A MULTI-LABORATORY ASSESSMENT OF THE PRECISION ID GLOBALFILER NGS STR PANEL

Jennifer D. Churchill[1], Marie-Louise Kampmann[2], Claus Børsting[2], Kevin M. Kiesler[3], Sarah Riman[3], Lisa A. Borsuk[3], Peter M. Vallone[3], Ryo Hasegawa[4], Robert Lagace[4], Fabricio Gonzalez-Andrade[5], Jonathan L. King[1], Bruce Budowle[1]

[1]Center for Human Identification, University of North Texas Health Science Center
[2]Section of Forensic Genetics, Department of Forensic Medicine, Faculty of Health and Medical Sciences, University of Copenhagen
[3]National Institute of Standards and Technology, Biomolecular Measurement Division
[4]Thermo Fisher Scientific
[5]Central University of Ecuador

The use of MPS technologies in forensic genetic labs has become increasingly feasible due to the generation of streamlined and automated workflows, enhanced data analysis options, and availability of relevant genetic marker panels. The Precision ID GlobalFiler NGS STR Panel v2 (Thermo Fisher Scientific) allows for amplification of 35 markers including the current required set of CODIS and European System core loci. However, extant DNA databases contain length-based allelic data and typically are limited to those loci that are core markers. Expanding loci that may increase the success of DNA typing would be invaluable, particularly for analysis of challenged samples. Large-scale studies on these markers from MPS-based typing are needed to provide allele frequencies for statistical calculations to fully exploit the power of STR typing with MPS technologies.

A set of 1021 samples were sequenced with the Precision ID GlobalFiler NGS STR Panel v2, Ion Chef, and Ion S5 workflow as part of a large multi-laboratory study. Data analysis was completed with the Ion Torrent Suite of software which uploaded data to Converge for more in-depth analyses. This large sample set included Ecuadorian, with Native Amerindians of Ecuador from three different ethnic groups, Greenlander, Eritrean, African American, European, U.S. Asian, and U.S. Hispanic individuals. Population specific genetic analyses were performed. Performance metrics such as read depth, strand balance, stutter ratios, and concordance to orthogonal capillary electrophoresis data also were evaluated for the large sample set. Finally, an evaluation of the increase in information derived from sequence-based allele calls versus length-based allele calls will be discussed. The information generated in this study demonstrates the efficacy of the Precision ID GlobalFiler NGS STR Panel v2 kit with reference samples and will be used to help facilitate continued bioinformatic development and future implementation efforts.