

GENETIC INCONSISTENCIES WITH STRs IN PATERNITY TESTING – EXPERIENCE AND RECOMMENDATIONS

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Genetic inconsistencies discovered during biological relationship testing can add complexity to the analysis and resolution of a case. Because of the low but not insignificant mutation rates in the VNTR and STR systems, an exclusion from paternity cannot be based on an exclusion in a single DNA system.

An exception is the case involving closely related alternative fathers where one is excluded in only one system and the other is excluded in none. Since more STR systems than VNTR systems are commonly used to resolve a paternity case, the chance of encountering mutations in STR systems increases.

Furthermore, resolving cases to determine if there is a true relationship with a genetic inconsistency versus, the detection of a close relative can be complex in the determination of biological relationship cases involving questions related to immigration.

We will present the mutation rates for our laboratory's VNTR and STR systems and how they are used to calculate a mutation PI and to obtain an overall result. We will also present information on the characteristics of exclusions in STR systems and how to utilize these characteristics so as to not falsely include nor exclude the tested individuals. We will also present our laboratory's immigration testing protocols which minimize the chance of falsely including or excluding the alleged relative.