

INFORMAZIONI PERSONALI

**Claudio Ottoni**

TITOLO DI STUDIO

**Dottore di ricerca in Ecologia e Biologia Evoluzionistica**

ESPERIENZA PROFESSIONALE

15/08/2016-31/10/2018

**Post-doc research assistant**

Centre for Ecological and Evolutionary Synthesis, University of Oslo, Norway.

01/02/2009-31/12/2008

**Post-doc research assistant**

Centre for Archaeological Sciences, University of Leuven, Belgium.

01/07/2008-31/12/2008

**Assistente scientifico**

Laboratorio di genetica veterinaria UnireLab, Pomezia (Rome), Italy.

ISTRUZIONE E FORMAZIONE

Settembre 1998 – Giugno 2004

**Laurea in Scienze Biologiche**

Università di Roma Tor Vergata.

Ottobre 2004 – Giugno 2008

**Dottorato in Biologia Evoluzionistica ed Ecologia**

Università di Roma Tor Vergata, ciclo XX.

Titolo della tesi: “ Holocene human peopling of Libyan Sahara. Molecular analysis of maternal lineages in ancient and extant populations of Fezzan”

COMPETENZE PERSONALI

Lingua madre

Italiano

Altre lingue

	COMPRESIONE		PARLATO		PRODUZIONE SCRITTA
	Ascolto	Lettura	Interazione	Produzione orale	
Inglese	Avanzato	Avanzato	Avanzato	Avanzato	Avanzato
Francese	Intermedio	Intermedio	Intermedio	Intermedio	Intermedio

**Competenze professionali**

Sampling of ancient biological tissues (bones, teeth, mummified tissues, dental calculus). Extraction of DNA from ancient (skeletal and mummified tissues, dental calculus) and modern biological tissues (blood, FTA, hair, nails and mouth swab).

Amplification of DNA through PCR: singleplex and multiplex PCR techniques. Primers design. Real-Time PCR techniques: SYBR-Green and Probe-based methods (7500 Fast System, Applied Biosystems).

Electrophoresis techniques: agarose, acrylamide, microchip electrophoresis system (MultiNA, Shimadzu Biotech).

Molecular techniques for the screening of genetic variation: RFLP (Restriction Fragment Length Polymorphisms); SNaPshot (Applied Biosystems); DNA automated sequencing and fragment analysis (instruments used: ABI Prism 3100 Avant, ABI Prism 3130); Pyrosequencing techniques (PSQ-96 Biotage, PSQ-24 Qiagen).

Cloning of PCR products (TOPO-TA cloning kit by Invitrogen).

Amplicon and genomic libraries preparation methods, Bioanalyser 2100 (Agilent), Caliper LabChip XT, BluePippin, analysis of Next-Generation Sequencing platform data (IonTorrent PGM, Illumina HiSeq, Pacific Bioscience).

## Competenze informatiche

Population genetics data-analysis: Genetic distance methods, Multivariate Analysis (Multidimensional Scaling, Correspondence Analysis, Principal Component Analysis), Analysis of Molecular Variance (AMOVA). Phylogenetic analysis (Network, Maximum-likelihood and Bayesian phylogenetic trees). Command languages: extensive knowledge of Bash (building pipelines for NGS data analysis), knowledge of Python (parsing dataset and basic scripting) and R (data analysis with packages MASS, Vegan, ggplot2).

NGS data quality control and filtering: AdapterRemoval, Cutadapt, FastQC

Metagenomic analyses of NGS data: Kraken, Diamond, MALT, MEGAN, MetaPhlan, MetaBIT, Blast+ Alignment of DNA reads to reference genomes and variant calling (BWA, Picard, Samtools, GATK, Vcftools, Bedtools, Bcftools) and aDNA damage assessment (mapDamage, PMDtools).

Microbial genomic analysis: Prokka, RAST, RepeatMasker, RepeatModeller, RepeatScout, Mauve. Circular visualization of genomic data with Circos (in particular bacterial genomes).

Software for DNA sequence data manipulation, phylogenetic and population genetic analysis: Bioedit, Geneious, Arlequin, MrBayes, PhyML, Phylip, FigTree, Network, Statistica (Statsoft).

Population genomic analyses: working with Eigensoft file formats (Converf, Mergeit), PCA of genomic data with Smartpca. Genotype likelihood and unfolded/folded site-frequency-spectrum (SFS) analysis with ANGSD. Admixture analysis with NGSadmix.

De-novo genome assembly and visualization: SPAdes, QUAST, REAPR, IGV, UGENE.

Experience with working in high-performance computing clusters (Abel HPC, University of Oslo) and the Slurm queue system.

Other software: Adobe Illustrator, Microsoft Office.

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 ULTERIORI INFORMAZIONI

## Pubblicazioni

1. Wrobel A, **Ottoni C**, Leo JC, Linke D (2018). *pYR4 from a Norwegian isolate of Yersinia ruckeri is a putative virulence plasmid encoding both a type IV pilus and a type IV secretion system*. *Frontiers in Cellular and Infection Microbiology* 8, 373.
2. Larmuseau MHD & **Ottoni C** (2018). *Mediterranean Y-chromosome 2.0 – why the Y in the Mediterranean is still relevant in the postgenomic era*. *Annals of Human Biology*, 45 (1), 20-33. <https://doi.org/10.1080/03014460.2017.1402956>
3. Wrobel A, **Ottoni C**, Leo JC, Gulla S, Linke D (2017). *The repeat structure of two paralogous genes, Yersinia ruckeri invasin (yrlnv) and a “Y. ruckeri invasin-like molecule”(yrlim) sheds light on the evolution of adhesive capacities of a fish pathogen*. *Journal of Structural Biology*, 201 (2) , 171-183. <https://doi.org/10.1016/j.jsb.2017.08.008>
4. **Ottoni C**, Van Neer W, De Cupere B, Daligault J, Guimaraes S, Peters J, Spassov N, Prendergast ME, Boivin N, Morales A, Bălăşescu A, Becker C, Benecke N, Boronenant A, Buitenhuis H, Chahoud J, Crowther A, Llorente L, Manaseryan N, Monchott H, Onar V, Osypińska M, Putelat O, Quintana Morales E, Studer J, Wierer U, Decorte R, Grange T, Geigl EM (2017). *The paleogenetics of cat dispersal in the ancient world*. *Nature Ecology & Evolution*, 1 (7), 0139. Doi: 10.1038/s41559-017-0139
5. Primativo G, **Ottoni C**, Biondi G, Serafino S, Martínez-Labarga C, Larmuseau MHD, Scardi M, Decorte R, Rickards O (2017). *Bight of Benin: a maternal perspective of four Beninese populations and their genetic implications on the American populations of African ancestry*. *Annals of Human Genetics*. 81 (2), 78-90. Doi: 10.1111/ahg.12186
6. Thieren E, **Ottoni C**, Popović D, and Van Neer W (2016). *Inter- and intraspecific variation in the surface pattern of the dermal bones of two sturgeon species*. *Journal of Applied Ichthyology*, 32 (4), 609-628. doi: 10.1111/jai.13091
7. **Ottoni C**, Rasteiro R, Willet R, Claeys J, Talloen P, Van de Vijver K, Chikhi L, Poblome J, Decorte R (2016) *Comparing maternal genetic variation across two millennia reveals the demographic history of an ancient human population in southwest Turkey*. *R Soc Open Sci*, 3, 150250. doi: 10.1098/rsos.150250
8. Ivanova S, Gurova M, Spassov N, Hristova L, Tzankov N, Popov V, Marinova E, Makedonska J, Smith S, **Ottoni C**, Lewis M (2016) *Magura Cave, Bulgaria: a multidisciplinary study of Late Pleistocene human palaeoenvironment in the Balkans*. *Quaternary International*, 415, 86-108. doi:10.1016/j.quaint.2015.11.082
9. Larmuseau M, Vessi A, Jobling M, Van Geystelen A, Primativo G, Biondi G, Martínez-Labarga C, **Ottoni C**, Decorte R, Rickards O (2015) *The paternal landscape along the Bight of Benin – Testing regional representativeness of West-African population samples using Y-chromosomal markers*. *PLoS One*, 10 (11), e0141510.
10. Purps J, Siegert S, Willuweit S, Nagy M, Alves C, Salazar R, Angustia SM, Santos LH, Anslinger K, Bayer B, Ayub Q, Wei W, Xue Y, Tyler-Smith C, Bafalluy MB, Martinez-Jarreta B, Egyed B, Balitzki B, Tschumi S, Ballard D, Court DS, Barrantes X, Bassler G, Wiest T, Berger B, Niederstatter H, Parson W, Davis C, Budowle B, Burri H, Borer U, Koller C, Carvalho EF, Domingues PM, Chamoun WT, Coble MD, Hill CR, Corach D, Caputo M, D'Amato ME, Davison S, Decorte R, Larmuseau MH, **Ottoni C**, Rickards O, Lu D, Jiang C,

- Dobosz T, Jonkisz A, Frank WE, Furac I, Gehrig C, Castella V, Grskovic B, Haas C, Wobst J, Hadzic G, Drobnic K, Honda K, Hou Y, Zhou D, Li Y, Hu S, Chen S, Immel UD, Lessig R, Jakovski Z, Ilievka T, Klann AE, Garcia CC, de Knijff P, Kraaijenbrink T, Kondili A, Miniati P, Vouropoulou M, Kovacevic L, Marjanovic D, Lindner I, Mansour I, Al-Azem M, Andari AE, Marino M, Furfuro S, Locarno L, Martin P, Luque GM, Alonso A, Miranda LS, Moreira H, Mizuno N, Iwashima Y, Neto RS, Nogueira TL, Silva R, Nastainczyk-Wulf M, Edelmann J, Kohl M, Nie S, Wang X, Cheng B, Nunez C, Pancorbo MM, Olofsson JK, Morling N, Onofri V, Tagliabracci A, Pamjav H, Volgyi A, Barany G, Pawlowski R, Maciejewska A, Pelotti S, Pepinski W, Abreu-Glowacka M, Phillips C, Cardenas J, Rey-Gonzalez D, Salas A, Brisighelli F, Capelli C, Toscanini U, Piccinini A, Pigionica M, Baldassarra SL, Ploski R, Konarzewska M, Jastrzebska E, Robino C, Sajantila A, Palo JU, Guevara E, Salvador J, Ungria MC, Rodriguez JJ, Schmidt U, Schlauderer N, Saukko P, Schneider PM, Sirker M, Shin KJ, Oh YN, Skitsa I, Ampati A, Smith TG, Calvit LS, Stenzl V, Capal T, Tillmar A, Nilsson H, Turrina S, De Leo D, Verzeletti A, Cortellini V, Wetton JH, Gwynne GM, Jobling MA, Whittle MR, Sumita DR, Wolanska-Nowak P, Yong RY, Krawczak M, Nothnagel M, and Roewer L. (2014). *A global analysis of Y-chromosomal haplotype diversity for 23 STR loci*. *Forensic Sci Int Genet* 12:12-23. doi: [10.1016/j.fsigen.2014.04.008](https://doi.org/10.1016/j.fsigen.2014.04.008)
11. **Ottoni C**, Flink LG, Evin A, Geörg C, De Cupere B, Van Neer W, Bartosiewicz L, Linderholm A, Barnett R, Peters J, Decorte R, Waelkens M, Vanderheyden N, Ricaut FX, Hoelzel AR, Mashkour M, Mohaseb Karimlu AF, Sheikh Seno S, Daujat J, Brock F, Pinhasi R, Hongo H, Perez-Enciso M, Rasmussen M, Frantz L, Megens HJ, Crooijmans R, Groenen M, Arbuckle B, Benecke R, Strand Vidarsdottir U, Burger J, Cucchi T, Dobney K, Larson G. (2013) *Pig domestication and human-mediated dispersal in western Eurasia revealed through ancient DNA and geometric morphometrics*. *Mol Biol Evol*, 30 (4), 824-32. doi: 10.1093/molbev/mss261
  12. Linsele V, Riemer H, Baeten J, De Vos D, Marinova E, **Ottoni C**. (2013) *Species identification of archaeological dung remains. A critical review of possible methods*. *Env Archaeol*, 18 (1), 5-17. doi: 10.1179/1461410313Z.00000000019
  13. Larmuseau MHD, **Ottoni C**, Raeymaekers JAM, Vanderheyden N, Larmuseau HFM, Decorte R. (2011) *Temporal differentiation across a West-European Y-chromosomal cline – genealogy as full tool in human population genetics*. *Eur J Hum Genet* 20: 434-440. doi: 10.1038/ejhg.2011.218
  14. **Ottoni C**, Larmuseau MHD, Vanderheyden N, Martínez-Labarga C, Primativo G, Biondi G, Decorte R, Rickards O (2011) *Deep into the roots of the Libyan Tuareg: a genetic survey of their paternal heritage*. *Am J Phys Anthr* 145 (1): 118-124. doi: 10.1002/ajpa.21473
  15. **Ottoni C**, Ricaut FX, Vanderheyden N, Brucato N, Waelkens M, Decorte R (2011) *Mitochondrial analysis of a Byzantine population reveals the differential impact of multiple historical events in South Anatolia*. *Eur J Hum Genet* 19: 571-576. doi:10.1038/ejhg.2010.230
  16. **Ottoni C**, Primativo G, Kashani BH, Achilli A, Martínez-Labarga C, Biondi G, Torroni A, Rickards O (2010) *Mitochondrial haplogroup H1 in North Africa: An Early Holocene arrival from Iberia*. *Plos One* 5 (10), e13378. doi:10.1371/journal.pone.0013378
  17. Predazzi IM, Martínez-Labarga C, Vecchione L, Mango R, Ciccacci C, Amati F, **Ottoni C**, Crawford M, Rickards O, Romeo F, Novelli G (2009) *Ethnic differences in allele frequencies at the OLR1 locus may suggest geographic disparities in cardiovascular risk events*. *Ann Hum Biol* 37 (2): 136-148. doi: 10.3109/03014460903393857
  18. **Ottoni C**, Koon H, Collins MJ, Rickards O, Craig OE (2009) *Preservation of ancient DNA in (thermally) damaged archaeological animal bones*. *Naturwissenschaften* 96 (2): 267-278. doi: 10.1007/s00114-008-0478-5
  19. **Ottoni C**, Martínez-Labarga C, Vitelli L, Scano G, Fabrini E, Contini I, Biondi G, Rickards O (2009) *Human mitochondrial DNA variation in Southern Italy*. *Ann Hum Biol* 36 (6): 785-811. doi: 10.3109/03014460903198509
  20. **Ottoni C**, Martínez-Labarga C, De Angelis F, Trucchi E, Contini I, Biondi G, Di Lemia S, Loogväli EL, Pennarun E, Achilli A, Rickards O (2009) *First genetic insight into Libyan Tuareg: a maternal perspective*. *Ann Hum Genet* 73 (4): 438-448. doi: 10.1111/j.1469-1809.2009.00526.x
  21. Martínez-Labarga C, Lelli R, Tarsi T, Babalini C, De Angelis F, **Ottoni C**, Giambra V, Pepe G, Azzebi E, Frezza D, Biondi G, Rickards O (2007) *Polymorphism of the COL1A2, CYP1A1 and HS1,2 Ig enhancer in the Libyan Tuaregs from Libya*. *Ann Hum Biol* 34 (4): 425-436. doi: 10.1080/03014460701362356

- Corsi**
- "An introduction to bioinformatics tools for population genomic data analysis", University of Gothenburg, Tjällmo, Sweden, 6-10 November 2017.
  - "One-day workshop on automating tasks using Make", University of Oslo, Oslo, 9 Nov 2016.
  - "BBASH Next-Generation Sequencing Workshop", University of Leicester, Leicester, 1-3 Feb 2016.
  - "Image editing for scientific publications", University KU Leuven, Leuven, June 2015.
  - "Palaeogenomics", Summer school of CNRS (France), Cargese, France, 17-21 Oct 2011.
  - "Real Time PCR-SDS 7500" (Applied Biosystems). University of Rome "Tor Vergata", Rome, Italy.
  - Chemical and Biological risk". University of Rome "Tor Vergata", Rome, Italy.
  - "R and basic statistic in bio-medical sciences". University of Rome "Tor Vergata", Rome, Italy.
  - "R and Multivariate Analysis in bio-medical sciences". University of Rome "Tor Vergata", Rome, Italy.
  - "Writing scientific papers". University of Rome "Tor Vergata", Rome, Italy.