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AN INDIVIDUAL WITH A RARE HOMOZYGOUS NULL PHENOTYPE

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Aim: The short tandem repeat (STR) loci are PCR-based genetic markers used in human identity testing. Commercial kits for multiplex typing of STR loci are available. However, kits from different manufacturers use different primer sets. Null alleles are typically the result of a mutation in one of the PCR primer binding sites. Consequently, a sample may demonstrate allele dropout when typed by a primer set from one manufacturer's kit and not when typed by another manufacturer's kit. Null alleles can lead to significant challenges in paternity establishment, as parent and child can appear to be homozygous for different alleles. In other words, the allele dropout may cause a heterozygous specimen to appear falsely as a homozygote.
We report the presence of a null allele at the D13S317 locus in an African American Alleged Father, his daughter, and the two children resulting from the rape/incest of the daughter. One of the children had an extremely rare homozygous null phenotype, resulting in no visible bands. The other three individuals appeared phenotypically homozygous. The presence of a mutant site was confirmed when the samples, originally amplified using Promega Corporation primers, revealed an additional band when reamplified with different primers manufactured by Applied Biosystems.

Methods: Highly polymorphic regions that have short repeat sequences of DNA known as STR loci were targeted with sequence-specific primers and amplified using PCR. The resulting DNA fragments were then separated and detected using gel electrophoresis. We used a polyacrylamide gel to separate the DNA fragments. Following electropheresis, the bands were detected with silver stain. Results were analyzed and interpreted.

Scope: The frequency of null alleles is difficult to determine, as their presence is suspected only in cases where parent-child data is available. The most recent AABB data shows that 3 null alleles were suspected in the black population in D13S317. However, the total number of independent samples run in all reporting laboratories is unclear.

Conclusions: The current primer sets from commercial manufacturers do not produce considerable number of null alleles. This may in part be due to the fact that the laboratories routinely submit the variant alleles to the AABB for the Annual Survey. In order to reduce such challenges, the respective manufacturers should be notified to modify the primers such that the amplification of the recognized mutants is achieved.