



PhD Program between the Freie Universität Berlin (FUB) and the China Scholarship Council (CSC)

**Open PhD Position at Freie Universität Berlin,
offered only to Chinese CSC scholarship candidates 2025**

Department/Institute: | Institute for Biology |

Subject area: | Human Evolution |

Name of Supervisor: | Prof. Katja Nowick |

Number of open PhD positions: | 2 |

Type of the PhD Study: | Full-time |

Project title: | Molecular evolution of humans |

PhD Project description:

Our group “Human Biology and primate Evolution“ investigates the molecular evolution of humans using state-of-the art experimental and computational methods. Our focus is on differences in gene regulation, evolution of transcription factors and non-coding RNAs and their influence on the evolution of the human brain, its development and functions.

The PhD student can perform either a project on 1) the comparative functional analysis of selected transcription factors, on 2) the computational analysis of the evolution of transcription factors and their networks, or combining both aspects depending on interests and expertise.

1) Our group has identified several transcription factors that are specific to humans or have human specific sequence differences. Some of these transcription factors are known to be important for proper development of cognitive skills. We want to investigate, which genes are regulated by these transcription factors and how their target genes differ between humans and other great apes. To this end, we are using induced pluripotent stem cells from several great ape species. These cells will be differentiated into neurons. The transcription factors will be knocked-out or overexpressed during the course of neuronal differentiation. We will investigate how this experimental manipulation effects neuronal phenotypes on a developmental and evolutionary basis. We will identify target genes using ChIP-Seq, CUT&RUN, and RNA-Seq methods. The aim with this project is to reveal how changes in transcription factor genes contribute to the development of human specific cognitive skills.

2) Cognitive skills are complex traits and as such determined by a combination of genetic and other factors. To fully unravel the molecular basis of cognition it is thus important to study the networks of genes involved in cognition and not individual genes. Our group has developed

methods for the comparative analysis of co-expression networks, with a focus on interactions of transcription factors and non-coding RNAs. We want to investigate how the gene regulatory network involved in cognition has changed during evolution enabling distinct human cognitive skills. To this end, we will examine brain transcriptome data from several primates as well as from humans with certain cognitive disorders. We expect to gain valuable insight into the complex molecular changes that may underlie cognitive differences between humans and other primates.

Language requirements:

- IELTS: 6,5 oder TOEFL: 95 ibt

Oder

- Test Daf 16 bzw. DSH 2

Academic requirements:

Completed University studies (Diplom or Master) in Biology or Bioinformatics or another relevant field.

Required: Strong interest in human molecular evolution

Desired:

- Experience with working with stem cell and molecular biology techniques, such as conducting research with induced pluripotent stem cells, differentiation into neuronal cells, CRISPR/Cas9, functional investigation of transcription factors and non-coding RNAs, CUT&RUN, ChIRP-Seq, RNA-Seq

and/or

- Experience with bioinformatics methods for the analysis of genomics and transcriptomics data, such as ChIP-Seq, CUT&RUN-Seq and RNA-Seq data, computational analysis of gene regulatory networks, programming in R or Python

Information of the professor or research group leader (website, awards etc.):

Research Focus of our lab:

Our group studies the **evolution of primates**. We are especially interested in the **molecular forces that shape phenotypic differences between primate species**. What makes us human? Why does a chimpanzee look like a chimpanzee? While the genomic information of several primate species is available, we are still far from translating genomic differences into specific phenotypic effects.

Our main focus is on the impact of **transcription factors (TFs)** on differences in transcriptomes, gene regulatory networks, and ultimately the phenotype. TFs are proteins that form gene regulatory networks to regulate the expression of all genes. TFs typically bind to specific DNA sequence motives to control the expression of a few to many other genes. Therefore, evolutionary changes in TFs can potentially have **large impacts on the phenotype** of a species. Indeed, we demonstrated that some TF genes show significantly more sequence and expression differences between humans and chimpanzees than other types of

genes. Intriguingly, some of these **fast evolving** TFs seem to play a role in **brain** and **cognitive functions**.

For more information, visit our website: <http://www.nowick-lab.info>

Information about the PI:

I did my PhD at the Max-Planck-Institute for Evolutionary Anthropology in Leipzig, Germany. Under the supervision of Prof. Svante Paabo, I studied the functions and evolution of FOXP2, a transcription factor gene involved in language acquisition, in primates. Inspired by the big impact a sequence change in one gene can have on human evolution, I joined the lab of Prof. Lisa Stubbs in the USA for my postdoc, to investigate the largest group of transcription factor genes, the Kruppel-type zinc finger genes, in primates. My work lead to a higher recognition of the importance of gene regulation and the factors regulating it for the evolution of phenotypes, among them cognition in humans.

Since 2011, I lead my own independent research group; in 2016, I became a university professor. I have already supervised 4 postdocs, 10 PhD students, more than 20 Bachelor and Master students.

Please note:

In a first step, the complete application should be uploaded to the online portal (<https://fuberlin.moveon4.de/form/60acfece5d328710e40bdbd5/eng>) for evaluation by January 15th, 2025.