

International Society for Forensic Genetics Short-term Fellowship Report

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On the 3rd – 10th April 2019 I visited the Małopolskie Centrum Biotechnologii (MCB) of the Jagiellonian University in Kraków to carry out work with Professor Wojciech Branicki and his team. The first aim was for us to identify areas for collaboration on the microbiome and metagenomics for use in forensics. We are currently in the process of writing a paper evaluating the current methods and tools applied to this field along with the challenges and considerations to ensure these methods are fit-for-purpose for the forensic community. The paper benefits from the input of forensic scientists, microbiologists and bioinformaticians to try and exhibit a well-rounded overview and strategy from sample collection through to data analysis.

Bioinformatics resources are very limited, but MCB are fortunate to have a dedicated team lead by Dr. Paweł Łabaj. Dr. Łabaj and I are part of the Metagenomics and Metadesign of Subways and Urban Biomes (MetaSUB) international consortium. The aims of the consortia are; to create geospatial metagenomic and forensic genetic maps, to identify and track antimicrobial resistance markers (AMRs) and identify novel biosynthetic gene clusters (BCGs) for drug discovery. Global city sampling day (gCSD) takes place on the 21st June annually where cities across the world take samples from their transit systems. My role within the consortium is as the sampling co-ordinator for London and we have been collecting samples since 2017. In London, 270 stations are sampled at 3 locations; a bench on the platform, a handrail or elevator button and a ticket machine. These swabs are then sent to the USA for sequencing. Currently we have all the sequencing data and some analysis of the samples has been carried out. Promising results have been obtained from the MetaSUB data both by ongoing analysis within the consortium as well as by external scientists taking part in the Metagenomic Forensics Challenge at the Critical Assessment of Massive Data Analysis (CAMDA) conference. Whilst I was at MCB, we started to construct a bioinformatics pipeline that could be used to analyse not only the MetaSUB data but could be used for any metagenomic or microbial sequencing data. Our priorities included ensuring the use of curated databases and full step-by-step documentation and tracking of each process. Once this has been finalised, the modelling team will help to create a model to try to predict the geolocation of where a sample originated from.

The work has already been presented internally at the King's College London Analytical, Environmental and Forensic Science PhD Symposium, where it was awarded best oral presentation. The work will be presented as a poster at the International Society for Forensic Genetics (ISFG) Conference in Prague and has been selected for an oral presentation at the International Symposium on Human Identification (ISHI), Palm Springs, California.