

## **Newsletter September 2023**

Welcome to the 29<sup>th</sup> edition of the PopGen ALUMNI newsletter!

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Join our Tuesday webinars: <a href="https://www.popgen-vienna.at/news/seminars/">https://www.popgen-vienna.at/news/seminars/</a>

#### Recent events and news

## September 2023: "Stormy" gettogether

Our **new cohort** of students (from Iran, Turkey, Lebanon, India and Austria) was welcomed to the PopGen Vienna crowd by Christian Schlötterer, enjoying mild September weather with "Sturm" - partially fermented, new wine. A reason why PopGen and the harvest season is a meaningful combination: several



projects run at the program use pomace at the vinyards as *Drosophila* Eldorado for collecting flies.

#### July 2023: Poster award



**Elif Bozlak** (Wallner group) received a poster award at the 39th ISAG (International Society for Animal Genetics) conference 2023 in Cape Town, South Africa. Her poster's title: "The first Rangifer tarandus Y chromosomal phylogeny"

#### July 2023: PhD defense

Congratulations to **Filip Wierzbicki** (Kolfer group) – he successfully defended his PhD thesis "*Transposable elements and piRNA clusters in* Drosophila".



#### June 2023: PhD defense



**Ben Wölfl** (Hermisson group) successfully defended his PhD thesis "A theory of oligogenic adaptation of a quantitative trait". Congratulations!

## Alumni portraits

We feature a brief report about one of PopGen's graduate and faculty alumni in the Newsletter. This time, PopGen Vienna graduate alumnus **Florian Schwarz** (former PhD student of the Kofler group) gives us some insight into his work at Eurofins Genomics in Munich (DE):



"I started my PhD in 2017 with Robert Kofler. Our main goal throughout my PhD was to unravel previously unknown dynamics of Transposable Elements, mainly within *Drosophila*.

I graduated in January 2022, on the tail end of the COVID period.

While preparing my graduation I applied for a variety of different positions, mainly in industry.

In February 2022 I was offered my current position as "Business Development Manager NGS" with

the company *Eurofins Genomics*. I accepted the position, moved from Vienna back to my hometown of Munich, and started on March 1st 2022.

*Eurofins Genomics*, part of the *Eurofins Group*, is a company focused on providing a full array of genomic solutions to their customers. In my role I exclusively focus on the Next Generation Sequencing and Third Generation Sequencing applications offered by the company.

I usually act as an intermediary between our Sales and our Production teams. Common tasks in my role include:

- Collecting information on new projects
- Discussing project details (often directly with the customer)
- Evaluating feasibility and turnaround times together with the Production Team (Our services include not only sequencing, but often also extraction and bioinformatic analysis)
- Calculating all relevant costs for a given project
- Discussing larger projects and discounts with Management
- Evaluating profitability of establishing new technologies and solutions
- Observing trends within the NGS market

I enjoy this role as it offers a broad perspective on the various different applications of NGS in Research, Pharma, Agriculture, Food testing etc.

The variety of customers with different goals and needs as well as the quick developments in technology lead to a dynamic environment where it is my job to recognize and act on trends quickly to be ahead of the competition, which is a challenge I enjoy.

While many daily tasks are not directly related to my PhD studies, the knowledge and skills I gained during the PhD (both technical as well as theoretical) are invaluable, and without them I would be incapable of fulfilling my current tasks.

Moving back to my hometown has also proven to be a blessing as it allows me to be close to friends and family once again."

# Out of sight, out of mind? Experiences of our students abroad

Many of our students choose to spend three to six months abroad during their study time. **Clara Groot Crego** (advisor Ovidiu Paun) spent 6 months at the University of Antwerp, hosted by Hannes Svardal.

"A little over a year ago, I stepped on the west-bound Night Jet with a big suitcase and a 13-hour long train ride ahead of me - destination Antwerp. I slept badly and was still a bit worried that my accommodation would be a scam, but 15 hours later I did arrive at said address to find it real and comfortable to call home for the next six months. The next day, I found my way to my new institute shrouded by a forest of oak trees at the edge of an old castle moat on the southern edge of the city.



Finally arrived at the beautiful train station of Antwerp!

I joined the research group of Hannes Svardal to develop a method for studying the link between interspecific gene flow and ecological overlap of species under the support of the PopGen Vienna graduate school and an EMBO Scientific Exchange Grant. While I work on the neotropical plant subgenus Tillandsia back at home (Bromeliaceae, related to pineapple), I got to work on the fascinating African Lake cichlid fish radiations here. I was closely collaborating with Sophie Gresham, one of Hannes' PhD students, which I believe was a great experience to learn how to work as a team. She has been working on a truly large dataset of more than 2,000 individuals and 700 species of cichlids, to characterize gene flow in the radiation.

While in Antwerp, I got to discover a parallel rapid radiation to the one I work on at home, by looking up ecological traits in thick old books, talking to cichlid specialists, and at the same time thinking about general evolutionary questions such as speciation and gene flow. The work I was doing was pushing me uncomfortably far into the statistical realm, but being in a large group with more than 7 PhD students and about 4 postdocs, I got the help I needed (especially from Russian postdocs Valya and Ilya). Even better was that I got to apply the same methodology on *Tillandsia* as well, and get a broader idea of

how this method could work in different systems.



Getting statistical support from Ilya and Valya.

Finally, I got to meet a lot of bright and clever people, got to think about different topics than in my day-to-day life in Vienna, got to degustate delicious beers in good company and even spend a fun retreat in Den Haag (primarily on the beach) with a group of people I can now happily call collaborators and friends. I think the opportunity provided by the Graduate School is very enriching and I am very grateful to all the people and agencies that made this experience possible for me."



The Svardal group + me (ESEB 2022, Prague)



Svardal lab group photo at an ancient oak tree in The Hague.



Games on the beach at the retreat in The Hague.

#### **Upcoming seminars**

Our Tuesday seminars are arranged as hybrid (or online) seminars, so you can join us from all over the world! Join us for seminars by R. Stelkens, H. Ringbauer, N. Galtier, S. Wigby, I. Arkhipova, C. Aquadro, M. Malinsky, J. Crocker, M. Phillips, M. Fagny, N. Chen and D. Bolnick during the winter term!

Sign up here to receive reminders and Zoom links: <a href="https://forms.gle/N2mZ2QCdyzLFsV746">https://forms.gle/N2mZ2QCdyzLFsV746</a>

## Have a successful Autumn!

## Publications of our students this year

Signor S, Vedanayagam J, Kim BY, **Wierzbicki F**, Kofler R and Lai EC. Rapid evolutionary diversification of the flamenco locus across simulans clade Drosophila species. PLoS Genet. 19(8), e1010914. (2023) doi: 10.1371/journal.pgen.1010914

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**Chen H, Pelizzola M** and Futschik A. Haplotype based testing for a better understanding of the selective architecture. BMC Bioinformatics 24(1), 322. (2023) doi: 10.1186/s12859-023-05437-3 https://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-023-05437-3

**Yıldırım B** and Vogl C. Purifying selection against spurious splicing signals contributes to the base composition evolution of the polypyrimidine tract. J. Evol. Biol. n/a(n/a). (2023) doi: 10.1111/jeb.14205 https://onlinelibrary.wiley.com/doi/10.1111/jeb.14205

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**Scarpa A**, **Pianezza R**, **Wierzbicki F** and Kofler R. Genomes of historical specimens reveal multiple invasions of LTR retrotransposons in Drosophila melanogaster populations during the 19th century. bioRxiv 2023.06.06.543830. (2023) doi: 10.1101/2023.06.06.543830

 $\underline{https://www.biorxiv.org/content/10.1101/2023.06.06.543830v1}$ 

**Bozlak E, Radovic L**, Remer V, Rigler D, Allen L, Brem G, Stalder G, Castaneda C, Cothran G, Raudsepp T, Okuda Y, Moe KK, Moe HH, Kounnavongsa B, Keonouchanh S, Van NH, Vu VH, ... Wallner B. Refining the evolutionary tree of the horse Y chromosome. Sci. Rep. 13(1), 8954. (2023) doi: 10.1038/s41598-023-35539-0 <a href="https://rdcu.be/ddALX">https://rdcu.be/ddALX</a>

**Lai W-Y**, Otte KA and Schlötterer C. Evolution of metabolome and transcriptome support a hierarchical organization of adaptive traits. Genome Biol. Evol. evad098. (2023) doi: 10.1093/gbe/evad098 <a href="https://academic.oup.com/gbe/advance-article/doi/10.1093/gbe/evad098/7180075">https://academic.oup.com/gbe/advance-article/doi/10.1093/gbe/evad098/7180075</a>

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Borges R, **Kotari I**, **Bergman J**, Chase MA, Mugal CF and Kosiol C. Traditional phylogenetic models fail to account for variations in the effective population size. bioRxiv 2022.09.26.509598. (2023) doi: 10.1101/2022.09.26.509598 https://www.biorxiv.org/content/10.1101/2022.09.26.509598v2

See all publications <u>here</u>