# STR ANALYSIS OF A FORENSICALLY INFORMATIVE STR AND SNP MULTIPLEX USING NEXT GENERATION SEQUENCING

Ashley L. Silvia[1], Nathan Shugarts[1], Carey Davis[2], Cydne Holt[2], Joe Varlaro[2], Jenifer Smith[1]
[1]Forensic Science Program, Pennsylvania State University
[2]Illumina

Since the mid 1980's forensic scientists have been utilizing the discriminating power of DNA profiling to link individuals to criminal acts and also identify decomposed human remains. Short Tandem Repeat (STR) analysis is used in forensic DNA typing, but without a suspect to compare it to, or a resulting CODIS match to a profile from one of the state or national DNA databases; the results are not often informative. Accessing additional information from evidentiary body fluid stains by exploiting single nucleotide polymorphisms (SNPs) could assist in generating leads in investigations by determining possible ancestry or phenotypic characteristics of the source. There are several approaches that may be utilized to identify SNPs however not all platforms are suitable for low levels of DNA that are often obtained from evidentiary stains or samples. This poster demonstrates that the MiSeq (Illumina), a Next Generation Sequencing (NGS) platform can successfully determine both STRs and autosomal SNPs of interest using the "pre-release" version of the ForenSeq DNA Signature Prep Kit (Illumina). SNPs and STRs were sequenced from generated amplicons consisting of a multiplex with 62 STRs (29 autosomal (including 13 CODIS loci), 9 X-STRs, and 24 Y-STRs) along with 176 SNPs (56 ancestry-informative, 24 phenotypic-informative, and 96 identity-informative). The ForenSeq DNA Signature Prep Kit (Illumina) successfully generated concordant STR genotypes as compared to genotypes generated by Identifiler (Applied Biosystems) and Y filer (Applied Biosystems) using the 3130xl Genomic Analyzer (Applied Biosystems). These results were reproducible and successfully obtained from quantities of DNA ranging from 1 ng to 100 pgms. Parameters such as stutter percentage and heterozygote signal intensity ratios within loci will be presented.