

## **ARE INDIVIDUALS FROM POPULATIONS WITH LOW GENETIC DIVERSITY MORE LIKELY TO BE WRONGLY IDENTIFIED AS CONTRIBUTORS TO DNA MIXTURES ?**

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Forensic tools are routinely used to analyze low template DNA mixtures from multiple contributors. Genetic crime scene profiles (CSPs) are analyzed to determine if a particular suspect contributed to a mixture. The likelihood of observing the CSP is compared under two hypotheses: a prosecutor's hypothesis where the suspect did indeed contribute to the mixture, and a defense hypothesis where the suspect did not contribute to the mixture. The likelihood of observing the CSP under these hypotheses depends on the frequency of the observed alleles in the population. Here, we use a simulation approach to investigate if individuals from populations with low genetic diversity are more likely to be mistakenly identified as contributors to DNA mixtures. We created an algorithm using Forensim to simulate DNA mixtures of 2-8 individuals based on allele frequencies from 11 populations. We then used Forensim again to calculate likelihood ratios (LRs) for each mixture; first where the suspect was a true contributor to the mixture, next where the suspect was not a contributor in the mixture. From these results we estimated power and false positive rate across population groups and number of contributors. We found that statistical power decreases as the number of contributors to a mixture increases. Additionally, non-contributors from populations with low genetic diversity were mistakenly identified as contributors to the mixture more often than non-contributors from populations with high genetic diversity.