

ITC CONFERENCE GRANT SCIENTIFIC REPORT

This report is submitted for approval by the grantee to the MC Chair.

Action number: CA15203

Conference title: The 2018 Meeting of the English Speaking Working Group (ESWG)

Conference start and end date: 12/09/2018 to 15/09/2018

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Grantee name: Joanna Vella

ACTIVITIES DURING YOUR ATTENDANCE AT THIS CONFERENCE:

(max.500 words)

I attended the 2018 Meeting of the English Speaking Working Group (ESWG) of the International Society of Forensic Genetics (ISFG) in Saint Petersburg, Russia where I represented the University of Malta and delivered an oral presentation, "Mitochondrial DNA typing of the Maltese" which is part of my doctoral research. I am tracing the origins of the Maltese population through mitochondrial DNA analysis. This was the first time I was invited to deliver an oral presentation about my doctoral research at an international meeting. It gave me the opportunity to inform international colleagues of the COST Action MITOEAGLE and I acknowledged the ITC Conference Grant in my presentation.

I participated in three educational workshops about the use of non-autosomal DNA markers, the use of Massive Parallel Sequencing (MPS) in DNA testing and kinship analysis, and forensic reasoning. I also attended the members meeting of the ISFG English Speaking Working Group (ESWG).

Dr Martin Bodner from the Medical University of Innsbruck delivered the mitochondrial part of the non-autosomal DNA markers workshop which focused on mitochondrial DNA analysis, from sample collection, analysis, evaluation of sequencing results and the use of the English DNA Profiling (EDNAP) Group Mitochondrial DNA Population Database (EMPOP).

The oral presentations at the meeting covered the evolution and gender aspects of 'MITOEAGLE' Mitochondrial mapping: Evolution – Age – Gender – Lifestyle – Environment, with presentations covering population genetic research about different ethnic groups and the diversity of the most common european mitochondrial DNA haplogroup 'H'.

Attending the meeting and workshops was a golden opportunity for me to meet and hear world experts in the field of population genetics. It also proved to be an excellent chance to network with fellow researchers in the field of genetics with over 80 attendees from around the globe where I was the only Maltese.



IMPACT ON YOUR RESEARCH AND FUTURE COLLABORATIONS (if applicable)

(max.500 words)

Attending the non-autosomal DNA workshop was useful to learn more about the techniques used for mitochondrial DNA analysis including the use of Next Generation Sequencing (NGS) technology to research the mitochondrial genome.

I had the opportunity to meet my collaborator, Dr Martin Bodner from the Medical University of Innsbruck and had the opportunity to discuss further analysis of the complete mitochondrial genome to molecularly dissect the sub-clades of mitochondrial haplogroup 'H' of 34 Maltese samples which share the same mitochondrial control region haplotype using Next Generation Sequencing (NGS).

Dr Sascha Willuwit from Charite, Berlin and custodian of the Y-STR Haplotype Reference Database (YHRD) delivered the other part of the non-autosomal DNA markers workshop. He provided training on the use of the YHRD and how to estimate population frequencies of Y chromosome profiles. This will aid me in the analysis of Maltese Y chromosome haplotypes and how to upload data on the YHRD which is another part of my PhD project.

Dr David Ballard from King's College London, delivered the workshop on the use of Massive Parallel Sequencing (MPS) technology in DNA testing and kinship analysis with a focus on microhaplotype marker systems. Short Tandem Reapeat (STR) sequence data in population genetics and STR nomenclature were also discussed. This enhanced my understanding of the different NGS platforms available and I would like to use MPS technology and use some of the markers in my future laboratory work.

I also had the opportunity to speak to Dr Ballard and Prof Denise Syndercombe-Court from King's College London to discuss mitochondrial DNA analysis of my Maltese population cohort and the possibility of collaboration.

