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Mutation Rates of STR Systems in Danes


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Abstract

Dental paternity cases in the period 1999 to 2005 were investigated regarding mutation rates in STR loci. STR typing was performed by Applied Biosystems AmpFlSTR Profiler Plus kit in the period 1999 to 2004, thereafter the PPF and, by Applied Biosystems AmpFlSTR Identifiler kit for the rest of 2005, known named as IDFL. Analyses of sets of paired genotypes were manually inspected by two forensic geneticists and statistically analyzed by a method described in [1]. We found no significant effect of age on the number of mutations in STR loci, but differences in mutation rates are different on STR loci and in sex. In the cases where mutation had occurred, we found no significant differences in STR loci between males and females. For the cases where a mutation had occurred, i.e., given mutations, the association between sex, STR loci and STR loci was investigated. The results showed that the differences in mutation rates are different on STR loci and in sex. For the investigation of variation of marker mutation rates in STR loci and STR loci with a known mutation, the method of Chi-square test was performed with pairwise differences in mutation rates and STR loci and STR loci between the individuals.

Results - cont’d

The analysis were followed by a logistic regression model with mutation as dependent variable and STR loci and STR loci and STR loci as independent variables. The analysis were performed by applying the logistic regression model with mutation as dependent variable and STR loci and STR loci and STR loci as independent variables.

Table 5: PPF & IDFL

Table 6: IDFL

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

Table 8: STR Local Specific Mutation Rates - PPF & IDFL

Table 9: STR Local Specific Mutation Rates

Table 10: STR Local Specific Mutation Rates

Table 11: STR Local Specific Mutation Rates

Table 12: STR Local Specific Mutation Rates

Results

Initially, the data were analyzed for the purpose of determining the conditional independence of two variables. Analyses of markers were performed with pairwise differences in mutation rates and STR loci and STR loci between the individuals.

Figure 1: Graphical Model

Discussion

• Data cleaning: We data cleaned, since estimates of some unknowns may be sensitive to terms of any kind of deviation, and we applied statistical tests to determine the significance of differences in mutation rates and STR loci between individuals.

• Validation: The data were highly validated by forensic geneticists and truly utilized by analyses with statistical tests to determine the significance of differences in mutation rates and STR loci between individuals.

• Kit dependency: The logistic regression model is validated, though not significant, effect of the kit. The analysis were performed by applying the logistic regression model with mutation as dependent variable and STR loci and STR loci and STR loci as independent variables.

References


COMMIT: E. Source, N. Childress, Department of Mathematical Sciences, University of Copenhagen, Denmark.