

**MAX-PLANCK INSTITUTE FOR
DEVELOPMENTAL BIOLOGY**

Department for Integrative Evolutionary Biology

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Open PhD position in Evolutionary Genomics

Have you ever had a burning question that would not let you sleep until you had the answer? Have you always had the feeling that understanding is more important than application? Are you thrilled by the prospect to find something that no one else in the world has seen before? If you additionally have the incentive to combine molecular and computational biology, have excellent communication skills, and you want to dedicate the next 3-5 years of your life to basic research, then join our department for Integrative Evolutionary Biology.

Our team: We are a highly interdisciplinary team working on the interface between molecular biology, developmental biology, population genetics, ecology, and evolutionary biology. Our model system is a nematode related to *Caenorhabditis elegans* which is one of the most important model organism in biomedical research. Our lab has established a second nematode species, *Pristionchus pacificus*, as model for comparative studies with *C. elegans*. Our current focus is on studying how environmental cues influence developmental decisions and how these processes drive speciation and genome evolution. To this end, we are investigating chemical signaling between nematodes, interactions with bacteria and we try to get mechanistical insights into the genetic basis of these and various other traits. Our Evolutionary Genomics and Bioinformatics group integrates analysis of next generation sequencing data and statistical analysis to find associations between genotype and phenotype and provides comparative and functional genomic analyses for further characterizing regulatory networks and selective forces acting on the underlying genomic loci.

Your profile: We are looking for a highly motivated student with a Masters or equivalent degree from any biomedical field. The applicant must be willing to acquire basic computational skills (familiarity with a command line interface and good knowledge in one scripting language) and spend at least 50% of the time in the dry lab. Furthermore, excellent communication skills are essential to successfully interact in this highly interdisciplinary environment.

Our offer: We have one open PhD position (initial contract for three years with salary according to the German public service pay scale) in the Evolutionary Genomics and Bioinformatics Group. This includes access to the working environment and resources of one of the world's most successful organizations in basic research. Two research proposals for

potential PhD projects are briefly described below, but we highly encourage applicants to propose their own research projects and are happy to discuss these during the interview.

To apply: Please send coverletter, CV, and name and contact details of two references to christian.roedelsperger@tuebingen.mpg.de

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Further information

<http://www.sommerlab.org/>

<http://www.eb.tuebingen.mpg.de/>

Project 1: Systems biology of the interaction between nematode and their microbiome

The fact, that depending on environmental cues, nematode larvae of *C. elegans* and *P. pacificus* make irreversible developmental decisions, such as the entry into an alternative long-lived dauer stage, highlights the influence of environmental factors on development. Nematodes of the *Pristionchus* lineage display a second developmental plasticity that allows them to develop into two different morphs that are specialized to either bacterial or predatory feeding. Studies from both nematodes have shown that pheromones controlling both decisions are derived from primary metabolism, suggesting that worms communicate their nutritional status to themselves as well as to the environment. In this study, we want to investigate how the microbiome influences the nutritional state of the bacterial feeding nematode and the associated consequences on development and other traits? Previous studies in our lab have established a collection of more than 100 bacterial isolates (Akduman et al. 2018) and we have started to characterize the development and behavior of worms that are grown on different diets (Sangvhi et al. 2016). The goal of this project is to combine genome sequencing of bacteria with expression profiles and phenotyping of nematodes to ask:

- To what extent does the microbiome affect nematode development and fitness?
- Which nematode genes respond to differences in the microbiome?
- Which bacterial components cause these responses?

Tasks/Techniques: basic worm handling and staging, library preparation for next generation sequencing, physiological assays and stainings, reporter constructs, EMS and transposon mutagenesis, genome assembly and annotation, comparative genomic and gene expression analysis.

References

Sangvhi, Baskaran, Röseler, Sieriebriennikov, Rödelsperger, Sommer. (2016):
Life History Responses and Gene Expression Profiles of the Nematode *Pristionchus pacificus*
Cultured on *Cryptococcus* Yeasts.

PLoS One:e0164881. doi: 10.1371/journal.pone.0164881.

Akduman, Rödelsperger, Sommer (2018):

Culture-based analysis of *Pristionchus*-associated microbiota from beetles and figs for studying nematode-bacterial interactions.

PLoS One:e0198018. doi: 10.1371/journal.pone.0198018.

Project 2: Comparative genomics of gene gain and loss in nematodes

In the preface of his visionary book “Evolution by Gene Duplication”, Susumu Ohno wrote: “*Yet, being an effective policeman, natural selection is extremely conservative by nature. Had evolution been entirely dependent upon natural selection, from a bacterium only numerous forms of bacteria would have emerged. The creation of metazoans, vertebrates and finally mammals from unicellular organisms would have been quite impossible, for such big leaps in evolution required the creation of new gene loci with previously nonexistent functions.*”. He postulated that only gene duplication could generate the redundancy that would allow organisms to accumulate formerly forbidden mutations. When the *P. pacificus* genome was sequenced and compared to *C. elegans*, we found that only 20% of genes had an exact correspondence in *C. elegans* and around 45% of genes have undergone duplication events in either of the lineages. Due to the overwhelming abundance of gene duplications, we are strongly interested in studying their role as a potential driver of phenotypic diversity. Previously, we observed that many developmental genes have undergone duplications possibly to increase the total gene dosage. However, when investigating duplication events at an intraspecies level, preliminary analyses suggest that in a majority of cases, one of the copies appears to be transcriptionally silent (Rödelsperger. 2018). We have recently established a phylogenomic data set (Prabh et al. 2018) that can be used to study duplication processes and at various time-scales asking the following questions:

- How does duplication affect gene dosage?
- Are both duplicate copies equal or is there an ancestral and a daughter copy?
- Are both copies functional?
- How does duplication change evolutionary rates?

Tasks/Techniques: Analysis of evolutionary constraints with PAML, gene expression profiling, comparison of synteny across species, population genomic analysis

References

Rödelsperger. (2018):

Comparative Genomics of Gene Loss and Gain in *Caenorhabditis* and Other Nematodes. *Methods Mol Biol.* 1704:419-432. doi: 10.1007/978-1-4939-7463-4_16.

Prabh, Roeseler, Witte, Eberhardt, Sommer, Rödelsperger. (2018): Deep taxon sampling reveals the evolutionary dynamics of novel gene families in *Pristionchus* nematodes. *Genome Research.* gr.234971.118. doi: 10.1101/gr.234971.118.