JOHNNY'S GOT A GUN, OR IS IT TOM, OR MAYBE BILL: COMBATING COMPLEX DNA MIXTURES OBTAINED FROM GUN SWABS UTILIZING THE PROBABILISTIC GENOTYPING SOFTWARE STRMIX™

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INTRODUCTION

Improvements in forensic deoxyribonucleic acid (DNA) analysis in recent years has led to the ability to produce DNA profiles from a wider variety of samples, including touch DNA. Touch DNA samples from swabbing of firearms are common submissions for forensic DNA laboratories in the United States. The nature of gun crime lends to frequent exchange of firearms and as such, DNA profiles obtained from firearms are often mixtures of two or more individuals. The combination of the low quantity of DNA obtained from touch samples and the numerous contributors to DNA profiles obtained from gun samples, results in complex DNA profiles that are often difficult to analyze using methods previously employed by DNA analysts. STRmix™ software uses a fully continuous approach to probabilistic genotyping to analyze mixtures that may have previously been reported as inconclusive.

DNA Labs International (DLI) acquired a STRmix™ license in May of 2015 and subsequently validated the software for casework use in accordance with the 2015 Scientific Working Group on DNA Analysis Methods (SWGDAM) guidelines for validation of probabilistic genotyping systems[1]. The validation of STRmix™ with the AmpF/STR® Identifiler® Plus profiling system was completed in December of 2015 and subsequently the first report utilizing the software was released in January of 2016. To date STRmix™ has been used by DNA Labs International in criminal cases covering eighteen jurisdictions and three countries. The effect of the implementation of STRmix™ on DNA mixture analysis of DNA profiles obtained from firearms will be discussed as well as an overview of results obtained from the first sixty-seven samples reported.

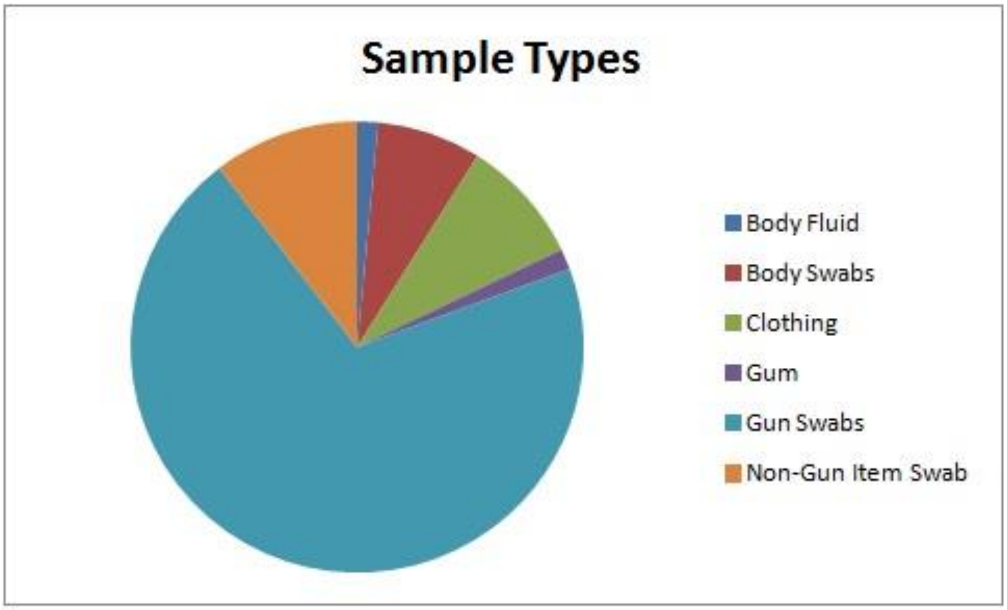
METHODS

All samples were extracted using Chelex® extraction process followed by phenol chloroform and Microcon® concentration or PrepFiler™ extraction on a Tecan Freedom EVO® 150 robotic workstation. Quantification was achieved utilizing the Applied Biosystems Quantiiler® Duo real time quantification platform. Amplification was carried out with the AmpF/STR® Identifiler® Plus using a full reaction with 28 cycles on a GeneAmp® PCR System 9700 Thermal Cycler. The amplification product was typed on an Applied Biosystems 3130*xl* Genetic Analyzer. Profile data was analyzed using the *GeneMapperID-X* analysis software version 1.4. The probabilistic genotyping software used was STRmix™ version 2.3.

RESULTS

To date fifty total cases have been reported that utilized STRmix™ analysis. A total of sixty-seven samples have been reported and of the sixty-seven samples, forty-seven were touch DNA swabs sampled from guns (see Figure 1). Furthermore, sixty-five of the sixty-seven samples would have been mixed profiles deemed completely inconclusive, or in which the major was suitable for comparison but the minor was inconclusive, without probabilistic genotyping capabilities. Many of the samples were analyzed against multiple persons of interest with STRmix™ analysis allowed for fifty-seven likelihood ratios that favored inclusion and nine likelihood ratios that favored exclusions of the person of interest. Additionally, two unknown offender profiles were developed from STRmix™ mixture deconvolution. Ninety-eight percent of cases that employ STRmix™ analysis result in a likelihood ratio (LR) with the remaining cases encompassing mixtures that will remain with the inconclusive determination.

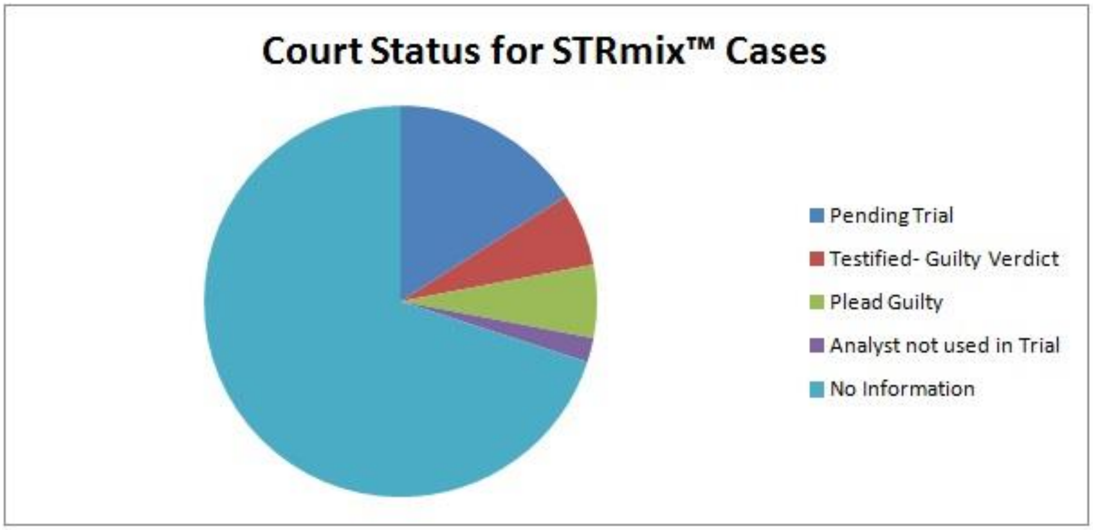
FIGURE 1: BREAKDOWN OF SAMPLE TYPES ANALYZED USING STRMIX™



STATUS IN THE LEGAL SYSTEM

All eyes in the forensic DNA community are on the pending probabilistic genotyping cases making their way through the legal system throughout the world currently. It is recognized by most that probabilistic genotyping is the future of DNA mixture interpretation[2,3] and now it is a matter of the technology being accepted in the court systems throughout the US and the rest of the world. Of the fifty cases reported by DLI thus far, two analysts have provided courtroom testimony in a total of three cases in three Florida counties. Four analysts have participated in numerous depositions and pre-trial hearings on STRmix™ evidence. Numerous cases still have trials pending where STRmix™ evidence will be presented (See Figure 2).

FIGURE 2: COURT STATUS FOR STRMIX™ CASES AT DLI



CONCLUSIONS

Laboratories across the nation frequently do not process samples from gun possession cases due to the limited and complex nature of the DNA profiles obtained. The experiences of DLI thus far with gun samples, after implementation of a probabilistic genotyping system, demonstrate that these often previously overlooked samples can now provide evidential value with current methods. Looking on to the future, DNA Labs International is working to accommodate profiling systems that support the expanded core set of short tandem repeat (STR) loci required by the Combined DNA Index System (CODIS) by January of 2017. Current validations of STRmix™ v2.4 with Promega PowerPlex® Fusion, Promega PowerPlex® Fusion 6C, Qiagen Investigator® 24plex QS, and the AmpF/STR® GlobalFiler® profiling systems are slated for completion by the end of the 2016 calendar year. Additionally, the AmpF/STR® Identifiler ® Plus kit will be revalidated for v2.4 of STRmix™. As more laboratories transition to using probabilistic genotyping systems and as these cases make their way through the legal system it will be the responsibility of DNA scientists to educate the criminal justice community, including police, attorneys and judges, on the changes in DNA mixture interpretation.

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