

Robert Kofler

Curriculum Vitae

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Personal data

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

Education

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

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

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.

Scientific impact

Citations	2266
h-index	23
i10-index	26
Publications	34
Source	Google Scholar

Publications

- [1] **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.
- [2] **R. Kofler**, "SimulaTE: Simulating complex landscapes of transposable elements of populations," *Bioinformatics*, vol. 34, no. 8, pp. 1419–1420, 2018.
- [3] 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.
- [4] 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.
- [5] 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.
- [6] **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.
- [7] **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.
- [8] **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.
- [9] **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.
- [10] **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.
- [11] 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.

- [12] 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.
- [13] 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.
- [14] **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.
- [15] 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.
- [16] 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.
- [17] 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.
- [18] **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.
- [19] 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.
- [20] 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.
- [21] **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.
- [22] 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.
- [23] **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.
- [24] **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.

- [25] 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.
- [26] A. Esteve-Codina, **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.
- [27] 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.
- [28] 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.
- [29] **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.
- [30] **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.
- [31] 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.
- [32] 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.
- [33] **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.
- [34] **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 **Einführung in das wissenschaftliche Arbeiten**, *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

- 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 genómico (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

Reviewer

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

Supervised Students

- 2018– Lukas Weilguny; M.Sc. Student
- 2017 Lukas Weilguny; Lab rotation
- 2017– Florian Schwarz; Ph.D. Student
- 2017– Odontsetseg Cannalonga; M.Sc. Student
- 2017– Filip Wierzbicky; Ph.D. Student
- 2017 Filip Wierzbicky; M.Sc. Student
- 2016– Divya Selvaraju; Ph.D. Student
- 2016– Christos Vlachos; Ph.D. Student
- 2016– Anna Maria Langmüller; PhD Student; co-supervised with Christian Schlötterer
- 2015 Magdalena Ploir; Molecular biology Intern
- 2014 Anna Maria Jakoby; Bioinformatics Intern
- 2008 Veronika Resch; M.Sc. student; co-supervised with Tamas Lelley

Computer skills

Java	Multi-threaded object-oriented programming	+++
Python	Object-oriented dynamic programming	+++
Perl	Dynamic programming	+++
R	Statistical data analysis	+++
C/C++	Low level programming	+
C#	GUI development, object-oriented programming	++
SQL	Data base design	+
UNIX tools	grep, awk, sed, ssh, diff, sort, join, cut, zsh,...	+++

NGS tools	bwa, samtools, Picard, IGV, bedtools, TopHat, ABySS...	+++
Adobe Illustrator	Professional graphics	++
\LaTeX	Professional type setting	+++
Version control	subversion, git	++

Interests

- Science
- History
- Running
- Bouldering

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**, *SNF Professor*.
 Department of Ecology and Evolution
 University of Lausanne
 Contact: Thomas.Flatt@unil.ch
- Ph.D. supervisor **Dr. Tamas Lelley**, *Professor of Molecular Plant Breeding*.
 Department of Plant breeding
 BOKU Vienna
 Contact: tamas.lelley@boku.ac.at