

**Allele Distribution for Six VNTR Markers
in the Caucasian Population from Uruguay
Compared With Regional Data**

J.P. Moisan¹, M.G. Le Roux¹, O. Pascal¹, F. Guidet¹, B. Mechoso², A. Vaglio², S. Pagano³, A. Pérez³,
E. Viera⁴, R. Quadrelli² (Head)

¹ Laboratoire de Génétique Moléculaire, Institut de Biologie, Hôtel Dieu, Nantes, France

² Instituto de Genética Médica, Hospital Italiano, Montevideo, Uruguay

³ Dirección Nacional de Policía Técnica, Laboratorio, Montevideo, Uruguay

⁴ Instituto Técnico Forense, Poder Judicial, Montevideo, Uruguay



Preliminary allele distributions were determined for six VNTR loci (D2S44, D10S28, D17S26, D4S139, D5S110, D8S358) in the Caucasian populations from Uruguay. Allele distributions are highly polymorphic in all populations sampled. Alleles were directly assigned according to analytical size markers ranging from 0.9 to 14 kilobases with twenty four subdivisions. This data was compared with one of the two nearest countries: Argentina. For this purpose the VNTR group mentioned above was employed, except for locus D8S358. The behavior of curve profiles shows several similarities in spite of the fact that the population from Argentina ranged from 0.6 to 13 kilobases with thirty one subdivisions. Samples tested varied in number from approximately one hundred to one hundred and fifty.