

The Krämer lab is inviting applications for Postdoctoral Researcher (TV-L E14, 3 years) Evolutionary and Comparative Computational Plant Genomics

At the Chair of Molecular Genetics and Physiology of Plants, we pursue genome-enabled computational approaches as well as experimental molecular functional analyses to develop an integrated understanding of plant evolutionary adaptations to rapid environmental change. Our goal is to decipher the underlying molecular mechanisms and evolutionary processes (e.g. recent and ongoing projects ERC-Advanced Grant „LEAP-EXTREME“, Transregio TRR 341 „Plant Ecological Genetics“, Research Priority Programme SPP 1819 „Rapid Evolutionary Adaptation“). Team members take advantage of large existing datasets from genome re-sequencing (ca. 1000 edaphically and ionomically indexed individuals), methylome sequencing, high-quality de novo genome assemblies (ca. 50) and extensive transcriptome datasets (tissue-based and single-cell) of the Zn/Cd-hyperaccumulating extremophile *Arabidopsis halleri*. *A. halleri* is a diploid stoloniferous perennial and obligate outcrosser with exceptionally large genetic and phenotypic diversity, well-suited for comparisons with closely related species including *Arabidopsis thaliana*.

PROJECT: You will answer biological questions by employing computer-based analyses of nucleotide sequence data, partly together with environmental and/or phenotypic parameters, population genomics (e.g. demographic analyses and simulations, population genetic studies based on individual genes or gene groups, genome-wide selection scans), possibly also genome analyses (e.g. assembly, annotation, analysis of structural variation), or analysis of regulatory/co-expression networks based on transcriptome data, in *Arabidopsis halleri* and closely related plant species. Additional experimental components are possible.

Additional tasks: Publications and presentations; teaching and supervision of students (4th semester undergraduates to doctoral students); organization and management of computational resources; working in interdisciplinary teams; acquisition of third-party funding.

YOUR PROFILE: PhD degree in population genetics, evolutionary/comparative genomics, genome analysis, bioinformatics, or related; programming skills and experience in R, Python and/or Perl, as well as in the computational analysis and the management of large nucleic acid sequence data sets ("short read" and "long read"); excellent oral and written communication skills (either at least C1 equivalent in both German and English, or alternatively C2 equivalent in English); first or senior authorship on at least one published (or accepted) peer-reviewed original scientific publication; outstanding ability and motivation for scientific work and excellence; creative, analytical, independent, well-structured and well-documented working style; excellent background in (population) genetics.

WE OFFER: Team-oriented supportive cutting-edge distinguished international research group in a campus University setting (> 35,000 students) that includes a large Botanical Garden; city (~ 300,000 people) located within a metropolitan region (5 mio. people) in northwestern Germany; several large Universities and research centers within 1 h travel; 45 min from Düsseldorf airport; adjacent to the Ruhr river valley bordering rural mountain/forest region; contract extension possible (depending on success).

Please address your application including a cover letter (describing your current research interests, how you envisage to contribute, and your career goals), CV, list of publications, and scans of academic degree certificates to **Professor Dr. Ute Krämer** (mgpp@rub.de; „ANR:4362“). We will begin to evaluate applications immediately (closing date: 7 April 2025, starting: between May and September 2025).



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