F841 CONSTRUCTION OF NEW QUADRUPLEX AMP-FLP SYSTEMS FOR AUTOSOMAL STR LOCI

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We introduce the development of two quadruplex systems, which are autosomal (D5S818-D13S317-D19S253-D3S2406, D2S1371-D8S1477-D12S391-D20S470). For efficient forensic case work and construction of national DNA database in Korea, it is necessary to use multiplex STR systems which fit Korean population. As a preliminary study, we have evaluated over 30 STR loci for suitable marker some of which are universally used and some are not yet. Allelic distribution in Korean populatuion was surveyed for each locus and validated through statistical analyses. Firstly, we constucted three triplex STR system with high discriminating power and stability, which are D3S1744-D12S391-D20S470, D5S818-D13S317-D19S253, D8S1132-D13S325-D3S2406. All the repeating units and size of each locus were determined by nucleotide sequence analysis using ABI 377 DNA sequencer. Eight loci which are not overlapped were selected. Through PCR optimization, ladder construction, two quadruplex STR systems described above were developed and sequence analyzed to verify the number of repeats of each locus. Validation study showed that these two systems were useful to not only fresh samples but also complicated forensic samples. The average discrimation power was much higher than that of commercially available multiplex typing kit in Korean population.

F842 Human Mitochondrial DNA Sequence variations in Korean Population

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From 136 unrelated Koreans, we have analyzed nucleotide sequence variation of 715 base pair region of the human mitochondrial DNA encompassing the D-loop (16021-16400 as HV1, 66-400 as HV2). As results, 92 and 45 mutation spots were detected in HV1 and HV2 respectively when compared with original Anderson sequence. 129 unique sequence haplotypes were defined indicating that sequence of 7 samples were overlapped. Especially in HV1 region, there were two spots which showed significant differnces from prevously reported caucacian database. They were 16223 and 16362, in which spot high C to T (>70%) and T to C (>50%) transition rate were observed respectively, while it proved to be common in most oriental populations. The average number of muatations were 4.6 and 5.0 in HV1 and HV2, respectively. Most frequent mutation type was transition (76% among the muatations) except that C base addition in 309 and 315 region of HV2 was observed frequently. The pedigree anlysis showed that no significant deviations between mother and child. As conclusion, it is considered that Mt DNA sequencing could be applicable to human identification combined with conventional STR analysis.