

P48

**Gene Analysis of Y chromosome in Humans and Apes**

Kyoung-Won Hong<sup>1</sup>, Jae-Won Huh<sup>1</sup>, Myung-Sook Kim<sup>1</sup>,  
Tae-Hyung Kim<sup>1</sup>, Joo-Mi Yi<sup>1</sup>, Osamu Takenaka<sup>2</sup>,  
Won-Ho Lee<sup>1</sup> and Heui-Soo Kim<sup>1</sup>

<sup>1</sup>Division of Biological Sciences, College of Natural Sciences, Pusan National University, Pusan 609-735, Korea

<sup>2</sup>Department of Cellular and Molecular Biology, Primate Research Institute, Kyoto University, Inuyama, Aichi 484-8506, Japan.

Non-recombining portion of the Y chromosome (NRY) have advantages in hominoid evolutionary studies - the absence of the reshuffling effect of recombination simplifies the historical record contained within the molecule. In order to understand hominoid evolutionary features, we have sequenced three Y specific genes (CDY, XKRY, TSPY) and one X-homologous gene (DBY). We also analyzed those sequences with the Y chromosomal genes (SRY, ZFY, PABY) that obtained from GenBank database. Compared to the X-Y homologous genes (PCDHX/Y, DBX/Y, DFFRX/Y, ZFX/Y, UTX/Y, SMCX/Y, RBMX/Y), the PCDHX and PCDHY genes showed high degree of sequence similarity, indicating that PCDHX and PCDHY genes were proliferated recently. Dotplot analysis of the genes indicated that RBMX and RBMY showed rather different sequences. Evolutionary rate of nucleotide substitutions per site per year were higher in the TSPY intron 5 than in the other introns and exons of the Y chromosomal genes. Examining of the relative internode in Home-Pan-Gorilla trichotomy indicated that TSPY last intron showed high value, suggesting that the TSPY last intron could be of great use for further study of the primate phylogeny and evolution.