ALLELE FREQUENCIES FOR FIVE DIFFERENT SINGLE LOCUS PROBES IN A POPULATION OF SOUTH-WEST GERMANY

W. Pflug*, G. Bäßler, G. Mai, U. Keller, S. Aab,
B. Eberspächer, G. Wahl
Landeskriminalamt Baden-Württemberg, Stuttgart, Germany

Introduction

In forensic science case work DNA analysis of restriction fragment length polymorphisms (RFLP's) has become the most powerful method. Nearly all labs working in the field of stain analysis prefer single locus probes (SLP's) because these probes have a better sensitivity than multilocus probes and offer the possibility of building a database for the alleles frequency. In routine case work in our lab we use 4 - 5 single locus probes and the results of DNA analysis are reported as frequency data. The precision of measuring fragment lengths i. e. the differences that may occur for the same individual on different blots was determined and is subsequently taken into consideration. For calculating the frequency we use the "sliding window" routine, a conservative method of frequency determination (Gill et al.). Up to now the only frequency data for a german population come from the area of Düsseldorf (Henke et al.). To compare the frequency data from Henke with the distribution in our area of South-West Germany, we analyzed about 360 unrelated individuals.

Methods

DNA extraction and separation of **HinfI** restricted DNA fragments was carried out by standard methods. Hybridization was done according to Smith et al. Single locus probes MS 1, MS 31, MS 43 A and G 3 (Wong et al.) from ICI/Cellmark and YNH 24 (Nakamura et al.) from Promega were used sequentially.
Length of DNA fragments was calculated by reference to a standard curve of size markers labelled with ^{35}S (Amersham).

Results

Allele sizes and the allele frequency distributions were determined for the 5 hypervariable loci D1S7, D7S21, D12S11, D7S22 and D2S44 detected by minisatellite probes MS 1, MS 31, MS 43 A, G 3 and YNH 24. The determination of allele sizes is limited by the resolution of the electrophoresis system. Fragments differing in mobility by 0,5 mm could be resolved. The resolution limit and measurement reproducibility ranges from ±100 bp in the 1,5 - 3,0 kb region of the gel to ±600 bp in the 12 - 15 kb region. The reproducibility of measurements was confirmed by including an aliquot of known control-DNA on every gel. For comparison with other statistical data, actual fragment sizes were approximated to 0,1 kb steps (bins). For probes MS 1, MS 31, MS 43 A, G 3 and YNH 24 restriction fragments could be registrated in 151, 78, 87, 116 and 46 bins. In fact this does not give

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the allele number, but can serve to estimate the variability of each system. The observed homozygosity was 4,1 % (MS 1), 5,3 % (MS 31), 8,5 % (MS 43), 6,1 % (G 3) and 4,6 % (YNH 24). The frequency profile of all SLP's is in good accordance with the profiles established by Henke et al., Smith et al. and Promega Corp. USA. Differences could only be noticed in the profile of MS 43 (Henke et al.) at about 8 kb and the profile of YNH 24 (Promega Corp. USA) at 3,5 kb.

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Single locus probe profiles obtained from HinfI restricted DNA of a south-west German population