Sonja Lecic

Curriculum Vitae

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Education

2022– **Ph.D. in *Wolbachia* Population Genomics and Cline Modeling**, *BOKU, Vienna*, Austria.

2018–2020 stopped **Ph.D. in Population Genetics**, *University of Veterinary Medicine / Vienna Graduate School of Population Genetics*, Austria.

2010–2012 **Master in Entomology**, *University of Belgrade*, Serbia.

2006–2010 **Bachelor in Biology**, *University of Belgrade*, Serbia.

Publications

Mueler SA, **Lečić S**, Merondun J, Wolf JB. Quantifying epigenetic variation with relevance to evolution. Submitted to *Nature Review Genetics*

Lečić S, Wolfe TM, Gosh A, Serdar S, Beraldo CS, Schuler H, Stauffer C, Hood G. Passengers blaze a trail: *Wolbachia* reveals invasion origin of the European cherry fruit fly in North America. Submitted to *Evolution Letters*.

Wolfe TM, Bruzzese DJ., Klasson L, Corretto E, **Lečić S**, Stauffer C, Feder, JL, Schuler H. Comparative genome sequencing reveals insights into the dynamics of *Wolbachia* in native and invasive cherry fruit flies. *Molecular Ecology* 30(23), 6259-6272 (2021).

Lečić S, Curčić S, Vujisić L, Curčić B, Curčić N, Nikoliić Z, Andelković B, Milosavljević, S, Tesević V, Makarov S. Defensive secretions in three ground-beetle species (insecta: Coleoptera: Carabidae). *Annales Zoologici Fennici* 51, 285–300 (2014).

Work Experience

2021-2022 **Prof. Jochen Wolf group**, *Division of Evolutionary Biology, Faculty of Biology, LMU Munich, Planegg-Martinsried*, Munich, Germany.
My work aimed at looking the evolutionary significance of epigenetic variation in natural populations of the Blue and Great tit species.

2018-2020 **Prof. Christian Schlötterer group**, *Institute for Population Genetics, University of Veterinary Medicine*, Vienna, Austria.
The project aimed at looking at temperature-dependent genomic signatures of insecticide resistance in an insecticide-free environment.

2017 **Prof. Wolfgang Miller group**, *Scholarship of Medical University of Vienna*, Vienna, Austria.
The internship aimed at investigating *Wolbachia* infection status and over-replication of *Wolbachia* titer in parents vs. hybrids of the *Drosophila yakuba* species group. I set-up inter-species crosses to generate inter-species hybrids.

2017 **Prof. Christian Schlötterer group**, *Scholarship of the Institute for Population Genetics, University of Veterinary Medicine*, Vienna, Austria.
My project aimed at testing the performance of different mapping and variant calling algorithms. To do this, I simulated time-series genomic data of evolved *Drosophila melanogaster* populations.

2014–2017 **Prof. Academic Marko Andjelkovic group**, *Research assistant at the Institute for Biological Research Sinisa Stankovic, Department for Population Genetics*, Belgrade, Serbia.
My work aimed at investigating altitudinal pattern of chromosomal inversion variability in *Drosophila subobscura* populations.

2013–2014 **Prof. Srecko Curcic group**, *Internship at the University of Belgrade, Insitute of Zoology*, Serbia.
The aim of the project was to investigate chemical composition of defensive secretions in ground beetle species.

Leaves

2020-2021 **Maternity leave**, *Vienna, Austria*.

Computer Skills

Linux, iOS, Windows, Office (Word, Excel, PowerPoint), LaTeX, GitLab, SLURM, conda environment, snakemake

Programing languages: R, Python, Bash, Awk, Julia

UNIX tools: grep, sed, vim, nano, emacs, sort, ssh, cut, diff, cat, mv, rm

Genomics tools: FastQC, IGV, Picard Tools, ReadTools, TrimGalore!, SAMtools, RepeatMasker, bismark, bwa, bowtie2, Novoalign, GSNAP, bbmap, freebayes, GATK, Guppy, Flye assembler, canu, Medaka, Racon/Rebaler, pilon, vcftools, bcftools, bedtools, PoPoolation2, vcflib, SHAPEIT2, IMPUTE2, TCS software, BreakDancer, SRA toolkit

R Libraries: poolSeq, CIRCOS, LDJump, heatmap2, dplyr, tydir, tidyverse, tsibble, stringr, data.table, vcfR, BioConductor, RMarkdown, cn.MOPS , BioAwk, seqtk, fastIndep, adegenet, kinship2, fshet, SIMrad, lme4, qvalue, HTSeq, DEXseq, methylKit, ggplot2, ggpubr

Python Libraries: pandas, numpy, math, stats, argparse, matplotlib, multiprocessing, datetime, pytorch

Simulation tools: MimicrEE2, poolSeq, Slim, ART

Statistics: Linear & non-linear models, generalized linear models, parametric & non-parametric testing, spatial modeling, randomized experimental design

NGS platforms: Illumina short-reads, Pool-Seq, RNA-seq, WGBS, RRBS, Nanopore

Laboratory Skills

Molecular Biology: DNA & RNA extraction, PCR, Real-time PCR, Electrophoresis, Primers and Probe design, Sanger sequencing

Evolutionary Experiments: *Drosophila* experimental evolution, common garden experiments, genotyping, fitness assays (fitness components: fecundity, developmental time and egg-to-adult viability), insecticide bioassays, behavioral/locomotor activity experiments using DAM system, *Drosophila* brain/gut/gonad dissections

Talks

2021-May Division of Evolutionary Biology, Faculty of Biology, LMU Munich, Planegg-Martinsried; Munich, Germany; Title: Epigenetic variation in natural populations and its relevance to ecology and evolution

2021-January Max Planck Intitute of Ornithology - Invited talk; Munich, Germany; Title: Navigating microsatellites and pedigrees to identify independent blue tit individuals for Pool-Seq

2019-May Scientific Advisory Board meeting (Members: Prof. Andy Clark, Prof. Nick Barton, Prof. John Parsh and Dr. Virginie Courtier-Orgogozo) - Vienna, Austria; Title: Neuronal signaling homeostasis modulates temperature-dependent cost of *Ace* insecticide resistance alleles

2019-April Intitute of Population Genetics, First Year Evaluation; Vienna, Austria; Title: Neuronal signaling homeostasis modulates temperature-dependent cost of *Ace* insecticide resistance alleles

2019-Jan PopGroup52 - Oxford, UK; **Sonja Lecic**, Rodolphe Poupardin, Viola Nolte, Agnes Jónás, Christian Schlötterer. Measuring the fitness cost of insecticide resistance with Evolve and Resequence: A case study with *Ace* resistance in *Drosophila simulans*.Link to the Abstract Book

2018-Sep Vienna Graduate School of Population Genetics, Retreat; Altaussee, Austria; Title: Accuracy of computational haplotype phasing in evolved *Drosophila simulans* populations

Courses & Workshops

2019-May **Molecular population genetics: making sence of sequence data**, *Vienna Graduate School of Population Genetics*, Vienna, Austria.

2018-Sep **Population Genetics Introductory Course**, *Vienna Graduate School of Population Genetics*, Vienna, Austria.

2018-May **Generalised Linear Models with R**, *University of Veterinary Medicine*, Vienna, Austria.

2018-April **Statistical Analysis with R**, *University of Veterinary Medicine*, Vienna, Austria.

2016-Sep **Programing in Evolutionary Biology (PEB)**, *Institite for Biological Research*, Belgrade, Serbia.

Teaching & Outreach

2019 **Experimental evolution: bringing theory and practice together**, *Vienna Graduate School of Population Genetics*, Vienna, Austria.
Part of the organization cometee and assistance with exercises

2019 **Special Statistics**, *University of Veterinary Medicine*, Vienna, Austria.
Assistance with statistical problems and exercises

2015-2017 **Population Genetics**, *University of Belgrade*, Serbia.
Assistance with population genetic problems and exercises

2015-Dec **Belgrade Science Festival**, *Science communicator*, Serbia.
Explaining scientific concepts to the general public

2015-Sep **European Researcher's Night**, *Science communicator*, Belgrade, Serbia.
Explaining scientific concepts to the general public

Languages

English	**Fluent**	*Daily usage*
Serbian	**Mothertongue**	*Mother's language*
French	**Basic**	*Basic words and phrases*
German	**Basic**	*Basic words and phrases*

Interests

- Amateur Astronomy
- Cartoon Drawing
- Writing
- Reading

References

Thomas Wolfe, PhD, *Postdoctoral Fellow*
Institute of Forest Entomology, Forest Pathology and Forest Protection (IFFF), Boku
Peter-Jordan-Straße 82 / I, 1190 Vienna, Austria
Contact: thomas.m.wolfe@boku.ac.at