Robert Kofler

Curriculum Vitae

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Personal data

Birth	03.02.1977 in Gmunden
Citizenship	Austria
Languages	german (mother tongue), english (fluent)
Children	Nils Matthias (2013)

Education

2018	**Habilitation in Population Genetics**, *Vetmeduni*, Vienna.
2005–2008	**Ph.D in Molecular plant breeding and Genetics**, *BOKU*, Vienna. with honors
1999–2005	**Dipl.-Ing. in Agriculture**, *BOKU*, Vienna. with honors

Professional Experience

2018	**Full Faculty of the Vienna Graduate School of Population Genetics**.
2016–	**Group Leader in Genome Evolution**, *Vetmeduni*, Wien.
2016	**Associated Faculty of the Vienna Graduate School of Population Genetics**.
2009–2016	**PostDoc and Senior PostDoc**, *Vetmeduni*, Wien.
2008–2009	**PostDoc**, *Max Planck Institute of Molecular Genetics*, Berlin/Barcelona.

Awards

2012	**Most cited young researcher**, *Vetmeduni*, Vienna.

Grants

2024-2028	**SFB Polygenic Adaptation**, ***451.578€ of 3,939,387€*** , FWF Austria, with Neda Barghi (Speaker), Joachim Hermisson (Deputy Speaker), Nicholas Barton, Magnus Nordberg, Christian Schlötterer, Kelly Swarts, Himani Sachdeva.
2022-2026	**Unravelling the Dynamics of Transposable Elements with Long-read Sequencing**, ***403,816.09 €*** , FWF Austria.
2021-2025	**Does the size of piRNA clusters predict the abundance of transposable element insertions?**, ***396,724.65 €*** , FWF Austria.

2018-2022	**Vienna Graduate School of Population Genetics**, ***11% of 2,800,182.00€*** , FWF Austria, with Christian Schlötterer (Speaker), Joachim Hermisson (Deputy Speaker), Magnus Nordberg, Reinhard Bürger, Andreas Futschik, Christian Lexer, Ovidiu Paun, Barbara Wallner, Claus Vogel.
2016-2019	**Optimizing novel, Next Generation Sequencing based, methods for linking genotype to phenotype**, ***337,900.50€*** , FWF Austria.
2017-2020	**Dynamics of a Natural Transposable Element Invasion in Experimentally Evolving Populations**, ***388,509.98€*** , FWF Austria.
2016-2020	**Profillinien**, ***108,961.60€*** , Vetmeduni Wien.

Scientific impact

Citations	5289
h-index	30
i10-index	43
Publications	47
Source	Google Scholar

Publications

* shared first author
\# shared last author

[1] **R. Kofler**, V. Nolte, and C. Schlötterer, "The transposition rate has little influence on the plateauing level of the p-element," ***Molecular Biology and Evolution***, vol. 39, no. 7, p. msac141, 2022.

[2] F. Wierzbicki, F. Schwarz, O. Cannalonga, and **R. Kofler**, "Novel quality metrics allow identifying and generating high-quality assemblies of pirna clusters," ***Molecular Ecology Resources***, vol. 22, no. 1, pp. 102–121, 2022.

[3] F. Wierzbicki, **R. Kofler**, and S. Signor, "Evolutionary dynamics of pirna clusters in drosophila," ***Molecular ecology***.

[4] F. Schwarz, F. Wierzbicki, K.-A. Senti, and **R. Kofler**, "Tirant stealthily invaded natural drosophila melanogaster populations during the last century," ***Molecular Biology and Evolution***, vol. 38, no. 4, pp. 1482–1497, 2021.

[5] A.-M. Waldvogel, B. Feldmeyer, G. Rolshausen, M. Exposito-Alonso, C. Rellstab, **R. Kofler**, T. Mock, K. Schmid, I. Schmitt, T. Bataillon, *et al.*, "Evolutionary genomics can improve prediction of species responses to climate change," ***Evolution Letters***, vol. 4, no. 1, pp. 4–18, 2020.

[6] S.-K. Hsu, A. M. Jakšić, V. Nolte, M. Lirakis, **R. Kofler**, N. Barghi, E. Versace, and C. Schlötterer, "Rapid sex-specific adaptation to high temperature in drosophila," *Elife*, vol. 9, p. e53237, 2020.

[7] **R. Kofler**, "piRNA clusters need a minimum size to control transposable element invasions," *Genome Biology and Evolution*, vol. 12, no. 5, pp. 736–749, 2020.

[8] C. Vlachos and **R. Kofler**, "Optimizing the power to identify the genetic basis of complex traits with Evolve and Resequence studies," ***Molecular Biology and Evolution***, pp. 1–21, 2019.

[9] L. Weilguny and **R. Kofler**, "DeviaTE: Assembly-free analysis and visualization of mobile genetic element compositions," ***Molecular Ecology Resources***, vol. advance access, pp. 1–21, 2019.

[10] **R. Kofler**, "Dynamics of transposable element invasions with piRNA clusters," ***Molecular Biology and Evolution***, vol. 36, no. 7, pp. 1457–1472, 2019.

[11] C. Vlachos, C. Burny, M. Pelizzola, R. Borges, A. Futschik, **R. Kofler**$^{\#}$, and C. Schlötterer$^{\#}$, "Benchmarking software tools for detecting and quantifying selection in evolve and resequencing studies," ***Genome Biology***, 2019.

[12] N. Barghi, R. Tobler, V. Nolte, A. M. Jakšić, F. Mallard, K. A. Otte, M. Dolezal, T. Taus, **R. Kofler**, and C. Schlötterer, "Genetic redundancy fuels polygenic adaptation in drosophila," ***PLoS biology***, vol. 17, no. 2, p. e3000128, 2019.

[13] C. Vlachos and **R. Kofler**, "MimicrEE2: Genome-wide forward simulations of Evolve and Resequencing studies," ***PLoS Computational Biology***, vol. 14, no. 8, pp. 1–10, 2018.

[14] **R. Kofler**, K.-A. Senti, V. Nolte, R. Tobler, and C. Schlötterer, "Molecular dissection of a natural transposable element invasion," ***Genome Research***, p. gr.228627.117, 2018.

[15] **R. Kofler**, "SimulaTE: Simulating complex landscapes of transposable elements of populations," ***Bioinformatics***, vol. 34, no. 8, pp. 1419–1420, 2018.

[16] A. M. Oppold, H. Schmidt, M. Rose, S. L. Hellmann, F. Dolze, F. Ripp, B. Weich, U. Schmidt-Ott, E. Schmidt, **R. Kofler**, T. Hankeln, and M. Pfenninger, "Chironomus riparius (Diptera) genome sequencing reveals the impact of minisatellite transposable elements on population divergence," ***Molecular Ecology***, vol. 26, no. 12, pp. 3256–3275, 2017.

[17] A. M. Jakšić, **R. Kofler**, and C. Schlötterer, "Regulation of transposable elements: interplay between TE-encoded regulatory sequences and host-specific *trans-* acting factors in *Drosophila melanogaster*," ***Molecular Ecology***, 2017.

[18] S. Franssen, **R. Kofler**, and C. Schlötterer, "Uncovering the genetic signature of quantitative trait evolution with replicated time series data," ***Heredity***, vol. 118, pp. 42–51, 2017.

[19] **R. Kofler***, A. M. Langmüller*, P. Nohaud, K. A. Otte, and C. Schlötterer, "Suitability of different mapping algorithm for genome-wide polymorphism scans with pool-seq data," ***Genes|Genomes|Genetics***, vol. 6, no. 11, pp. 3507–3515, 2016.

[20] **R. Kofler**, D. G. Sanchez, and C. Schlötterer, "Popoolationte2: Comparative population genomics of transposable elements using pool-seq," ***Molecular Biology and Evolution***, vol. 33, no. 10, pp. 2759–2764, 2016.

[21] **R. Kofler**, V. Nolte, and C. Schlötterer, "Tempo and mode of transposable element activity in *Drosophila*," ***PLoS Genetics***, vol. 11, no. 7, p. e1005406, 2015.

[22] **R. Kofler**, V. Nolte, and C. Schlötterer, "The impact of library preparation protocols on the consistency of allele frequency estimates in pool-seq data," ***Molecular Ecology Resources***, 2015.

[23] **R. Kofler**, T. Hill, V. Nolte, A. J. Betancourt, and C. Schlötterer, "The recent invasion of natural drosophila simulans populations by the p-element," ***Proceedings of the National Academy of Sciences***, vol. 112, no. 21, pp. 6659–6663, 2015.

[24] H. Topa, Á. Jónás, **R. Kofler**, C. Kosiol, and A. Honkela, "Gaussian process test for high-throughput sequencing time series: application to experimental evolution," ***Bioinformatics***, p. btv014, 2015.

[25] C. Schlötterer, **R. Kofler**, E. Versace, R. Tobler, and S. Franssen, "Combining experimental evolution with next-generation sequencing: a powerful tool to study adaptation from standing genetic variation," ***Heredity***, 2014.

[26] C. Schlötterer, R. Tobler, **R. Kofler**, and V. Nolte, "Sequencing pools of individuals – mining genome-wide polymorphism data without big funding," ***Nature Reviews Genetics***, 2014.

[27] **R. Kofler** and C. Schlötterer, "A guide for the design of evolve and resequencing studies," ***Molecular Biology and Evolution***, vol. 31, pp. 474–83, 2014.

[28] R. Tobler, S. U. Franssen, **R. Kofler**, P. Orozco-terWengel, V. Nolte, J. Hermisson, and C. Schlötterer, "Massive habitat-specific genomic response in *D. melanogaster* populations during experimental evolution in hot and cold environments," ***Molecular Biology and Evolution***, vol. 31, pp. 364–375, 2014.

[29] F. Llorens, M. Hummel, L. Pantano, X. Pastor, A. Vivancos, E. Castillo, H. Matllin, A. Ferrer, M. Ingham, M. Noguera, **R. Kofler**, J. C. Dohm, R. Pluvinet, M. Bayés, H. Himmelbauer, J. A. del Rio, E. Martí, and L. Sumoy, "Microarray and deep sequencing cross-platform analysis of the mirRNome and isomiR variation in response to epidermal growth factor," ***BMC Genomics***, vol. 14, no. 1, p. 371, 2013.

[30] S. Boitard, **R. Kofler**, P. Françoise, D. Robelin, C. Schlötterer, and A. Futschik, "Pool-hmm: a Python program for estimating the allele frequency spectrum and detecting selective sweeps from next generation sequencing of pooled samples," ***Molecular Ecology Resources***, p. n/a, 2013.

[31] **R. Kofler***, A. J. Betancourt*, and C. Schlötterer, "Sequencing of Pooled DNA Samples (Pool-Seq) Uncovers Complex Dynamics of Transposable Element Insertions in Drosophila melanogaster.," ***PLoS Genetics***, vol. 8, no. 1, p. e1002487, 2012.

[32] V. Nolte, R. V. Pandey, **R. Kofler**, and C. Schlötterer, "Genome-wide patterns of natural variation reveal strong selective sweeps and ongoing genomic conflict in Drosophila mauritiana," ***Genome Research***, vol. 23, pp. 99–110, 2013.

[33] P. Orozco-Terwengel, M. Kapun, V. Nolte, **R. Kofler**, T. Flatt, and C. Schlötterer, "Adaptation of Drosophila to a novel laboratory environment reveals temporally heterogeneous trajectories of selected alleles.," ***Molecular ecology***, vol. 21, pp. 4931–4941, 2012.

[34] **R. Kofler** and C. Schlötterer, “Gowinda: unbiased analysis of gene set enrichment for Genome Wide Association Studies.,” ***Bioinformatics***, vol. 28, no. 15, pp. 2084–2085, 2012.

[35] D. K. Fabian, M. Kapun, V. Nolte, **R. Kofler**, P. S. Schmidt, C. Schlötterer, and T. Flatt, “Genome-wide patterns of latitudinal differentiation among populations of Drosophila melanogaster from North America,” ***Molecular Ecology***, vol. 21, pp. 4748–4769, 2012.

[36] **R. Kofler**, R. V. Pandey, and C. Schlötterer, “PoPoolation2: identifying differentiation between populations using sequencing of pooled DNA samples (Pool-Seq),” ***Bioinformatics***, vol. 27, no. 24, pp. 3435–6, 2011.

[37] **R. Kofler***, P. Orozco-terWengel*, N. De Maio, R. V. Pandey, V. Nolte, A. Futschik, C. Kosiol, and C. Schlötterer, “PoPoolation: a toolbox for population genetic analysis of next generation sequencing data from pooled individuals.,” ***PLoS ONE***, vol. 6, no. 1, p. e15925, 2011.

[38] A. Esteve-Codina, **R. Kofler**, N. Palmieri, G. Bussotti, C. Notredame, and M. Pérez-Enciso, “Exploring the gonad transcriptome of two extreme male pigs with RNA-seq.,” ***BMC Genomics***, vol. 12, p. 552, 2011.

[39] A. Esteve-Codina, R. **R. Kofler**, H. Himmelbauer, L. Ferretti, A. P. Vivancos, M. A. M. Groenen, J. M. Folch, M. C. Rodríguez, and M. Pérez-Enciso, “Partial short-read sequencing of a highly inbred Iberian pig and genomics inference thereof.,” ***Heredity***, vol. 107, no. 3, pp. 256–64, 2011.

[40] R. V. Pandey, **R. Kofler**, P. Orozco-terWengel, V. Nolte, and C. Schlötterer, “PoPoolation DB: a user-friendly web-based database for the retrieval of natural polymorphisms in Drosophila.,” ***BMC Genetics***, vol. 12, p. 27, 2011.

[41] F. Llorens, M. Hummel, X. Pastor, A. Ferrer, R. Pluvinet, A. Vivancos, E. Castillo, S. Iraola, A. M. Mosquera, E. González, J. Lozano, M. Ingham, J. C. Dohm, M. Noguera, **R. Kofler**, J. A. del Río, M. Bayés, H. Himmelbauer, and L. Sumoy, “Multiple platform assessment of the EGF dependent transcriptome by microarray and deep tag sequencing analysis.,” ***BMC Genomics***, vol. 12, p. 326, 2011.

[42] **R. Kofler**, T. Teixeira Torres, T. Lelley, and C. Schlötterer, “PanGEA: identification of allele specific gene expression using the 454 technology.,” ***BMC Bioinformatics***, vol. 10, p. 143, 2009.

[43] **R. Kofler**, J. Bartos, L. Gong, G. Stift, P. Suchánková, H. Simková, M. Berenyi, K. Burg, J. Dolezel, and T. Lelley, “Development of microsatellite markers specific for the short arm of rye (Secale cereale L.) chromosome 1.,” ***Theoretical and Applied Genetics***, vol. 117, no. 6, pp. 915–26, 2008.

[44] J. Bartos, E. Paux, **R. Kofler**, M. Havránková, D. Kopecký, P. Suchánková, J. Safár, H. Simková, C. D. Town, T. Lelley, C. Feuillet, and J. Dolezel, “A first survey of the rye (Secale cereale) genome composition through BAC end sequencing of the short arm of chromosome 1R.,” ***BMC Plant Biology***, vol. 8, p. 95, 2008.

[45] L. Gong, G. Stift, **R. Kofler**, M. Pachner, and T. Lelley, “Microsatellites for the genus Cucurbita and an SSR-based genetic linkage map of Cucurbita pepo L.,” ***Theoretical and Applied Genetics***, vol. 117, no. 1, pp. 37–48, 2008.

[46] **R. Kofler**, C. Schlötterer, E. Luschützky, and T. Lelley, "Survey of microsatellite clustering in eight fully sequenced species sheds light on the origin of compound microsatellites.," ***BMC Genomics***, vol. 9, p. 612, 2008.

[47] **R. Kofler**, C. Schlötterer, and T. Lelley, "SciRoKo: a new tool for whole genome microsatellite search and investigation.," ***Bioinformatics***, vol. 23, no. 13, pp. 1683–5, 2007.

Teaching experience

University

2017–present **Introduction to scientific work**, *Vetmeduni*, Vienna, B.Sc. Veterinary Medicine **1ECTS**.

2016–present **Excercises in Population Genetics**, *Vetmeduni*, Vienna, M.Sc. Evolutionary Systems Biology **2.5ECTS**.
Coalescent, PAML, Drift, Quantitative Traits,

2013–present **Introduction to programming**, *Vetmeduni*, Vienna, B.Sc. Biomedicine **3ECTS**.
Introduction to programming in Python; Basic command line skills

2011–present **Analysis of NGS data**, *Vetmeduni*, Vienna, Graduate School of Population Genetics **2ECTS**.
Unix commands; NGS software (IGV, BWA, samtools); Python

International Workshops

2014 **Experimental Evolution**, *Practical Course on Next Generation Sequencing for Population Genetics and Experimental Evolution*, Vienna.
3 units; Mapping of reads; Design of experimental evolution; Best practices of Pool-Seq

2014 **Population Genomics with sequenced pools**, *Workshop on the analysis of whole-genome sequence data*, Neuchâtel (Switzerland).
1 day; PoPoolation1, PoPoolation2 and Gowinda

2011 **Analysis of NGS data from pools**, *Next generation sequencing workshop*, Vienna.
1 day

2010 **PoPoolation**, *Workshop on Population Genomics*, Sandbjerg (Denmark).
3 hours; Estimating natural variation in pooled populations

2009 **PanGEA**, *Summer School Ecological Genomics*, Bertinoro (Italy).
1 hour; Identification of allele specific gene expression using PanGEA

Talks

2022 KITP Adapt22 Workshop (Santa Barbara; USA): Silencing of transposable element invasions - a curious case of polygenic adaptation? Link to recorded talk

2022 Comparative Medicine Symposium 2022 (Vienna; Austria): Genome dynamics of parasitic DNA

2019 SEBES Seminar (Zurich; Switzerland): Dynamics of transposable element invasion in Drosophila; **invited speaker**

2019 ACAD Seminar Series (Adelaide; Australia): Dynamics of transposable element invasion in Drosophila; **invited speaker**

2019 ESEB (Turku; Finland): Polygenic adaptation fuels temperature adaptation in Drosophila

2019 EBI Hinxton Seminar Series (Cambridge; GB): Dynamics of transposable element invasions; **invited speaker**

2019 SMBE Satellite Meeting (Vienna; Austria): Optimizing the power to identify QTLs with Evolve and Resequence

2018 Symposium Genomic Basis of Climate Adaptation (Frankfurt; Germany): Influence of temperature on the dynamics of transposable element invasions; **invited speaker**

2017 KITP EcoEvo17 Workshop (Santa Barbara; USA): An open problem with transposable element abundance Link to recorded talk

2017 Drosophila Conference (San Diego; USA): Dynamics of a natural P-element invasion in experimentally evolving populations of *D. simulans*

2016 Mind The Gap 2016 (Vienna; Austria): Dynamics of a natural Transposable Element invasion

2016 SMBE 2016 (Brisbane; Australia): Dynamics of a natural Transposable Element invasion

2015 SMBE 2015 (Vienna; Austria): Tempo and Mode of Transposable element activity in *Drosophila*

2012 Gregor Mendel Institute (Vienna; Austria): Population Genomics in *Drosophila*

2011 Centro Nacional de Analisis genomico (Barcelona; Spain): Population Genomics in *Drosophila* using Next Generation Sequencing

2011 Symposium Sequencing in Vienna (Vienna; Austria): Population Genomics in *Drosophila melanogaster*

2011 Vall d'Hebron Institute of Oncology (Barcelona; Spain): Population Genomics using Next Generation Sequencing

2011 Summer School Ecological Genomics (Bertinoro; Italy): Identification of positive selection in *D. melanogaster* using short read sequencing

2007 COST Meeting (Teneriffa; Spain): Identification of microsatellite markers specific for the chromosome arm 1RS

Services

Reviewer Journals

Genome Research, Molecular Biology and Evolution, Nature Communications, PLoS Genetics, Nucleic Acids Research, Bioinformatics, BMC Biology, Molecular Plant, Molecular Ecology, Genetics, Evolution, Genome Biology and Evolution, Proceedings of the Royal Society B, Biology, BMC Genomics, Mobile DNA, Molecular Ecology Resources, BMC Bioinformatics, Ecology and Evolution, Computers in Biology and Medicine, PLoS One, Frontiers in Plant Science, Biology Letters, Genes, Current Genetics, Plant Communications, Peer J, Canadian Journal of Microbiology

Reviewer Funding Agencies

ANR (France), BBSRC (Great Britain)

Editor

- Editorial Board Member: Genes

Conferences

- ESEB; Symposium on Selfish Genetic Elements

Supervised Students

as main supervisor

2019	Madeleina Maria Eller; B.Sc. Student
2018-2019	Elisabeth Salbaba; B.Sc. Student
2018-2019	Lukas Weilguny; M.Sc. Student
2017-2021	Florian Schwarz; Ph.D. Student
2017-2018	Odontsetseg Cannalonga; M.Sc. Student
2017–	Filip Wierzbicky; Ph.D. Student
2017	Filip Wierzbicky; M.Sc. Student
2016–	Divya Selvaraju; Ph.D. Student
2016–2019	Christos Vlachos; Ph.D. Student
2015	Magdalena Ploir; Molecular biology Intern
2014	Anna Maria Jakoby; Bioinformatics Intern

as co-supervisor

2018-2022	Mimmi Eriksson; PhD student; with Ovidiu Paun
2016-2021	Anna Maria Langmüller; PhD Student; with Christian Schlötterer
2008	Veronika Resch; M.Sc. student; with Tamas Lelley

Interests

- Running
- Climbing
- History

References

PostDoc supervisor	**Dr. Christian Schlötterer**, *Full Professor of Population Genetics*. Institute of Population genetics Vetmeduni Vienna Contact: schlotc@gmail.com
Collaborator	**Dr. Thomas Flatt**, *Professor*. Department of Biology University of Fribourg Contact: flatt.thomas@gmail.com
Ph.D. supervisor	**Dr. Támas Lelley**, *Professor of Molecular Plant Breeding*. Department of Plant breeding BOKU Vienna Contact: tamas.lelley@boku.ac.at