Eco O 109 reveals two polymorphic sites in the human inter-alpha-trypsin inhibitor light chain gene, ITI L

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SOURCE AND DESCRIPTION OF CLONE : The 1.2 kb Eco RI/Sma I fragment (1) of lambda HuLITI-2 (2) used as a probe is a full length cDNA clone coding for the light chain of human inter-alpha-trypsin inhibitor. This cDNA encodes both the N-terminal alpha-1-microglobulin and the C-terminal protease inhibitory domains of ITI L chain (3).

POLYMORPHISMS : Eco O 109 (Dra II) (PuG/GNCCPy) identifies four invariant bands at 1.9 kb, 0.95 kb, 0.8 kb, 0.7 kb and two diallelic polymorphisms, one A1,A2 with DNA fragments at 4.3 kb or 4.0 kb and the other B1,B2 at 1.0 kb or 0.6 kb.

FREQUENCY : Studied in 70 unrelated healthy white caucasians

A1 4.3 kb allele	(0.10)	B1 1.0 kb allele	(0.05)
A2 4.0 kb allele	(0.90)	B2 0.6 kb allele	(0.95)

NOT POLYMORPHIC FOR : Ava II, Nco I, Nde II, Nhe I, Rsa I, Sty I, and 28 other enzymes already listed in (1).

CHROMOSOMAL LOCALISATION : The ITI L gene has been mapped in 9q32-q33 by in situ hybridization (4).

MENDELIAN INHERITANCE : Mendelian segregation of alleles A1,A2 (fig. 1) and B1,B2 (fig. 2) was observed in two informative families.

PROBE AVAILABILITY : Available from J.P. Martin.

OTHER COMMENTS : A or B polymorphisms are located in the parts of the gene coding for alpha-1-microglobulin or the protease inhibitory domains respectively.

REFERENCES :

- (1) Léveillard et al. Nucl. Acids Res. 1988, **16**, 2744.
- (2) Salier et al. Proc. Natl. Acad. Sci. USA, 1987, **84**, 8272-8276.
- (3) Kaumeyer et al. Nucl. Acids Res. 1986, **14**, 7839-7850.
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Fig. 1 : **Fig. 2 :**