

RESEARCH INTERESTS Evolutionary Genomics | Phylogenomics | Molecular Evolution | Chordates and Mammals

EDUCATION

- 2009 PhD in Evolutionary Biology | **University of Montpellier 2, Montpellier, France**
2006 MSc in Evolutionary Biology and Ecology | **University of Montpellier 2, Montpellier, France**
2004 BSc in Biochemistry and Biotechnology | **University of Thessaly, Larissa, Greece**

ACADEMIC BACKGROUND

- 2013-18 PostDoc with Prof SJ Rossiter | **School of Biological and Chemical Sciences, Queen Mary University of London, London, UK**
2011-13 PostDoc with Prof SJ Rossiter, Dr JA Cotton and Dr E Stupka | **School of Biological and Chemical Sciences, Queen Mary University of London, London, UK**
2010-11 PostDoc with Dr N Galtier | **Institute of Evolutionary Sciences CNRS/UMR 5554, University of Montpellier 2, Montpellier, France**
2006-09 PhD with Dr F Delsuc and Prof EJP Douzery | **Institute of Evolutionary Sciences CNRS/UMR 5554, University of Montpellier 2, Montpellier, France**
2006 MSc with Dr F Delsuc and Prof EJP Douzery | **Institute of Evolutionary Sciences CNRS/UMR 5554, University of Montpellier 2, Montpellier, France**

PUBLICATIONS

Citations = 1353; h-index=13 (Metrics based on Google Scholar, May 2018)

- 2018 F Delsuc†, H Philippe†, G Tsagkogeorga†, P Simion, MK Tilak, X Turon, S López-Legentil, J Piette, P Lemaire, EJP Douzery. A phylogenomic framework and timescale for comparative studies of tunicates. *BMC Biol*, 16: 39 †Equal contributors
- 2017 X Mao, G Tsagkogeorga, SE Bailey, SJ Rossiter. Genomics of introgression in the Chinese horseshoe bat (*Rhinolophus sinicus*) revealed by transcriptome sequencing. *Biol J Lin Soc*, blx017. doi: 10.1093/biolinnean/blx017
- 2017 G Tsagkogeorga, S Müller, C Dessimoz, SJ Rossiter. Comparative genomics reveals contraction in olfactory receptor genes in bats. *Sci Rep*, 7(11): 259
- 2016 SE Bailey, X Mao, M Struebig, G Tsagkogeorga, G Csorba, LR Heaney, J Sedlock, W Stanley, JM Rouillard, SJ Rossiter. The use of museum samples for large-scale sequence capture: a study of congeneric horseshoe bats (family Rhinolophidae). *Biol J Lin Soc*, 117(1): 58
- 2015 G Tsagkogeorga, MR McGowen, KTJ Davies, S Jarman, A Polanowski, MF Bertelsen, SJ Rossiter. A phylogenomic analysis of the role and timing of molecular adaptation in the aquatic transition of cetartiodactyl mammals. *R Soc Open Sci*, 2(9): 150156
- 2015 KTJ Davies, NC Bennett, G Tsagkogeorga, SJ Rossiter, CG Faulkes. Family wide molecular adaptations to underground life in african mole-rats revealed by phylogenomic analysis. *MBE*, 32(12): 3089
- 2014 KTJ Davies, G Tsagkogeorga, SJ Rossiter. Divergent evolutionary rates in vertebrate and mammalian specific conserved non-coding elements (CNEs) in echolocating mammals. *BMC Evol Biol*, 14(1): 261
- 2014 KTJ Davies, G Tsagkogeorga, NC Bennett, LM Davalos, CG Faulkes, SJ Rossiter. Molecular evolution of growth hormone and insulin-like growth factor 1 receptors in long-lived, small-bodied mammals. *Gene*, 549(2): 228
- 2014 J Romiguier, P Gayral, M Ballenghien, A Bernard, V Cahais, A Chenuil, Y Chiari, R Derrat, L Duret, N Faivre, E Loire, JM Lourenco, B Nabholz, C Roux, G Tsagkogeorga, AA Weber, LA Weinert, K Belkhir, N Bierne, S Glmin, N Galtier. Comparative population genomics in animals uncovers the determinants of genetic diversity. *Nature*, 515(7526): 261
- 2013 G Tsagkogeorga*, J Parker*, JA Cotton, E Stupka, SJ Rossiter. Phylogenomic analyses elucidate the evolutionary relationships of bats. *Curr Biol*, 23(22): 2262 *Joint first authors
- 2013 J Parker*, G Tsagkogeorga*, JA Cotton, Y Liu, P Provero, E Stupka, SJ Rossiter. Genome-wide signatures of convergent evolution in echolocating mammals. *Nature*, 502(7470): 228 *Joint first authors
- 2013 C Roux, G Tsagkogeorga, N Bierne, N Galtier. Crossing the species barrier: genomic hotspots of introgression between two highly divergent *Ciona intestinalis* species. *MBE*, 30(7): 1574
- 2012 G Tsagkogeorga, V Cahais, N Galtier. The population genomics of a fast evolver: high levels of diversity, functional constraint and molecular adaptation in the tunicate *Ciona intestinalis*. *GBE*, 4(8): 852
- 2012 V Cahais, P Gayral, G Tsagkogeorga, J Melo-Ferreira, M Ballenghien, LA Weinert, Y Chiari, K Belkhir, V Ranwez, N Galtier. Reference-free transcriptome assembly in non-model animals from next-generation sequencing data. *Mol Ecol Res*, 12(5): 834
- 2011 P Gayral, L Weinert, Y Chiari, G Tsagkogeorga, M Ballenghien, N Galtier. Next-generation sequencing of transcriptomes: a guide to RNA isolation in nonmodel animals. *Mol Ecol Res*, 11(4): 650
- 2010 F Denoeud, S Henriot, S Mungpakdee, JM Aury, CD Silva, H Brinkmann, J Mikhaleva, LC Olsen, C Jubin, C Canestro, JM Bouquet, G Danks, J Poulain, C Campsteijn, M Adamski, I Cross, F Yadetie, M Muffato, A Louis, S Butcher, G

- Tsagkogeorga, A Konrad, S Singh, MF Jensen, EH Cong, H Eikeseth-Otteraa, B Noel, V Anthouard, BM Porcel, R Kachouri-Lafond, A Nishino, M Ugolini, P Chourrout, H Nishida, R Aasland, S Huzurbazar, E Westhof, F Delsuc, H Lehrach, R Reinhardt, J Weissenbach, SW Roy, F Artiguenave, JH Postlethwait, JR Manak, EM Thompson, O Jaillon, LD Pasquier, R Boudinot, DA Liberles, JN Volff, H Philippe, B Lenhard, HR Crollius, P Wincker, D Chourrout. Plasticity of animal genome architecture unmasked by rapid evolution of a pelagic tunicate. *Science*, 330(6009): 1381
- 2010 G Tsagkogeorga, X Turon, N Galtier, EJP Douzery, F Delsuc. Accelerated evolutionary rate of housekeeping genes in tunicates. *J Mol Evol*, 71(2): 153
- 2009 TR Singh†, G Tsagkogeorga†, F Delsuc, S Blanquart, N Shenkar, Y Loya, EJP Douzery, D Huchon. Tunicate mitogenomics and phylogenetics: peculiarities of the *Herdmania momus* mitochondrial genome and support for the new chordate phylogeny. *BMC Genom*, 10: 534 †Equal contributors
- 2009 G Tsagkogeorga, X Turon, RR Hopcroft, MK Tilak, T Feldstein, N Shenkar, Y Loya, D Huchon, EJP Douzery, F Delsuc. An updated 18S rRNA phylogeny of tunicates based on mixture and secondary structure models. *BMC Evol Biol*, 9: 187
- 2008 F Delsuc, G Tsagkogeorga, N Lartillot, H Philippe. Additional molecular support for the new chordate phylogeny. *Genesis*, 46(11): 592

SELECTED CONFERENCES, SEMINARS & WORKSHOPS

- 11/2017 Invited seminar: “Genomics of adaptation in bats and mammals” | Laboratoire Evolution, Génomes, Comportement, Ecologie (EGCE), CNRS, Gif-sur-Yvette, France.
- 01/2017 PopGroup50 - The 50th Population Genetics Group | Churchill College, Cambridge, UK.
- 11/2015 Dating species divergences using rocks and clocks | The Royal Society, London, UK.
- 09/2014 Ensembl Gene Annotation Workshop | Cambridge University, Cambridge, UK.
Introduction to Ensembl gene annotation pipeline, including Ensembl genebuild system, core database schema, job tracking, Runnable and RunnableDB modules.
- 06/2014 G Tsagkogeorga, M McGowen, A Foote, T Gilbert, S Jarman, A Polanowski, M Bertelsen and SJ Rossiter. “Genome-wide scan for molecular adaptations in the common ancestor of hippos and whales.” Poster in SMCB, San Juan, Puerto Rico.
- 12/2013 Ensembl API Workshop | Cambridge University, Cambridge, UK.
Workshop aimed at researchers and developers interested in exploring Ensembl beyond the website. The workshop covered the core, compara, variation and functional genomics (regulation) databases and APIs.
- 07/2013 G Tsagkogeorga, J Parker, JA Cotton, E Stupka and SJ Rossiter. “Phylogenomic analyses resolve the evolutionary relationships of bats (Chiroptera).” Poster in SMCB, Chicago, Illinois.
- 03/2013 Generic Model Organism Database (GMOD) Community Meeting | The Hauser Forum, Cambridge, UK.
- 06/2009 G Tsagkogeorga, X Turon, EJP Douzery and F Delsuc. “Tunicate phylogenomics from the 454 high-throughput sequencing of non-model species transcriptomes”. Talk in one-day conference with subject: “New high-throughput sequencing technologies and their applications in the domain of biodiversity” | Montpellier, France.
- 07/2007 Workshop on Molecular Evolution | Marine Biological Laboratory (MBL), Woods Hole, Massachusetts, USA.
Two-week course in molecular evolution and comparative genomics.

ACHIEVEMENTS, GRANTS & FELLOWSHIPS

- 12/2018 Shortlisted among 15 candidates across the UK for the David Phillips Fellowships | **Biotechnology and Biological Sciences Research Council, BBSRC, UK**
- 07/2007 International Mobility Grant for Ph.D. Students | **PhD School of Integrative Systems in Biology, Agronomy, Geosciences, Hydrosociences and Environment, SIBAGHE, France**
- 10/2006 PhD Fellowship | **Ministry of National Education, Advanced Instruction and Research, France**
- 03/2004 ERASMUS Scholarship | **State Scholarship’s Foundation IKY, Greece**

REVIEWER

BMC Evolutionary Biology | Gene | Genome Biology and Evolution | Molecular Biology and Evolution | Molecular Ecology Resources | Molecular Phylogenetics and Evolution | Nature Ecology Evolution

MEMBERSHIPS

Athena SWAN Committee | STEMNET London | The Genetics Society

TRAINING & TEACHING

Advised and trained PhD students and early career researchers in bioinformatics and large-scale ‘omic’ data analysis. I have also done some lecturing of Phylogenetics and Phylogenomics to MSc students at Queen Mary University of London.

SKILLS

Human languages: Greek, English, French | **Computer languages:** Bash, Perl, R, LATEX | **Bioinformatics:** Expertise in large-scale analysis of high-throughput sequencing data in parallel computing environments. Up-to-date with most assembly, mapping and gene annotation tools. Thorough knowledge of phylogenetics and molecular evolution analyses.