

Personal Data

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Education

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

Employment

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

Publication summary

35 publications (for details see <https://scholar.google.ch/citations?user=fjDDI8AAAAJ&hl=en>)
 1957 citations (January 2020); h-index 18

Approved research projects

Since 09/2015 PI on SNSF grant (SNSF 31003A_163446 / 1): “*Speciation genomics of the Swiss
 Alpine whitefish radiation*” (co-PI Ole Seehausen)
 327 808 CHF (3 years duration)

Since 08/2015 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)
 193 876 CHF + 285 996 CHF (3 + 3 years duration)

Since 06/2018 Co-PI on sub-project: “*Reconstruction of the genome of the extinct Lake
 Constance whitefish and characterisation of the genetic bases of habitat
 adaptation to the profundal zone*” in EU Interreg Project “SeeWandel” (co-PI Ole
 Seehausen)
 324 954 CHF (4 years duration)

Supervision

PhD projects

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

Rishi De-Kayne (co-advised with Ole Seehausen, started 2016):

Speciation genomics of the Swiss Alpine whitefish radiation

Cas Retel (co-advised with Lutz Beck, University advisor Ole Seehausen, started 2015):

Genomics of rapid adaptation in host-virus coevolution

Yun Huang (co-advised with Frédéric Chain and Manfred Milinski, finished 2018):

Transcriptome variation and evidence for adaptation in threespined sticklebacks

MSc projects

David Frei (co-advised with Ole Seehausen, 2018):

Genomic analysis of the whitefish diversity of Lake Constance

Recent teaching

Since 2014	BSc lecture with practical (joint lecture): Scientific methods in ecology and evolution (University Bern), 6 contact hours; ~30 students
2016 & 2017	MSc summer practical: Aquatic ecology and evolution (University Bern); 20 contact hours, 1 student
2016	PhD training course: Bioinformatics and Population Genomics (Swiss Institute for Bioinformatics SIB course); 2 contact hours, 32 students

Recent editorial activities

2016 - 2017	Guest editor Philosophical Transactions B on “ <i>Evolutionary causes and consequences of recombination rate variation in sexual organisms</i> ” together with Jessica Stapley, Susan Johnston, Anna Santure, Carole Smadja
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Recent peer-reviewed publications in international scientific journals

2019

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.

2018De-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: 3745-3755Frickel 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: 2411-2420Matthews 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**2017**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**2016**Huang Y., Chain F.J.J., Panchal M., Eizaguirre C., Kalbe M., Lenz T.L., Samonte I.E., Stoll M., Bornberg-Bauer E., Reusch T.B.H., Milinski M., **Feulner P.G.D.** (2016)

Transcriptome profiling of immune tissues reveals habitat-specific gene expression between lake and river sticklebacks.

Molecular Ecology 25: 943-958Lamanna F., Kirschbaum F., Ernst A.R.R., **Feulner P.G.D.**, Mamonekene V., Paul C., Tiedemann R. (2016)Species delimitation and phylogenetic relationships in a genus of African weakly-electric fishes (Osteoglossiformes, Mormyridae, *Campylomormyrus*).*Molecular Phylogenetic and Evolution* 101: 8-18**2015**Paul C., Mamonekene V., Vater M., **Feulner P.G.D.**, Engelmann J., Tiedemann R., Kirschbaum F. (2015)Comparative histology of the adult electric organ among four species of the genus *Campylomormyrus* (Teleostei: Mormyridae).*Journal of Comparative Physiology A* 201: 357-374**Feulner P.G.D.** †, Chain F.J.J. †, Panchal M. †, Huang Y., Eizaguirre C., Kalbe M., Lenz T.L., Samonte I.E., Stoll M., Bornberg-Bauer E., Reusch T.B.H., Milinski M. (2015)

Genomics of divergence along a continuum of parapatric population differentiation.

PLoS Genetics 11: e1004966*Recent oral contributions to international conferences**Invited lectures at international symposia*

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
- 2016, 08. - 11.05., EMBO|EMBL Symposium: New Model Systems for Linking Evolution and Ecology, Heidelberg, Germany
Adaptation and speciation genomics: a fish perspective

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
- 2015, 12. - 16.07., Society for Molecular Biology and Evolution SMOBE, Vienna, Austria
Genomics of divergence along a continuum of incipient speciation

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

Other artefacts with documented use

- De-Kayne R., Zoller S., **Feulner P.G.D.**
 AWG_v1 assembly for *Coregonus sp.* 'Balchen'
 Assembly: GCA_902175075.1; available on ENA and NCBI
- De-Kayne R., Zoller S., **Feulner P.G.D.**
 A *de novo* chromosome-level genome assembly of *Coregonus sp.* "Balchen": one representative of the Swiss Alpine whitefish radiation.
bioRxiv: 771600 doi: 10.1101/771600
- 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

†‡ authors contributed equally