

# THOMAS WOLFE

## Biostatistician - Bioinformatics - Population Geneticist

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## EXPERIENCE

### Post Doctoral Fellow

#### Boku

📅 2019 - Ongoing

📍 Vienna

- Project supervision
- Experimental design
- Statistical analysis
- Modelling
- NGS sequencing
- System administration

### Doctoral student

#### University of Vienna

📅 2015 - 2019

📍 Vienna

- Transcriptomic pipelines
- Haplotype phasing
- Epigenetics pipelines
- Communication skills

## PROJECTS

### Wolbachia spread

#### FWF project P35327 / Awarded to Chrisitan Stauffer (co-written )

📅 2022 - 2026

📍 Austria

In collaboration with Nick Barton (IST) and Michael Turelli (UC Davis), this work uses mathematical models to characterise the speed and nature of the spread of a new *Wolbachia* strain along a transect. With data spanning over a decade, I examine the genomes of both flies and bacteria to unveil positive and negative interactions between both organisms. In this project, I wrote the genomics section for the FWF proposal. Now, I am involved in the supervision and elaboration of experiments to quantify the phenotypic effects of the symbiont on its host, genome assemblies, and model fitting using Bayesian statistical methods.

### Wolbachia evolution

#### FWF project P31441 / Awarded to Hannes Schuler

📅 2018 - 2022

📍 Austria

Using genomic data that from whole *Wolbachia* genomes, I explored the relevance of *Wolbachia* horizontal transfers for the invasive potential of a cherry fruit fly pest species. I developed the Nanopore pipelines in-house and used Illumina sequencing to assemble whole *Wolbachia* genomes, quantified levels of diversity at the SNP and structural levels between various strains and populations, and measured phenotypic effects of the horizontally acquired strain. The main challenge in this project was separating coinfecting bacterial strains, which required me to establish haplotype phasing bioinformatic pipelines. I also implemented statistical analyses to measure the effects of the new symbiont on the host reproductive success.

## STRENGTHS

Creative    Curious    Methodical

Critical Thinking    Open Minded

Cooperative

## SKILLS

### Statistics

Experimental Design    randomized designs

block designs    optimal design of experiments

D-optimal designs    I-optimal designs

Causal Inference    Mendelian randomization

graphical models    do-calculus    backdoor criterion

frontdoor criterion

Statistical Analysis    generalized linear models

parametric and non-parametric testing

Bayesian statistics

### Programming

R    terra    ggplot2    tidyverse    lubridate    skpr

glmm    rstan    brms    rethinking    variancePartition

dreamlet    edgeR    DESeq2    adegnet    shiny

Python    snakemake    Nextflow    Biopython

PyVCF    numpy    panda    matplotlib    whatshap

library

Stan    Slim    Julia    Golang

Awk    bioawk

Scripting    my github    Jupyter Notebook    latex

rmarkdown    bookdown

System Admin    Linux    bash scripting    tmux

slurm    LSF    ssh    server management

## Polyploid evolution

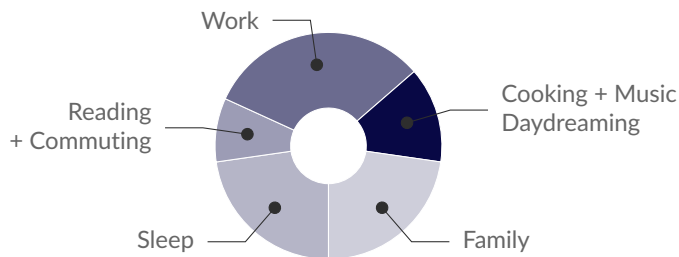
FWF project Y661 / Awarded to Ovidiu Paun

📅 2015 - 2019

📍 Austria

Here, I researched the long-term evolutionary significance of repeated allopolyploidization, mainly for two phenotypically distinct Orchid lineages maintained separately despite sharing the same parental genetic material and ongoing gene flow. I used transcriptomics and epigenetics to study the evolution of duplicated genes, levels of diversity resulting from repeated allopolyploidization, and the correlation between gene expression and phenotypes leading to biodiversity increase. For this work, I developed bioinformatic pipelines to analyse transcriptomic data, measure levels of small RNAs, assemble genomes, and read phasing.

## A DAY IN MY LIFE



## EDUCATION

Ph.D. in Evolutionary Genomics

University of Vienna / Vienna Graduate School of Population Genetics

📅 2015 - 2019

📍 Austria

Thesis title: *Dactylorhiza* Allopolyploidization, from Ecological Differentiation to Molecular Evolution.

M.Sc. in Molecular Life Sciences

University of Lausanne

📅 2014 - 2015

📍 Switzerland

Thesis title: The long term effect of polyploidization on transposable element activity.

B.Sc. in Biology

University of Lausanne

📅 2010 - 2014

📍 Switzerland

## COMMUNICATION

### 📄 Journal Articles (\* top contributions)

\* Balao, Francisco, Emiliano Trucchi, **Wolfe, Thomas M**, Bao-Hai Hao, Maria Teresa Lorenzo, Juliane Baar, Laura Sedman, Carolin Kosiol, Fabian Amman, Mark W Chase, et al. (2017). "Adaptive sequence evolution is driven by biotic stress in a pair of orchid species (*Dactylorhiza*) with distinct ecological optima". In: *Molecular ecology* 26.14, pp. 3649-3662.

**Contributions:** sRNA data analysis, SNP analysis, GO enrichments, ecological divergence analysis, visualisation, writing and result interpretation.

## Modelling

### Population genetics

population structure linkage disequilibrium  
signatures of selection horizontal gene transfers  
spatial modelling  
fluctuating selection diffusion theory

### Quantitative genetics

QTL mapping  
dominant effects epistatic effects additive effects  
pleiotropic effects polygenic adaptation

## Methods

### Spatial Data Analysis

kriging GeoJSON  
OSM

### Bioinformatics

AlphaFold vcfilter vcflib  
BCFtools bedtools freebayes flye pilon  
last minimaps2 Busco Trinity prokka  
RepeatMasker RepeatModeler panaroo seqkit  
fastsimcoal2 locator2 GADMA GMASS ...

### Genomics

Nanopore Illumina PacBio  
RADseq

### Transcriptomics

RNAseq GO enrichments  
qPCR

### Epigenetics

WGBS RRBS miRNA sRNA

## REFEREES

Assoc. Prof. Ovidiu Paun

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Prof. Christian Stauffer

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Institute of Forest Entomology, Forest Pathology and Forest Protection

Peter-Jordan-Straße 82

1190 Vienna, Austria

\* **Wolfe, Thomas M.**, Martin Pontz, Claus Vogl, Christian Lexer, and Ovidiu Paun (in prep). "Genomic interactions and ecological divergence in sibling allopolyploid marsh orchids". In: *MBE*.

**Contributions:** RNAseq read classification (phasing), bioinformatic pipelines, data analysis, coordination, sampling, writing, and result interpretation.

\* **Wolfe, Thomas M.**, Lukas Von Metz, Moussa Abd El-Hameed, Daniel J. Bruzese, Jeffrey L. Feder, Lisa Klasson, Erika Corretto, Liliya Š. Serbina, Kata Tuba, Ulrike Holz, Christian Stauffer, and Hannes Schuler (in prep). "Horizontally acquired Wolbachia, and its role in the success of the invasive cherry fruit fly pest *Rhagoletis cingulata*." In: *Current Biology*.

**Contributions:** Genome assemblies, Nanopore sequencing, crossing experiment design, structural variation analysis, sampling, writing, and result interpretation.

Bruzese, Daniel J, Hannes Schuler, **Wolfe, Thomas M**, Mary M Glover, Joseph V Mastroni, Meredith M Doellman, Cheyenne Tait, Wee L Yee, Juan Rull, Martin Aluja, et al. (2022). "Testing the potential contribution of Wolbachia to speciation when cytoplasmic incompatibility becomes associated with host-related reproductive isolation". In: *Molecular Ecology* 31.10, pp. 2935–2950.

**Contributions:** Statistical analysis, result interpretation.

Szukala, Aglaia, Jessica Lovegrove-Walsh, Hirzi Luqman, Simone Fior, **Wolfe, Thomas M**, Božo Frajman, Peter Schönschwetter, and Ovidiu Paun (2023). "Polygenic routes lead to parallel altitudinal adaptation in *Heliosperma pusillum* (Caryophyllaceae)". In: *Molecular Ecology* 32.8, pp. 1832–1847.

**Contributions:** Statistical analysis, bioinformatic pipeline supervision, result interpretation.

**Wolfe, Thomas M**, Francisco Balao, Emiliano Trucchi, Gert Bachmann, Wenjia Gu, Juliane Baar, Mikael Hedrén, Wolfram Weckwerth, Andrew R Leitch, and Ovidiu Paun (2023). "Recurrent allopolyploidizations diversify ecophysiological traits in marsh orchids (*Dactylorhiza majalis* sl)". In: *Molecular Ecology* 32.17, pp. 4777–4790.

**Contributions:** RNAseq analysis, bioinformatic pipelines, data analysis, coordination, sampling, writing, and result interpretation.

**Wolfe, Thomas M**, Daniel J Bruzese, Lisa Klasson, Erika Corretto, Sonja Lečić, Christian Stauffer, Jeffrey L Feder, and Hannes Schuler (2021). "Comparative genome sequencing reveals insights into the dynamics of Wolbachia in native and invasive cherry fruit flies". In: *Molecular Ecology* 30.23, pp. 6259–6272.

**Contributions:** Experimental design, Nanopore in-house sequencing, genome assemblies and polishing, writing and result interpretation.

**Wolfe, Thomas M**, Stephanie Hembach, Andrius Petrašiūnas, Sigita Juzėnas, Christian Stauffer, and Hannes Schuler (2022). "First report of the American eastern cherry fruit fly *Rhagoletis cingulata* (Loew)(Diptera: Tephritidae) in Lithuania". In: *BiolInvasions records* 11, pp. 1–7.

**Contributions:** Screening, data analysis, writing and result interpretation.

**Wolfe, Thomas M.**, Callum Thomas, José L. Bella, Rute R. da Fonseca, Frieder Mayer, and Ricardo Pereira (in prep). "Wolbachia distribution in the *Chorthippus* complex follows ecology and geography rather than species." In: *Microbial Ecology*.

**Contributions:** Metagenome analysis, statistical analysis, writing and result interpretation.

Zečić, Sonja, **Wolfe, Thomas M.**, Animesh Gosh, Serdar Satar, Camilla Souza Beraldo, Emily Smith, Jason J. Dambroskie, Glen Ray Emily Jernigan Hood, Hannes Schuler, and Christian Stauffer (in prep).

## LANGUAGES

English	● ● ● ● ●
French	● ● ● ● ●
German	● ● ● ● ●
Serbian	● ● ● ● ●

“Spatially varying Wolbachia frequencies predict the invasion origin of an agricultural pest recently introduced from Europe to North America.” In: *Evolutionary Applications*.

**Contributions:** Spatial analysis (kriging), result interpretation.

## Conference

“Genomic drivers of ecological divergence after recurrent allopolyploidization in *Dactylorhiza* (Orchidaceae).” (Oct. 2017). In: [Plant Genome Evolution](#). Barcelona, Spain. Poster presentation.

“Genomic interactions and their eco-physiological implications for the evolution of allopolyploid marsh orchids.” (May 2019). In: [Institute of Science and Technology Austria \(EvoLunch\)](#). Klosterneuburg, Austria. Invited speaker.

“Genomic interactions and their eco-physiological implications for the evolution of allopolyploid marsh orchids.” (May 2021). In: [Dobby Meeting](#). LMU, Germany (online). Invited speaker.

“Macro and microevolutionary drivers of allopolyploid evolution in *Dactylorhiza*” (Sept. 2018). In: [GFÖ](#). Vienna, Austria. Oral presentation.

“Molecular basis of phenotypic divergence between two orchid species (*Dactylorhiza*) with distinct ecological optima.” (Jan. 2017). In: [PopGroup 50](#). Cambridge, England. Oral presentation.

“Revisiting Wolbachia diversity between invasive and native *Rhagoletis* cherry fruit flies in the light of comparative genomics.” (Jan. 2021). In: [PopGroup 54](#). Liverpool, UK (online). Oral presentation.

“The influence of horizontally acquired Wolbachia on invasive cherry fruit fly populations: A multi-perspective study.” (Aug. 2022). In: [ESEB](#). Prague, Czechia. Poster presentation.

“The influence of horizontally acquired Wolbachia on invasive cherry fruit fly populations: A multi-perspective study.” (Mar. 2023a). In: [SEEB](#). Poznan, Poland. Invited speaker.

“The influence of horizontally acquired Wolbachia on invasive cherry fruitfly populations: A multi-perspective study.” (June 2023b). In: [Wolbachia 2023](#). Kolympari, Greece. Oral presentation.

“The macro- and microevolutionary processes driving allopolyploid evolution in *Dactylorhiza* (Orchidaceae).” (Aug. 2018). In: [ESEB](#). Montpellier, France. Poster presentation.

“The transcriptomic drivers of ecological divergence after recurrent allopolyploidization in *Dactylorhiza* (Orchidaceae).” (May 2016). In: [International Conference on Polyploidy, Hybridization and Biodiversity](#). Rovinj, Croatia. Oral presentation.

“The transcriptomic drivers of ecological divergence after recurrent allopolyploidization in *Dactylorhiza* (Orchidaceae).” (Sept. 2017a). In: [Plant Epigenetics](#). Vienna, Austria. Poster presentation.

“The transcriptomic drivers of ecological divergence after recurrent allopolyploidization in *Dactylorhiza* (Orchidaceae).” (June 2017b). In: [Botany 2017](#). Fort Worth, USA. Oral presentation.

“Unveiling Wolbachia’s influence on cherry fruit fly *Rhagoletis* species in Europe.” (Sept. 2023). In: [Natural History Museum \(NHM\)](#). Vienna, Austria. Invited speaker.

“Wolbachia infection dynamics in the invasive *Rhagoletis cingulata*.” (June 2021a). In: [CNIE](#). Turin, Italy (online). Oral presentation.

“Wolbachia infection dynamics in the invasive *Rhagoletis cingulata*.” (May 2021b). In: [Symbiosis Meeting](#). Emory, USA (online). Oral presentation.