Detection of familial LPL deficiency by PvuII RFLP

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Familial LPL deficiency is a rare autosomal recessive disease, and its genetic defects remains unknown. To investigate the basis for this disease and its detection, RFLPs(restriction fragment length polymorphisms) analyses were carried out using human LPL cDNA which was cloned from placental cDNA library(manuscript in preparation). With the 1.6 kb cDNA fragment containing full length of coding region as a probe, we analysed 8 patients(1) and 50 controls. As reported in Caucasians previously(2), there are a two allele polymorphism(A1 ; 7.9 kb, A2 ; 5.1 and 2.8 kb) in Japanese population which were identified by PvuII digestion(Fig.1). In 50 unrelated controls, 28 showed A2A2 genotype(A2 homozygote), 22 had A1A2 genotype(A1A2 heterozygote), but no A1A1 genotype was found(Table-1). Frequencies of A1 and A2 allele in controls were 0.22 and 0.78, respectively. In contrast, 4 of 8 familial LPL deficient patients were demonstrated to be A1 homozygotes and the rest were A2 homozygotes. No A1A2 heterozygote was found among the patients. Moreover, all parents of 4 A1 homozygous patients were A1A2 heterozygotes and the co-dominant inheritance was observed in all families(Fig.2). These results indicate that the PvuII RFLP is a useful marker to analyse the genetic defects in the patient families.

1 2 3 (kb)

Fig.1 Detection of 3 genotypes by PvuII RFLP.

lane 1. A1A1
lane 2. A1A2
lane 3. A2A2

P F M (kb)

Fig.2 A co-dominant inheritance observed for all the A1 homozygous patients. The 3'half fragment of 1.6 kb cDNA was used as a probe. P=patient, F=father, M=mother

Table-1
Distribution of 3 genotypes in Japanese.

	A1A1	A1A2	A2A2
P	4	0	4
C	0	22	28

P=patients
C=controls

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References

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