B3 Evaluation of Y-STR Markers Using a Cajun Population

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Do the eight minimal haplotype Y-STR markers provide enough discrimination in a population that is potentially highly related? In this study, it can be demonstrated that in related populations, eight markers do not provide enough discrimination of the individuals in that population.

This presentation will impact the forensic community by demonstrating how the eight minimal haplotype Y-STR markers alone may be insufficient to reach individual characterization; therefore, additional markers may need to be used to discriminate some populations.

The Cajun population of southern Louisiana has a long history. The original population consisted of only a few family units that were continuously displaced from France to Canada to Louisiana. This population had sustained geographical and social isolation from the 1700s until the mid-late 1900s. Given the history of the Cajuns and since Y-STR's are inherited virtually unchanged from father to son(s), the possibility of observing a minimal number of different profiles form the Cajun population is greater than in the general population. Samples from the southern Louisiana area Cajun and non-Cajun populations were collected and processed. These samples were organically extracted, quantified, amplified, and analyzed using capillary electrophoresis. The eight minimal haplotype STR's plus two additional Y-STR's were analyzed. Even with ten loci, the results show more similarities and exact matches in the Cajun population than in a non-Cajun population.

Y-STR, Related Population, Discriminating Power

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