



Michael Jahn

Curriculum vitae

Personal information

Name Michael Jahn, PhD
Date of birth Dec 31, 1985
Born in Dresden, Germany
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Current position

Post-doctoral fellow, Group of Prof. Paul Hudson, Science For Life Laboratory, Stockholm. Topic: Systems biology and metabolic engineering of photoautotrophic bacteria.

Education

July 10, 2015 **Graduated *Doctor rerum naturalium***, at the University of Leipzig, Germany, with *summa cum laude* (1.0).
2011–2015 **PhD studies**, Group of Prof. Susann Müller, Dept. Environmental Microbiology, Helmholtz-Centre for Environmental Research, Leipzig.
Thesis: 'Characterization of population heterogeneity in a model biotechnological process using *Pseudomonas putida*'.
2005–2011 **Diploma studies, biology**, Dresden University of Technology (TUD), main subjects: genetics, biochemistry, immunology.
Diploma thesis: 'Dynamic mating pheromone gradients for induction of mating projection and fluorescence in yeast', group of Prof Gerhard Rödel, grade 1.2.
1996–2004 **High school**, Romain-Rolland-Gymnasium, Dresden, Abitur with grade 1.6.
1992–1996 **Elementary school**, Dresden.

Work experience

- 5/2016–now **Post-doctoral researcher**, Systems biology analysis of cyanobacteria at the group of Prof. Paul Hudson, Science For Life Laboratory, Stockholm (belongs to KTH).
- 8–12/2009 **Erasmus internship**, Center of Excellence in Evolutionary Genetics and Physiology at the group of Prof. Mikko Nikinmaa, Dept. of Biology, University of Turku, Finland.
- 2008–2009 **Student assistant**, Institute of Genetics, group of Prof. Gerhard Rödel, Dept. of Biology, Dresden University of Technology (TUD).
- 2007–2008 **Student assistant**, Mitteldeutscher Praxisverbund Humangenetik, Dresden.
- 2004–2005 **Voluntary service 'Freiwilliges Ökologisches Jahr'**, national park 'Sächsische Schweiz', tour guide and education.

Leaves

- 11/2019–5/2020 Parental leave with 2nd child Sophie
- 9/2015–5/2016 Parental leave with 1st child Simon

Awards

- Nov 25, 2015 **PhD-Award 2015** by the Helmholtz-Centre for Environmental Research, Leipzig. Awarded annually for excellence of the dissertation, prize money 1,000 Euro.

Awarded grants

- Nov 11, 2019 **Investigation of protein resource allocation in the model CO₂ fixing bacterium *Ralstonia eutropha*** (Swedish: Undersökning av proteiners resursfördelning i en modell för CO₂-fixerande bakterier, *Ralstonia eutropha*).
Funding agency: FORMAS. Project number: 2019-01491. Project leader: Dr. Michael Jahn. Awarded funding for period 2020-01-01-2021-12-31. Total funds: 2,000,000 SEK (equals around 200,000 Euro).

Teaching and supervision

- Teaching Planned teaching activity for the course **CB2030 'Systems biology'** at Kungliga Tekniska Högskolan (KTH, together with Prof. Lukas Käll), study period winter 2019 – spring 2020. Teaching activity was unfortunately postponed due to parental leave and COVID-19 outbreak. It is intended to resume teaching activity as soon as possible. Topics covered for this course among others: Pathway Analysis, Genome-scale metabolic models, Flux Balance Analysis.
- Supervision Supervised several master and intern students during my PhD and postdoctoral studies:
- Alexander Mattausch, intern biotechnology, University of Heidelberg, 2019
 - Timothy Bergmann, master student biotechnology (KTH, Stockholm), 2019
 - Raquel Perruca, master student, Lund Technical University, 2018
 - Carsten Vorpahl, master student University of Leipzig, 2015
 - Dominique Türkowsky, master student University of Leipzig, 2014

Scientific interests and expertise

Sustainability	Current overuse of (fossil) planetary resources and disposal of non-degradable waste into the environment makes the shift towards a sustainable economy mandatory. The concept of the bioeconomy entails that conventional chemical processes or materials be replaced with sustainable ones. Autotrophic microbes can play their roll as a versatile, efficient and biodegradable catalyst.
Metabolic modeling, data science and visualization	High-throughput methods generate larger amounts of biological data than ever before. This poses problems, but also opportunities. I envision a close integration of experiments and data with predictive mathematical models , such as genome scale metabolic models. This allows to integrate the current state of knowledge into a coherent system, spot contradictions or errors, and identify overarching themes in metabolism.
Metabolic engineering	Microbial cells are 'programmed' for production of biomass, not fine chemicals. Rational design and engineering of pathways is necessary to turn photo-autotrophic bacteria into 'solar power plants'.
Proteomics & other 'omics	Proteomics, transcriptomics and metabolomics are probing the whole 'system' of the cell instead of isolated parts. This allows to discover biological relationships that were not considered in the original hypothesis, and gives an unbiased picture.
Single cell variability	Previous work regarding single cell variability of <i>S. cerevisiae</i> , <i>E. coli</i> , and <i>Pseudomonas putida</i> showed me that a population is never uniform but varies extensively in size, shape, productivity, and plasmid copy number. Future projects aiming to build improved cellular catalysts have to consider this variability. Flow cytometry and cell sorting can be used to select the most productive mutants.
Reproducibility and Transparency	Adopting open standards, sharing protocols and resources , and depositing data and apps on publicly available sites has great advantages. It increases reach, trust of the scientific community, and reproducibility of results.

Qualifications and skills

Courses	Approved project manager for genetic works, according to German laws (§ 14,15 GenTSV), 2015. Laser scanning microscopy, 1 week course, 2013. Scientific writing and project proposal writing, 2 week course , 2013.
Model organisms	Experienced in cultivation and molecular biology works of cyanobacteria (e.g. <i>Synechocystis sp.</i> , <i>Synechococcus</i>), <i>Cupriavidus necator</i> , <i>Pseudomonas putida</i> , <i>E. coli</i>)
Important techniques	Bioreactor cultivation, chemostat, turbidostat Mass spectrometry, proteomics Flow cytometry, cell sorting, automated imaging Metabolic mapping, data mining, visualization Molecular biology work (DNA and proein extraction, cloning)
Programming lanuguages	R (advanced), Python (moderate)

Authored R packages	<p>SysbioTreemaps – visualizing gene expression with treemaps</p> <p>ShinyMC – interactive app to monitor bioreactor cultivations</p> <p>ShinyProt – interactive app to visualize proteomics data</p> <p>ShinyLib – interactive app to visualize gene knockout library data</p>
Metabolic models	<p>Improved <i>Synechocystis</i> coarse grained (simplified) resource allocation model, for GAMS, and ported to python.</p> <p>Improved and updated genome scale model (GEM) for <i>Cupriavidus necator</i> a.k.a. <i>Ralstonia eutropha</i>.</p> <p>Constructed new genome scale resource balance (RBA) model for <i>Cupriavidus necator</i> a.k.a. <i>Ralstonia eutropha</i></p>

Peer review and outreach

Peer review	Active reviewer for several journals including Microbial Cell Factories, Frontiers in Microbiology, Photosynthesis Research, and others. The full list of my review contributions is available via Publons.org
Platforms	<p>My home page ↗</p> <p>My github page ↗</p> <p>My ORCID page ↗</p> <p>My Publons page ↗</p> <p>My ResearchGate page ↗</p> <p>My Twitter page ↗</p>

Languages

German	Native language.
English	Proficient user , CEF level C1.
Swedish	Vantage user , CEF level B2.

Publications

- Yao L, Shabestary K, Björk SM, Asplund-Samuelsson J, Joensson HN, **Jahn M**, Hudson EP. *Pooled CRISPRi screening of the cyanobacterium Synechocystis sp PCC 6803 for enhanced industrial phenotypes*. Nature Communications, **2019**.
- Karlsen J, Asplund-Samuelsson J, Thomas Q, **Jahn M**, Hudson EP. *Ribosome Profiling of Synechocystis Reveals Altered Ribosome Allocation at Carbon Starvation*. MSystems 3, e00126-18, **2018**.
- **Jahn M**, Vialas V, Karlsen J, Maddalo G, Edfors F, Forsström B, Uhlén M, Käll L, Hudson EP. *Growth of Cyanobacteria Is Constrained by the Abundance of Light and Carbon Assimilation Proteins*. Cell Reports 25, 478–486.e8., **2018**.
- Shabestary K, Anfelt J, Ljungqvist E, **Jahn M**, Yao L, Hudson EP. *Targeted Repression of Essential Genes To Arrest Growth and Increase Carbon Partitioning and Biofuel Titters in Cyanobacteria*. ACS Synthetic Biology, 7, 1669–1675, **2018**.
- **Jahn M**, Vorpahl C, Hübschmann T, Harms H, Müller S. *Copy number variability of expression plasmids determined by cell sorting and Droplet Digital PCR*. Microbial Cell Factories, **2016**.
- Lindmeyer M, **Jahn M**, Vorpahl C, Müller S, Schmid A, Bühler B. *Variability in subpopulation formation propagates into biocatalytic variability of engineered Pseudomonas putida strains*. Frontiers in microbiology 6, **2015**.
- Lieder S, **Jahn M**, Koepff J, Müller S, Takors Ralf. *Environmental stress speeds up DNA replication in Pseudomonas putida in chemostat cultivations*. Biotechnology journal, **2015**.
- **Jahn M**, Günther S, Müller S. *Non-random distribution of macromolecules as driving forces for phenotypic variation*. Current Opinion in Microbiology. 25:49-55, **2015**.
- Rödiger S, Burdukiewicz M, Blagodatskikh K, **Jahn M**, Schierack P. *R as an environment for reproducible analysis of DNA amplification experiments*. R Journal 7/1:127-150, **2015**.
- **Jahn M**, Vorpahl C, Türkowsky D, Lindmeyer M, Bühler B, Harms H, Müller S. *Accurate determination of plasmid copy number of flow-sorted cells using droplet digital PCR*. Analytical Chemistry 86:5969-76, **2014**.
- Lieder S, **Jahn M**, Seifert J, von Bergen M, Müller S, Takors R. *Subpopulation-proteomics reveal growth rate, but not cell cycling, as a major impact on protein composition in Pseudomonas putida KT2440*. AMB Express 4:71, **2014**.
- **Jahn M**, Seifert J, von Bergen M, Schmid A, Bühler B, Müller S. *Subpopulation-proteomics in prokaryotic populations*. Current Opinion in Biotechnology 24:79-87, **2013**.
- **Jahn M**, Seifert J, Hübschmann T, von Bergen M, Harms H, Müller S. *Comparison of preservation methods for bacterial cells in cytomics and proteomics*. Journal Of Integrated Omics 3:1-9, **2013**.
- **Jahn M**, Mölle A, Rödel G, Ostermann K. *Temporal and spatial properties of a yeast multi-cellular amplification system based on signal molecule diffusion*. Sensors 13:14511-22, **2013**.

Conference contributions

- May 22–24, 2019 **NPC 14** - Nordic congress on photosynthesis, Turku, Finland. Short presentation.
- Oct 24–26, 2018 **4th Applied Synthetic Biology meeting** - Toulouse, France. Presentation.
- Jul 20–22, 2015 **Single Cell VI** – 6th International Conference on Analysis of Microbial Cells at the Single Cell Level, Retz (Austria), presentation.
- Oct 15–17, 2014 **DGFZ** – 24th Annual Conference of the German Society for Cytometry, Dresden, presentation.
- Jul 13–16, 2014 **ECB16** – 16th European Congress on Biotechnology, Edinburgh, presentation.
- May 26–28, 2014 **DECHEMA** – Biomaterials Made in Bioreactors, Dresden, poster.
- Mar 06–08, 2013 **RPP7** – 7th European Conference on Recombinant Protein Production, Ulm, presentation.
- Jul 21–25, 2013 **FEMS** – 5th Congress of European Microbiologists, Leipzig, poster.
- Oct 10–12, 2012 **DGFZ** – 22nd Annual Conference of the German Society for Cytometry, Bonn, presentation.
- Jun 23–27, 2012 **CYTO 2012** – 27th Congress of the International Society for Advancement of Cytometry, Leipzig, presentation.