



B34 Study on Mutation Rate of CODIS 13, D2S1338, D19S433 and X STR Loci and its Influence to CPI Value

Meng Yi Chen, MS, Ministry Justice Investigation Bureau, PO Box 340, Hsin-Tien, Taipei 231, Taiwan; Ling-Leng Ming, MS, and Chang-En Pu, MS, Forensic Medicine Section, Scientific and Technical Research Center, Ministry Justice Investigation Bureau, Taiwan, Republic of China

After attending this presentation, attendees will understand that the mutation rate of STR profiling should be considered in paternity examinations.

This presentation will impact the forensic community and/or humanity by demonstrating mutation rate of STR profiling should be noticed when building paternity.

Paternity determination is conducted according to the Mendelian Inheritance laws by examining STR genotypes between child and alleged father or mother. This is currently tested at the STR systems CODIS 13, D2S1338, D19S433 and 7 X STR loci. But when mutations occur at those loci, it will interfere with the judgment of paternity or non-paternity between individuals. This study was concerned about mutation rate in these STR loci and the influence to the value of CPI in paternity test.

We observed total 737 cases containing 633 duo cases and 104 trio cases. In 12,150 parent/child allelic transfers (meioses) at CODIS 13, D2S1338, D19S433 and X STR loci, 33 isolated STR mismatches were observed.

Paternal meioses mutation rates: D3S1358 and FGA were 0.00469

vWA, D8S1179 and D19S433 were 0.00313

CSF1PO, D13S317, D7S820, D21S11 and D18S51 were 0.0015

No paternal meioses mutations were observed in TH01; TPOX; D5S818 and D16S539.

Maternal meioses mutation rates only observed in D5S818, D8S1179, D21S11, and D16S539 with the value of 0.00498.

X STR linked mutation only observed in DXS10011, DXS7132 and AR loci with the value of 0.02174, 0.01538 and 0.01961 respectively. Null alleles were observed in D8S1179 locus only.

CPI value of 97 real parenthood trio cases and 33 single mutation cases were calculated according to published formula. This study suggested that?

1. If one single STR mismatch was observed and concluded that the inconsistency was a mutation, then the mutation result must be also incorporated into the reported results.
2. Using the mutation rate divided by the average probability of exclusion to calculate the mutation loci paternity index (PI) according to AABF annual report summary 2003
3. For the duo cases (mother didn't want to be tested or she didn't want to pay), it was suggested that mother should be sampled for further tests if in a low CPI or mutation situation.
4. With regards to null allele cases, the sample could be tested with other commercial kits and the null alleles might be revealed.

Forensic Science, STR, Mutation Rate