

Hypervariable lengths of human DNA associated with a human satellite III sequence found in the 3.4kb Y-specific fragment

C.Fowler, R.Drinkwater, L.Burgoyne and J.Skinner

School of Biological Sciences, Flinders University, Bedford Park, SA 5042, Australia
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Human Satellite III DNA contains a degenerate, pentameric tandem repeat sequence TTCCA (1). A probe (Seq.228S below) isolated from a human sperm library enriched in repeat sequences, has disclosed that such sequences are associated with hypervariable lengths of DNA upon Taq 1 digestion of human genomes. The resulting restriction fragments are highly discriminating of individuals, (Fig. 1) a major cause apparently being random C-G point mutations in the pentamer (TTCCA) thus creating Taq 1 sites (TCGA), though further mutations of the resultant (CpG) dinucleotide may be contributory. Equality of Taq 1 restrictions was checked by reprobing with centromeric tandem repeat sequences where invariate patterns were obtained. Probe 228S also identifies the 3.4 kb Y-specific fragment (2) and other unspecified autosomal fragments upon EcoRI digestion of human genomes. Comparison of Taq 1/228S patterns with mini-satellite probe patterns (3) produced different but similarly complex restriction patterns for individual genomes. Mini-satellite hypervariation is revealed by enzymes restricting in regions flanking the short tandem repeats. By contrast, this hypervariation is revealed only by Taq 1 apparently restricting within the pentameric repeat.

- References: (1) Prosser, J., et.al., (1986) J.Mol.Biol. 187, 145-155.
 (2) Nakahori, Y., et.al., (1986) Nuc.Acids Res. 14, 7569-7580.
 (3) Jeffreys, A.J., et.al., (1985) Nature. 314, 67-73.

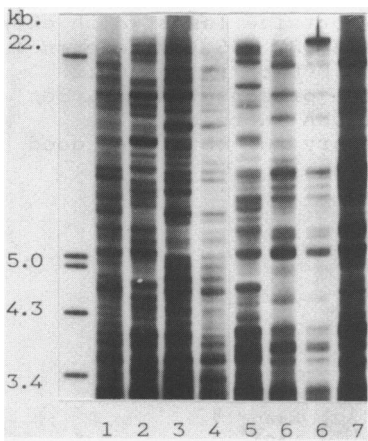


Fig 1. Taq 1/228S analysis of individuals 1-7: persons 1-4 are related, 5-7 are unrelated and duplicate 6 is germline/somatic tissue compared.

SEQ-228S: Satellite III sequence related DNA.
 G.G.A.A.T.G.G.A.A.T.G.G.A.A.T.G.G.A.A.T.G.G.A.A.T.G.G.A.A.T.G.G.A.A.T. (30)
 G.G.A.A.T.G.G.A.A.T.T.C.A.A.C.C.C.G.A.A.T.G.G.A.A.T.G.G.A.A.A. (60)
 G.G.A.A.T.G.G.A.A.T.A.A.A.C.C.C.G.A.G.T.G.G.A.A.T.G.G.A.A.T. (90)
 G.G.A.A.T.G.G.A.G.T.G.G.A.A.T.G.G.A.A.T.G.T.A.A.T.G.G.A.A.G. (120)
 G.G.A.A.T.G.G.T.A.C.G.G.A.A.T.G.G.A.A.T.G.G.A.A.T.G.G.A.A.C. (150)
 T.A.A.A.T.G.A.A.A.T.G.G.A.A.T.G.G.A.A.T.G.G.A.A.T.G.G.A.A.T. (180)
 G.G.A.A.T.G.G.A.A.T.G.G.A.A.T.G.G.A.A.T.G.G.A.A.C.C.C.G.T.G.T. (210)
 G.C.A.A.T.T.G.A.A.T.G.G.A.A.T.C.G.A.A.T.G.G.A.A.T.G.G.A.A.T. (240)
 G.C.C.A.A.T.G.G.A.A.T.G.G.A.T.T.C.A.C.T.A.G.A.T.G.G.A.A.T.G. (270)
 G.A.A.G.G.A.A.T.G.G.A.A.T.C.A.A.C.C.A.G.T.G.G.A.A.T.G.G.C.A. (300)
 A.T.G.G.C.A.T.G.G.A.A.T.G.G.A.A.T.C.G.A.A.T.G.G.A.A.T.G.C.A. (330)
 G.T.