Mutation Rates of STR Systems in Danes
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Mutation Rates of STR Systems in Danes


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Abstract

Double paternity cases in the period 1999 to 2005 were investigated regarding mutations at STR loci. STR typing was performed by two different Polymerase Chain Reaction Amplification Profiler+ kits in the period 1999 to May 2005, thereafter the PAP kit, and by Applied Biosystems Amplifier kit for the rest of the period of study. The results were consistent with the data found. Analysis of the STR loci at the end of 2005 was performed by the PAP kit. A total of 4,479 cases were analyzed at 9 STR loci and for 152 cases, STR loci were analyzed at 35 STR loci, in total 4,524 cases.

As the mutations rates are expected to be small, i.e. due to random events, we set the type I error at 0.05. We investigated the possible association between mutations and STR loci, mutations and sex, and the strategy local variables. For the cases where a mutation had occurred, i.e. given mutations, the association between sex, sex and STR loci was investigated. The results are shown in Table 1. The mutation rates for STR loci were calculated in Table 5.

The reliability of the given mutations being paternal significant different from maternal, with the 95% confidence intervals for male mutations, the probability did not contain the value 0.05.

Results - cont’d

The analysis were followed by a logistical regression with mutations as dependent variable, using the PAP kit. By sex, the dominant null hypothesis was not rejected. By sex, the dominant null hypothesis was not rejected.

Table 7: STR Local Specific Mutation Rates - PAP & IDFL

Table 8: STR Local Specific Mutation Rates - IDFL

Discussion

• Data cleaning: We used a data cleaning, since estimates of any occurrence are very sensitive to terms of any kind, e.g. clipping terms in the negative of data.

Validation: The data were highly validated by forensic geneticists and thoroughly analyzed by statisticians, seeking high confidence to the mutations rates.

References


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