ERC-CZ funded postdoctoral position in genomics of convergent adaptation

Start date: negotiable
Duration: 2 years with possibility for extension
Place: Department of Botany, Charles University, Prague, Czech Republic, EU
Group: https://www.plantecologicalgenomics.cz/

We seek a highly motivated, independent early career researcher interested in leading a research program within the context of a newly starting competitive ERC-CZ Consolidator project. The projects addresses genomic drivers of repeated adaptation through analysis of available structural and population genomic data of multiple plant species (for details see below). The successful candidate will join the team of Ecological Genomics at Charles University in Prague lead by Filip Kolář and will be integrated into a network of local and international collaborators.

Requirements

- keen interest in leading an independent research program in a collaborative research group
- a strong background in structural, statistical, and/or population genomics
- PhD in evolutionary biology, genetics, bioinformatics, or related fields

We offer

- competitive salary well-exceeding the Prague city average
- work in a dynamic international environment, located in an inspiring historical city centre
- additional interdisciplinary experience through international collaboration in polyploid genomics (Levi Yant, SLU Uppsala) and comparative genomics (Sam Yeaman, U Calgary)

Optional - further possibilities for strengthening academic career

- taking part in teaching relevant courses
- supervision of master project(s) in the Bioinformatics or Evolutionary Biology program
- opportunity to develop independent follow-up research projects
- application for additional self-funded projects in national and international funding schemes (e.g. Marie Curie, EMBO fellowship, GA CR) is highly encouraged and supported

Project details

Evolution is driven by a combination of deterministic forces and stochasticity, whose relative importance remains a matter of debate. Knowing how predictable is evolution can provide insights into evolution-informed treatment of crops, pathogens or species under climate change.

This project will address repeated genome evolution in natural environments. By leveraging fascinating natural diversity of Brassicaceae plants which repeatedly naturally adapted to exceptionally strong selective pressures we aim at uncovering general mechanisms determining which portion of the genome evolves in a predictable manner. The successful candidate will work with a dozen of species for which we have recently established reference assemblies and original catalogs of natural population genomic and transcriptomic variation including repeated adaptive candidate genes. By combining already available short- and long-read sequencing data with information from public databases, the candidate will derive structural genomic and gene expression (pleiotropy) predictors across these species and will test whether genomic context or functional constraints determine the probability the same gene is reused in adaptation.

Building on our research in natural *Arabidopsis* populations (e.g. Bohutínská et al. 2021, Celestini et al. 2025, Vlček et al. 2025) the project will extend well beyond this system in order to discern generality. The candidate is expected to be fully involved in the further project design and leading the analytical part of the project. Possibility for development of further spin-off project(s) and collaborations within the interdisciplinary team and with our collaborators will be supported.

Please send your CV, contact for two referees and a half-page motivation letter in a single pdf file to Filip Kolář (filip.kolar@natur.cuni.cz). Review of the applications will begin **September 5th 2026**.

References

Bohutínská M, Vlček J, Yair S, Laenen B, Konečná V, Fracassetti M, Slotte T, Kolář F (2021): Genomic basis of parallel adaptation varies with divergence in Arabidopsis and its relatives. – *Proceedings of the National Academy of Sciences. doi:10.1073/pnas.2022713118.*

Celestini S, Lipánová V, Vlček J, Kolář F (2025): Whole-genome duplication reshapes adaptation: Autotetraploid Arabidopsis arenosa leverages its high genetic variation to compensate for selection constraints. – *Molecular Biology and Evolution. doi:10.1093/molbev/msaf298*

Vlček J, Hämälä T, Vives Cobo C, Curran E, Šrámková G, Slotte T, Schmickl R, Yant L, Kolář F (2025): Whole-genome duplication increases genetic diversity and load in outcrossing Arabidopsis. – *Proceedings of the National Academy of Sciences. doi: 10.1073/pnas.2501739122*