



## **Thomas Wolf**

Phone: +49 3641 532-1457 Email: [thomas.wolf@leibniz-hki.de](mailto:thomas.wolf@leibniz-hki.de)

## **Bioinformatic investigation and prediction of gene regulatory elements in pathogenic fungi**

Understanding and modeling of gene regulation in fungi requires knowledge about transcription factors (TFs) and transcription factor binding sites (TFBSs). The increasing number of sequenced genomes and the huge amount of gene expression data together with the availability of computational methods allow to predict TFs and TFBSs.

Novel methods for TFBS prediction will be applied and improved by integration the experimental findings stored in databases. A novel tool integrating RNA-Seq data with prior knowledge to reverse engineer regulatory networks will be created. RNA-Seq from fungal data will be exploited to refine the understanding of the organization of regulatory elements. These elements will be studied and modeled in pathogenic fungi. A special emphasis will be made on the regulation of secondary metabolite gene clusters, which are in the research focus of the HKI.

### **Publications**

Rischer M, Klassen JL, Wolf T, Guo H, Shelest E, Clardy J, Beemelmans C (2016) Draft Genome Sequence of *Shewanella* sp. Strain P1-14-1, a Bacterial Inducer of Settlement and Morphogenesis in Larvae of the Marine Hydroid *Hydractinia echinata*. *Genome Announc* 4(1), [Details PubMed](#)

Klassen JL, Rischer M, Wolf T, Guo H, Shelest E, Clardy J, Beemelmans C (2015) Genome Sequences of Three *Pseudoalteromonas* Strains (P1-8, P1-11, and P1-30), Isolated from the Marine Hydroid *Hydractinia echinata*. *Genome Announc* 3(6), [Details PubMed](#)

Klassen JL, Wolf T, Rischer M, Guo H, Shelest E, Clardy J, Beemelmans C (2015) Draft Genome Sequences of Six *Pseudoalteromonas* Strains, P1-7a, P1-9, P1-13-1a, P1-16-1b, P1-25, and P1-26, Which Induce Larval Settlement and Metamorphosis in *Hydractinia echinata*. *Genome Announc* 3(6), [Details PubMed](#)

Wolf T, Shelest V, Nath N, Shelest E (2015) CASSIS and SMIPS: promoter-based prediction of secondary metabolite gene clusters in eukaryotic genomes. *Bioinformatics* 32(8), 1138. [Details PubMed](#)

Wartenberg A, Linde J, Martin R, Schreiner M, Horn F, Jacobsen ID, Jenull S, Wolf T, Kuchler K, Guthke R, Kurzai O, Forche A, d'Enfert C, Brunke S, Hube B (2014) Microevolution of *Candida albicans* in macrophages restores filamentation in a nonfilamentous mutant. *PLoS Genet* 10(12), e1004824. [Details PubMed](#)

## **Supervisor**

[Reinhard Guthke](#)

## **Co-Supervisors**

[Axel A. Brakhage](#)

## **Start of PhD**

May 15, 2012

## **Doctoral Disputation**

May 12, 2017