AN EVALUATION AND COMPARISON OF LOCUS-SPECIFIC AND ALLELE-SPECIFIC ALTERNATE STUTTER ARTIFACTS FREQUENTLY ENCOUNTERED IN GLOBALFILER™ DNA PROFILES

Oluwakemi Sowemimo[1], MSFS; Thomas V. Walsh, MSFS[2]; Fabio Oldoni, PhD1; Megan M. Foley, MSFS[2]
[1]Arcadia University
[2]The Center for Forensic Science Research and Education

Forensic DNA analysts commonly encounter stutter during data interpretation. Stutter is a DNA artifact caused by strand slippage of Taq polymerase during polymerase chain reaction (PCR) most commonly resulting in the deletion of a single repeat unit. Stutter has the potential to create serious challenges during DNA interpretation especially when the evidence profile is a DNA mixture of multiple individuals. Misinterpreting a stutter artifact can lead to the false inclusion or exclusion of a person of interest. Therefore, it is critical that stutter is thoroughly understood and accurately identified when present. Both locus-specific and allele-specific stutter have been studied and percentages have been developed to help predict and identify stutter when the stutter peak is one repeat unit shorter in length compared to the parent allele. However, limited information exists to assist with the accurate identification of alternate stutter peaks. In this study, we identified and evaluated the most common alternate stutter artifacts in one hundred and sixty-five single-source GlobalFiler™ DNA profiles encompassing African American, Caucasian, and Hispanic population datasets. Locus-specific and allele-specific stutter percentages were calculated, graphed, and compared to determine if an alternate stutter filter is necessary and if so, the most appropriate stutter values to use when interpreting DNA profiles. The most common alternate stutter products were observed at SE33 (N – 2, N – 6, and N – 8), D1S1656 (N – 2), and FGA (N + 2). The slope of the linear trendline indicated the allele-specific stutter percentages for SE33 (N – 6 and N – 8) and D1S1656 (N – 2) were more appropriate to accurately identify stutter. At SE33 (N – 2) and FGA (N + 2), the linear trendline slope indicated the locus-specific stutter percentages may be used. Overall, the results demonstrate the importance of implementing stutter filters for alternate stutter artifacts. In addition, the results support the use of an allele-specific stutter filter at some loci rather than a locus-specific stutter filter. An allele-specific stutter percentage will allow for the more accurate identification of alternate stutter products and decrease the possibility of incorrectly labeling a stutter peak as a true allele or incorrectly removing a true allele as stutter.