

INCONSISTENCIES IN PARENTAGE TESTING: WHAT HAPPENS WHEN ALLELES DON'T MATCH

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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 a single exclusion. 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 as opposed to the detection of a close relative can be complex in the determination of biological relationship cases involving questions related to immigration.

The mutation rates for various STR systems obtained through the American Association of Blood Bank's most recent annual survey of parentage testing laboratories will be presented. The recommend PI calculation for incorporating mutations will be reviewed. An immigration testing protocol will be presented which minimizes the chance of falsely including or excluding the alleged relative.