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Polymorphism of LPL Locus in Japanese and Comparison of PCR Amplification Efficiency from Degraded DNA between LPL Locus and the D21S11

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Abstract: The short tandem repeat (STR) polymorphism of the lipoprotein lipase (LPL) locus was amplified by PCR and analyzed using denaturing polyacrylamide gel electrophoresis followed by silver staining. Among 158 DNA samples from the Japanese population, six alleles were observed. When the sequences of the allelic products were compared, each allelic segment contained 7 and 9-13 TTTA tetranucleotide repeat motifs. Genotypic distribution met Hardy-Weinberg expectations, and included heterozygosity was 48.8%. Most of the Japanese genotypes allele 10. When PCR amplification efficiency for the LPL locus from degraded DNA was compared with that for the D21S11 locus in terms of amplification size, increase in amplification size showed a considerable influence on amplification efficiency, producing inaccurate amplification, such as unbalanced amplification, or amplification of non-target PCR products. These results suggest that reduction in amplification size increases the accuracy and efficiency of PCR amplification from highly degraded DNA.

Key words: Short tandem repeat (STR), LPL, Japanese population, D21S11, Degraded DNA

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