conditions associated with depression. Codon context analysis revealed the abundance of identical GTG-GTG and CTG-CTG pairs, and the rarity of methionine-initiated codon pairs. Information based on codon usage, preferred codons, rare, and codon context might be used in constructing a deliverable synthetic construct to correct the gene expression level of the human body, which is altered in the depressive state. Other molecular signatures also revealed the role of evolutionary forces in shaping codon usage.

Keywords: Depression-associated genes Codon usage analysis Differential gene expression Single nucleotide polymorphisms (SNPs) Codon context

<https://www.nature.com/articles/s41598-024-51909-8#:~:text=The%20CAI%20values%20of%20the,codon%20bias%20is%20present58.>