Universiteit
Leiden
The Netherlands

Comparative genomics of the balanced lethal system in Triturus newts

France, J.M.

Citation
France, J. M. (2025, April 3). *Comparative genomics of the balanced lethal system in Triturus newts*. Retrieved from https://hdl.handle.net/1887/4210100

Version:	Publisher's Version
License:	Licence agreement concerning inclusion of doctoral thesis in the Institutional Repository of the University of Leiden
Downloaded from:	https://hdl.handle.net/1887/4210100

Note: To cite this publication please use the final published version (if applicable).

Curriculum Vitae

James France was born on 7th April 1990 in Bolton, Lancashire, United Kingdom. After completing his secondary education at Queen Elizabeth's Grammar School, Blackburn, he pursued an integrated master's degree at the University of Durham (2008–2013), graduating with joint honours in chemistry and biology. During his undergraduate studies he completed a research internship at the University of Washington, Seattle, USA, characterizing lateral line regeneration in zebrafish. For his master's thesis, *Characterisation of Nucleotide Binding Dynamics in the IRE1 Kinase Domain*, James investigated the activation mechanism of the enzyme IRE1, which regulates the response to misfolded proteins.

After earning his degree James became a research assistant at the University of Central Lancashire's School of Medicine and Dentistry. His research focussed on developing cell culture models of Alzheimer's disease to investigate the biochemical mechanisms that make oral bacteraemia a risk factor for dementia. Additionally, James taught as part of master's programmes, including research methods, literature appraisal and biochemistry.

James grew fascinated with the processes that might drive the evolution of apparently harmful traits. In 2019 he was given the opportunity to begin his PhD studies in the laboratory of Dr. Ben Wielstra at the Institute of Biology Leiden, Leiden University and Naturalis Biodiversity Center. These studies focus on the genomics and evolution of the mysterious balanced lethal system found in newts of the genus *Triturus*. His research has involved optimising a target capture sequencing protocol to obtain large scale genomic data from hundreds of samples of *Triturus* and other newt species. He analysed these data to construct high-density genetic maps which revealed the rearrangements that created the balanced lethal system, as well as allowing for the identification of a recent sex chromosome turnover within European newts. He then developed simulations to model the spread and paradoxical survival of the balanced lethal system. Alongside research, James was also involved in lecturing on sequencing technology and genomic architecture as part of bachelor's and master's programs, developing teaching lab protocols that explore genetic linkage, and supervising a total of twenty bachelor's and master's internship students.

After completing his PhD thesis, James hopes to continue his research into evolutionary mysteries with the genome of another European amphibian, the Edible Frog (*Pelophylax kl. Esculentus*), and its bizarre mode of reproduction, known as hybridogenesis.

List of Publications

Published

J. Mars, S. Koster, W. Babik, **J. France**, K. Kalaentzis, C. Kazilas, I. Martínez-Solano, M. C. de Visser, B. Wielstra, Phylogenomics yields new systematic and taxonomical insights for *Lissotriton* newts, a genus with a strong legacy of introgressive hybridization. *Molecular Phylogenetics and Evolution* **204**, 108282 (2025).

K. Kalaentzis, S. Koster, J. W. Arntzen, S. Bogaerts, **J. France**, M. Franzen, C. Kazilas, S. N. Litvinchuk, K. Olgun, M. de Visser, B. Wielstra, Phylogenomics resolves the puzzling phylogeny of banded newts (genus *Ommatotriton*). *Molecular Phylogenetics and Evolution* **203**, 108237 (2025).

C. Kazilas, C. Dufresnes, **J. France**, K. Kalaentzis, I. Martínez-Solano, M. C. de Visser, J. W. Arntzen, B. Wielstra, Spatial genetic structure in European marbled newts revealed with target enrichment by sequence capture. *Molecular Phylogenetics and Evolution* **194** (2024).

W. Meilink, F. D. van Beek, I. van de Breevaart, S. de Geus, C. Hellendoorn, F. Jahangier, A. Lim, M. Sluimers, A. M. Wali, J. J. C. W. van Delft, J. E. Herder, **J. France**, B. Wielstra, Difficulties in species identification in water frogs (genus *Pelophylax*) using morphological and molecular markers in The Netherlands. *Alytes* **41**, 49–55 (2024).

K. Kalaentzis, J. W. Arntzen, A. Avcı, V. van den Berg, W. Beukema, **J. France**, K. Olgun, I. van Riemsdijk, N. Üzüm, M. C. de Visser, B. Wielstra, Hybrid zone analysis confirms cryptic species of banded newt and does not support competitive displacement since secondary contact. *Ecology and Evolution* **13** (2023).

J. Robbemont, S. van Veldhuijzen, S. J. R. Allain, J. Ambu, R. Boyle, D. Canestrelli, E. O. Cathasaigh, C. Cathrine, A. Chiocchio, D. Cogalniceanu, M. Cvijanović, C. Dufresnes, C. Ennis, R. Gandola, D. Jablonski, A. Julian, D. Kranzelic, S. Lukanov, I. Martínez-Solano, R. Montgomery, B. Naumov, M. O'Neill, A. North, M. Pabijan, R. Pushendorf, D. Salvi, B. Schmidt, K. Sotiropoulos, F. Stanescu, D. Stankovic, S. Stapleton, E. Sunje, M. Szabolcs, E. Vacheva, D. Willis, A. Zimic, **J. France**, W. R. M. Meilink, T. Stark, R. P. J. H. Struijk, A. Theodoropoulos, M. C. de Visser, B. Wielstra, An extended mtDNA phylogeography for the alpine newt illuminates the provenance of introduced populations. *Amphibia Reptilia* **44**, 347–361 (2023).

J. D. Brouwer, B. Helder, **J. France**, M. C. de Visser, R. P. J. H. Struijk, B. Wielstra, An isolated crested newt population in Dutch coastal dunes: distribution relict or introduction? *Amphibia Reptilia* **44**, 19–26 (2022).

S. Koster, N. Prins, C. Dufresnes, **J. France**, M. C. de Visser, R. P. J. H. Struijk, B. Wielstra, The conservation paradox of an introduced population of a threatened species: spadefoot toads in the coastal dunes of the Netherlands. *Amphibia Reptilia* **44**, 11–18 (2022).

M. Kuijt, L. Oskam, I. D. Boer, C. Dufresnes, **J. France**, M. J. Gilbert, M. C. de Visser, R. P. J. H. Struijk, B. Wielstra, The introduction of three cryptic tree frog species in the Dutch coastal dunes challenges conservation paradigms. *Amphibia Reptilia* **44**, 1–10 (2022).

C. Vliegenthart, M. V. D. Vrede, I. D. Boer, M. J. Gilbert, P. Lemmers, **J. France**, M. C. de Visser, R. P. J. H. Struijk, B. Wielstra, The limits of mtDNA analysis for determining the provenance of invasive species: a midwife toad example. *Amphibia Reptilia* **44**, 27–33 (2022).

C. J. Carter, **J. France**, S. Crean, S. K. Singhrao, The *Porphyromonas gingivalis*/Host Interactome Shows Enrichment in GWASdb Genes Related to Alzheimer's Disease, Diabetes and Cardiovascular Diseases. *Frontiers in Aging Neuroscience* **9** (2017).

Under Review or in Revision

J. France, W. Babik, M. Cvijanović, K. Dudek, A. Ivanović, T. Vučić, B. Wielstra, Identification of Y-chromosome turnover in newts fails to support a sex chromosome origin for the *Triturus* balanced lethal system.

J. France, W. Babik, K. Dudek, M. Marszałek, B. Wielstra, Linkage mapping vs Association: A comparison of two RADseq-based approaches to identify markers for homomorphic sex chromosomes in large genomes.

J. France, M. C. de Visser, J. W. Arntzen, W. Babik, M. Cvijanović, A. Ivanović, J. Smith, T. Vučić, B. Wielstra, The balanced lethal system in *Triturus* newts originated in an instantaneous speciation event.

M. C. de Visser, **J. France**, E. McCartney-Melstad, G. M. Bucciarelli, A. Theodoropoulos, H. B. Shaffer, B. Wielstra, NewtCap: an efficient target capture approach to boost genomic studies in Salamandridae (True Salamanders and Newts).

M. de Visser, **J. France**, O. Paulouskaya, T. Brown, M. Fahrbach, C. van der Ploeg, B. Wielstra, Conserved gene content and unique phylogenetic history characterize the 'bloopergene' underlying *Triturus'* balanced lethal system.

S. Koster, R. Polanen, A. Avcı, S. Bogaerts, E. Bozkurt, F. Goudarzi, M.-R. Hemami, K. Olgun, F. Pasmans, S. Steinfartz, N. Üzüm, M. C. de Visser, **J. France**, A. Theodoropoulos, B. Wielstra, Discordance between Phylogenomic Methods Due to Introgression in Near Eastern Mountain Newts (*Neurergus*, Salamandridae).

Acknowledgements

While pursuing a PhD does not come without its challenges, it has been an enjoyable and at times extremely satisfying experience. This is due in no small part to the brilliant people I have been lucky enough to work alongside during my time in Leiden. I must express my most sincere gratitude to all those without whose knowledge, experience and effort the completion of this thesis would not have been possible.

I am particularly indebted to my supervisor Dr. Ben Wielstra. Thank you for laying the foundation of a research topic I have found completely fascinating, and for offering immensely helpful guidance and support throughout all phases of this project. I am exceptionally fortunate to have been able to work in such an open and friendly environment. I am also very grateful to my promotor Prof. Micheal Richardson for his essential and insightful contributions to this project. I must also mention and thank the other members of the Wielstra lab, none more so than my fellow PhD student Manon de Visser, with who I have worked especially closely over the last five years. From fieldwork to DNA extractions to bioinformatics, I could have not wished for a more helpful and enthusiastic colleague. To my other lab mates, Notis, Tijana, Olga and Willem, I have hugely appreciated your help, friendship and support. During my time in this lab, I have been proud to supervise a group of bachelor's and master's students, Konstantinos, Christos, Julia, Nienke, Stephanie and Lisanne to name just a few, whose infectious enthusiasm has been a joy to behold.

The work presented in this thesis is almost entirely dependent on several large sample sets. I am thus extremely grateful to Prof. Ana Ivanović and all her colleagues at the University of Belgrade for their years of effort in establishing and maintaining the *Triturus* colony which forms the basis of so much of this research. I am equally thankful to Prof. Wiesław Babik and his group at Jagiellonian University in Krakow for providing the huge number of *Lissotriton* samples which were essential to this project, and also generating the vast amount of RADseq data necessary for the identification of sex-chromosomes.

The major portion of the lab work I performed during my PhD project was undertaken at the facilities of Naturalis. None of this could have been accomplished without the help of the fantastically talented technician team, including Marina, Elza, Bertie Joan, Marcel, Roland and many others. I would also like to thank the team at the Sylvius laboratories, in particular Kees and Emilie, for their invaluable assistance. Outside of the labs I have thoroughly enjoyed being a part of the Understanding Evolution group at Naturalis and would like to acknowledge my appreciation for all the useful and fascinating discussions I've had with Vincent, Jeremy, Luis, Jorinde, Brigida, Panji and everyone else.

Of course, I cannot go without mentioning so many of my friends and colleagues within the PhD and postdoc community at Naturalis. To Ryan, Andrés, Lizzie, Kevin, Mike, Deyi, Esther, Werner, Roderick, Niels, Cas, Jada, Sjoerd, Vicky, Giovanni, Elsa, Panos, Merijn, Dewi, Kasper, Hector, Isaak, Nemi, Anabelle and everyone else who has played their part in making my time working on this research as enjoyable as it has been interesting, I am truly grateful.

Finally, I must express my immense love and gratitude to my fiancée Franziska, whose unbounded kindness and support has been so vital for me over the last seven years. Without Fran, I doubt I would have even considered taking up this project, and I certainly wouldn't have completed it. To my love, your endless belief in me and patience during even the most frustrating moments have carried me along this journey in a way that I will never be fully able to put into words. Thank you.