THE USABILITY OF THE FORENSEQ KINTELLIGENCE WORKFLOW IN GENERATING INVESTIGATIVE LEADS IN THE CONTEXT OF FORENSIC GENETIC GENEALOGY

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The identification of Joseph DeAngelo as a suspect on the Golden State Killer Investigation initiated the use of forensic genetic genealogy (FGG) as an investigative lead for violent crimes, crimes against children and missing persons. The identification of DeAngelo was possible due to the use of direct to consumer tests, where hundreds of thousands of SNPs (single-nucleotide polymorphisms) are analyzed with the use of commercial microarrays that were initially developed for medical research. Commercial microarrays interrogate a vast number of SNPs, some of which can raise privacy concerns [1]. In addition, forensic laboratories do not have the ability or instrumentation to perform SNP array analysis[2], therefore samples are often outsourced and there is no standardization of use of such SNP microarrays between laboratories. To address these concerns, Verogen developed the ForenSeq® Kintelligence Library Prep Kit and Universal Analysis Software for MiSeq FGx™ Sequencing System. The ForenSeq Kintelligence Kit interrogates 10,230 SNPs specifically selected for forensic use, which exclude information regarding disease diagnosis. Moreover, the kit is designed to prepare libraries from forensic DNA samples. The libraries can be sequenced in the MiSeq FGx and data analyzed using the Universal Analysis Software (UAS). The kit and software were designed for use in forensic laboratories with forensic gDNA samples (low input/degraded) and casework protocols and workflows. The software allows the generation and download of sample reports, phenotype and ancestry reports and GEDmatch PRO™ reports in a format supported by GEDmatch PRO for DNA samples from multiple origins.

In this report, we share how the ForenSeq Kintelligence Library Prep kit and software can provide kinship information in the context of investigative leads. Using the Control DNA available in the kit and samples with whole genome sequencing data or microarray results, we performed developmental validation experiments to establish the robustness of the Kintelligence workflow. Using samples with known genotypes allowed us to determine the presence of artifacts (such as rare unexpected alleles or missing alleles) in the results. These artifacts, which increased proportionally with the decrease of DNA available for the workflow, are flagged in the software with QC indicators. Additionally, we evaluated the usability of UAS to manage the forensic genetic data generated with the Kintelligence workflow. Specifically, we evaluated the ability to generate easy-to-read sample reports and GEDmatch PRO reports, which can be directly uploaded to GEDmatch PRO.

Overall, we established that the Kintelligence workflow can respond to the specific needs of forensic sciences laboratories interested in performing FGG analysis.

References

[1] – Kennett, D. Using genetic genealogy databases in missing persons cases and to developsuspect leads in violent crimes. Forensic Sci. Int., 301 (2019) 107-117

[2] – Philips, C. The Golden State Killer investigation and the nascent field of forensic genealogy. Forensic Sci. Int. Genet., 36 (2018) 186-188