In the group

Molecular Cell Dynamics, Jun. Prof. Dr. M. Simon

Saarland University, Centre for Human and Molecular Biology, a PhD student position is available in the DFG funded Project

An integrative epigenomic approach to discover small RNA mediated regulatory programs in *Paramecium tetraurelia*

We offer a three year position (65% TV-L 13) in this project which is in close collaboration with the group of Dr. M. Schulz, Multi-Modal Computing and Interaction (Saarland University). For the wet-lab part of the project, we search for a highly motivated student with outstanding knowledge in RNAi, siRNAs and siRNA induced heterochromatin formation. Handling of NGS data and experience in ciliate genetics is welcome. The methodological focus of the project lies on siRNA sequencing, ChIP/ChIPseq, and immunoprecipitation procedures.

Please send applications including a detailed curriculum vitae, a synopsis of your diploma thesis, a publication list (if available), and two addresses for reference per e-mail to

martin.simon@uni-saarland.de

Deadline is July, 8th 2016.

Project description:

Recent advances in RNA Biology show that small RNA molecules control phenotypic variation at the epigenetic level either by post-transcriptional or transcriptional inactivation of gene expression. However, the ongoing work mostly focuses on individual loci and individual mechanisms rather than estimating the extent to which such mechanisms contribute to transcriptome dynamics, and as a consequence, to phenotypic plasticity or phenotypic robustness. The epigenetic model organism Paramecium allows us to study genome wide RNA and chromatin dynamics to get an insight into small RNA controlled short-term regulation of gene expression and long-term manifestation of gene expression patterns by epigenetic mechanisms. Recently, we described different RNA-mediated silencing pathways acting at different levels. Now, we will analyse genome wide small RNA/chromatin associations in different metabolic states dissecting post-transcriptional and transcriptional silencing pathways. This will be achieved by an integrative approach using bioinformatics to differentiate between newly identified siRNA clusters associated or not associated with heterochromatin formation, as well as biochemical analysis of siRNAs and dissection of their genetic requirements such as RNAi components involved in post-transcriptional or transcriptional silencing. Further, a new integrative analysis approach will be used to associate short RNA abundance and chromatin modifications with gene expression. We will model trans acting siRNA networks enabling coordinated activation and silencing of gene groups, as well as identification of trans acting RNAs derived from gene duplicates. We will not only be able to describe the extent of epigenetic pathways controlling gene expression and adaptation of this unicellular organism during vegetative growth, we will moreover analyse which of these epigenetic characters can be passed on to sexual progeny. We will identify genetic requirements for epigenetic inheritance and manifestation of positively selected gene expression patterns by small RNAs, which are mobile elements between generations. This will be the key to understand short-time Lamarckian adaptation in contrast to long-term Darwinian evolution.