



D43 CPI Distribution and Cut-Off Value for Duo Paternity Building

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Attendees will learn that CPI can be very low for real duo paternity cases and CPI could be very high for random pairs (duo). The presentation will demonstrate that a suitable CPI range should be developed for determining paternity.

The STR loci comprising CODIS has an average power of paternity exclusion larger than 0.9999 based upon mother, child and father combinations (a trio case). This figure is true for many populations. In cases requiring the identification of human remains if only one living relative (either of the parents or of offspring) is available, this represents a duo case for parentage building. In duo cases when allele sharing is found in all the 13 loci, the probability of parentage could be determined. However, it is hard to avoid a false parentage evaluation if the pair happened to share an allele at all 13 loci. In Taiwan, the National Unidentified Bodies CODIS 13 STR Database has approximately 1250 bodies and 350 families for comparison originally. Using STR typing and blood-relative comparing instances a body first-degree matched to more than one individual was rarely found, however the CPI (Cumulated Paternity Index) was extremely low. It is necessary to evaluate the false parentage rate and set a cut-off value of CPI and vice versa to analyze the distribution of CPIs from real paternity cases, hope to help evaluate the paternity and lead to identification.

According to the published frequencies of STR alleles, the cumulated power of exclusion (PE) for duo for Chinese in Taiwan is 98.13%. The data showed that about 1.87 % random individuals could not be excluded from being a first-degree blood relative to the population. For proving this, CODIS 13 population data of 1,000 Chinese in Taiwan was collected and paired resulting in 499,500 pairs. Microsoft Excel Macros controlled by a Visual Basic program written by authors was used to handle the allele sharing comparison and CPI calculation. There were 462 (0.0925%) pairs found with all 13 allele sharing loci. False parentage relation was noted when the CPI for pairs ranged from 2.56 to 6,835,432.78, and the median CPI was 484.69 meaning that if the CPI of 484.69 were used as the cut-off, 50% of the false pairs would not be recognized as first-blood-relative, and if the CPI cut-off increased to 1,000, 62.9% false pairs could be eliminated, however the false exclusion rate for real duos was 5.7%(cut-off = 484.69) and then increased to 10.8%(cut-off = 1,000) respectively. The dilemma could be resolved by profiling more STR systems when duos were found with low CPI or adding anthropology and other information to make the confirmation. This is especially the case for mass and open comparing operation of STR database for the unidentified bodies.

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