

David Díez-del-Molino

Postdoctoral Researcher at the Swedish Museum of Natural History (NRM) (Updated 04/05/2016)

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Research Interests

I am interested in the study of animal and human populations using a wide range of methods from **population genetics** to **computational genomics**. My current research is focused on two main fields: (1) studying the genetic and demographic history of **invasive fish species** aiming to discover **evolutionary processes that shape the genomes of invaders** and drive its success in novel environments, and (2) using genomic tools to shed light on the **origin and history of human and animal populations** by investigating their genomes and modelling **ancient DNA**.

Skills

- Languages: Spanish/English/Catalan
- Wet-lab work: techniques related to molecular markers such as microsatellite loci, SNPs, mtDNA, and NGS.
- Software (Plink, ADMIXTURE, TreeMix, etc...) and analyses (FST, He, IBD, Tajima's D, PSMC, etc...) related with population genetics/genomics.
- Bioinformatics and genomic data analysis: from handling big sequence files to variant calling and filtering.
- Computer simulations and modelling DNA data using either custom scripting or standard software such as *ms* or *FastSimCoal2*.
- R (scripting and plotting), Python (scripting) and the GNU/Linux environment (including shell and cluster scripting).
- Experience supervising undergraduate and master students.
- Experience in writing projects and technical reports, communicating results in conferences and publishing in journals.

Education and training

2016—Present: **Postdoctoral Researcher**. Swedish Museum of Natural History.

2014—2016: **Postdoctoral Researcher**. University College London.

2010 — 2015: **Ph.D. in Population Genetics**. University of Girona.

2008 — 2009: **Master in Biological Conservation**. The Complutense University of Madrid.

2003 — 2008: **Bachelor degree in Biological Sciences**. University of Salamanca.

Other Training/ Recent Courses

- 2015 — *Population Genetics and Demographic History: model-based approaches*. Instituto Gulbenkian de Ciência. Oeiras, Portugal (4 days)
- 2015 — *Variant Analysis with GATK*. The Broad Institute/University of Cambridge. Cambridge, UK (2 days)
- 2015 — *Genomic data analysis using Hapmap and the 1000 Genomes projects*. Transmitting Science. Sabadell, Spain (5 days)
- 2014 — *Introduction to High Performance High Throughput Computing*. ISD/University College London. London, UK. (2 days)
- 2013 — *Next-Generation Sequencing data analysis* (38 hours). COMAV/Polytechnic University of Valencia, Valencia, Spain.

Teaching Experience

2013/2014: **Adjunct Professor**. University of Girona.

- *Integrated Scientific Techniques*
- *Conservation Genetics*
- *Genetics*
- *Population Genetics*

2015/2016: **Adjunct Professor**. University of Girona.

- *Introduction to Bioinformatics*
- *Applied Bioinformatics*

Research Projects

2014-2016: **Bridging European and Anatolian Neolithic (BEAN) - International Training Network**.

PI: Mark G. Thomas. The 7th Framework Program of the European Commission. Code 289966.

FP7-PEOPLE-2011-ITN

2010-2012: **River invasibility of introduced freshwater fish: population structure of the introduced *Gambusia holbrooki***. PI: Jose-Luis García-Marín. Spanish Ministry of Science and Innovation (MICINN) CGL2009-12877-C02-02

Awards and scholarships

- 2014-2016: **Marie-Curie ITN – Experienced Researcher**. University College London, UK.
- 2013: **Travel grant** to visit Bryan Neff's Laboratory at the University of Western Ontario in London, Ontario, Canada, for 3 months. University of Girona.
- 2010 - 2013: **Ph.D. Scholarship** from the University of Girona (BR12/2010)

Publications

- PEČNEROVÁ P, **DÍEZ-DEL-MOLINO D**, VARTANYAN S, DALÉN L. (2016) [Changes in variation at the MHC class II DQA locus during the final demise of the woolly mammoth](#). Scientific Reports. doi: 10.1038/srep25274
- VERA M, **DÍEZ-DEL-MOLINO D**, GARCÍA-MARÍN JL. (2016) [Genomic data provide insights on the evolutionary changes of the invasive mosquitofish \(*Gambusia holbrooki*\)](#). Molecular Ecology. doi: 10.1111/mec.13545
- **DÍEZ-DEL-MOLINO D**, ARAGUAS RM, VERA M, VIDAL O, SANZ N, GARCÍA-MARÍN JL. (2016) [Temporal genetic dynamics among mosquitofish \(*Gambusia holbrooki*\) populations in invaded watersheds](#). Biological Invasions. doi:10.1007/s10530-016-1055-z
- ZUZANA HOFMANOVÁ, SUSANNE KREUTZER, GARRETT HELLENTAL, CHRISTIAN SELL, YOAN DIEKMANN, **DAVID DÍEZ-DEL-MOLINO** et al. (2015) [Early farmers from across Europe directly descended from Neolithic Aegeans](#). In press & BioRxiv. doi: <http://dx.doi.org/10.1101/032763>
- **DÍEZ-DEL-MOLINO D** (2015) [Genetic diversity and population structure of the non-native Eastern mosquitofish \(*Gambusia holbrooki*\) in Mediterranean streams](#). PhD. Thesis. University of Girona.
- **DÍEZ-DEL-MOLINO D**, CARMONA-CATOT G, ARAGUAS RM, VIDAL O, GARCÍA-BERTHOUE, SANZ N, GARCÍA-MARÍN JL (2013) [Gene flow and maintenance of genetic diversity in invasive mosquitofish \(*Gambusia holbrooki*\)](#). PLoS ONE 8(12): e82501. doi:10.1371/journal.pone.0082501
- SANZ N, ARAGUAS RM, VIDAL O, **DÍEZ-DEL-MOLINO D**, FERNÁNDEZ-CEBRIAN R, GARCÍA-MARÍN JL. (2013) [Genetic characterization of the invasive mosquitofish \(*Gambusia* spp.\) introduced to Europe: population structure and colonization routes](#). Biological Invasions. doi:10.1007/s10530-013-0456-5
- VIDAL O, SANZ N, ARAGUAS RM, FERNÁNDEZ-CEBRIÁN R, **DÍEZ-DEL-MOLINO D**, GARCÍA-MARÍN JL. (2012) [SNP diversity in introduced populations of the invasive *Gambusia holbrooki*](#). Ecology of Freshwater Fish. 21:100-108.

Workshops and Conferences

- [Symposium organizer] SMBE15: The Annual Meeting of the Society for Molecular Biology and Evolution. **SMBE**. Vienna, 2015.
- [Conference organizer] BEAN Workshop 'Simulating the Neolithic'. **University College London/Institute of Archaeology**. London, 2015.
- [Attendance] I Workshop on Bioinformatics and Computational Biology. **Bioinformatics Barcelona (BIB)**. Barcelona, 2013.
- [Conference organizer & poster] Temporal genetic dynamics in invasive populations of mosquitofish (*Gambusia holbrooki*). **XXXIX Congress of the Spanish Society of Genetics (SEG)**. Girona, 2013.
- [Poster] Comparative genetic diversity patterns of mosquitofish populations among invaded watersheds. **VII European Conference on Biological Invasions (NEOBIOTA2012)**. Pontevedra, 2012.
- [Poster] Population structure of mosquitofish (*Gambusia holbrooki*) along a highly polluted river. **IV Iberian Workshop of Ichthyology (SIBIC)**. Girona, 2012. *Best poster award*
- [Oral communication] Population structure of *Gambusia holbrooki* along a highly polluted river. **XIX Workshop in Population Genetics and Evolution (SEGPE)**. Orduña, 2012.
- [Poster] Population structure of the invasive species *Gambusia holbrooki* in rivers of the Iberian Peninsula. **XXVIII Congress of the Spanish Society of Genetics (SEG)**. Murcia, 2011.

Scientific societies and other roles

- Spanish Society for Conservation and Study of Mammals (SECEM), Spanish Society of Genetics (SEG), Iberian Society of Ichthyology (SIBIC), Society for Molecular Biology and Evolution (SMBE)
- 2011-2015: Ph.D. students' representative at the University of Girona.
- Reviewer for JCR journals: PLoS ONE, Hydrobiologia.

Science outreach

2015-present: Personal blog (<https://medium.com/@indianadiez>)

2013-2015: Social media strategy coordinator of the profiles of the Laboratory of Genetic Ichthyology in Twitter (https://twitter.com/LIG_UdG) and Facebook (<https://www.facebook.com/lig.genetica.udg>)

2013-2015: Creator and editor of the Laboratory of Genetic Ichthyology's blog (<http://coolgenes.wordpress.com/>)

Additional information can be supplied upon request