

## PERSONAL INFORMATION

- Bertorelle, Giorgio, Associate Professor in Genetics, University of Ferrara, Italy
- Scopus Author ID: 7004271582
- Email: ggb@unife.it; Website of the group: [is.gd/popgg](http://is.gd/popgg)

## RESEARCH INTERESTS AND PROJECTS

The study of genetic and genomic variation to i) reconstruct evolutionary and demographic processes in different species, and ii) identify the impact of human activities on genetic biodiversity in different species and suggest management and conservation strategies. Some current projects are described at <https://sites.google.com/unife.it/popgg/home/research>. A recently funded projects started in 2020 on the genomic susceptibility to extinction in five Italian endemic species, with the creation of an Italian consortium in conservation genomics, is described at [www.endemics.it](http://www.endemics.it).

## PUBLICATIONS

101 scientific publication, 94 in ISI journals (cited 4319 times according to Scopus) 7 book chapters, and 1 edited book; H-index: 36 (according to Scopus)

## RESEARCH ACHIEVEMENTS

Theoretically, I contributed to the transition in population genetics from the analysis of classical allozyme markers, to DNA sequences and microsatellites, and to the most recent genomic data, especially with the use of computer simulations (e.g. Approximate Bayesian Computation). I also analysed the potential risks of using genetic data to infer demographic patterns when the model assumed by a statistical method (e.g. a neutrality test) is violated (e.g. the mutational model is wrong or the family size is not Poisson distributed), and I contributed to the development of efficient and user-friendly methods to facilitate the use of genetics in conservation biology (e.g. the online software SPOTG).

Empirically, I provided new hypotheses regarding the evolutionary history, the demographic dynamic, and the selective pattern, in several species using both modern and ancient data on genetic and genomic variation. Examples include the study of human migrations, the impact and the history of domestication in cattle, pigs and beans, the effects of the glaciations on the genetic structure and the geographic patterns in three Antarctic fish species, the genetic risks of extinction in a toad and a tortoise species affected by recent human activities, the identification of the genes under selection during the transition from oviparity to ovo-viviparity in a lizard and during the bean domestication, and the reconstruction of the impact of drift and selection drift on genes and genomes in the Apennine brown bear.

Management. I have a long-term experience in managing multi-packages projects involving several people and co-authors (research, citizen science, spin-off, scientific societies, workshops and schools; see below)

### Grant evaluation panels

2020 European Commission, ERC Synergy Grants

2020 Vinci Grant, Université Franco-Italienne

2020 PhD grants, National Institute of Marine Biology Ecology and Biotechnology, Italy

2018 University of Camerino, Italy

2016 FNRS, Belgium; Royal Society, UK; BBSRC, Research Council, UK

2015 DFG, Deutsche Forschungsgemeinschaft; Italian Research Evaluation System (VQR 2011-2014)

2014 Danish Agency for Science, Technology and Innovation; EPHE, France; University of Padova; University of Insubria

2012 DFG, Deutsche Forschungsgemeinschaft

2011 NERC, Natural Environment Research Council, UK; Austrian Science Fund; Italian Ministry for Education, University and Research (PRIN funds); Italian Research Evaluation System (VQR 2004-2010)

2010 Austrian Science Fund; Marsden Fund, New Zealand Government

2009,2008 University of Padova, Italy

2007 European Commission, Seventh Framework Programme, Projects Ideas; Estonian Science Foundation

2005 Netherlands Organization for Scientific Research

2004 European Commission, Sixth Framework Programme. Projects NEST

## PUBLICATIONS

Iannucci A, Benazzo A, Natali C, Arida EA, Arifin Zein MS, Jessop TS, Bertorelle G, Ciofi C. 2021. Population structure, genomic diversity and demographic history of Komodo dragons inferred from whole-genome sequencing. *Molecular Ecology*, Accettato per la pubblicazione (si veda Allegato X).

Torres Villaca S, Piccinno R, Rota-Stabelli O, Gabrielli M, Benazzo A, Matschiner M, Soares LS, Bolten AB, Bjorndal KA, Bertorelle G. 2021. Divergence and hybridization in sea turtles: inferences from genome data show evidence of ancient gene flow between species. *Molecular Ecology*, Accettato per la pubblicazione (si veda Allegato X).

Trucchi E, Benazzo A, Lari M, Iob A, Vai S, Nanni L, Bellucci E, Bitocchi E, Xu C, Jackson S, Lema V, Babot P, Oliszewski N, Gil A, Neme G, Michieli Catalina T, De Lorenzi M, Calcagnile L, Caramelli D, Star B, de Boer H, Boessenkool S, Papa R, Bertorelle G. 2021. Ancient genomes reveal early Andean farmers selected common beans while preserving diversity. *Nature Plants*, 7, 123-128.

Trucchi E, Gratton P, Mafessoni F, Motta S, Cicconardi F, Bertorelle G, D'Annessa I, Di Marino D. 2021. Population dynamics and structural effects at short and long range support the hypothesis of the selective advantage of the G614 SARS-Cov2 spike variant. *Molecular Biology and Evolution*, 38:1966-1979.

Biello R, Zampiglia M, Corti C, Deli G, Biaggini M, Crestanello B, Delaugerre M, Di Tizio L, Leonetti Francesco L, Stefano C, Olivieri O, Pellegrino F, Romano A, Sperone E, Hauffe Heidi C, Trabalza-Marinucci M, Bertorelle G, Canestrelli D. 2021. Mapping the geographic origin of captive and confiscated Hermann's tortoises: A genetic toolkit for conservation and forensic analyses. *Forensic Science International: Genetics*, 2021, 51, 102447.

Jike W, Li M, Zadra N, Barbaro E, Sablok G, Bertorelle G, Rota-Stabelli O, Varotto C. 2020 Phylogenomic proof of recurrent demipolyploidization and evolutionary stalling of the "triploid bridge" in arundo (Poaceae). *International Journal of Molecular Sciences*, 21, 1-22.

Raffini F, Bertorelle G, Biello R, D'Urso G, Russo D, Bosso L. 2020. From Nucleotides to Satellite Imagery: Approaches to Identify and Manage the Invasive Pathogen *Xylella fastidiosa* and Its Insect Vectors in Europe. *Sustainability*, 12, 4508.

Jike W, Sablok G, Bertorelle G, Li M, Varotto C. 2018. In silico identification and characterization of a diverse subset of conserved microRNAs in bioenergy crop *Arundo donax* L. *Scientific Reports*, 8, 16667.

Barlow A, Cahill JA, Hartmann S, Theunert C, Xenikoudakis G, Fortes GG, Paijmans JLA, Rabeder G, Frischauf C, Grandal A, Garcia-Vazquez A, Murtskhvaladze M, Saarma U, Anijalg P, Skrbinsek T, Bertorelle G, Gasparian B, Bar-Oz G, Pinhasi R, Slatkin M, Dalen L, Shapiro B, Hofreiter M. 2018. Partial genomic survival of cave bears in living brown bears. *Nature Ecology and Evolution*, 2, 1563–1570.

Fuselli S, Baptista RP, Panziera A, Magi A, Guglielmi S, Tonin R, Benazzo A, Bauzer LG, Mazzoni CJ, Bertorelle G. 2018. A new hybrid approach for MHC genotyping: high-throughput NGS and long read MinION nanopore sequencing, with application to the non-model vertebrate Alpine chamois (*Rupicapra rupicapra*). *Heredity*, 121, 293–303.

Cornetti L, Griffith OW, Benazzo A, Panziera A, Whittington CM, Thompson MB, Vernesi C, Bertorelle G. 2018. Candidate genes involved in the evolution of viviparity: a RAD sequencing experiment in the lizard *Zootoca vivipara* (Squamata: Lacertidae). *Zoological Journal of the Linnean Society*, 183, 196-207.

Benazzo A, Trucchi E, Cahill JA, Maisano Delser P, Mona S, Fumagalli M, Bunnefeld L, Cornetti L, Ghirotto S, Girardi M, Ometto L, Panziera A, Rota-Stabelli O, Zanetti E, Karamanlidis A, Groff C, Paule L, Gentile L, Vilà C, Vicario S, Boitani L, Orlando L, Fuselli S, Vernesi C, Shapiro B, Ciucci P, Bertorelle G. 2017. Survival and divergence in a small group: The extraordinary genomic history of the endangered Apennine brown bear stragglers. *Proceedings of the National Academy of Science USA*, 114: E9589-E9597.

Bitocchi E, Rau D, Benazzo A, Bellucci E, Goretti D, Biagetti E, Panziera A, Laidò G, Rodriguez M, Gioia T, Attene G, McClean P, Lee RK, Jackson SA, Bertorelle G, Papa R. 2016. High level of nonsynonymous changes in common bean suggests that selection under domestication increased functional diversity at target traits. *Frontiers in Plant Science*, 7, n.2005.

Canu A, Villaca ST, Iacolina L, Apollonio M, Bertorelle G, Scandura M. 2016. Lack of polymorphism at the MC1R wild-type allele and evidence of domestic allele introgression across European wild boar populations. *Mammalian Biology*, 81, 477-479.

Cristofari R, Bertorelle G, Ancel A, Benazzo A, Le Maho Y, Ponganis PJ, Stenseth NC, Trathan PN, Whittington JD, Zanetti E, Zitterbart DP, Le Bohec C, Trucchi E. 2016. Full circumpolar migration ensures evolutionary unity in the Emperor penguin. *Nature Communications*, 7, n.11842.

Cornetti L, Benazzo A, Hoban S, Vernesi C, Bertorelle G. 2016. Ancient, but not recent, population declines have had a genetic impact on alpine yellow-bellied toad populations, suggesting potential for complete recovery. *Conservation Genetics*, 17, 727-743.

Zenboudji S, Cheylan M, Arnal V, Bertolero A, Leblois R, Astruc G, Bertorelle G, Pretus JL, Lo Valvo M, Sotgiu G, Montgelard C. 2016. Conservation of the endangered Mediterranean tortoise *Testudo hermanni hermanni*: The contribution of population genetics and historical demography. 2016. *Biological Conservation*, 195, 279-291.

Vernesi C, Hoban SM, Pecchioli E, Crestanello B, Bertorelle G, Rosà R, Hauffe HC. 2016. Ecology, environment and evolutionary history influence genetic structure in five mammal species from the Italian Alps. *Biological Journal of the Linnean Society*, 117, 428-446.

Vai S, Vilaça ST, Romandini M, Benazzo A, Visentini P, Modolo M, Bertolini M, MacQueen P, Austin J, Cooper A, Caramelli D, Lari M, Bertorelle G. 2015. The Biarzo case in northern Italy: is the temporal dynamic of swine mitochondrial DNA lineages in Europe related to domestication? *Scientific Reports*, 5, art. no. 16514.

Fusco G, Leśniewska M, Congiu L, Bertorelle G. 2015. Population genetic structure of a centipede species with high levels of developmental instability. *PLoS ONE*, 10, art. no. e0126245.

Cornetti L, Belluardo F, Ghielm, S, Giovine G, Ficetola GF, Bertorelle G, Vernesi C, Hauffe HC. 2015. Reproductive isolation between oviparous and viviparous lineages of the Eurasian common lizard *Zootoca vivipara* in a contact zone. *Biological Journal of the Linnean Society*, 114, 566-573.

Benazzo A, Panziera A, Bertorelle G. 2015. 4P: fast computing of population genetics statistics from large DNA polymorphism panels. *Ecology and Evolution*, 5, 172-175.

Hoban S, Arntzen W, Bruford M, Godoy J, Hoelzel A, Segelbacher G, Vilà C, Bertorelle, G. 2014. Comparative evaluation of potential indicators and temporal sampling protocols for monitoring genetic erosion. *Evolutionary Applications*, 7, 984-998.

Scliar MO, Gouveia MH, Benazzo A, Ghirotto S, Fagundes NJ, Leal TP, Magalhães WC, Pereira L, Rodrigues MR, Soares-Souza GB, Cabrera L, Berg DE, Gilman RH, Bertorelle G, Tarazona-Santos, E. 2014. Bayesian inferences suggest that Amazon Yunga Natives diverged from Andeans less than 5000 ybp: Implications for South American prehistory. *BMC Evolutionary Biology*, 14, art. no. 174.

Kutanan,W, Ghirotto S, Bertorelle G, Srithawong S, Srithongdaeng K, Pontham N, Kangwanpong D. 2014. Geography has more influence than language on maternal genetic structure of various northeastern Thai ethnicities. *Journal of Human Genetics*, 59, 512-520.

Bellucci E, Bitocchi E, Ferrarin, A, Benazzo A, Biagetti E, Klie S, Minio A, Rau D, Rodriguez M, Panziera A, Venturini L, Attene G, Albertini E, Jackson SA, Nanni L, Fernie AR, Nikoloski Z, Bertorelle G, Delledonne M, Papa R. 2014. Decreased Nucleotide and Expression Diversity and Modified Coexpression Patterns Characterize Domestication in the Common Bean. *The Plant Cell*, 26, 1901–1912.

Vilaça ST, Biosa D, Zachos F, Iacolina L, Kirschning J, Alves P C, Paule L, Gortazar C, Mamuris Z, Jedrzejewska B, Borowik T, Sidorovich VE, Kusak J, Costa S, Schley L, Hartl GB, Apollonio M, Bertorelle G\*, Scandura M\*. 2014. Mitochondrial phylogeography of the European wild boar: the effect of climate on genetic diversity and spatial lineage sorting across Europe. *Journal of Biogeography*, 41, 987–998. \*Equal contribution

Perez M, Livoreil B, Mantovani S, Boisselier M-C, Crestanello B, Abdelkrim J, Bonillo C, Goutner V, Lambourdière J, Pierpaoli M, Sterijovski B, Tomovic L, Vilaça ST, Mazzotti S, Bertorelle G. 2014. Genetic Variation and Population Structure in the Endangered Hermann's Tortoise: The Roles of Geography and Human-Mediated Processes. *The Journal of Heredity*, 105, 70-81.

Hoban S, Arntzen JW, Bertorelle G, Bryja J, Fernandes M, Frith K, Gaggiotti O, Galbusera P, Godoy JA, Hauffe HC, Rus Hoelzel A, Nichols RA, Pérez-Espona S, Primmer C, Russo IRM, Segelbacher G, Siegismund HR, Sihvonen M, Sjögren-Gulve P, Vernesi C, Vilà C, Bruford MW. 2013. Conservation Genetic Resources for Effective Species Survival (ConGRESS): Bridging the divide between conservation research and practice. *Journal for Nature Conservation*, 21, 433-437.

Hoban SM, Mezzavilla M, Gaggiotti OE, Benazzo A, van Oosterhout C, Bertorelle G. 2013. High variance in reproductive success generates a false signature of a genetic bottleneck in populations of constant size: a simulation study. *BMC Bioinformatics*, 14, art. no. 309.

Marino, I, Benazzo A, Agostini C, Mezzavilla M, Hoban SM, Patarnello T, Zane L, Bertorelle G. 2013. Evidence for past and present hybridization in three Antarctic icefish species provides new perspectives on an evolutionary radiation. *Molecular Ecology*, 22, 5148–5161.

Hoban SM, Gaggiotti OE, Bertorelle G. 2013. The number of markers and samples needed for detecting bottlenecks under realistic scenarios, with and without recovery: A simulation-based study. *Molecular Ecology*, 22, 3444-3450.

Hoban SM, Hauffe HC, Pérez-Espona S, Arntzen JW, Bertorelle G, Bryja J, Frith K, Gaggiotti OE, Galbusera P, Godoy JA, Hoelzel AR, Nichols RA, Primmer CR, Russo I-R, Segelbacher G, Siegismund HR, Sihvonon M, Vernesi C, Vilà C, Bruford MW. 2013. Bringing genetic diversity to the forefront of conservation policy and management. *Conservation Genetics Resources*, 5, 593-598.

Hoban S, Gaggiotti EO, CONGRESS Consortium, Bertorelle G. 2013. Sample Planning Optimization Tool for conservation and population Genetics (SPOTG): a software for choosing the appropriate number of markers and samples. *Methods in Ecology and Evolution*, 4, 299–303.

Casonato A, Daidone V, Barbon G, Pontara E, Di Pasquale I, Gallinaro L, Marullo L, Bertorelle G. 2013. A common ancestor more than 10,000 years old for patients with R854Q-related type 2N von Willebrand's disease in Italy. *Haematologica*, 98, 147-152.

Hoban S, Bertorelle G, Gaggiotti OE. 2012. Computer simulations: tools for population and evolutionary genetics. *Nature Reviews Genetics*, 13, 110–122.

Kutanan W, Kampuansai J, Fuselli S, Nakbunlung S, Seielstad M, Bertorelle G, Kangwanpong, D. 2011. Genetic structure of the Mon-Khmer speaking groups and their affinity to the neighbouring Tai populations in Northern Thailand. *BMC Genetics*, 12, art. no. 56.

Silvertown J, Cook L, Cameron R, Dodd M, McConway K, Worthington J, Skelton P, Anton C, Bossdorf O, Baur B, Schilthuizen M, Fontaine B, Sattmann H, Bertorelle G, Correia M, Oliveira C, Pokryszko B, Ożgo M, Stalažs A, Gill E, Rammul Ü, Sólymos P, Féher Z, Juan X. 2011. *PLoS One*, 6, art. no. e18927.

Kutanan W, Kampuansai J, Nakbunlung S, Lertvicha P, Seielstad M, Bertorelle G, Kangwanpong D. 2011. Genetic structure of Khon Mueang populations along a historical Yuan migration route in Northern Thailand. *Chiang Mai Journal of Science*, 38, 295-305.

Kutanan W, Kampuansai J, Colonna V, Nakbunlung S, Lertvicha P, Seielstad M, Bertorelle G, Kangwanpong D. 2011. Genetic affinity and admixture of northern Thai people along their migration route in northern Thailand: evidence from autosomal STR loci. *Journal of Human Genetics*, 56, 130-137.

Lari M, Rizzi E, Mona S, Corti G, Catalano G, Chen K, Vernesi C, Larson G, Boscato P, De Bellis G, Cooper A, Caramelli D, Bertorelle G. 2011. The complete mitochondrial genome of an 11,450-year-old aurochs (*Bos primigenius*) from Central Italy. *BMC Evolutionary Biology*, 11, art. no. 32.

Fuselli S, de Filippo C, Mona S, Sistonen J, Fariselli P, Destro-Bisol G, Barbujani G, Bertorelle G, Sajantila A. 2010. Evolution of detoxifying systems: The role of environment and population history in shaping genetic diversity at human CYP2D6 locus. *Pharmacogenetics and Genomics*, 20, 485-499.

Bertorelle G, Benazzo A, Mona S. 2010. ABC as a flexible framework to estimate demography over space and time: some cons, many pros. *Molecular Ecology*, 19, 2609-2625.

Mona S, Catalano G, Lari M, Larson G, Boscato P, Casoli A, Sineo L, Di Patti C, Pecchioli E, Caramelli D, Bertorelle G. 2010. Population dynamic of the extinct European aurochs: genetic evidence of a north-south differentiation pattern and no evidence of post-glacial expansion. *BMC Evolutionary Biology*, 10, art. no. 83.

Flanagan JM, McMahon G, Brendan Chia SH, Fitzpatrick P, Tighe O, O'Neill C, Briones P, Gort L, Kozak L, Magee A, Naughten E, Radomyska B, Schwartz M, Shin JS, Strobl W, Tyfield LA, Waterham HR, Russell H, Bertorelle G, Reichardt JKV, Mayne PD, Croke DT. 2010. The Role of Human Demographic History in Determining the Distribution and Frequency of Transferase-Deficient Galactosaemia Mutations. *Heredity*, 104, 148-154.

Valsecchi E, Corkeron PJ, Galli P, Sherwin W, Bertorelle G. 2010. Genetic evidence for sex-specific migratory behaviour in the western south Pacific humpback whales. *Marine Ecology Progress Series*, 398, 275-286.

Alboni P, Alboni M, Bertorelle G. 2010. Origin and evolution of vasovagal syncope. *Giornale Italiano di Cardiologia*, 11:20-27.

Crestanello B, Pecchioli E, Vernesi C, Mona S, Martinkova N, Janiga M, Hauffe HC, Bertorelle G. 2009. The genetic impact of translocations and habitat fragmentation in *Rupicapra* spp. *Journal of Heredity*. 100, 691-708.

Barbisan F, Savio C, Bertorelle G, Patarnello T, Congiu L. 2009. Duplication polymorphism at MHC class II DRB1 locus in the wild boar (*Sus scrofa*). *Immunogenetics* 61,145-151.

Gabriele G, Vernesi C, Vicario S, Pecchioli E, Caccone A, Bertorelle G, Sbordoni V. 2009. Mitochondrial DNA variation in roe deer (*Capreolus capreolus*) from Italy: evidence of admixture in one of the last *C. c. italicus* pure populations from central-southern Italy. *Italian Journal of Zoology* 76, 16-27.

Mona S, Crestanello B, Bankhead-Dronnet S, Pecchioli E, Ingrosso S, D'Amelio S, Rossi L, Meneguz PG, Bertorelle G. 2008. Disentangling the effects of recombination, selection, and demography on the genetic variation at a major histocompatibility complex class II gene in the alpine chamois. *Molecular Ecology* 17, 4053-4067.

Alboni P, Alboni M, Bertorelle G. 2008. The origin of the vasovagal syncope: to protect the heart or to escape predation? *Clinical Autonomic Research*, 18, 170-178.

Caramelli D, Milani L, Vai S, Modi A, Pecchioli E, Girardi M, Pilli E, Lari M, Lippi B, Ronchitelli A, Mallegni F, Casoli A, Bertorelle G, Barbujani G. 2008. A 28,000 years old Cro-Magnon mtDNA sequence differs from all potentially contaminating modern sequences. *PLoS ONE*, 3, art. no. e2700.

Vernesi C, Bruford MW, Bertorelle G, Pecchioli E, Rizzoli A, Hauffe HC. 2008. Where's the Conservation in Conservation Genetics? *Conservation Biology*, 22, 802-804.

Scandura M, Iacolina L, Crestanello B, Pecchioli E, Di Benedetto MF, Russo V, Davoli R, Apollonio M, Bertorelle G. 2008. Ancient vs. recent processes as factors shaping the genetic variation of the European wild boar: are the effects of the last glaciation still detectable? *Molecular Ecology* 17, 1745-1762.

Kampuansai J, Bertorelle G, Castri L, Nakbunlung S, Seielstad M, Kangwanpong D. 2007. Mitochondrial DNA Variation of Tai Speaking Peoples in Northern Thailand. *ScienceAsia*, 33, 443-448.

Caramelli D, Vernesi C, Sanna S, Sampietro L, Lari M, Castri L, Vona G, Floris R, Francalacci P, Tykot R, Casoli A, Bertranpetit J, Lalueza-Fox C, Bertorelle G, Barbujani G. 2007. Genetic variation in prehistoric Sardinia. *Human Genetics*, 122, 327- 336.

Genovart M, Oro D, Juste J, Bertorelle G. 2007. What genetics tell us about the conservation of the critically endangered Balearic Shearwater? *Biological conservation*, 137, 283-293.



Pellecchia M, Negrini R, Colli L, Patrini M, Milanese E, Achilli A, Bertorelle G, Cavalli-Sforza LL, Piazza A, Torroni A, Ajmone-Marsan P. 2007. The mystery of Etruscan origins: novel clues from *Bos taurus* mitochondrial DNA. *Proceedings of the Royal Society B*, 274, 1175-1179.

Besaggio D, Fuselli S, Srikumool M, Kampuansai J, Castrì L, Tyler-Smith C, Seielstad M, Kangwanpong D, Bertorelle G. 2007. Genetic variation in Northern Thailand Hill Tribes: origins and relationships with social structure and linguistic differences. *BMC Evolutionary Biology*, 7, art. no. S12.

Caramelli D, Lalueza-Fox C, Condemi S, Longo L, Milani L, Manfredini A, de Saint Pierre M, Adoni F, Lari M, Giunti P, Ricci S, Casoli A, Calafell F, Mallegni F, Bertranpetit J, Stanyon R, Bertorelle G, Barbujani G. 2006. A highly divergent mtDNA sequence in a Neandertal individual from Italy. *Current Biology*, 16, R630-R632

Beja-Pereira A, Caramelli D, Lalueza Fox C, Vernesi C, Ferrand N, Sampietro L, Casoli A, Goyache F, Luis Royo L, Conti S, Lari M, Martini A, Ouragh L, Magid A, Atash A, Boscato P, Triantophylidis C, Ploumi K, Sineo L, Mallegni F, Taberlet P, Erhardt G, Bertranpetit J, Barbujani G, Luikart G, Bertorelle G. 2006. The origin of European cattle: evidence from modern and ancient DNA. *Proceedings of the National Academy of Science USA*, 103, 8113-8.

Coelho M, Luiselli D, Bertorelle G, Lopes IA, Seixas S, Destro-Bisol G, Rocha J. 2005. Microsatellite variation and evolution of human lactase persistence. *Human Genetics*, 117, 329-339.

Forlani A, Crestanello B, Mantovani S, Livoreil B, Zane L, Bertorelle G, Congiu L. 2005. Identification and characterization of microsatellite markers in Hermann's tortoise (*Testudo hermanni*, Testudinidae). *Molecular Ecology Notes*, 5, 228-230

Barbujani G, Vernesi C, Caramelli D, Castrì L, Lalueza-Fox C, Bertorelle G. 2004. Etruscan Artifacts: Much Ado about Nothing. *American Journal of Human Genetics*, 75, 923-927.

Dupanloup I, Bertorelle G, Chikhi L, Barbujani G. 2004. Estimating the Impact of Prehistoric Admixture on the Europeans' Genome. *Molecular Biology and Evolution*, 21, 1361-1372.

Bertorelle G, Bruford M, Chemini C, Vernesi C, Hauffe HC. New flexible bayesian approaches to revolutionize conservation genetics. 2004. *Conservation Biology*, 18, 584.

Vernesi C, Caramelli D, Dupanloup I, Bertorelle G, Lari M, Cappellini E, Moggi-Cecchi J, Chiarelli B, Castri L, Casoli A, Mallegni F, Lalueza-Fox C, Barbujani G. 2004. The Etruscans: a population-genetic study. *American Journal of Human Genetics*, 74, 694-704.

Mirimin L, Vernesi C, Bertolucci C, Mazzotti S, Bertorelle G. 2004. Mitochondrial DNA variation and divergence in three Hermann's tortoise (*Testudo hermanni*) populations. *Italian Journal of Zoology*, 71, 199-201.

Beja-Pereira A, Luikart G, England PR, Bradley DG, Jann OC, Bertorelle G, Chamberlain AT, Nunes TP, Metodiev S, Ferrand N, Erhardt G. 2003. Gene-culture coevolution between cattle milk protein genes and human lactase genes. *Nature Genetics*, 35, 311-313.

Barbujani G, Bertorelle G. 2003. Were Cro-Magnons too like us for DNA to tell? *Nature*, 424, 127.

Dupanloup I, Pereira L, Bertorelle G, Calafell F, João Prata M, Amorim A, Barbujani G. 2003. A recent shift from polygyny to monogamy in humans is suggested by the analysis of worldwide Y-chromosome diversity. *Journal of Molecular Evolution*, 57, 85-97.

Caramelli, C, Lalueza-Fox C, Vernesi C, Lari, M, Casoli A, Mallegni F, Chiarelli B, Dupanloup I, Bertranpetit J, Barbujani G, Bertorelle G. 2003. Evidence for a genetic discontinuity between Neandertals and Cro-Magnons. *Proceedings of the National Academy of Science USA*, 100, 6593-6597.

Tighe O, Dunican D, O'Neill C, , Bertorelle G, et other 24 authors. 2003. Genetic diversity within the R408W phenylketonuria mutation lineages in Europe. *Human Mutation*, 21, 387-393.

Vernesi C, Crestanello B, Pecchioli E, Tartari D, Caramelli D, Hauffe H, Bertorelle G. 2003. The genetic impact of population decline and reintroduction in the wild boar (*Sus scrofa*): a microsatellite analysis. *Molecular Ecology*, 12, 585-595.

Zerjal T, Xue Y, Bertorelle G, and other 20 authors. 2003. The genetic legacy of the Mongols. *American Journal of Human Genetics*, 72, 717-721.

Manni F, Rotola A, Caselli E, Bertorelle G, Di Luca D. 2002. Detecting recombination in TT virus: a phylogenetic approach. *Journal of Molecular Evolution*, 55, 563-572.

Vernesi C, Fuselli S, Castrì L, Bertorelle G, Barbujani G. 2002. Mitochondrial diversity in linguistic isolates of the Alps: a reappraisal. *Human Biology*, 74, 725-730.

O'Donnell KA, O'Neill C, Tighe O, Bertorelle G, Naughten E, Mayne PD, Croke DT. 2002. The mutation spectrum of hyperphenylalaninaemia in the Republic of Ireland: the population history of Irish revisited. *European Journal of Human Genetics*, 10, 530-538.

Vernesi C, Pecchioli E, Caramelli D, Tiedemann R, Randi E, Bertorelle G. 2002. The genetic structure of natural and reintroduced roe deer (*Capreolus capreolus*) populations in the Alps and Central Italy, with reference to the mitochondrial DNA phylogeography of Europe. *Molecular Ecology*, 11, 1285-1297.

Rannala B, Bertorelle G. 2001. Using linked markers to infer the age of a mutation. *Human Mutation*, 18, 87-100.

Slatkin M, Bertorelle G. 2001. The use of intra-allelic variability for testing neutrality and estimating selection intensity and population growth rate, with applications to human genetic diseases. *Genetics*, 158, 865-874.

Di Benedetto G, Erguven A, Stenico M, Castrì L, Bertorelle G, Togan I, Barbujani G. 2001. DNA diversity and population admixture in Anatolia. *American Journal of Physical Anthropology*, 115, 144-156.

Dupanloup de Ceuninck, I., Bertorelle, G. 2001. Inferring admixture proportions from molecular data: extension to any number of parental populations. *Molecular Biology and Evolution*, 18, 672-675.

Barbujani G, Bertorelle G. 2001. Genetics and the population history of Europe. *Proceedings of the National Academy of Science USA*, 98, 22-25.

Bertorelle G, Bucchini L, Pilastro A, Matessi C. 1999. DNA fingerprinting data and the analysis of population genetic structure by comparing band-sharing patterns. *Molecular Ecology*, 8, 1851-1866.

Bertorelle G, and Rannala B. 1998. Using rare mutations to estimate population divergence times: A maximum likelihood approach. *Proceedings of the National Academy of Science USA*, 95, 15452-15457.

Bertorelle G, Excoffier L. Inferring admixture proportions from molecular data. 1998. *Molecular Biology and Evolution*, 15, 1298-1311.

Chikhi L, Destro-Bisol G, Bertorelle G, Pascali V, Barbujani G. 1998. Molecular clines suggest a recent, Neolithic ancestry of European populations. *Proceedings of the National Academy of Science USA*, 95, 9053-9058.

Barbujani G, Bertorelle G, Chikhi L. 1998. Evidence for Palaeolithic and Neolithic gene flow in Europe. *American Journal of Human Genetics*, 62, 488-491.

Bertorelle G, Bisazza A, Marconato A. 1997. Computer simulation suggests that the spatial distribution of males influences female visiting behaviour in the river bullhead. *Ethology*, 103, 999-1014.

Bertorelle G, Barbujani G. 1997. Expected effects of mass screening policies on the frequency of cystic fibrosis homozygotes. *Human Genetics*, 100, 666-668.

Bertorelle G, Barbujani G. 1997. What do intragenic microsatellites tell us about the overdominance hypothesis at the cystic fibrosis gene? *Annals of Human Genetics*, 61:532-533.

Stenico M, Nigro L, Bertorelle G, Calafell F, Capitanio MA, Corrain C, Barbujani G. 1996. High mitochondrial sequence diversity in linguistic isolates of the Alps. *American Journal of Human Genetics*, 59, 1363-1375.

Debraekeleer M, Chaventrè A, Bertorelle G, Verlingue C, Raguene O, Mercier B, Ferec C. 1996. Linkage disequilibrium between the four most common cystic fibrosis mutations and microsatellite haplotypes in the Celtic population of Brittany. *Human Genetics*, 98, 223-227.

Bertorelle G, Calafell F, Francalacci P, Bertranpetit J, Barbujani G. 1996. Geographic homogeneity and non-equilibrium patterns of mtDNA sequences in Tuscany, Italy. *Human Genetics*, 98, 145-150.

Barbujani G, Bertorelle G, Capitanio G, Scozzari R. 1995. Geographical structuring in the mtDna of Italians. *Proceedings of the National Academy of Science USA*, 92, 9171-9175.

Bertorelle G, Slatkin M. 1995 The number of segregating sites in expanding human populations, with implications for estimates of demographic parameters. *Molecular Biology and Evolution*, 12, 887-892.

Bertorelle G, Bertranpetit J, Calafell F, Nasidze IS, Barbujani G. 1995. Do Basques- and Caucasian-speaking populations share non-Indo-European ancestors? *European Journal of Human Genetics*, 3, 256-263.

Bertorelle G, Barbujani G. 1995. Analysis of DNA diversity by spatial autocorrelation. *Genetics*, 140, 811-819.

Pilastro A, Bertorelle G, Marin G. 1995 Winter fattening strategies in two sympatric insectivorous passerines: analysis of environmental and social determinants. *Journal of Avian Biology*, 26, 25-32.

Barbujani G, Whitehead GN, Bertorelle G, Nasidze I.S. 1994 Testing hypotheses on processes of genetic and linguistic change in the Caucasus. *Human Biology*, 66,843-864.

Pilastro A, Farinello F, Bertorelle G, Marin G. 1994. Winter fattening strategies in two sympatric passerines: Effects of territoriality. *Bollettino di Zoologia*, 61:64-65.