

P38

## Comparative analyses of genomic sequences in human chromosome 21 and chimpanzee chromosome 22

Dae-Soo Kim, Tae-Hyung Kim, Yeo-Jin Jeon, Kyung-Won Hong<sup>1</sup>,  
Jae-Won Huh<sup>1</sup>, Woo-Young Kim<sup>1</sup>, Won-Ho Lee<sup>1</sup>  
and Heui-Soo Kim<sup>1</sup>

Pusan Bioinformatics & Biocomplexity Research Center, Pusan National University  
<sup>1</sup>Dept of Biology, College of Natural Sciences, Pusan National University

The identifying the types and extent of DNA of DNA sequence variation existing between human chromosome 21 and chimpanzee chromosome 22 will be important for understanding the genetic basis of recently evolved human and chimpanzee specific traits. To obtain chimpanzee sequences derived from the BAC clones, assembly were generated by using the megablast program. The resulting alignments were checked by eye to remove poorly aligned regions. This set was used to analyze the degree of conservation of noncoding and coding sequences between chimpanzee and human. Orthologous chimpanzee sequences were obtained by performing pipmaker server against the human genome. Human and chimpanzee specific repetitive sequences were identified by Repeatmasker. We compared human chromosome 21 to chimpanzee chromosome 22 sequences, and analysed rearrangement event between two species. The result showed that a variety retroelements are almost present at the deletion boundaries in the human and chimpanzee genome, respectively, suggesting that duplication, translocation. insertion, and deletion events could be actively associated with retroelements.