



Kurdish population data for the STR loci ACTBP2, CSF1PO, FGA, TH01, TPOX, VWA, D3S1358, D5S818, D7S820, D13S317 and D21S11

I. Shimada^{a,b,*}, C. Hohoff^b, S. Rand^b, B. Brinkmann^b

^a*Department of Legal Medicine, Toyama Medical and Pharmaceutical University,
2630 Sugitani, Toyama 930-0194, Japan*

^b*Institut für Rechtsmedizin, Universität Münster, Münster, Germany*

The short tandem repeat (STR) systems D3S1358, VWA, FGA, TH01, TPOX, CSF1PO, D5S818, D13S317, D7S820 (as part of the AmpFISTR® Profiler™ PCR Amplification Kit (ABI)) were studied in a Kurdish population sample (950 unrelated individuals mainly from Northern Iraq).

DNA from the buccal swabs was extracted by the Proteinase K/Chelex-100 method and amplified according to the recommendations of the manufacturer (ABI). PCR products were separated by capillary gel electrophoresis on an ABI PRISM 310 Genetic Analyzer (ABI) with laser-induced fluorescence (LIF) detection.

The aim of this study was to establish a database for immigration cases. Since the combined MEC of the Profiler kit was not sufficient for all, especially deficiency cases (99.94%), a duplex PCR composed of the polymorphic loci ACTBP2 and D21S11 was set up and a combined MEC of 99.998% was achieved. No deviation from Hardy–Weinberg equilibrium was observed.

The investigated loci cover six of the eight systems from the German DNA database stored at the Bundeskriminalamt (BKA). These loci possess a combined power of discrimination (PD) of 0.999999996, while the combined PD of all 11 STR systems is 0.9999999999994 in the Kurdish population.

* Corresponding Author. Department of Legal Medicine, Toyama Medical and Pharmaceutical University, 2630 Sugitani, Toyama 930-0194, Japan.