

Codon evolution and conservation of the reading phase in genetic code translation

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The description of the optimized evolution of a code based on 4 nucleotides involves a sequential transition of codons, formed firstly by monomers evolving to dimers and then to triplets, in accordance with the progressive increase of the number of amino acids to be coded. The successive increase in the size of these codons during evolution implies changes in the phase reading of the genetic message, which could become chaotic. In order to overcome this constraint, this paper proposes a codon evolution where two things occur simultaneously: codons change in size and there is an alternation of the molecule which holds the information. For example, the nucleotides of the original oligonucleotide are read as monomers when they are translated to an oligopeptide, but further on, this oligopeptide which is read as amino acid dimers, is translated to a nucleotide form (oligonucleotide). Finally, amino acids conforming a peptide are translated from this oligonucleotide, through a reading of tr