B52 Evaluating the False Parentage Rate and CPI Cut-off of CODIS 13 STR for Seven Populations

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After attending this presentation, attendees will be able to recognize that false parentage determination after DNA test is possible.

This presentation will impact the forensic community and/or humanity by demonstrating the cutoff value of CPI for parentage could be established to avoid false parentage, especially important for unidentified body recognition on immigration blood relative testing.

We report on the use of STR typing for the genetic linkage of unidentified human remains and the problems associated with false paternity results. STR loci are chosen and used on based upon their power of discrimination and ability to multiplex with other STR loci. Most of the STR loci used in forensic science both for criminal and civil investigations. The CODIS 13 core STR systems has an average power of paternity exclusion (PE, to exclude a random man) larger than 0.9999(in trio cases) in many populations. In the identification of unidentified bodies only one relative (either of parents or either of son/daughter) is available for testing. This results in duo cases for parentage building. When allele sharing is found in all the 13 loci, the probability of parentage could be determined preliminarily. However it is hard to avoid a false confirmation of the alleged father or false identification of the unidentified bodies. In Taiwan, the national unidentified bodies CODIS 13 STR database has approximately 680 bodies and 200 families. Sometimes a body matches to more than one individuals (from different families) and cases with extremely low Cumulated Paternity Index (CPI) were found. It is necessary to evaluate the false parentage rate and set a cut-off value of CPI for avoiding false determination of parentage.

The CODIS 13 population data of 177 African American, 194 US Caucasian, 202 Southwestern Hispanic, 153 Bahamian, 157 Jamaican, 76 Trinidadian and 1,000 Chinese in Taiwan was collected from published websites of FBI USA or by authors. The cumulated power of exclusion (PE) for duo for African America = 98.31%, US Caucasian = 98.23%, Southwestern Hispanic = 97.97%, Bahamian = 98.48%, Jamaican = 98.32%, Trinidadian = 98.61% and Chinese in Taiwan = 98.13%. The data showed that about 1.4 % to 2% of random men could not be excluded from being an alleged father for the studied populations. A matching test model was designed to evaluate the practically possible false parentage rate.

All the collected individuals were paired resulting in 15,576, 18,721, 20,301, 11,628, 12,246, 2,850, and 499,500 pairs for each population respectively. Each pair was checked for allele sharing locus by locus and the CPI for those pairs with 13 loci sharing was also calculated. Microsoft Excel Macros controlled by a program written by the authors were used to handle the comparison and calculation. CPI calculations were based on the distribution frequencies for the respective populations. These were 8(0.0514%), 10(0.0534%), 9(0.0443%), 3(0.0258%), 7(0.0572%), 3(0.1053%) and 250(0.0501%) pairs found
with 13 allele sharing loci for the seven populations. False parentage was noted when the CPI for pairs ranged from 1.76 to 1,950,430. These were 4.48% CPI lower than 100, and 78.27 % lower than 1,000. If the suitable CPI cut-off value were used such as CPI=1,000, there would be less of false parentage.

Though we could reduce the false positive rate by increasing the cut-off value, the false exclusion rate (a real father excluded as a random man) would be increased accordingly. In this study many duo paternity cases in Taiwan were found with CPI lower than 1,000 when only CODIS 13 STRs were typed. If CPI=1,000 was suggested as the cut-off value these low CPI cases could be classified as false parentage cases. More real paternity cases have to be observed to set an optimum range of value for CPI cut-off, or more STR systems are required when matches were found with low CPI. This is especially the case for mass and open matching operation of STR database for the unidentified bodies. If less than 13 STR typing were obtained from the unknown skeleton owing to degradation of DNA, the CPI would be much lower, and the risk of false identification would be much higher. In such cases mtDNA sequencing and other investigating techniques should be added to enhance the discrimination.

Short Tandem Repeat, CODIS 13, Parentage Test

 ** Presenting Author*