Taql polymorphism in the 3' flanking region of the human aortic smooth muscle actin gene

Hisao Ueyama and Rie Ohsugi Department of Medical Biochemistry, Shiga University of Medical Science, Seta, Otsu 520-21, Japan

Source and Description of Clone: A 2 kb EcoRI fragment from the 3' flanking region of the human aortic smooth muscle actingene that was subcloned into pUC18¹ (pASMDe).

Polymorphism: Taql identifies two alleles with DNA fragments at 8.5 kb or at 5 kb and 3.5 kb.

Frequency: Unrelated individuals (26 Japanese and 5 Caucasians) studied: 24 males, 7 females (62 chromosomes).

8.5 kb allele

0.81

5 kb and 3.5 kb allele

0.19

Not Polymorphic For: Banl, Banll, Bgll, Dral, EcoRl, HindIII, Mspl, Ncol, Pstl, Pvall, Scal, Xbal.

Chromosome Localization: 10q22 to 10qter2.

Mendelian Inheritance: Co-dominant segregation in five families.

Probe Availability: Available for collaboration.

Other Comments: Low background under usual stringency conditions. Final wash at 0.1×SSC at 65°C.

References: 1. Kamada, S. et al. (1989) Gene, in press. 2. Ueyama, H. et al. in preparation.

Scrfl restriction fragment length polymorphism at the D7S23 locus (probe pKM.19), closely linked to cystic fibrosis

V.Nunes, M.Ramsay¹, T.Casals, M.Chillón, N.Lench¹, M.Schwartz² and X.Estivill Molecular Genetics Department, Fundació d'Investigació Sant Pau, Barcelona, Spain, ¹Molecular Genetics Department, St Mary's Hospital Medical School, London and ²Clinical Genetics Unit, Royal Manchester Children's Hospital, Manchester, UK

Source/Description: pKM.19 is a 1.0 kb EcoRI genomic fragment in pUC13 (ref. 1, 2), pPI was isolated independently but contains the same fragment as pKM.19 (ref. 3).

Polymorphism: Serfl (CC/NGG) identifies a two affele polymorphism with bands at 0.86 kb (A1) and $0.61 \pm 0.27 \text{ kb}$ (A2), and a constant band of 0.52 kb.

Frequency:		CF			non-CF	
Population	11	ΑI	A2	n	ΑI	A2
Spanish	80	0.63	0.36	80	0.04	0.96
British	32	0.78	0.22	31	0.06	0.94

Not Polymorphic For: BamFII, HindIII, PvuII, XbaI, EcoRI, TaqI, HincII.

Chromosomal Localisation: To chromosome 7q31 by linkage analysis and using a panel of somatic human/rodent cell hybrids (1, 2).

Mendelian Inheritance: Co-dominant segregation was demonstrated in 100 families.

Probe Availability: Freely available from X. Estivill.

Other Comments: The same probe detects a PstI polymorphism which was previously described (2).

References: 1. Estivill et al. (1987) Nature 326, 840-845. 2. Estivill et al. (1987) Genomics 1, 257-263. 3. Ramsay et al. (1990) Genomics in press.

Acknowledgements: Supported by the Spanish Ministry of Education and Science (PB87-0074). M.R. was supported by the South African Medical Research Council and the Institute for Medical Research.

