Dra I polymorphism in the human inter-alpha-trypsin inhibitor heavy chain gene ITIH1

T.Léveillard, J.P.Salier, R.Sesboué, J.Bourguignon, M.Diarra-Mehrpour and J.P.Martin

Institut National de la Santé et de la Recherche Médicale, INSERM Unité 295, Faculté de Médecine-Pharmacie de Rouen, Avenue de l'Université, BP 97, 76803 St Etienne Rouvray Cédex, France

SOURCE AND DESCRIPTION OF CLONE : The 1.0 kb insert of lambda HuHITI-19 (1) used as a probe codes for the heavy chain H1 of the human inter-alpha-trypsin inhibitor (2).

POLYMORPHISM : Dra I (TTT/AAA) identifies one invariant band at 5.8 kb and a diallelic polymorphism with DNA fragments at 4.0 kb or 2.4 kb and 1.6 kb.

FREQUENCY : Studied in 24 healthy caucasians.

4.0 kb allele	(0.56)
2.4 kb and 1.6 kb allele	(0.44)

NOT POLYMORPHIC FOR : Apa LI, Ban I, Ban II and 18 other enzymes already listed in (3) and (4).

CHROMOSOMAL LOCALISATION : The ITIH1 gene has been mapped to 3p211-p212 by in situ hybridization.

MENDELIAN INHERITANCE : Codominant segregation was found in three informative families (11 individuals).

PROBE AVAILABILITY : Available from J.P. Martin.

REFERENCES :

- (1) Salier J.P. et al. Proc. Natl. Acad. Sci. USA 1987, 84, 8272-8276.
- (2) Diarra-Mehrpour et al. Eur. J. Biochem. 1989, 179, 147-154.
- (3) Léveillard T. et al. Nucl. Acids Res. 1988, 16, 11852.
- (4) Léveillard T. et al. Nucl. Acids Res. 1989, 17, 2875.