

PhD Studentship

Plant genomics and transcriptional networks (65% TvL-E)

The research group of **Professor Dr. Ute Krämer** has an opening for a **PhD student** in **plant genomics** and the **analysis of transcriptional networks**. The successful candidate will independently contribute to **high-throughput sequencing-based transcriptomics** (experimental or *in silico*) under a variety of growth conditions and in multiple plant individuals of a **large in-house biodiversity collection** comprising ~850 individuals of the **plant species *Arabidopsis halleri***. Plants treatments will comprise a variety of **nutrient deficiency** and **mineral excess** conditions, as well as cultivation in **natural soils**. Among the closest wild relatives of the common genetic model *A. thaliana*, the ecological model *A. halleri* has strongly differing biological features including extraordinarily large within-species phenotypic variation, extreme traits as well as high genetic diversity (**1-3**). The focus will be on conditions such as **heavy metal toxicity** (zinc, cadmium, lead, copper), **pH extremes** or **low nutrient concentrations** (e.g. iron, zinc, phosphate) in **soil**. Our results will identify effective strategies for future **crop improvement**, phytoremediation and phytomining. The successful candidate will be a member of an interdisciplinary team of researchers in **experimental genetics, computational genetics/genomics, molecular physiology** and **field biology**. Funding is from an **ERC Advanced Grant** awarded for an ambitious and comprehensive approach employing *A. halleri* as a model for addressing **plant local adaptation**. The goal is to understand the **nature and origin of the underlying genetic variants** as well as **genotype-phenotype relationships** in a functional network context.

Knowledge and **practical experience** in **large-scale plant cultivation** under controlled conditions, in particular in **hydroponics**, or in large-scale **sequencing-based transcriptome data analysis**, including also **statistics** and the appropriate **software packages**, are highly advantageous. Experience in **transcriptional network** construction and analysis are beneficial. Applicants should have a keen interest in programming using **R/bioconductor, Python** or **Perl, data management, automation** (for example RNA extraction, preparation of libraries for sequencing), **experimental evolution** and the **integration of data** from different research approaches. Documented skills in one or several of these tasks are highly advantageous (see also https://www.ruhr-uni-bochum.de/mgpp/Downloads/job_ad_2018_05_15_ERC.pdf).

Our **research group** is diverse and international (<http://www.rub.de/mgpp/kraemer.html>). The **laboratory, office** and **plant growth infrastructure** is large and **outstanding**, and we have substantive **gardener** and other **technical and administrative support**. **Ruhr University Bochum (RUB)** is among the **leading research universities** in Germany. As a modern reform-oriented University hosting **ca. 40,000 students**, RUB bundles the entire scope of scientific disciplines on a **single campus**. Bochum is a medium-sized city of around 300,000 inhabitants positioned in the **heart of Central Europe**, within the Rhein-Ruhr metropolitan region of more than 5 million inhabitants. Short- and long-distance **public transport** is seamless, with fast access to neighbouring **mountains and forests** as well as the **cultural programme** in Bochum and nearby cities, for example **Essen** (10 minutes), **Dortmund** (10 minutes), **Düsseldorf** (30 minutes) and **Cologne** (1 h). The University has outstanding **family support** and **day-care facilities**.

Please send your application, including a **cover letter** summarizing your expertise and research interests, a **CV**, a list of **publications, degree certificates** and the **summary** of your Master thesis, to Prof. Dr. Ute Krämer (Ute.Kraemer@rub.de) by email, with the subject line "**Application PhD Studentship ERC PG-2018**". Projected start date 10/2019 (change possible)

1. Hanikenne M, *et al.* (2008) *Nature* **453**: 391-395. DOI: 10.1038/nature06877; **2.** Stein RJ, *et al.* (2017) *New Phytol* **213**: 1274-1286. DOI: 10.1111/nph.14219; **3.** Hanikenne M, *et al.* (2013) *PLoS Genet* **9**(8):e1003707. DOI: 10.1371/journal.pgen.1003707