## *Personal Data*


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## *Education*

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| 07/2006 | PhD in Evolutionary Biology at the University of Potsdam |
| 11/2002 | Diploma in Biology at the Christian-Albrechts-University, Kiel |

## *Employment history*

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| Since 08/2014 | Group leader (tenured since 04/2019) Fish Genomics at Eawag, Swiss Federal Institute of Aquatic Science and Technology |
| 01/2013 - 07/2014 | Postdoctoral researcher at the Max Planck Institute for Evolutionary Biology, Department Evolutionary Ecology, Plön |
| 01/2010 - 12/2012 | Postdoctoral researcher at the Westfälische Wilhelms University, Münster |
| 12/2007 - 11/2009 | Postdoctoral researcher on a Marie Curie Transfer of Knowledge host fellowship (PI Jon Slate) at University of Sheffield |
| 06/2006 - 11/2007 | Postdoctoral researcher at University of Potsdam |
| 01/2003 - 05/2006 | PhD student at University of Potsdam |

## *Institutional responsibilities (2017-2022)*

Eawag Strategy Commission (since 2021)
Eawag Seminar Committee Member (since 2015)
Eawag Database Committee (2014-2018)
Organisation of Eawag Symposium (2020, 2021, 2022)
Organisation of CEEB poster competition for young researcher (2017, 2019, 2021)

## *Approved research projects (2017-2022)*

***Science foundation grants***

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| 10/2016 - 11/2020 | PI on SNSF grant (SNSF 31003A_163446 / 1): "*Speciation genomics of the Swiss Alpine whitefish radiation*" (co-PI Ole Seehausen)<br>327 808 CHF (3 years duration + 1 year cost neutral extension) |
| 01/2016 - 10/2022 | PI on LEAD agency grants (assessed within the German Science Foundation Priority Program 1819 funded by SNSF; SNSF 310030E-160812 and SNSF 310030E_179637): "*Host virus coevolution - demography versus selection*" and continuation "*Host virus coevolution – demography versus selection in the face of multiple stressors*" (co-PI Lutz Becks, MPI Plön now University of Konstanz)<br>193 876 CHF + 285 996 CHF (3 + 3 years duration + 10 month cost neutral extension) |

***Other grants***

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| Since 06/2018 | Co-PI on sub-project: "*Reconstruction of the genome of the extinct Lake Constance whitefish and characterisation of the genetic basis of habitat adaptation to the profundal zone*" in EU Interreg Project "SeeWandel" (co-PI Ole Seehausen)<br>324 954 CHF + 22 725 CHF (4 years duration + 4 months extension) |

## *Supervision (2017-2022)*

***PhD projects***

Sofia L Mendes (co-advised with main advisor Vitor Sousa and Carla Sousa-Santos, started 2019):
*The role of hybridization in speciation and adaptation: insights from Iberian freshwater fish species*

David Frei (co-advised with Ole Seehausen, started 2018):
*Reconstructing the genome of the extinct whitefish species of Lake Constance and characterising the genetic basis of adaptation to the profundal habitat*

Linda Haltiner (co-advised with Piet Spaak, University advisor Bernhard Wehrli, started 2018)
*Competition between filter feeders in Lake Constance*

Rishi De-Kayne (co-advised with Ole Seehausen, finished 2020):
*Speciation genomics of the Swiss Alpine whitefish radiation*

Cas Retel (co-advised with Lutz Beck, University advisor Ole Seehausen, finished 2020):
*Genomics of rapid adaptation in host-virus coevolution*

Yun Huang (co-advised with Frédéric Chain, University advisor Manfred Milinski, finished 2018):
*Transcriptome variation and evidence for adaptation in threespined sticklebacks*

***MSc projects***

David Frei (University advisor Ole Seehausen, 2018):
*Genomic analysis of the whitefish diversity of Lake Constance*

***BSc projects***

Nicole Nesvadba (University advisor Ole Seehausen, 2020):
*Morphometric variation across a depth gradient in Lake Constance whitefish*

## *Teaching (2017-2022)*

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| Since 2014 | BSc lecture with practical: Scientific Methods in Ecology and Evolution (University Bern)<br>6 contact hours; ~30 students |
| 2021 | MSc Four-weeks research project in Bioinformatics & Computational Biology<br>20 contact hours, 1 student |
| 2019 | Adaptation Genomics co-instructed with Jessica Stapley (Physalia Course, Berlin, Germany)<br>40 contact hours, 22 students |
| 2016 & 2017 | MSc summer practical: Aquatic Ecology and Evolution (University Bern)<br>20 contact hours, 1 student |

## *Scientific reviewing activities (2017-2022)*

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| Since 2021 | Subject editor Molecular Ecology and Molecular Ecology Resources |
| 2020 | German Science Foundation Review Panel "Sequencing costs in projects" |
| 2016/2017 | Guest editor Philosophical Transactions B on "*Evolutionary causes and consequences of recombination rate variation in sexual organisms*" |

Reviewer for:

***Journals:***

Trends in Ecology and Evolution (2); Nature Ecology and Evolution (2); Science Advances (2); Molecular Ecology Resources (6); Methods in Ecology and Evolution (1); Molecular Ecology (9); Evolutionary Applications (2); Evolution (2); Genes (1); Genome Biology and Evolution (1); G3 (1); Journal of Evolutionary Biology (2); Aquatic Science (3); Book chapter: Methods in Fish Biology (1)

***Funding agencies:***

German Science Foundation (8); US National Science Foundation (1); Natural Science and Engineering Research Council of Canada (1); Wellcome Trust (1); Great Lakes Fishery Commission (1)

***PhD thesis:***

University of Aberdeen (thesis and oral examination), University of Helsinki (thesis pre-examination), University of Basel (thesis and oral examination)

## *Active memberships in scientific societies*

Member European Society of Evolutionary Biology
Council member ERGA (European Reference Genome Atlas)

## *Research output of the last five years (2017-2022)*

### *Peer-reviewed publications in international scientific journals*

Frei, D., De-Kayne, R., Selz, O. M., Seehausen, O., **Feulner, P. G. D.** (**2022**)
Genomic variation from an extinct species is retained in the extant radiation following speciation reversal.
*Nature Ecology & Evolution* https://doi.org/10.1038/s41559-022-01665-7

Retel C., Kowalik V., Becks L., **Feulner P.G.D.** (**2022**)
Strong selection and high mutation supply characterize experimental Chlorovirus evolution.
*Virus Evolution* 8: veac003

De-Kayne R. †, Frei D. †, Greenway R., Mendes S. L., Retel C., **Feulner P. G. D.** (**2021**)
Sequencing platform shifts provide opportunities but pose challenges for combining genomic data sets.
*Molecular Ecology Resources* 21: 653-660

Seppälä, O., Çetin, C., Cereghetti, T., **Feulner, P. G. D.**, Adema, C. M. (**2021**)
Examining adaptive evolution of immune activity: opportunities provided by gastropods in the age of 'omics'.
*Philosophical Transactions of the Royal Society B: Biological Sciences* 376: 20200158

De-Kayne R., Zoller S., **Feulner P.G.D**. (**2020**)
A *de novo* chromosome-level genome assembly of *Coregonus sp "Balchen"*: one representative of the Swiss Alpine whitefish radiation.
*Molecular Ecology Resources* 20: 1093-1109

Retel C. †, Kowalik V. †, Huang W., Werner B., Künzel S., Becks L.‡, **Feulner P.G.D.** ‡ (**2019**)
The feedback between selection and demography shapes genomic diversity during coevolution.
*Science Advances* 5: eaax0530

Huang Y., **Feulner P.G.D.**, Eizaguirre C., Lenz T.L., Bornberg-Bauer E., Milinski M., Reusch T.B.H., Chain F.J.J. (**2019**)
Genome-wide genotype-expression relationships reveal both copy number and single nucleotide differentiation contribute to differential gene expression between stickleback ecotypes.
*Genome Biology and Evolution* 11: 2344-2359

**Feulner P.G.D.**, Seehausen O. (**2019**)
Genomic insights into the vulnerability of sympatric whitefish species flocks.
*Molecular Ecology* 28: 615-629

Retel C. †, Märkle H. †, Becks L. ‡, **Feulner P.G.D.** ‡ (**2019**)
Ecological and evolutionary processes affecting viral genetic diversity.
*Viruses* 11 doi: 10.3390/v11030220

De-Kayne R., **Feulner P.G.D.** (**2018**)
A European whitefish linkage map and its implications for understanding genome-wide synteny between salmonids following whole genome duplication.
*G3: GENES, GENOMES, GENETICS* 8: 3745-3755

Frickel J., **Feulner P.G.D.**, Karakoc E., Becks L. (**2018**)

Population size changes and selection drive patterns of parallel evolution in a host–virus system.
*Nature Communications* 9: 1706

**Feulner P.G.D.** †, Schwarzer J. †, Haesler M.P., Meier J.I., Seehausen O. (**2018**)
A dense linkage map of Lake Victoria cichlids improved the *Pundamilia* genome assembly and revealed a major QTL for sex-determination.
*G3: GENES, GENOMES, GENETICS* 8: 2411-2420

Matthews B., Best R.J., **Feulner P.G.D.**, Narwani A., Limberger R. (**2018**)
Evolution as an ecosystem process: insights from genomics.
*Genome* 61: 298-309

Stapley J., **Feulner P.G.D.**, Johnston S.E., Santure A.W., Smadja C.M. (**2017**)
Variation in recombination frequency and distribution across eukaryotes: patterns and processes.
*Philosophical Transactions of the Royal Society B* 372: 20160455

**Feulner P.G.D.**, De-Kayne R. (**2017**)
Genome evolution, structural rearrangements and speciation. (Commentary)
*Journal of Evolutionary Biology* 30: 1488-1490

## *Oral contributions to international conferences*

***Invited lectures at international symposia***

**2022**, 14. - 19.03., The 69th Annual Meeting of the Ecological Society of Japan
*Gone but not forgotten: Alpine whitefish radiation retains genomic fragments from their extinct sister species*
**2021**, 12. & 14.04., 2nd Genetic Diversity Monitoring Workshop
*Spatial and temporal genomic variation in the Alpine whitefish radiation*
**2019**, 04. - 07.03., Spring Symposium organised by the Doctoral Programme in Wildlife Biology Research, Helsinki, Finland
*Genomics of rapid adaptation*
**2018**, 07. - 09.03., Wild Genomics Meeting, Bielefeld, Germany
*Genomics of the whitefish adaptive radiation in Swiss lakes*
**2017**, 10. - 15.09., German Zoological Society DZG, Section Evolutionary Biology, Bielefeld, Germany
*Genomics of ecological speciation across the Swiss Alpine whitefish radiation*
**2017**, 19. - 24.02., Gordon Research Conference Speciation, Lucca, Italy
*Whitefish genomics: divergence of large duplicated genomes*

***Contributed lectures at international symposia***

**2018**, 19. - 22.08., II Joint Congress on Evolutionary Biology, Montpellier, France
*Co-genomic signature of rapid antagonistic co-evolution*

***Invited international seminars***

**2022**, 24.01., University of Innsbruck Ökologisches Kolloquium, online (Innsbruck, Austria)
**2021**, 10.12., University of Massachusetts Lowell, online (Lowell, US)
**2021**, 02.03., Museum Koenig MEEGene Seminar, online (Bonn, Germany)
**2020**, 14.01., University of Edinburgh Roslin Institute (Edinburgh, Scotland)
**2019**, 10.04., Norwegian University of Life Sciences Cigene seminar series (As, Norway)
**2018**, 08.02., University of Lisbon (Lisbon, Portugal)
**2018**, 09.02., Instituto Gulbenkian de Ciencia Seminar Series (Oeiras, Portugal)

### *Outreach activities*

Alexander T.J., Vonlanthen P., Périat G., Selz O.M., **Feulner P.G.D.**, Seehausen, O. (**2017**)
Artenvielfalt und Zusammensetzung der Fischgemeinschaft im Zürichsee.
Projet Lac Report, Eawag, Kastanienbaum

As an advisory board member of the Seewandel project (https://seewandel.org/en/startseite/), I contribute to numerous activities associated with sustainable management of the Lake Constance ecosystem. I discuss our research with local authorities and managers of Lake Constance, and respond on a regular basis to questions from international commissions (e.g. the Internationale Gewässerschutzkomission für den Bodensee, IGKB, and Internationale Bevollmächtigtenkonferenz für den Bodensee). At the National level, I also routinely discuss our progress with members of the Federal Office of the Environment and deliver yearly progress reports (FOEN).

### *General contributions to science*

Since January **2021**: Swiss representatives on the council of ERGA (European Reference Genome Atlas; https://www.erga-biodiversity.eu/)

### *Other artefacts with documented use*

De-Kayne R., Selz O. M., Marques D. A., Frei D., Seehausen O., **Feulner P. G. D.** (**2022**)
Hybridization and a mixture of small and large-effect loci facilitate adaptive radiation.
*bioRxiv* https://doi.org/10.1101/2022.02.18.481029

Thorburn D., Sagonas K., Lenz T., Chain F., **Feulner P.G.D.**, Bornberg-Bauer E., Reusch T, Milinski M., Eizaguirre C. (**2022**)
Systematic genome scans reveal common population-specific signals of balancing selection.
Research Square https://doi.org/10.21203/rs.3.rs-1092984/v2

Stapley J., **Feulner P.G.D.**, Johnston S.E., Santure A.W., Smadja C.M. (**2017**)
Recombination: the good, the bad and the variable. (Editorial)
*Philosophical Transactions of the Royal Society B* 372: 20170279

De-Kayne R., Zoller S., **Feulner P.G.D**. (**2019**)
AWG_v1 assembly for *Coregonus sp. 'Balchen'*
Assembly: GCA_902175075.1; available on ENA and NCBI

7 data packages on ERIC (Eawag Research Data Institutional Collection):
Frei, D., De-Kayne, R., Selz, O., Seehausen, O., & **Feulner, P.** (**2021**).
Data for: Genomic variation from an extinct species is retained in the extant radiation following speciation reversal (Version 1.0). Eawag: Swiss Federal Institute of Aquatic Science and Technology.
https://doi.org/10.25678/0005AP
Retel, C., Kowallik, V., Becks, L., & **Feulner, P.** (**2021**).
Data for: Strong selection and high mutation supply characterize experimental Chlorovirus evolution (Version 1.0) [Data set]. Eawag: Swiss Federal Institute of Aquatic Science and Technology.
https://doi.org/10.25678/0005BQ
Retel, C., Kowallik, V., Huang, W., Werner, B., Künzel, S., Becks, L., & **Feulner, P. G. D.** (**2021**).
Data for: The feedback between selection and demography shapes genomic diversity during coevolution (Version 1.0) [Data set]. Eawag: Swiss Federal Institute of Aquatic Science and Technology.
https://doi.org/10.25678/00031Q

De-Kayne, R., Zoller, S., & **Feulner, P. G. D.** (**2021**).
Data for: A de novo chromosome-level genome assembly of Coregonus sp. "Balchen": one representative of the Swiss Alpine whitefish radiation (Version 1.0) [Data set]. Eawag: Swiss Federal Institute of Aquatic Science and Technology.
https://doi.org/10.25678/00034T

De-Kayne, R., & **Feulner, P. G. D.** (**2021**).
Data for: A European whitefish linkage map and its implications for understanding genome-wide synteny between salmonids following whole genome duplication (Version 1.0) [Data set]. Eawag: Swiss Federal Institute of Aquatic Science and Technology.
https://doi.org/10.25678/00033S

**Feulner, P. G. D.**, Schwarzer, J., Haesler, M. P., Meier, J. I., & Seehausen, O. (**2021**).
Data for: A dense linkage map of Lake Victoria cichlids improved the Pundamilia genome assembly and revealed a major QTL for sex-determination (Version 1.0) [Data set]. Eawag: Swiss Federal Institute of Aquatic Science and Technology.
https://doi.org/10.25678/00032R

**Feulner, P. G. D.**, & Seehausen, O. (**2019**).
Data for: Genomic insights into the vulnerability of sympatric whitefish species flocks (Version 1.0) [Data set]. Eawag: Swiss Federal Institute of Aquatic Science and Technology.
https://doi.org/10.25678/00030P

† ‡ authors contributed equally