

STR Polymorphism at the HumCD4 Locus in an Italian Population

N. Cerri, E. Nassuato and F. De Ferrari

Institute of Forensic Medicine- University of Brescia, P.le Spedah Civili, 1 25100 Brescia



INTRODUCTION

Analysis of DNA loci by PCR technique is a very powerful tool in criminal investigation and paternity testing; however forensic application of any genetic marker requires a study to carry out a data base of the relevant population for a correct use of the analysis results.

In order to obtain data from a Northern Italian population, allele frequencies and genotype distribution of STRs HumCD4 (Edwards *et al*; 1991) were studied in a sample from Brescia area (Lombardy).

MATERIALS AND METHODS

DNA was extracted from blood samples by the phenol chloroform isoamyl alcohol method. Standard PCR amplification was carried out in a total volume of 50ul containing 5-15 ng template DNA, 10pmol each primer, 100uM each dNTP, 1.5mM MgCl₂ and 1U *Taq* polymerase at the conditions of 96°C 2 min, 94°C 1 min, 64°C 1 min, 70°C 1.5 min 10 cycles then 90°C 1 min, 64°C 1 min, 70°C 1.5 min for 20 cycles. The amplification products were separated by 6% denaturing PAGE and visualized by silver staining.

RESULTS

The preliminary results show a total of 12 different genotypes corresponding to 5 common alleles, the most frequent alleles were 5 and 6 with a similar frequency value (0.32) and 10 (0.31). The data obtained are in accordance with the prediction of Hardy Weinberg equilibrium and the allele frequencies were consistent with those previously reported in other Italian and Caucasian populations.

In conclusion, this study confirms that HumCD4 for its sensitivity, its polymorphicity and its satisfactory electrophoretic resolution is a very useful marker in forensic investigation.