A105

Identification and Phylogeny of L1PA4 Elements Belonging to the LINE-1 Family in Primates

Heui-Jeong Park[P], Joo-Mi Yi[1], Tae-Hyung Kim[2], Won-Ho Lee[1], Heui-Soo Kim[C]

[PC1]Division of Biological Sciences, Pusan National University, Pusan 609-735; [2]Interdisciplinary Program of Bioinformatics, Pusan National University, Pusan 609-735

L1(LINE-1) elements are mammalian long interspersed nuclear elements that replicated by retrotransposition. Five major families (L1PA5, L1PA4, L1PA3B, L1PA2, and L1PA1) of elements have succeeded each other from common ancestor. These elements are useful to understnad evolutionary history in primates including our humans. Here, we investigated evolution dynamic of primate L1PA4 elements from LINE-1 family. In hominoids (chimpanzee, gorilla, orangutam, gibbon) and Old World monkeys (crab-eating monkey, rhesus monkey, Japanese monkey) the L1PA4 elements of the LINE-1 families were examined by PCR amplification and sequencing. One hundred forty-five L1PA4 elements from hominoid and Old World monkeys showed a high degree of sequences similarity to those of humans. Deletion or insertion events of the L1PA4 elements were severely appeared in primates, especially chimpanzee and rhesus monkey. Phylogenetic analysis using the sequence data by neighbor-joining method indicated that L1PA4 elements showed random cluster in primate species. Taken together, the findings suggest that L1PA4 elements have evolved independently during primate evolution. The data could be of great use for future studies primates speciation and human evolution.

A106

Incongruous Evolution and Phylogeny Using 16SrRNA Sequences of Mitochondrial DNA for Platyrrhini Systematics

Kyung-Won Hong[P], Tae-Hyung Kim[2], Joo-Mi Yi[1], Jae-Won [1]Huh[1], Osamu Takenaka[3], Won-Ho Lee[1], Heui-Soo Kim[C]

[PC1]Division of Biological Sciences, Pusan National University, Pusan 609-735; [2]Interdisciplinary Program of Bioinformatics, Pusan National University, Pusan 609-735; [3]Department of Cellular and Molecular Biology, Primate Research Institute, Kyoto University, Inuyama, Japan

We sequenced 16S ribosomal RNA sequences (16SrRNAs) of mitochondrial DNA (mtDNA) from five New World monkeys (squirrel monkey, night monkey, titi monkey, spider monkey and common marmoset). These sequences were aligned and analyzed with orthologous sequences from humans and capuchin monkeys. Phylogenetic analysis of 16SrRNAs was not agreed with other molecular data sets, -globin, IRBP, G6PD and 12SrRNA. This discrepancy indicates the alternative mutations among secondary structures (stem, loop, bulge and others) of 16SrRNA in New World monkeys. Estimating the incongruence length difference (ILD) among the five molecular data sets using the partition homogeneity test showed incongruent P-value between genomic DNA (IRBP--globin-G6PD) and Mitochondrial genome (12SrRNA-16SrRNA). We also calculated the costs for change between each base type (A, T, G and C). The ribosomal sequences (16SrRNA and 12SrRNA) showed that T,G and G,C transversions were rarely occurred than nuclear genomic sequences, whereas A,T and A,C transversions were frequently occurred than nuclear genomic sequences. Taken together; our data suggest that 16SrRNA sequences of mtDNA should be exclude for construction of the natural tree from platyrrhini systematics.

A107

Molecular Phylogeny of *Hylobates* Based on *Alu* Elements of the Y Chromosome

Kyung-Won Hong[P], Jae-Won Huh[1], Woo-Young Kim[1], Tae-Hyung Kim[2], Joo-Mi Yi[1], Won-Ho Lee[1], Heui-Soo Kim[C]

[PC1]Division of Biological Sciences, Pusan National University, Pusan 609-735; [2]Interdisciplinary program of bioinformatics, Pusan National University, Pusan 609-735

The phylogenetic relationship among the *Hylobates*subgenera is one ofthe most controversial issues among primates. Using the PCR amplification and sequencing of AZF (AZoospermia Factor regions) gene in hominoid primates (chimpanzee, gorilla, orangutan and gibbon), we found the *Alu* elements (AluY*Hy*) on the genome of gibbon species only in orthologous locus of the EIF1AY (Eukaryote translation Initiation Factor 1A on Y chromosome). Therefore, we used the Alu sequences for understanding the phylogenetic relationship of gibbon species. It could be good marker on the Y chromosome because of male specificity and inheritance. Also, AluY*Hy*has splicing accept site (5'- TGAAA CGGAG-3'), suggesting the probability of exonization at Hylobate EIF1Ay last intron. Phylogenetic trees by neighbor-joining and maximum parsimony methods indicated that *H. agilis* and *H. muelleri* showed sister relationship and *H. lar*and *H. klossii*. This phenomenon was supported by the previous study from the mitochondrial DNA data.

A108

Molecular Evolution of Y-chromosomal Genes in Humans and Apes

Kyung-Won Hong[P], Jae-Won Huh[1], Eun-Sil Park[1], Heui-Soo Kim[C]

Division of Biological Sciences, Pusan National University, Pusan 609-735

The nonrecombining portion of the Y chromosome (NRY) makes up 95% of the length of Y chromosome. It suggests that the most of Y chromosome is paternally inherited and dose not recombine during male meiosis. These features have been increasingly used to investigate the human and primate evolution. We sequenced five Y-chromosomal genes (DFFRY, BPY, CDY, EIF1AY, DBY) from chimpanzee (*Pan troglodytes*), gorilla (*Gorilla gorilla*), orangutan (*Pongo pygmaeus*) and gibbon (*Hylobates agilis*). These genes have been known as candidate genes of azoospermia factors. Toestimate the evolutionary change, the sequences were compared with those of humans and with published Y-chromosomal DNAs of apes (PABY, SRY, ZFY, TSPY). The rate of nucleotide substitutions per site per year was higher in TSPY last intron than other genes. The phylogenetic trees constructed by the neighbor-joining and maximum parsimony methods from the combined dataset, suggesting that human and chimpanzee are more closely related to each other than either of them is to gorilla. Our data could be of great use for further study to understand human evolution during primate radiation.