ERC-CZ-funded postdoctoral position in polyploid structural genomics

<u>Start date</u>: Jan 2024 (negotiable if required) <u>Duration</u>: 2 years, minimum <u>Place</u>: Charles University, Prague, Czech Republic, EU Groups: https://www.yantlab.net/ and https://www.plantecologicalgenomics.cz/

We seek a motivated early career researcher interested in leading a research project as part of a wider programme broadly focused on addressing the *polyploid paradox*: what is the basis for the occasionally spectacular success of polyploids, against all odds?

The role is primarily computational/bioinformatic, but with optional field and wet lab components. You will have access to novel, very large-scale long-read-based population genomic data of various multiple-ploidy species. You will be formally a member of Prof Levi Yant's group, which is based in both Prague, CZ, and Nottingham, UK, and be fully integrated in the Plant Ecological Genomics group led by Filip Kolář. This role is based in vibrant Prague and integrated into a fantastic network of local and international collaborators.

We offer:

-Great science AND a competitive salary, well-exceeding the average for Prague

-A dynamic international science environment, located in an inspiring historical city centre.

-Involvement with and growth opportunities with many worldwide collaborations

Requirements:

-A passion for polyploids. Also, a strong interest in leading independent projects in a collaborative group

-Experience in handling large-scale (preferably long-read) sequence data

-A strong background in any kind of genomics or genome bioinformatics (PhD or computational MSc required)

Optional:

-Participation in teaching relevant courses and co-supervision of PhD students/junior researchers

- -Develop your independent research programme.
- -Application for additional projects (e.g. Marie Curie, EMBO, NERC, Leverhulme) is highly supported.

Project details

Whole genome duplication (WGD) occurs in all kingdoms and can promote adaptation. But WGD is traumatic to the cell, and commonly fatal for lineages. In autopolyploids (within-species WGD), sudden duplication of all chromosomes disrupts core processes, especially meiosis. Nevertheless, the rare hopeful monster that survives WGD is somehow special, occasionally experiencing runaway success. This gives rise to a 'polyploid paradox': WGD-mediated adaptability for some, despite challenges to core processes. Our work revealed the basis of adaptation to WGD with nimble, convergent evolution at WGD of genome management and DNA repair. Importantly, these processes likely affect genomic structural variation (SV) in young polyploids.

Here we leverage our discovery to ask a new question: is the post-WGD shakeup—the stumbling process of adaptation to WGD— itself the key engine for later evolutionary success? What are the exact mechanisms? That is, might WGD-mediated adaptability be grounded in adaptation to the very challenges WGD presents? Specifically, we test our hypothesis: is the (mis)management of core processes like DNA repair a key missed piece in the century-long quest to understand polyploid adaptation?

We test our hypothesis using SV-focussed graphical pangenomics on manipulated diversity in evolve-andresequence studies, using lines harboring specific candidate alleles from successful autopolyploids vs diploid alleles. I predict these candidates differentially regulate DNA repair, ion homeostasis, and stress response changes at WGD, boosting diversity at WGD and thus, adaptability. We assess functional consequences of these 'allelic shakeups' upon WGD in models spanning kingdoms, life history types, and genome diversity. Given the importance of WGD in processes ranging from crop resilience to cancer progression, by testing our hypothesis in a wide range of models in parallel, we aim to gain insight into this century-old mystery.

The project is led by Levi and three new postdoctoral researchers in Prague, collaborating with Filip Kolář, who is recruiting an additional researcher to Prague. Both candidates will be members of both labs and constitute a dynamic, interdisciplinary team focused on adaptive consequences of WGD.

Please send your CV, details for two referees, and a motivation statement in a single pdf file to Levi Yant (Levi.Yant@nottingham.ac.uk). Review of the applications begins **October 30th**, **2023**.

References/relevant examples of our work:

Konečná et al (2021) Serpentine adaptation in autopolyploid Arabidopsis arenosa is dominated by repeated recruitment of shared alleles. Nature Comm, https://rdcu.be/cutvo

Monnahan et al (2019) Pervasive population genomic consequences of genome duplication in *Arabidopsis arenosa. Nature Ecology & Evolution*, <u>https://rdcu.be/borZY</u>

Bohutínská et al (2021) Novelty and convergence in adaptation to whole genome duplication. *Molecular Biology and Evolution*, <u>https://doi.org/10.1093/molbev/msab096</u>