

Polymorphism at the FES locus detected by PFGE

Klaus Koch, M.Jücker, M.Michels, W.J.M.van de Ven¹ and H.Tesch

I. Med. Klinik, Universität Köln, J.Stelzmann Straße 9, D-5000 Köln 41, FRG and ¹Universitaire Ziekenhuizen, Leuven, Herestraat 49, B-3000 Leuven, Belgium

Source/Description: pFES.95 is a 0.95 kb EcoRI cDNA fragment containing sequences of exons 15–19 of the human c-fes gene, subcloned in pUC18 (1).

Polymorphism: NruI digestion yields two bands of 550 and 500 kb.

Frequency: Studied in 15 European Caucasians:

500 kb allele: 0.46

550 kb allele: 0.54

Heterozygosity frequency.

Not Polymorphic For: BamHI, BglII, EcoRI, KpnI, NotI.

Chromosomal Localisation: 15q25-qter (2).

Mendelian Inheritance: Codominant segregation has been shown in two families.

Probe Availability: Contact W.J.M. van de Ven.

Acknowledgements: This work was supported by the Deutsche Forschungsgemeinschaft and the Deutsche Krebshilfe.

References: 1) Roebroek *et al.* (1986) *Mol. Biol. Rep.* **11**, 117. 2) Harper *et al.* (1983) *Nature* **304**, 169–171.

Nru I RFLP



A BstXI polymorphism at the D5S116 locus

S.Cottrell and L.Varesco¹

Director's Laboratory and ¹Molecular Analysis of Mammalian Mutation Laboratory, Imperial Cancer Research Fund, Lincoln's Inn Fields, London WC2A 3PX, UK

Source/Description: Phage ECB20 (D5S116) was isolated from a library of end clones of >800 kb BssHII fragments (1).

Polymorphism: BstXI identifies a two allele polymorphism: A1: 16.8 kb

A2: 13.0 kb

There are two invariant bands at 6.0 and 3.3 kb.

Frequency: Estimated from 18 unrelated Caucasians.

A1: 0.36 PIC = 0.35

A2: 0.64

Not Polymorphic For: EcoRI, HindIII, MspI, BglII, PvuII, TaqI, PstI, all tested on a panel of 6 unrelated individuals.

Chromosomal Localisation: 5q11-qter by somatic cell hybrids PN/TS-1 (1) and HHW213 (2).

Mendelian Inheritance: Codominant segregation was observed in 5 families.

Probe Availability: Available from S.Cottrell.

Other Comments: This probe contains repetitive sequences and should be used in the presence of an excess of total human DNA in the hybridisation mixture.

Acknowledgements: We thank Dr H.Thomas for the somatic cell hybrid PN/TS-1 and Dr J.J.Wasmuth for HHW213.

References: 1) Varesco,L. *et al.* (1989) *Proc. Natl. Acad. Sci. USA* **86**, 10118–10122. 2) Carlock,L.R. and Wasmuth,J.J. (1985) *Somat. Cell. Mol. Genet.* **11**, 267–276.

