

L-Systems: a mathematical paradigm for designing full length human genes and genomes

Arunava Goswami^{1*}, Pabitra Pal Choudhury², Amita Pal³, R L Brahmachary¹, Sk Sarif Hassan²

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We have shown how L-Systems can generate both an exon (human OR) and a system containing both exons and introns (human mitochondria). Ligands for only two human olfactory (OR) receptors are known. One of them, OR1D2, binds to Bourgeonal, a volatile chemical constituent of the fragrance Lily of the valley (*Convallaria majalis*). OR1D2, OR1D4 and OR1D5 are three full-length olfactory receptors present in an olfactory locus in human genome. These receptors are more than 80% identical in DNA sequences and have 108 base pair mismatches among them. We have used L-system mathematics to show a closely related sub-family of OR1D2, OR1D4 and OR1D5. Craig Venter's group reported experimental construction of long DNA molecules adopting several working hypotheses. A mathematical rule for generating such long sequences would shed light on several fundamental problems in various areas of biology, for example evolution of long DNA chains in chromosomes, the reasons for existence of long stretches of non-coding regions, as well as usher in automated methods for the preparation of long DNA chains to enable chromosome engineering. However, this mathematical principle must have room for editing/correcting DNA sequences locally in the areas of genomes where mutation and/or DNA polymerase has introduced errors over millions of years of evolution. Here we present

the whole mitochondrial genome (exons and introns) generated by the L-Systems.

Author details

¹Biological Sciences Division, Indian Statistical Institute, 203 B. T. Road, Calcutta, 700108, India. ²Applied Statistics Unit, Indian Statistical Institute, 203 B. T. Road, Calcutta, 700108, India. ³Bayesian Interdisciplinary Research Unit (BIRU), Indian Statistical Institute, 203 B. T. Road, Calcutta, 700108, India.

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¹Biological Sciences Division, Indian Statistical Institute, 203 B. T. Road, Calcutta, 700108, India

Full list of author information is available at the end of the article

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