Rebecca Just
Report on Exchange Visit
ISFG Short-Term Fellowship, 2019

Rebecca Just traveled to Oslo, Norway August 3-10, 2019 to work at the Department of Forensic Sciences, Oslo University Hospital. The aim of the visit was to continue a collaborative project with Dr. Øyvind Bleka and Dr. Peter Gill (initiated in 2018) to develop and test methods for probabilistic genotyping of STR typing results developed using Massively Parallel Sequencing (MPS). During the visit, the researchers examined results from CaseSolver [1] interpretation of 60 mixtures (two, three and four-person, at a variety of total template inputs, donor template inputs and contributor ratios) typed using the ForenSeq DNA Signature Prep Kit (Verogen, Inc.). CaseSolver results obtained using both qualitative and quantitative interpretation models, and three different allele representations were compared to assess likelihood ratio changes for contributors and non-contributors, and the practical benefits of using differing amounts of sequence information. The researchers subsequently prepared a poster for presentation at the 28th Congress of the International Society for Forensic Genetics, as well as an extended abstract for the ISFG Congress Proceedings. On the basis of the results from this preliminary study, the researchers also discussed further collaborative work, including a) development of a web-accessible method for conversion of sequence strings to the LUS and LUS+ alleles [2,3] that can be interpreted in EuroForMix [4] and CaseSolver, and b) re-analysis of the mixture data using a static analytical threshold for re-interpretation in CaseSolver. The researchers are presently engaged in this work, and plan for future preparation of a full-length manuscript.

During the visit, Dr. Just also gave a presentation to researchers, caseworkers and other staff in the Department of Forensic Sciences, Oslo University Hospital on probabilistic interpretation of MPS-based STR typing results and the collaboration. Additionally, Dr. Just had the opportunity to meet with Dr. Eirik Hanssen to discuss results from Oslo University Hospital's validation of the ForenSeq system and considerations for casework use of the assay.

References

[1] Ø Bleka, L Prieto and P Gill. CaseSolver: An investigative open source expert system based on EuroForMix, Forensic.Sci.Int.Genet. 41 (2019) 83-92.

[2] RS Just and JA Irwin. Use of the LUS in sequence allele designations to facilitate probabilistic genotyping of NGS-based STR typing results, Forensic.Sci.Int.Genet. 34 (2018) 197-205.

[3] RS Just, J Le and JA Irwin. LUS+: Extension of the LUS designator concept to differentiate most sequence alleles for 27 STR loci, Submitted to Forensic.Sci.Int.Genet.

[4] Ø Bleka, G Storvik and P Gill, EuroForMix: An open source software based on a continuous model to evaluate STR DNA profiles from a mixture of contributors with artefacts, Forensic.Sci.Int.Genet. 21 (2016) 35-44.