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## Comparative genomics of the balanced lethal system in *Triturus newts*

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# Curriculum Vitae

James France was born on 7<sup>th</sup> 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. Üzümlü, 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).

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## 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. Üzümlü, M. C. de Visser, **J. France**, A. Theodoropoulos, B. Wielstra, Discordance between Phylogenomic Methods Due to Introgression in Near Eastern Mountain Newts (*Neurergus*, Salamandridae).

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