STUDY OF LATIUM REGION POPULATIONS: FROM ENEOLITIC TO 15TH CENTURY CE

PhD Student: Valentina Meloni/ *Supervisor*: Prof. Olga Rickards / *Co-supervisor*: Dr. Flavio De Angelis

35th Cycle - A.Y. 2019/2020

During historical and prehistorical times, ancient Italy was characterized by a variety of population groups with different cultures and traditions. Each population had experienced different cultural and biological influences, both from outside the country and from exchanges between local groups. In addition, the peculiar and heterogeneous presence of different environments, climates and resources led to cultural and/or biological differentiation and even to the isolation of different groups.

The aim of this work is to apply a multidisciplinary approach to the study of Latium populations during the long period that spans from Eneolitic to 15th century CE. Starting from 2425 individual remains collected from 21 archaeological sites, it will be carried out a careful selection of about 100 individuals on the basis of accurate archaeological and anthropological information.

DNA extraction will be carried out on petrous bones (Pinhasi et al., 2015) and teeth, applying a specific and consolidated DNA extraction protocol (Malmström et al., 2009) that allows an efficient small fragments recovery. Bone powdering and extraction will be performed in dedicated clear room in order to avoid contaminations.

Extracted DNA will be used to build up genomic libraries to be sequenced using Illumina technology (Mayer and Kirker, 2010). Libraries will be prepared in four steps: (a) Blunt-End-Repair, (b) Adapter ligation, (c) Adapter-Fill-In and (d) Indexing PCR. Then they will be purified (using AMpure XP) to make a size selection of aDNA fragments and to remove by-products of previous reactions. A microfluidic electrophoresis run will be performed on Agilent Bioanalyser 2100 using *DNA High Sensitivity* kit to verify library size selection, fragments quality and quantity. In this way it is possible to fill out an Excel spreadsheet with library concentration and molarity, in order to calculate the right library amount necessary to build up an equimolar pool of 12-15 samples. Genomic libraries will be sequenced on Illumina MiSeq for a mtDNA screening run, to obtain preliminary information on genomic coverage and geographic origin information.

The best libraries in terms of endogenous DNA concentration, DNA damage patterns and contaminations, will be submitted to whole genome sequencing on Illumina HiSeq3000. Applying several bioinformatic tools, the reads will be processed and analysed to investigate family relationships, migration phenomena, heterozygosis percentage, revealing of mutation and annotation variants in order to obtain a demographic analysis.

During the whole genome sequencing it will be also investigated residence mobility and migration, using Sr and Pb isotope analysis. For this phase of the work a small amount of enamel will be removed from the first permanent molars and then it will be submitted to the isotope determinations by ICP-MS. From this analysis it should be possible to identify individuals that moved to a different region during their lifetime, since Sr and Pb present in the tooth enamel are deposited during the tooth formation phase and therefore their proportion reflect the local geology where the individual spent its childhood.

Finally, sequencing results will be triangulated both with the information collected by archaeologists and anthropologists who have studied burials and with the results of isotopic analysis. In this way, this study will make possible to characterize changes and history of the populations that lived in the Lazium region for a so broad range of time.

CONTRIBUTED PRESENTATIONS

2019

Valentina Meloni, Laura Lombardi, Roberta Aversa, Andrea Berti, Filippo Barni. Optimization of STR amplification down to single cell after DEPArrayTM Isolation. Presented at The 28th Congress of the International Society for Forensic Genetics. Prague, 9-14th September 2019. Poster presentation.

Valentina Meloni, Ignazio Ciuna, Mirella Bucciaglia, Andrea Berti. Evaluation of the Bone DNA Extraction kit and the Maxwell Instrument in Bone samples analysis. 20th European DNA Working Goup Meeting. 5th-7th of November 2019, Hamburg. Oral presentation.

Valentina Meloni, Ignazio Ciuna, Andrea Berti. Identification of human skeletal remains from a Second World War mass grave. 20th European DNA Working Goup Meeting. 5th-7th of November 2019, Hamburg. Oral presentation.

2018

Valentina Meloni, Laura Lombardi, Roberta Aversa, Ignazio Ciuna, Marco Gigliucci, Adolfo De Meo, Cesare Rapone, Andrea Berti. Optimization of the amplification procedure down to single cell after DEPArrayTM Isolation. 19th European Forensic DNA Working Group Meeting. 6th – 8th of November 2018, Athens, Greece. Oral presentation.

Laura Lombardi, Valentina Meloni, Roberta Aversa, Ignazio Ciuna, Marco Gigliucci, Adolfo De Meo, Cesare Rapone, Andrea Berti. BLOOD IN BLOOD: isolation and typing of single contributors after DEPArray™ separation. 19th European Forensic DNA Working Group Meeting. 6th – 8th of November 2018, Athens, Greece. Poster presentation.

PUBBLICATIONS

Valentina Meloni, Laura Lombardi, Roberta Aversa, Andrea Berti, Filippo Barni. Optimization of STR amplification down to single cell after DEPArrayTM Isolation. Forensic Science International: Genetics Supplement Series. 2019

M. Baldoni, A. Nardi, R. Lelli, M. Gnes, F. Ferraresi, V. Meloni, P. Cerino, S. Greco, G. Manenti, M. Angle, O. Rickards, C. Martinez-Labarga. Archaeo-biological reconstruction of the Italian medieval population of Colonna (8th–10th centuries CE). Journal of Archeological Science. 2016