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Evolution of primate-specific and mammalian-specific highly conserved non-coding genomic region

We are interested in evolutionary changes toward human, and are conducting genome wide computational analyses both at protein coding and non-coding regions. Most of intergenic and intronic regions of eukaryote genomes are junk DNAs. Only small portion have some functional roles, and are evolutionarily conserved. We thus used noncoding DNA sequences that are relatively conserved between human and rhesus macaque genomes as queries to conduct BLAST searches for mammalian and nonmammalian genomic sequences. Primate specific and mammalian specific highly conserved regions were extracted, and characteristics of their neighboring protein coding genes were examined using Gene Ontology database. We found clear difference between mammalian and primate specific conserved regions.

CV

1979	Department of Biology, Faculty of Science, University of Tokyo, Tokyo, Japan (B.S. majoring in physical anthropology)
1979-1981	Department of Anthropology, Graduate School of Science, University of Tokyo, Tokyo, Japan (M.S.)
1982-1986	Center for Demographic and Population Genetics, Graduate School of Biomedical Sciences, University of Texas Health Science Center at Houston, USA (Ph.D.)
1987-1989	JSPS Postdoctoral Fellow at Section of Anthropology, Department of Biology, Faculty of Science, University of Tokyo, Tokyo, Japan
1989-1991	Assistant Professor, Section of Anthropology, Department of Biology, Faculty of Science, University of Tokyo, Tokyo, Japan
1991-2002	Associate Professor, Division of Evolutionary Genetics, National Institute of Genetics, Mishima, Japan
1993-2002	Adjunct Associate Professor, Department of Genetics, School of Life Science, Graduate University for Advanced Studies, Mishima, Japan
2002-Present	Professor, Division of Population Genetics, National Institute of Genetics, Mishima, Japan
2002-Present	Adjunct Professor, Department of Genetics, School of Life Science, Graduate University for Advanced Studies, Mishima, Japan
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