

Georgia Tsagkogeorga

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

EDUCATION

Sep 2006 – Dec 2009 PhD in Evolutionary Biology | **University of Montpellier 2, Montpellier, France**
Sep 2005 – Jun 2006 MSc in Evolutionary Biology and Ecology | **University of Montpellier 2, Montpellier, France**
Oct 2000 – Oct 2004 BSc in Biochemistry and Biotechnology | **University of Thessaly, Larissa, Greece**

ACADEMIC BACKGROUND

Mar 2013 – Present **School of Biological and Chemical Sciences, Queen Mary University of London, London, UK**
PostDoc position funded as part of an ERC grant to Prof SJ Rossiter
Research project in Evolutionary Genomics and Molecular Ecology:
“Dissecting the genetic basis of divergent and convergent evolution: from individuals to species radiations.”

Mar 2011 – Feb 2013 **School of Biological and Chemical Sciences, Queen Mary University of London, London, UK**
PostDoc position funded as part of a BBSRC grant to Prof SJ Rossiter, Dr JA Cotton and Dr E Stupka
Research project in Phylogenomics and Evolutionary Genomics:
“The molecular basis of convergence: a genome-wide approach in a novel mammalian model.”

Jan 2010 – Jan 2011 **Institute of Evolutionary Sciences CNRS/UMR 5554, University of Montpellier 2, Montpellier, France**
PostDoc position funded as part of an ERC grant to Dr N Galtier
Research project in Population Genetics and Phylogenomics:
“Population phylogenomics: linking molecular evolution to species biology.”

Sep 2006 – Dec 2009 **Institute of Evolutionary Sciences CNRS/UMR 5554, University of Montpellier 2, Montpellier, France**
PhD project with Dr F Delsuc and Prof EJP Douzery
Research project in Molecular Phylogenetics, Phylogenomics and Evolution:
“Molecular phylogeny and evolution of Tunicates (Urochordates): a phylogenomic approach.”

Jan 2006 – Jun 2006 **Institute of Evolutionary Sciences CNRS/UMR 5554, University of Montpellier 2, Montpellier, France**
MSc project with Dr F Delsuc and Prof EJP Douzery
Research project in Molecular Phylogenetics and Evolution:
“Molecular phylogeny and evolution of Tunicates: the contribution of the 18S ribosomal RNA.”

Mar 2004 – Jun 2004 **Institute of Genetics and Microbiology CNRS/UMR 8621 University of Paris-Sud XI, Orsay, France**
BSc project with Prof JP Rousset and C Stathopoulos
Research project in Molecular Genetics of Translation:
“Effects of rRNA modifications on translation accuracy in yeast *Saccharomyces cerevisiae*.”

PEER-REVIEWED PUBLICATIONS

Citations = 1112; h-index=12 (Metrics based on Google Scholar, May 2017)

19. X Mao, [G Tsagkogeorga](#), SE Bailey, SJ Rossiter (2017). Genomics of introgression in the Chinese horseshoe bat (*Rhinolophus sinicus*) revealed by transcriptome sequencing. *Biol J Lin Soc*, blx017. doi: 10.1093/biolinnean/blx017
18. [G Tsagkogeorga](#), S Müller, C Dessimoz, SJ Rossiter (2017). Comparative genomics reveals contraction in olfactory receptor genes in bats. *Sci Rep*, 7(11): 259
17. SE Bailey, X Mao, M Struebig, [G Tsagkogeorga](#), G Csorba, LR Heaney, J Sedlock, W Stanley, JM Rouillard, SJ Rossiter (2016). 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
16. [G Tsagkogeorga](#), MR McGowen, KTJ Davies, S Jarman, A Polanowski, MF Bertelsen, SJ Rossiter (2015). 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
15. KTJ Davies, NC Bennett, [G Tsagkogeorga](#), SJ Rossiter, CG Faulkes (2015). Family wide molecular adaptations to underground life in african mole-rats revealed by phylogenomic analysis. *MBE*, 32(12): 3089
14. KTJ Davies, [G Tsagkogeorga](#), SJ Rossiter (2014). Divergent evolutionary rates in vertebrate and mammalian specific conserved non-coding elements (CNEs) in echolocating mammals. *BMC Evol Biol*, 14(1): 261
13. KTJ Davies, [G Tsagkogeorga](#), NC Bennett, LM Davalos, CG Faulkes, SJ Rossiter (2014). Molecular evolution of growth

- hormone and insulin-like growth factor 1 receptors in long-lived, small-bodied mammals. *Gene*, 549(2): 228
12. J Romiguier, P Gayral, M Ballenghien, A Bernard, V Cahais, A Chenuil, Y Chiari, R Darnat, L Duret, N Faivre, E Loire, JM Lourenco, B Nabholz, C Roux, G Tsagkogeorga, AA Weber, LA Weinert, K Belkhir, N Bierne, S Glemin, N Galtier (2014). Comparative population genomics in animals uncovers the determinants of genetic diversity. *Nature*, 515(7526): 261
 11. G Tsagkogeorga*, J Parker*, JA Cotton, E Stupka, SJ Rossiter (2013). Phylogenomic analyses elucidate the evolutionary relationships of bats. *Curr Biol*, 23(22): 2262
*Joint first authors
 10. J Parker*, G Tsagkogeorga*, JA Cotton, Y Liu, P Provero, E Stupka, SJ Rossiter (2013). Genome-wide signatures of convergent evolution in echolocating mammals. *Nature*, 502(7470): 228
*Joint first authors
 9. C Roux, G Tsagkogeorga, N Bierne, N Galtier (2013). Crossing the species barrier: genomic hotspots of introgression between two highly divergent *Ciona intestinalis* species. *MBE*, 30(7): 1574
 8. G Tsagkogeorga, V Cahais, N Galtier (2012). 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
 7. V Cahais, P Gayral, G Tsagkogeorga, J Melo-Ferreira, M Ballenghien, LA Weinert, Y Chiari, K Belkhir, V Ranwez, N Galtier (2012). Reference-free transcriptome assembly in non-model animals from next-generation sequencing data. *Mol Ecol Res*, 12(5): 834
 6. P Gayral, L Weinert, Y Chiari, G Tsagkogeorga, M Ballenghien, N Galtier (2011). Next-generation sequencing of transcriptomes: a guide to RNA isolation in nonmodel animals. *Mol Ecol Res*, 11(4): 650
 5. 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 Yadatie, 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 (2010). Plasticity of animal genome architecture unmasked by rapid evolution of a pelagic tunicate. *Science*, 330(6009): 1381
 4. G Tsagkogeorga, X Turon, N Galtier, EJP Douzery, F Delsuc (2010). Accelerated evolutionary rate of housekeeping genes in tunicates. *J Mol Evol*, 71(2): 153
 3. TR Singh†, G Tsagkogeorga†, F Delsuc, S Blanquart, N Shenkar, Y Loya, EJP Douzery, D Huchon (2009). Tunicate mitogenomics and phylogenetics: peculiarities of the *Herdmania momus* mitochondrial genome and support for the new chordate phylogeny. *BMC Genom*, 10: 534
†Equal contributors
 2. G Tsagkogeorga, X Turon, RR Hopcroft, MK Tilak, T Feldstein, N Shenkar, Y Loya, D Huchon, EJP Douzery, F Delsuc (2009). An updated 18S rRNA phylogeny of tunicates based on mixture and secondary structure models. *BMC Evol Biol*, 9: 187
 1. F Delsuc, G Tsagkogeorga, N Lartillot, H Philippe (2008). Additional molecular support for the new chordate phylogeny. *Genesis*, 46(11): 592

CONFERENCE PRESENTATIONS

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| 8 – 12 Jun 2014 | <u>G Tsagkogeorga</u> , 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 Annual Meeting of the Society for Molecular Biology and Evolution, San Juan, Puerto Rico. |
| 9 – 24 Aug 2013 | KTJ Davies, NC Bennett, <u>G Tsagkogeorga</u> , J Parker, SJ Rossiter, CG Faulkes. Genetic insights into the behavioural and morphological diversity of African mole-rats (family: Bathyergidae). Poster in 14th Congress of the European Society for Evolutionary Biology, Lisbon, Portugal. |
| 7 – 11 Jul 2013 | <u>G Tsagkogeorga</u> , J Parker, JA Cotton, E Stupka and SJ Rossiter. "Phylogenomic analyses resolve the evolutionary relationships of bats (Chiroptera)." Poster in Annual Meeting of the Society for Molecular Biology and Evolution, Chicago, Illinois. |
| 22 Mar 2013 | SE Bailey, X Mao, <u>G Tsagkogeorga</u> , J Parker, B Lim, P Bates, SJ Rossiter (2012) Horseshoe bat diversification: A phylogenomic study of adaptation and discordance. Poster in BritBats: 2nd British Bat Research Symposium, Bristol, UK. |
| 23 – 26 Jun 2012 | J Parker, <u>G Tsagkogeorga</u> , JA Cotton, E Stupka and SJ Rossiter. "Signatures of genome-wide convergent molecular evolution: initial results." and P Gayral, V Cahais, <u>G Tsagkogeorga</u> , J Melo-Ferreira, M Ballenghien, L Weinert, Y Chiari, K Belkhir, V Ranwez, N Galtier. "How ecological factors influence population phylogenomics?" Posters in Annual Meeting of the Society for Molecular Biology and Evolution, Dublin, Ireland. |

- 4 – 8 Jul 2010 [G Tsagkogeorga](#), TR Singh, F Delsuc, S Blanquart, N Shenkar, Y Loya, EJP Douzery and D Huchon. “Tunicate mitogenomics and phylogenetics: the *Herdmania momus* mitochondrial genome and support for the new chordate phylogeny”. Poster in Annual Meeting of the Society for Molecular Biology and Evolution, Lyon, France.
- 18 Jun 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 focusing on: “New high-throughput sequencing technologies and their applications in the domain of biodiversity”, Montpellier, France.
- 25 – 29 Jun 2008 [G Tsagkogeorga](#), EJP Douzery and F Delsuc. “Updating tunicate phylogeny: Bayesian analysis of 18S rRNA sequences using mixture and secondary structure models”. Talk in “Bayesian Phylogeny Workshop”, Budapest, Hungary.
- 5 – 8 Jun 2008 F Delsuc, [G Tsagkogeorga](#), N Lartillot and H Philippe. “More data and better models provide further evidence that tunicates are the closest living relatives of vertebrates”. Poster in Annual Meeting of the Society for Molecular Biology and Evolution, Barcelona, Spain.
- 8 Apr 2008 [G Tsagkogeorga](#), EJP Douzery and F Delsuc. “Comparative genomics and evolution of tunicates”. Talk in one-day conference for PhD students of the Institute of Evolutionary Sciences of Montpellier (ISEM), Sète, France.
- 23 – 27 Jun 2007 [G Tsagkogeorga](#), MK Tilak, X Turon, EJP Douzery and F Delsuc. “Inferring tunicate phylogeny using 18S rRNA secondary structure models”. Talk in 4th International Tunicate Meeting, Villefrance-sur-Mer, France.
- 20 – 22 Sep 2006 [G Tsagkogeorga](#), MK Tilak, X Turon, EJP Douzery and F Delsuc. “Molecular phylogeny of Tunicates inferred from 18S rRNA sequences using secondary structure models”. Poster in 10th Evolutionary Biology Meeting, Marseille, France.

SELECTED MEETINGS & WORKSHOPS

- 4 – 7 Jan 2017 PopGroup 50 – The 50th Population Genetics Group meeting, Churchill College, Cambridge, UK.
- 8 Jun 2016 “War and Peace: the Dynamics of Evolutionary Conflict”, Centre for Ecology and Evolution (CEE) Summer Symposium, Imperial College London, London, UK.
- 19 Apr 2016 British Bats Research Symposium 2016, University College London, London, UK.
- 9 – 10 Nov 2015 “Dating species divergences using rocks and clocks”, The Royal Society, London, UK.
- 17 Mar 2015 Evolutionary Genetics and Genomics Symposium (EGGS), Cambridge University, Cambridge, UK.
- 19 – 20 Sep 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.
- 4 – 6 Dec 2013 “Ensembl API Workshop”, Cambridge University, Cambridge, UK.
Aimed at researchers and developers interested in exploring Ensembl beyond the website: core, compara, variation and functional genomics (regulation) databases and APIs.
- 5 – 6 Apr 2013 “Generic Model Organism Database (GMOD) Community Meeting”, The Hauser Forum, Cambridge, UK.
- 26 Mar 2013 “London NGS User Group - Next Generation Sequencing Conference”, Institute for Child Health - UCL, London, UK.
- 26 Apr 2012 “London NGS User Group - RNASeq”, MRC National Institute for Medical Research, London, UK.
- 17 Apr 2012 “Complete Genomics: Genomic Information for Research and Beyond Seminar”, Barts and The London School of Medicine, London, UK.
- 29 Mar 2012 “Sequence Capture For Next Gen Sequencing”, Barts and The London School of Medicine, London, UK.
- 10 - 12 Jun 2008 “MIEP’08: Mathematics and Informatics in Evolution and Phylogeny” Saint Martin de Londres, France.
- 22 Jul – 3 Aug 2007 “Workshop on Molecular Evolution”, Marine Biological Laboratory (MBL), Woods Hole, Massachusetts, USA.

GRANTS & FELLOWSHIPS

- Jul 2007 International Mobility Grant for Ph.D. Students | **PhD School of Integrative Systems in Biology, Agronomy, Geosciences, Hydrosociences and Environment, SIBAGHE, France**
I was awarded financial support during my PhD to attend the “Workshop on Molecular Evolution” in Woods Hole MA, USA.
- Oct 2006 PhD Fellowship | **Ministry of National Education, Advanced Instruction and Research, France**
I was awarded a three-year doctoral fellowship | ranked 11th in a multidisciplinary competition.
- Mar 2004 ERASMUS Scholarship | **State Scholarship’s Foundation IKY, Greece**

I received a three-month scholarship to undertake my final year research project in the University Paris-Sud XI in Orsay, France.

MEMBERSHIPS

- Feb 2013 – present **Athena SWAN Committee** | Athena SWAN is an Equality Challenge Unit for gender equality in science. I have been a member of the committee of the School of Biological and Chemical Sciences of Queen Mary University since 2013.
- Jul 2015 – present **STEMNET London** | Aiming to inspire students and young people in Science, Technology, Engineering and Mathematics, I joined the STEM London network last year as a volunteer STEM Ambassador.
- Aug 2015 – present **The Genetics Society**

REVIEWER

Biological Journal of the Linnean Society | Gene | Genome Biology and Evolution | Molecular Biology and Evolution | Molecular Ecology Resources | Molecular Phylogenetics and Evolution

TRAINING & TEACHING

I have been continually advising and training PhD students and PostDocs in bioinformatic and large-scale evolutionary analyses. I have also done some occasional lecturing to Master and Foundation students:

- 2014 – present **School of Biological and Chemical Sciences, Queen Mary University of London, London, UK**
MSc Module "Research Frontiers in Evolutionary Biology" | I give a lecture every year on Phylogenetics and Phylogenomics.
- 2016 **School of Biological and Chemical Sciences, Queen Mary University of London, London, UK**
MSc Module "Ecology and Evolutionary Biology Field Course" | Helped as teaching assistant in the tropical ecology field course that took place in Borneo. I ran small workshops in R, teaching how to estimate biodiversity and species accumulation curves.
- 2014 **School of Biological and Chemical Sciences, Queen Mary University of London, London, UK**
Foundation Programme Module "Diversity and Ecology" | I gave two lectures on using Phylogenies.

OTHER EXPERIENCE

Fieldwork:

- Jun 2010 Zaragosa - Salamanca, Spain | Five-day sampling across Spain of natural populations of invertebrate species for RNA-Seq analyses.
- Jun 2008 Villefrance-sur-Mer, France | Three-day stay in the Oceanography Laboratory of Villefrance (LOV: Laboratoire d'Océanographie de Villefranche) for planktonic tunicate species sampling. Participation in daily collections of zooplankton.

Other Professional Activities:

- Jul 2004 – Aug 2004 **Doping Control Center, Athens, Greece**
Volunteer Laboratory Assistant in ATHENS 2004 Olympic Games | Doping control analyses for anabolic and steroid substances.
- Jul 2003 – Aug 2003 **Department of Internal Medicine, Haematology Division, University Hospital of Patras, Patras, Greece**
Internship as a Trainee Laboratory Assistant.

SKILLS

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

LEISURE INTERESTS Modern Art, Yoga, Cycling, Running.

REFERENCES Available upon request.

London, 29 May 2017