# STATISTICS OF PARENTAGE ANALYSIS: CONSIDERATIONS OF MUTATIONS

**Ranajit Chakraborty**
*University of Texas School of Public Health, Houston, TX*

It is now well established that with the routine use of Short Tandem Repeat (STR) markers, parentage analysis has become more powerful as well as faster than before. However, as the STR markers are more mutable than the classical serological markers, parentage-testing laboratories are observing sporadic exclusions, caused by mutations during maternal or paternal meiosis events. While the logic of entertaining mutations in statistical interpretation of parentage testing data is relatively simple, there are occasions where paternal exclusions due to mutations are not easy to distinguish from actual non-paternity. A formal logic for such distinctions is described in this presentation, which requires the knowledge of locus-specific rates of mutations. This logic also justifies the recent AABB guidelines of using exclusions based on at least two loci as a criterion of non-paternity. Allele size change is also an additional criterion that is helpful in distinguishing mutations from non-paternity. Further, this analysis also demonstrates that when mutation rates are incorporated in the analysis, the number of loci showing apparent exclusions provides additional support of the inference of parentage, above and beyond the information provided by the modified paternity index. These analytical results call for more rigorous documentation of mutation events encountered in casework analyses, since with more refined data on locus-specific patterns of mutation rates, further refinement of statistical interpretation is possible.

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