

ALLELE FREQUENCIES AT THE D2S44, D10S28 AND D14S13 LOCI IN FOUR SOUTHERN AFRICAN POPULATIONS

J ROUSSEAU, S REAVIS, R MARTELL, E du TOIT & T SEWELL*

Provincial Laboratory for Tissue Immunology & *University of Cape Town Electron
Microscopy Unit
Cape Town, South Africa

Polymorphic DNA arising from variations in the number of short tandem repeats accounts for many of the hypervariable regions detected in the human genome (Nakumura et. al., 1987). For this preliminary study we have analysed 3 such loci and have determined the size range and frequency distribution of the VNTR alleles in the South African Caucasoid, Cape Coloured, Xhosa and Khoi-San populations.

The South African Caucasoids originate from a small genetic pool of Dutch, German and French ancestors with an admixture of approximately 7% Southern African and Asian genes (Botha et al., 1972). The Cape Coloureds are an anthropologically distinct population group possessing Western European, Southern African and Asian genes in significantly different proportions from those seen in South African Caucasoids. The Xhosa group are representative of the Nguni-speaking tribes. The Khoi-San are descended from people of the latter Stone Age and reside in Namibia.

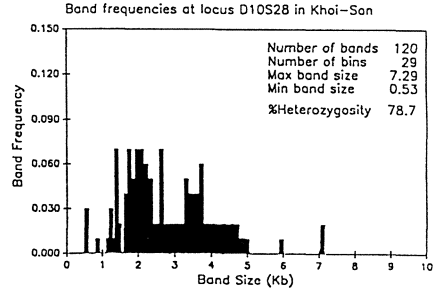
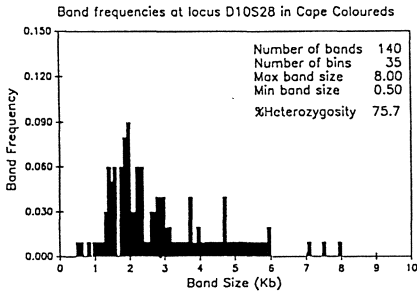
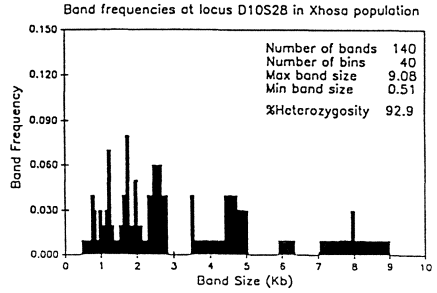
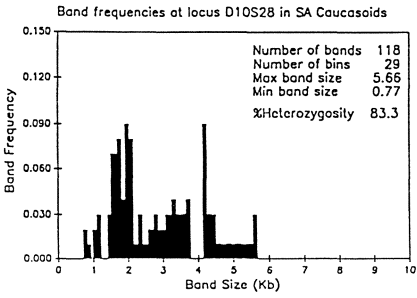
METHODS

Genomic DNA was prepared from peripheral blood samples by the salting-out method (Miller et. al., 1988). The DNA was digested with the restriction enzyme Hae III, Southern blotted and hybridised to the VNTR probes YNH24 (D2S44), TBQ7 (D10S28) and CMM101 (D14S13) (Promega). A previously standardised protocol was applied (Reavis et.al., 1992) and, in order to obtain reliable band frequencies the data were analysed using a digitised video-image system developed in this laboratory. Allele sizes (kb) were calculated from a curve fit (least squares method) of band size (kb) versus log [mobility]. Binning databases (dBaseIV, Borland) for each population group were created from which the histograms of the allele distributions were generated. A fixed-bin approach was used in which the bin increments were 6%.

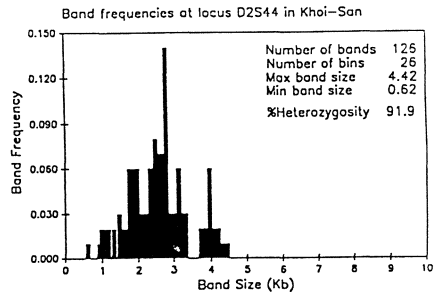
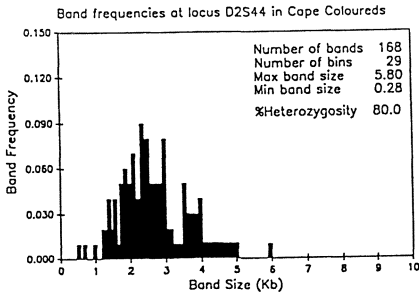
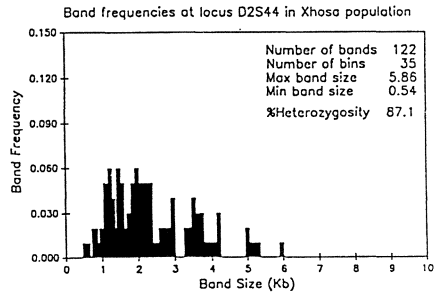
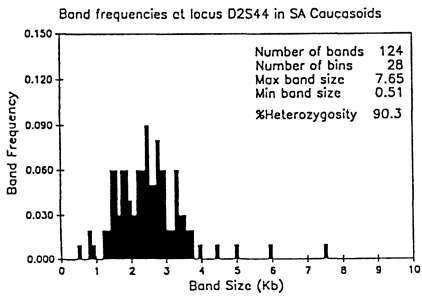
Table 1. Predominant allelic species seen in the different populations

Population Group	Genetic Locus		
	D2S44	D10S28	D14S13
Caucasoid	2.41 - 2.56	1.91 - 2.02	1.70 - 1.80
Cape Coloured	2.27 - 2.41	1.91 - 2.02	3.42 - 3.63
Khoi-San	2.71 - 2.87	2.02 - 2.15	Not done
Xhosa	1.91 - 2.02	1.70 - 1.80	1.70 - 1.80

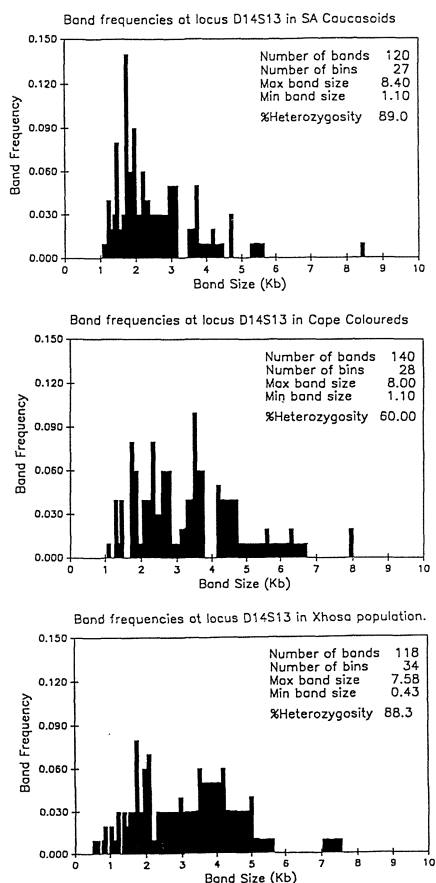
Distribution of D10S28 alleles in the South African Caucasoid, Cape Coloured, Khoi-San and Xhosa populations of Southern Africa.



Distribution of D2S44 alleles in the South African Caucasoid, Cape Coloured, Khoi-San and Xhosa populations of Southern Africa.



**Distribution of D14S13 alleles in the South African
Caucasoid, Cape Coloured and Xhosa populations
of Southern Africa.**



REFERENCES

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RESULTS & DISCUSSION

These ethnic groups demonstrate differences in their allele distributions as may be seen from the histograms. The size range for all the population groups studied was between 0.7kb and 9 kb and no single allelic form was present in an exceptionally high frequency although the most common allelic species differed in the populations as shown in Table 1.

The allele size range and frequency distribution of the four populations appeared similar at the D2S44 locus. At the D10S28 locus the range of allele sizes was greater in the Xhosas than in the Caucasoids with the Cape Coloureds midway between the two. The size range and distribution of alleles of the Khoi-San was similar to that of the Caucasoids. At the D14S13 locus the allele size range was similar for the three populations studied but the distribution was not, with the Xhosas having larger fragments whereas the Caucasoids had a preponderance of smaller sized fragments. As expected, the size range and frequency distribution of the fragments observed in the Cape Coloureds at this locus reflected features of both the South African Caucasoid and Xhosa populations.