Curriculum

Personal information

First name and Surname: Marco Rosario Capodiferro
Date and place of birth: 1987/04/25 Potenza (PZ) ITALY

Education

July 2014
Acquisition of licence to work as a Senior Biologist

October 2011–May 2014
Master's Degree in Applied Biomolecular Sciences at the University of Perugia, Italy. Vote 110/110 cum laude.
Thesis title: "The wild boar (*Sus scrofa*) mitogenome in Umbria: phylogenetic analyses of the 'Italian' clade D4 and a preliminary comparison with domestic pigs"
Supervisors: Prof. Alessandro Achilli and PhD Hovirag Lancioni

October 2006-October 2011
Bachelor's Degree in Biological Sciences at the University of Perugia, Italy. Vote 107/100.
Thesis title: "The Autophagy"
Supervisor: Prof. Carlo Cirotto

September 2001-July 2006
High School Degree at Scientific Lyceum "PierPaoloPasolini", Potenza, Italy.

Professional experience

October 2016-July 2018
Co-Supervisor for the Master's degree thesis of MSc. Nicola Rambaldi Migliore
▪ Master's Degree in "Molecular Biology and Genetics", University of Pavia.
▪ Thesis title: "Refining the genetic history of Panama through modern and ancient mitogenomes"

15 February 2018-15 April 2018
Scientific Visitor Estonian Biocentre, Tartu, Estonia
▪ Bioinformatic analysis of ancient whole genome row data
▪ Phylogenetic and phylogeographic analysis of Ancient genomes

24 July 2017–06 September 2017
Scientific Visitor University of Illinois, Urbana-Champaign, IL (USA)
▪Extraction of the DNA and building of the whole-genome library of 30 ancient samples from different kind of bones (petrous bones, femur, humerus and teeth)
▪Sequencing of 16 ancient complete genome with the Illumina HiSeq 4000
▪Preliminary bioinformatic approach to the study of the ancient complete genome

30 January 2017–30 March 2017
Scientific Visitor Institute for Legal Medicine, Innsbruck Medical University, Innsbruck (Austria)

▪Sequencing of 210 complete mitogenomes using the Ion Torrent PGM (Personal Genome Machine).
▪Analysis of NGS output data, following the guidelines of the International Society for Forensic Genetics (ISFG).
▪Phylogenetic analysis of 330 mitogenomes using various software, such as Mtphyl, PamlX, Beauti and Beast.

2017–Present
Subject Expert (Cultore della materia) for the course in "Molecular Genetics" Bachelor's degrees in Biotechnology
University of Pavia, Department of Biology and Biotechnology "L. Spallanzani"

2017–Present
Subject Expert (Cultore della materia) for the course in "Molecular Genetics Methodologies" Master degrees in Biological Sciences
University of Pavia, Department of Biology and Biotechnology "L. Spallanzani"

2017–2018
Tutor for the course in "Molecular Genetics Methodologies" Master degrees in Biological Sciences
University of Pavia, Department of Biology and Biotechnology "L. Spallanzani"

2017–2018
Tutor for the course in "Molecular Genetics" Bachelor's degrees in Biotechnology
University of Pavia, Department of Biology and Biotechnology "L. Spallanzani"

2016–2017
Tutor for the course in "Molecular Genetics" Bachelor's degrees in Biotechnology
University of Pavia, Department of Biology and Biotechnology "L. Spallanzani"

2016–2018
Lecture Speaker during the "Conservation Genetics" course
University of Pavia, Department of Earth and Environmental Sciences

April 2015-September 2015
Research contract (6 month) into the Laboratory of Population Genetics and Molecular Evolution, Department of Chemistry, Biology and Biotechnology, University of Perugia, Italy.
Project title: "Study and development of experimental protocols for the genetic characterization of wild boar in Umbria"

October 2013-May 2014
Internship into the Laboratory of Population Genetics and Molecular Evolution, Department of Chemistry, Biology and Biotechnology, University of Perugia, Italy.

January 2013-May 2013
Lab mentor's for biology class by the University of Perugia, Italy.

May 2011-October 2011
Internship into the laboratory of Cytology and Histology, Department of Cellular and Environmental Biology, University of Perugia, Italy.

Technical skills

▫ Human and animal DNA extraction
▫ Ancient DNA extraction
▫ DNA quantification
▫ DNA amplification (PCR)
▫ Electrophoresis analysis
▫ Sanger sequencing
▫ NGS sequencing (MiSeq, Ion PGM, HiSeq)
▫ NGS output analysis
▫ Sequence analysis
▫ Phylogenetic analysis (Network and Phylogenetic tree)
▫ Preparation of histological samples
▫ Histological staining

Computer skills

▪ Operating System Windows and Ubuntu
▪ Office Platform and R bases
▪ Competences in the use of the principal scientific search engine and database
▪ Competences in the use of software for sequence and phylogenetic analysis: ANGSD, GATK, Samtools, Bamtools, VFCtools, Plink, AdmixTools, Sequencer, Network, Mega, DNAsp, BioEdit, GenSyn, Beast, Beauty, PamelX, Geneious and other

Languages

Native language: Italian
Second language: English

Pavia, 31/07/2018
Marco Rosario Capodiferro