

## **AUTOSOMAL STRS ALONE OFTEN MAY NOT BE SUFFICIENT FOR THE IDENTIFICATION OF HUMAN REMAINS**

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DNA analysis of unidentified human remains (UHR's) often yields partial (<13 core loci) short tandem repeat (STR) profiles. This can be due to the age of the remains, environmental conditions, and/or the presence of PCR inhibitors in the sample. When searching these partial profiles against family reference samples (FRS) in a DNA database, such as the FBI's Combined DNA Index System (CODIS), adventitious associations may result. We demonstrate two cases with associations by STR typing which were excluded with the use of mitochondrial DNA (mtDNA) analysis and an additional case which was excluded with the use of Y-STR's. The need for multi-technology DNA testing is highlighted for filtering candidate associations and providing statistical weight to associations. Because of the sheer number of FRS that will be searched, caution should be exercised when placing undue significance on a genetic profile association. Lineage based genetic systems, such as mtDNA and Y-STRs will in many cases serve as efficient filters to reduce the number of adventitious associations. The same issues apply to those who attempt to use familial searching of DNA databases for developing investigative leads.