

SL801

The Y *Alu* Insertion Polymorphism in Korean Population

Wook Kim and Kyung-Wha Yu

Department of Biology, Dankook University

The *Alu* family of short interspersed repeats(SINEs) is found in all primate species, with about 500,000 copies per haploid genome present in humans that have accumulated in their genomes via retrotransposition from a few master gene. Some of the 500,000 *Alu* element in the human genome have arisen so recently that not all chromosomes carry an *Alu* element at a particular locus. Once an *Alu* element insertion occurs, it appears not to be subject to loss or rearrangement, and the probability of independent insertion at the exact same position is negligible(Deininger, 1989). Thus, *Alu* insertion polymorphisms at specific loci have been shown to be valuable for human population studies. Based on the mapping data(Hammer, 1994), the *Alu* element, referred to as the Y *Alu* polymorphic(*YAP*) element, is present at a specific site on the non-recombining portion of the Y chromosome(Yq11) in some individuals and absent in others. The frequency of Y chromosomes containing the *YAP* element(*YAP*⁺) is highest in sub-Saharan African population, followed by North African and European populations (Hammer, 1994). Most Asian populations(India, China, Papua New Guinea) reported so far lack the *YAP*⁺ element. An exception to this pattern was the finding of the *YAP*⁺ element in Japanese populations(42%)(Hammer and Horai, 1995). We have examined the Y *Alu* insertion polymorphism using a PCR based assaying method in Korean population. A total of 180 unrelated males were analyzed to raise the possibility of tracing paternal lineages and male-mediated gene flow between Korea and Japan. The frequency of *YAP*⁺ element was found to be 1.1%(2/180). We also cloned these two *YAP*⁺ elements derived from PCR products by ligating into PCRTMII and subsequently sequenced to determine the length of the 3'-terminal poly(A) region of the sequence. The first clone, designated p[*YAP*⁺]KB-1 was found to have 41 dA-nucleotides and the second one, p[*YAP*⁺]KK-1 appeared to have 50 dA-nucleotides. Nucleotide sequence comparison with the 3'-terminal poly(A) region in other *YAP* elements revealed that they seem to belong to the type 3a which is frequently found in Japanese population. It might be suggested that these *YAP*⁺ chromosomes provide an explanation for the admixtures recently from Japan. Therefore, it is suggested that a large infusion of *YAP*⁺ chromosomes entered Japan with the Yayoi migration starting 2,300 years ago from Korea and a very few *YAP*⁺ chromosome admixed into Korean population so recently from modern Japanese originated from Jomon people who lived in Japan more than 10,000 years ago.