## Molecular Characterization of a Highly Variable Short Tandem Repeat Polymorphism at the D2S1241 Locus

B. Reichenpfader<sup>1</sup>, R. Zehner<sup>2</sup>, M. Klintschar<sup>1</sup>

<sup>1</sup>Department of Forensic Medicine, Karl-Franzens-Universität, Universitätsplatz 4, 8010 Graz, Austria <sup>2</sup>Zentrum der Rechtsmedizin, J.W. Goethe-Universität, Kennedyalle 104, 60596 Frankfurt, Germany



We report the analysis of the STR locus D2S1242 (GDB ID G00-309-429), which was investigated by PCR amplification, native and denaturating polyacrylamide gel electrophoresis in a total of 146 unrelated Austrians.

No deviations from Hardy-Weinberg expectations were observed. The mean exclusion chance (MEC) was 0.669, the discriminating power (DP) was 0.947 and the observed heterozygosity rate was 0.856. An allelic ladder consisting of nine sequenced alleles (141-175bp) was constructed. Sequence analysis revealed that the locus comprised two repeat motifs varying in number between alleles: GAAA and GAAG. According to the number of repeats, the smallest allele was designated 15 and the largest allele 23.

Allele	Frequency
15	0.014
16	0.048
17	0.137
18	0.137
19	0.164
20	0.212
21	0.226
22	0.048
23	0.014

ജ