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Codon based co-occurrence network motifs in human mitochondria

Pramod Shinde, Camellia Sarkar and Sarika Jalan*

Complex Systems Lab, Discipline of Physics, Indian Institute of Technology Indore, Khandwa road, Simrol, Indore 453552, INDIA

Presenting author: pramodshinde119@gmail.com

Abstract

The nucleotide polymorphism in human mitochondrial genome (mtDNA) tolled by codon position bias plays an indispensable role in human population dispersion and expansion. Herein, we constructed genome-wide nucleotide co-occurrence networks using a massive data consisting of five different geographical regions and around 3000 samples for each region. We developed a powerful network model to describe complex mitochondrial evolutionary patterns between codon and non-codon positions. It was interesting to report a different evolution of Asian genomes than those of the rest which is divulged by network motifs. We found evidence that mtDNA undergoes substantial amounts of adaptive evolution, a finding which was supported by a number of previous studies. The dominance of higher order motifs indicated the importance of long-range nucleotide co-occurrence in genomic diversity. Most notably, codon motifs apparently underpinned the preferences among codon positions for co-evolution which is probably highly biased during the origin of the genetic code. Our analyses manifested that codon position co-evolution is very well conserved across human sub-populations and independently maintained within human sub-populations implying the selective role of evolutionary processes on codon position co-evolution. Ergo, this study provided a framework to investigate cooperative genomic interactions which are critical in underlying complex mitochondrial evolution.

References

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