

Abstract

Chargaff's first parity rule for the contents of the four nucleotides in DNA is easily understood based on the double-stranded DNA structure. However, the second parity rule, based on similar nucleotide relationships in single-stranded DNA, has been a puzzle in molecular biology, because it is impossible to imagine how pairs of G and C, and A and T are formed in the single DNA strand or intra-strand. Research works are going on to find all the factors that are responsible for the intra-strand parity (ISP) in the chromosomes. The present work constitutes an attempt to accommodate the findings of the intra-strand frequency distribution parity (ISFDP) which supports the parity but there is a weak correlation with intra-strand-parity (ISP). According to Nussinov-Forsdyke hypothesis formation of stem-loop structures is a selection factor for ISP in genomes. In stem loop complementary nucleotides pair with each other and therefore frequencies of complementary nucleotides is maintained in a single strand of DNA. Generally stem-loops are found to be at the transcription termination site as a hairpin structure followed by a short uracil-rich region in DNA. While several bacterial chromosomes maintain ISP, fairly large number of chromosomes has been reported to be violating ISP. In this study we also analyze the potential stem-loop region in bacterial genome with a suitable Dynamic programming, which outcomes that lesser is the parity deviation higher is the percentage of nucleotides paired in stem-loop structures.