Two RFLPs generated by Taq I at the human HRAS1 locus

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SOURCE/DESCRIPTION: pbc-N1 (Pulciani et al., 1982), contains a 6.4 Kb Bam HI fragment of the human proto-oncogene HRAS1 (Harvey-ras 1) subcloned in pBR322 from a library of human fetal liver DNA.

POLYMORPHISM: Taq I detects three invariant bands at 2.3, 1.7 and 0.45 Kb and two polymorphisms. The first is a multiallele polymorphism related to the already reported MspI/HpaII polymorphism (Krontiris et al., 1985) with bands ranging from 2.5 to 4.35 Kb (Figure, lanes 1, 2 and 5). The second is a novel polymorphism which identifies a variant allele characterized by three fragments of 2.3, 0.8 and 0.65 Kb (Figure, lanes 3 and 4).

FREQUENCY: The variant allele has been found in 17.21% of the alleles from 61 European Caucasians.

NOT POLYMORPHIC FOR: ----

CHROMOSOMAL LOCALISATION: Chromosome 11p15.

MENDELIAN INHERITANCE: Co-dominant segregation shown in 4 families (22 individuals).

PROBE AVAILABILITY: Commonly available.

OTHER COMMENTS: Our data indicate that besides the known polymorphism due to the variable number of repetitions in the VTR region of the human HRAS1 gene, Taq I digestion reveals a variant allele which has two additional Taq I restriction sites within the region itself. The generation of the variant allele appears to be linked to the duplication processes of VTR sequence.

REFERENCE: Pulciani et al. (1982) J. Cell. Biochemistry, 20: 51-61.

Krontiris et al. (1985) Nature, 313: 369-374.

ACKNOWLEDGEMENTS: Supported by CNR "Progetto Finalizzato Oncologia" Grant No. 85.02304.44.