TaqI RFLP identified by probe VK17A (DXS294) at Xq26

G.K.Suthers, V.J.Hyland, E.Baker, K.E.W.Fernandez, D.F.Callen, G.R.Sutherland

Cytogenetics Unit, Department of Histopathology, Adelaide Children's Hospital, North Adelaide, SA 5006, Australia

SOURCE/DESCRIPTION : A 3.3 kb *TaqI* fragment (VK17A) of single-copy human DNA was blunt-ligated into the *SmaI* site of pUC19. VK17A was a subclone of VK17 (DXS294) which was derived from a 16,X-specific library described by Hyland, VJ et al (submitted). The only region of the human X-chromosome represented in this library was Xq26->qter.

POLYMORPHISM : *TaqI* (New England Biolabs) identified a two allele polymorphism with band sizes 3.3 kb (A1) and 3.8 kb (A2). No constant bands were detected.

FREQUENCY : In a sample of 21 unrelated Australians and 21 unrelated Utah individuals the following allele frequencies were obtained :

		A1	A2
Australian	(29 chromosomes)	0.86	0.14
Utah	(30 chromosomes)	0.70	0.30
Total	(59 chromosomes)	0.78	0.22

The difference in allele frequencies between the two populations was not statistically significant. The PIC (over 59 chromosomes) was 0.34.

NOT POLYMORPHIC FOR : *MspI*, *RsaI*, *BglII*, *PstI*, *Sau3A*, *HincII*, *SacI*, *EcoRI*, *HindIII*, *PvuII* or *BamHI* (12 chromosomes each).

CHROMOSOMAL LOCALISATION : Examination of a 3-point crossover in Utah pedigree K-1329 (individual 7058) indicated that VK17A was distal to *DXS11* (located at Xq24-26). *In situ* hybridisation of VK17A against cell line GM08121 (karyotype 46,X,del(X)(q26qter)) showed that the probe was proximal to the breakpoint and thus proximal to *DXS105* (Patterson et al, 1987). Therefore VK17A lies in a region bound by *DXS11* and *DXS105*.

MENDELIAN INHERITANCE : Co-dominant inheritance was shown in two three-generation Utah pedigrees, K-1329 and K-1340.

PROBE AVAILABILITY : The probe has been lodged with the American Type Culture Collection.

OTHER COMMENTS : Reliable overnight result after ³²P- labelling by nick translation.

REFERENCE : Patterson, M et al (1987), *Genomics* 1: 297-306.

ACKNOWLEDGEMENTS : GKS is the recipient of a National Health and Medical Research Council scholarship. The Adelaide Children's Hospital Research Trust provided support.