A TECHNOLOGICAL EVALUATION OF NEXT-GENERATION SEQUENCING FOR THE FIGHT AGAINST HUMAN TRAFFICKING

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In the next-generation sequencing (NGS) era, it is now possible to generate larger, more informative genetic data sets from single samples. Forensic assays that previously were laborious, expensive and implemented as stand alone protocols may now be analyzed in tandem using this new technology. Forensic markers can include traditional short tandem repeats (STRs) and mitochondria that are currently used in forensic databases. For victim identification, additional markers may be of value, including single nucleotide polymorphisms (SNPs) that provide kinship, ancestry, and physical feature descriptions. These additional markers will augment DNA databases for high-risk populations, such as migrant families and minor and adult victims of human trafficking. To move this technology into routine use, NGS performance, quality assurances, informative genetic markers, database applications, community support, and legal and ethical aspects must be evaluated. To support this effort, the Duke-NCSU Collaboratory for Science, Ethics, Identity and Human Rights (SEIHR) has been established to engage stakeholders and develop workflows for database development of high-risk populations. The first-phase technological efforts of this collaboratory include NGS system verification. In this study, we present data from numerous NGS sequencing systems for STR, SNP and mitochondria data, as applied to use in human trafficking. The system performance, database potential, and statistical power for each marker class were inspected. We show the current state of NGS technology and provide a path forward for second phase investigations of the Duke-NCSU SEIHR, principally exploring the feasibility, applicability and ethics of non-standard markers for victim identification and kinship analyses in human trafficking.