

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Cristian CAPELLI

eRA COMMONS USER NAME (credential, e.g., agency login):

POSITION TITLE: Associate Professor of Anthropology

EDUCATION/TRAINING (*Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.*)

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
University La Sapienza, Rome	BS	07/1996	Biology
Catholic University of Rome	PHD	02/2001	Medical Forensic Sciences
University College London	Postdoctoral	12/2001	Population genetics
Catholic University of Rome	Postdoctoral	12/2002	Population genetics

A. Personal Statement

I am Associate Professor of Anthropology, and my research is focused on the characterization of the genetic and genomic variation in populations of human and non-human primates, to reconstruct their structure and evolutionary history. My training includes molecular and computational biology and over the years I have conducted work in the field, to collect biological samples for DNA analysis. These experiences have given me an understating of the complexity of the different steps involved in developing and coordinating population/evolutionary genetics projects, from the gathering of samples to their data analysis. I have coordinated projects involving several national and international collaborators, postdocs and PhD students, which have led to high profile publications. The current proposal stems from ongoing projects and is based on expertise gathered from two decades of population genetics research; this has provided me with the theoretical, technical and managerial skills required for successfully carrying out the research here proposed. Ongoing and recently completed projects led as PI and relevant for this application include:

2017-2018	Boise Trust Fund (UK): "Modelling hominin gene-flow along the rift valley: baboon genome variation in Gorongosa National Park, Mozambique".
2019-2020	Boise Trust Fund (UK): "Modelling hominin population structure in Southern Africa: genome variation in <i>P. ursinus</i> morphotypes"
2019-2020	John Fell Fund (UK) "The evolutionary history of chacma baboons (<i>Papio ursinus</i>)"
2021-2022	EASI Genomics (European Consortium) "Mind the GAP: comparing genotypes and phenotypes in assigning specimen to species-insights from <i>Papio</i> "
2021-2022	Leakey Foundation (USA) "The Y chromosome evolutionary history of <i>Papio</i> "
2024-2025	Leakey Foundation (USA) "The evolutionary history of <i>Theropithecus gelada</i> : population structure, gene flow and climatic changes"

B. Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments

- 2020-ongoing Associate Professor of Anthropology, Department of Chemistry, Life Sciences and Environmental Sustainability, University of Parma
Honorary Fellow, St Hugh's College, Oxford
- 2014-2020 Associate Professor of Human Evolution, Dept. of Zoology, University of Oxford, UK
- 2006-2014 Lecturer in Human Evolution, Dept. of Zoology, University of Oxford, UK
- 2006-2020 Tutorial Fellow and Director of Studies for Human Sciences, St Hugh's College, Oxford, UK
- 2004-2006 Technical Support Scientist, Genetic Identity Europe, Promega Corporation, Italy
- 2003-2004 Technician, Institute of Legal Medicine, Università Cattolica, Rome, Italy
- 2002-2003 Field Force, Abbott Laboratories, Italy
- 2001-2002 Postdoctoral Research Fellow, Institute of Legal Medicine, Università Cattolica, Rome, Italy
- 2001 Postdoctoral Research Fellow, Galton Laboratory, UCL, UK
- 1999-2000 PhD Visiting student, Galton Laboratory, UCL, London, UK (Supervisor: GB Goldstein)
- 1998 PhD Visiting Student, Dept. of Zoology, LMU, Munich, Germany (Supervisor: S Paabo)

Honors

- 2010 International Prize for Physical Anthropology "Fabio Frassetto", Accademia Nazionale dei Lincei, Italy

C. Contributions to Science

1. My early publications focused on the analysis of uniparental markers, primarily Y chromosome, in human populations. These publications on African and European populations provided the ground for developing subsequent genome-wide projects, building upon related results and collaborations. Among these, the most significant (as first or last author) have been:
 - a. Marks, S.J., Montinaro, F., Levy, H., Brisighelli, F., Ferri, G., Bertoncini, S., Batini, C., Busby, G.B.J., Arthur, C., Mitchell, P., Stewart, B.A., Oosthuizen, O., Oosthuizen, E., D'Amato, M.E., Davison, S., Pascali, V., **Capelli, C.** Static and Moving Frontiers: The Genetic Landscape of Southern African Bantu-Speaking Populations (2015) *Molecular Biology and Evolution*, 32 (1), pp. 29-43.
 - b. Marks, S.J., Levy, H., Martinez-Cadenas, C., Montinaro, F., **Capelli, C.** Migration distance rather than migration rate explains genetic diversity in human patrilocal groups (2012) *Molecular Ecology*, 21 (20), pp. 4958-4969.
 - c. Busby, G.B.J., Brisighelli, F., Sánchez-Diz, P., Ramos-Luis, E., Martinez-Cadenas, C., Thomas, M.G., Bradley, D.G., Gusmão, L., Winney, B., Bodmer, W., Vennemann, M., Coia, V., Scarnicci, F., Tofanelli, S., Vona, G., Ploski, R., Vecchiotti, C., Zemunik, T., Rudan, I., Karachanak, S., Toncheva, D., Anagnostou, P., Ferri, G., Rapone, C., Hervig, T., Moen, T., Wilson, J.F., **Capelli, C.** The peopling of Europe and the cautionary tale of Y chromosome lineage R-M269 (2012) *Proceedings of the Royal Society B: Biological Sciences*, 279 (1730), pp. 884-892.
 - d. Batini, C., Ferri, G., Destro-Bisol, G., Brisighelli, F., Luiselli, D., Sánchez-Diz, P., Rocha, J., Simonson, T., Brehm, A., Montano, V., Elwali, N.E., Spedini, G., D'Amato, M.E., Myres, N., Ebbesen, P., Comas, D., **Capelli, C.** Signatures of the preagricultural peopling processes in sub-

saharan africa as revealed by the phylogeography of early y chromosome lineages (2011) *Molecular Biology and Evolution*, 28 (9), pp. 2603-2613.

- e. **Capelli, C.**, Onofri, V., Brisighelli, F., Boschi, I., Scarnicci, F., Masullo, M., Ferri, G., Tofanelli, S., Tagliabracci, A., Gusmao, L., Amorim, A., Gatto, F., Kirin, M., Merlitti, D., Brion, M., Vereza, A.B., Romano, V., Cali, F., Pascali, V. Moors and Saracens in Europe: Estimating the medieval North African male legacy in southern Europe (2009) *European Journal of Human Genetics*, 17 (6), pp. 848-852.
 - f. **Capelli, C.**, Brisighelli, F., Scarnicci, F., Arredi, B., Caglia', A., Vetrugno, G., Tofanelli, S., Onofri, V., Tagliabracci, A., Paoli, G., Pascali, V.L. Y chromosome genetic variation in the Italian peninsula is clinal and supports an admixture model for the Mesolithic-Neolithic encounter (2007) *Molecular Phylogenetics and Evolution*, 44 (1), pp. 228-239.
 - g. **Capelli, C.**, Redhead, N., Abernethy, J.K., Gratrix, F., Wilson, J.F., Moen, T., Hervig, T., Richards, M., Stumpf, M.P.H., Underhill, P.A., Bradshaw, P., Shaha, A., Thomas, M.G., Bradman, N., Goldstein, D.B. A Y chromosome census of the British Isles (2003) *Current Biology*, 13 (11), pp. 979-984.
 - h. **Capelli, C.**, Wilson, J.F., Richards, M., Stumpf, M.P.H., Gratrix, F., Oppenheimer, S., Underhill, P., Pascali, V.L., Ko, T.-M., Goldstein, D.B. A predominantly indigenous paternal heritage for the Austronesian-speaking peoples of insular Southeast Asia and Oceania (2001) *American Journal of Human Genetics*, 68 (2), pp. 432-443.
2. Over the years I have worked on several occasion on the molecular characterizations of historical and ancient human and non-humans remains. These investigations have complemented my work on modern populations and have led to interesting developments at the interface between forensic and population genetics, still ongoing.
- a. Saupe T, Montinaro F, Scaggion C, Carrara N, Kivisild T, D'Atanasio E, Hui R, Solnik A, Lebrasseur O, Larson G, Alessandri L, Arienzo I, De Angelis F, Rolfo MF, Skeates R, Silvestri L, Beckett J, Talamo S, Dolfini A, Miari M, Metspalu M, Benazzi S, **Capelli C**, Pagani L, Scheib CL. Ancient genomes reveal structural shifts after the arrival of Steppe-related ancestry in the Italian Peninsula. *Curr Biol*. 2021 Jun 21;31(12):2576-2591.
 - b. Caramelli, D., Lalueza-Fox, C., **Capelli, C.**, Lari, M., Sampietro, M.L., Gigli, E., Milani, L., Pilli, E., Guimaraes, S., Chiarelli, B., Marin, V.T.W., Casoli, A., Stanyon, R., Bertranpetit, J., Barbujani, G. Genetic analysis of the skeletal remains attributed to Francesco Petrarca (2007) *Forensic Science International*, 173 (1), pp. 36-40.
 - c. Verginelli, F., **Capelli, C.**, Coia, V., Musiani, M., Falchetti, M., Ottini, L., Palmirotta, R., Tagliacozzo, A., De Grossi Mazzorin, I., Mariani-Costantini, R. Mitochondrial DNA from prehistoric canids highlights relationships between dogs and South-East European wolves (2005) *Molecular Biology and Evolution*, 22 (12), pp. 2541-2551.
 - d. **Capelli, C.**, Tschentscher, F., Pascali, V.L. "Ancient" protocols for the crime scene?: Similarities and differences between forensic genetics and ancient DNA analysis (2003) *Forensic Science International*, 131 (1), pp. 59-64.
 - e. Hofreiter, M., **Capelli, C.**, Krings, M., Waits, L., Conard, N., Münzel, S., Rabeder, G., Nagel, D., Paunovic, M., Jambresí, G., Meyer, S., Weiss, G., Pääbo, S. Ancient DNA analyses reveal high mitochondrial DNA sequence diversity and parallel morphological evolution of late pleistocene cave bears (2002) *Molecular Biology and Evolution*, 19 (8), pp. 1244-1250.
 - f. Krings, M., **Capelli, C.**, Tschentscher, F., Geisert, H., Meyer, S., Von Haeseler, A., Grossschmidt, K., Possnert, G., Paunovic, M., Pääbo, S. A view of Neandertal genetic diversity (2000) *Nature Genetics*, 26 (2), pp. 144-146.
 - g. Greenwood, A.D., **Capelli, C.**, Possnert, G., Pääbo, S. Nuclear DNA sequences from late pleistocene megafauna (1999) *Molecular Biology and Evolution*, 16 (11), pp. 1466-1473. e12. doi: 10.1016/j.cub.2021.04.022. Merry, R. & Jensen, J.L. (2015).
3. In the last decade I transitioned to genome-based investigation of human variation in African and European population. My main interest is characterizing the role of gene flow, ancient and recent, in shaping patterns

of distribution of variation across populations. Many of these investigations developed from fieldwork conducted in Lesotho, Namibia and South Africa. Key publications include:

- a. Daniels RJ, D'Amato ME, Lesaoana M, Kasu M, Ehlers K, Chauke PA, Lecheko P, Challis S, Rockett K, Montinaro F, González-Santos M, **Capelli C**. Genetic heritage of the Baphuthi highlights an over-ethnicized notion of "Bushman" in the Maloti-Drakensberg, southern Africa. *Am J Hum Genet*. 2023 May 4;110(5):880-894.
 - b. González-Santos M, Montinaro F, Grollemund R, Marnetto D, Atadzhanov M, May CA, Mabunda N, de Maret P, Oosthuizen O, Oosthuizen E, **Capelli, C**. Exploring the relationships between genetic, linguistic and geographic distances in Bantu-speaking populations. *American Journal of Biological Anthropology*, 2022 179(1), 104– 117.
 - c. Raveane A, Aneli S, Montinaro F, Athanasiadis G, Barlera S, Birolo G, Boncoraglio G, Di Blasio AM, Di Gaetano C, Pagani L, Parolo S, Paschou P, Piazza A, Stamatoyannopoulos G, Angius A, Brucato N, Cucca F, Hellenthal G, Mulas A, Peyret-Guzzon M, Zoledziewska M, BaaliA, Bycroft C, Cherkaoui M, Dina C, Dugoujon JM, Galan P, Gienza J, Kivisild T, Melhaoui M, Metspalu M, Myers S, Pereira L, Ricaut FX, Brisighelli F, Cardinali I, Grugni V, Lancioni H, Pascali VL, Torroni A, Semino O, Matullo G, Achilli A, Olivieri A, **Capelli C**. Population structure of modern-day Italians reveals patterns of ancient and archaic ancestries in Southern Europe. *Sci Adv*. 2019 Sep 4;5(9):eaaw3492.
 - d. Montinaro, F., Busby, G.B.J., Gonzalez-Santos, M., Oosthuizen, O., Oosthuizen, E., Anagnostou, P., Destro-Bisol, G., Pascali, V.L., **Capelli, C**. Complex ancient genetic structure and cultural transitions in Southern African populations (2017) *Genetics*, 205 (1), pp. 303-316.
 - e. González-Santos, M.G., Montinaro, F., Oosthuizen, O., Oosthuizen, E., Busby, G.B.J., Anagnostou, P., Destro-Bisol, G., Pascali, V., **Capelli, C**. Genome-Wide snp analysis of southern african populations provides new insights into the dispersal of bantu-Speaking groups (2015) *Genome Biology and Evolution*, 7 (9), pp. 2560-2568.
 - f. Montinaro, F., Busby, G.B.J., Pascali, V.L., Myers, S., Hellenthal, G., **Capelli, C**. Unravelling the hidden ancestry of American admixed populations (2015) *Nature Communications*, 6, art. no. 6596.
 - g. Busby, G.B.J., Hellenthal, G., Montinaro, F., Tofanelli, S., Bulayeva, K., Rudan, I., Zemunik, T., Hayward, C., Toncheva, D., Karachanak-Yankova, S., Nesheva, D., Anagnostou, P., Cali, F., Brisighelli, F., Romano, V., Lefranc, G., Buresi, C., Ben Chibani, J., Haj-Khelil, A., Denden, S., Ploski, R., Krajewski, P., Hervig, T., Moen, T., Herrera, R.J., Wilson, J.F., Myers, S., **Capelli, C**. The role of recent admixture in forming the contemporary West Eurasian genomic landscape (2015) *Current Biology*, 25 (19), pp. 2518-2526.
4. More recently I have opened a new line of research focusing on the evolutionary history of non-human primates. As part of this work we have investigated three main genera: *Papio*, *Theropithecus* and *Eulemur*. Our aim is to characterize the degree of population structure present within this genera, integrating genomic data with morphometric analysis and paleoclimate reconstruction. Our goal is to understand how population structure is reflected at morphological level within and across species, as well as identify population/species adaptive phenotypes ultimately shaped by climate.
- a. D'Ercole, J., S. Bertoncini, M. Gianni, L. Taglioli, F. Brisighelli, M. Campera, J.-B. Ramanamanjato, C. Tsagnangara, **C. Capelli**, G. Donati, and S. Tofanelli. 2024. Long-term genetic monitoring of a translocated population of collared brown lemurs. *Journal of Wildlife Management* 88:e22500
 - b. Mutti G, Oteo-Garcia G, Caldon M, da Silva MJF, Minhós T, Cowlshaw G, Gottelli D, Huchard E, Carter A, Martinez FI, Raveane A, **Capelli C**. Assessing the recovery of Y chromosome microsatellites with population genomic data using *Papio* and *Theropithecus* genomes. *Sci Rep*. 2023 Aug 24;13(1):13839.
 - c. Santander C, Molinaro L, Mutti G, Martínez FI, Mathe J, Ferreira da Silva MJ, Caldon M, Oteo-Garcia G, Aldeias V, Archer W, Bamford M, Biro D, Bobe R, Braun DR, Hammond P, Lüdecke T, Pinto MJ, Meira Paulo L, Stalmans M, Regala FT, Bertolini F, Moltke I, Raveane A, Pagani L, Carvalho S, **Capelli C**. Genomic variation in baboons from central Mozambique unveils complex evolutionary relationships with other *Papio* species. *BMC Ecol Evol*. 2022 Apr 11;22(1):44. doi: 10.1186/s12862-022-01999-7.

- d. Martinez FI, **Capelli C**, Ferreira da Silva MJ, Aldeias V, Alemseged Z, Archer W, Bamford M, Biro D, Bobe R, Braun DR, Habermann JH, Lüdecke T, Madiquida H, Mathe J, Negash E, Paulo LM, Pinto M, Stalmans M, Tátá F, Carvalho S A missing piece of the Papio puzzle: Gorongosa baboon phenostucture and their relationships with Papio species. J Hum Evol. 2019 May;130:1-20.
- e. Bertoncini S, D'Ercole J, Brisighelli F, Ramanamanjato JB, **Capelli C**, Tofanelli S, Donati G. Stuck in fragments: Population genetics of the Endangered collared brown lemur Eulemur collaris in the Malagasy littoral forest. (2017) American Journal of Physical Anthropology, 163(3):pp542-552.

The complete List of Publications (98) can be recovered from SCOPUS (ID: 7004189634).

ORCID: 0000-0001-9348-9084