Dr. Nicholas Jay Tobias

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Employment and Education

Group Leader	**Senckenberg Gesellschaft für Naturforschung** Metagenomics and Metabolomics of Insects	04/2020-present
Postdoctoral Researcher	**Goethe University** Supervisor: Prof. Helge Bode	07/2016-03/2020
Humboldt Fellow	**Goethe University** Supervisor: Prof. Helge Bode	07/2014-07/2016
Postdoctoral Researcher	**University of Melbourne** Supervisor: Prof. Timothy Stinear	07/2013-03/2014
Visiting Scientist	**University of Cambridge** Supervisor: Prof. Peter Leadley	03/2013-06/2013
Visiting Scientist	**Swiss Tropical Public Health Institute** Supervisor: Prof. Gerd Pluschke	05/2013-05/2013
Doctor of Philosophy	**Monash University** Supervisor: Prof. Timothy Stinear Thesis Title: Molecular studies of *Mycobacterium ulcerans*	03/2007-06/2013
Graduate Certificate Commercializing Research	**Monash University**	2010
Research Assistant	**Monash University** Supervisor: Prof. Timothy Stinear	2006-2007
Bachelor of Science (Honours)	**Monash University** Supervisor: Prof. John Davies & Prof. Timothy Stinear Major in Molecular Biology and Microbiology	2003-2006

Publications – peer reviewed

37. Neubacher N*, Tobias NJ*, Huber M*, Cai X, Glatter T, Pidot SJ, Stinear TP, Lütticke A, Papenfort K, Bode HB (2020) **Symbiosis, virulence and natural products biosynthesis in entomopathogenic bacteria are regulated by a small RNA.** *Nat Microbiol* (accepted).
***equal first author**

36. Mangas KM, Tobias NJ, Marion E, Babonneau J, Marsollier L, Porter JL, Pidot SJ, Wong CY, Jackson DC, Chua BY, Stinear TP (2020). **High antibody titres induced by protein subunit vaccines using *Mycobacterium ulcerans* antigens Hsp18 and MUL_3720 with a TLR-2 agonist fail to protect against Buruli ulcer in mice.** *PeerJ***. 8**:e9659. doi: 10.7717/peerj.9659.

35. Mangas KM, Buultjens AH, Porter JL, Baines SL, Marion E, Marsollier L, Tobias NJ, Pidot SJ, Quinn KM, Price DJ, Kedzierska K, Zeng W, Jackson DC, Chua BY, Stinear TP (2020). **Vaccine-Specific Immune Responses against Mycobacterium ulcerans Infection in a Low-Dose Murine Challenge Model.** *Infect Immun.* **88**(3):e00753-19. doi: 10.1128/IAI.00753-19.

34. Tobias NJ, Brehm J, Kresovic D, Brameyer S, Bode HB, Heermann R. (2020). **New Vocabulary for Bacterial Communication.** *Chembiochem*. doi: 10.1002/cbic.201900580

33. Tobias NJ*, Parra-Rojas C, Shi YN, Shi YM, Simonyi S, Thanwisai A, Vitta A, Chantratita N, Hernandez-Vargas EA*, Bode HB* (2019). **Cyclo(tetrahydroxybutyrate) production is sufficient to distinguish between *Xenorhabdus* and *Photorhabdus* isolates in Thailand.** *Environ Microbiol* (accepted). doi: 10.1111/1462-2920.14685

***co-corresponding author**

32. Tobias NJ, Bode HB (2019). **Heterogeneity in bacterial specialized metabolism**. *J Mol Biol* (in press). doi: 10.1016/j.jmb.2019.04.042

31. Grammbitter GLC, Schmalhofer M, Karimi K, Shi YM, Schöner T, Tobias NJ, Morgner N, Groll M, Bode HB (2019). **An uncommon type II PKS catalyzes biosynthesis of aryl polyene pigments.** *J Am Chem Soc*. doi: 10.1021/jacs.8b10776

30. Shi YM, Brachmann AO, Westphalen MA, Neubacher N, Tobias NJ, Bode HB (2019). **Dual phenazine gene clusters enable diversification during biosynthesis.** *Nat Chem Biol.* **15**(4):331-339.

29. Tobias NJ, Shi YM, Bode HB (2018). **Refining the natural product repertoire in entomopathogenic bacteria**. *Trends Microbiol*. **26**(10):833-840

28. Tobias NJ, Linck A, Bode HB (2018). **Natural product diversification mediated by alternative transcriptional starting**. *Angew Chem Int Ed Engl.* **57**(20):5699-5702

27. Bulltjens AH, Vandelannoote K, Meehan CJ, Eddyani M, de Jong BC, Fyfe JAM, Globan M, Tobias NJ, Porter JL, Tomita T, Tay EL, Seemann T, Howden BP, Johnson PDR, Stinear TP (2018). **Comparative genomics shows that *Mycobacterium ulcerans* migration and expansion preceded the rise of Buruli ulcer in Southeastern Australia.** *Appl Environ Microbiol* **84**(8): e02612-17.

26. Tobias NJ, Wolff H, Djahanschiri B, Grundmann F, Kronenwerth M, Shi YM, Simonyi S, Grün P, Shapiro-Ilan D, Pidot SJ, Stinear TP, Ebersberger I, Bode HB (2017). **Natural product diversity associated with the nematode symbionts *Photorhabdus* and *Xenorhabdus*.** *Nat Microbiol* **2**(12):1676-1685.

25. Muangpat P, Yooyangket T, Fukruksa C, Suwannaroj M, Yimthin T, Sitthisak S, Chantratita N, Vitta A, Tobias NJ, Bode HB, Thanwisai A (2017). **Screening of the Antimicrobial Activity against Drug Resistant Bacteria of *Photorhabdus* and *Xenorhabdus* Associated with Entomopathogenic Nematodes from Mae Wong National Park, Thailand.** *Front Microbiol* **8**:1142.

24. Kaempfer P, Tobias NJ, Ke LP, Bode HB, Glaeser SP (2017). ***Xenorhabdus thuongxuanensis* sp. nov. and *Xenorhabdus eapokensis* sp. nov., isolated from *Steinernema* species.** *Int J Syst Evol Microbiol* **67**(5):1107-1114.

23. Glaeser SP, Tobias NJ, Thanwisai A, Chantratita N, Bode HB, Kaempfer P (2016). ***Photorhabdus luminescens* subsp*. namnaoensis* sp. nov. isolated from *Heterorhabditis baujardi* nematodes in Nam Nao district of central Thailand.** *Int J Syst Evol Microbiol* **67**(4):1046-1051.

22. Tobias NJ (2016). **Insect vectors of disease: untapped reservoirs for new antimicrobials?** *Front Microbiol* **7**:2085.

21. Tobias NJ, Ahrendt T, Schell U, Miltenberger M, Hilbi H, Bode HB, 2016. ***Legionella* shows a diverse secondary metabolism dependent on a broad spectrum Sfp-type phosphopantetheinyl transferase.** *PeerJ* **4**:e2720.

20. Heinrich AK, Glaeser A, Tobias NJ, Heermann R, Bode HB, 2016. **Heterogeneous regulation of anthraquinone biosynthesis via the novel regulator AntJ in *Photorhabdus luminescens.*** *Heliyon.***2**(11):e00197.

19. Tobias NJ, Heinrich AK, Eresmann H, Wright PR, Neubacher N, Backofen R, Bode HB, 2017. ***Photorhabdus*-nematode symbiosis is dependent on *hfq*-mediated regulation of secondary metabolites.** *Environ Microbiol* 19(1):119-129. doi: 10.1111/1462-2920.13502.

18. Tobias NJ, Mishra B, Gupta DK, Phan Ke L, Thines M, Stinear TP, Bode HB, 2016. **Genome comparisons provide insights into the role of secondary metabolites in the pathogenic phase of the *Photorhabdus* life cycle** *BMC Genomics* **17**(1):537**.**

17. Tobias NJ, Amissah NA, Ahortor EK, Wallace JR, Ablordey AS, Stinear TP, 2016. **Systematic fecal survey suggests peridomestic animals in rural Ghana are not major reservoirs of *Mycobacterium ulcerans.*** *PeerJ* **4**:e2065.

16. Schöner TA, Gassel S, Osawa A, Tobias NJ, Okuno Y, Sakakibara Y, Shindo K, Sandmann G, Bode HB, 2016. **Aryl polyenes, one of the most widespread class of bacterial natural products, are functionally related to antioxidative carotenoids.** *Chembiochem* **17**(3):247-53**.**

15. Mulley G, Beeton ML, Wilkinson P, Ockendon-Powell N, Hapeshi A, Tobias NJ, Nollman FI, Bode HB, van den Elsen J, ffrench-Constant RH, Waterfield NR, 2015. **From insect to man: *Photorhabdus* sheds light on the emergence of human pathogenicity.** *PLoS One* **10**(12): e0144937.

14. Schimming O, Challinor VL, Tobias NJ, Adihou H, Grün P, Pöschel L, Richter C, Schwalbe H, Bode HB, 2015. **Structure, biosynthesis and occurrence of bacterial pyrrolizidine alkaloids.** *Angew Chem* **54**(43):12702-5.

13. Medema MH, Kottmann R, Yilmaz P, Cummings M, Biggins JB, Blin K, de Bruijn I, Chooi YH, Claesen J, Coates RC, Cruz-Morales P, Duddela S, Dusterhus S, Edwards DJ, Fewer DP, Garg N, Geiger C, Gomez-Escribano JP, Greule A, Hadjithomas M, Haines AS, Helfrich EJ, Hillwig ML, Ishida K, Jones AC, Jones CS, Jungmann K, Kegler C, Kim HU, Kotter P, Krug D, Masschelein J, Melnik AV, Mantovani SM, Monroe EA, Moore M, Moss N, Nutzmann HW, Pan G, Pati A, Petras D, Reen FJ, Rosconi F, Rui Z, Tian Z, Tobias NJ, Tsunematsu Y, Wiemann P, Wyckoff E, Yan X, Yim G, Yu F, Xie Y, Aigle B, Apel AK, Balibar CJ, Balskus EP, Barona-Gomez F, Bechthold A, Bode HB, Borriss R, Brady SF, Brakhage AA, Caffrey P, Cheng YQ, Clardy J, Cox RJ, De Mot R, Donadio S, Donia MS, van der Donk WA, Dorrestein PC, Doyle S, Driessen AJ, Ehling-Schulz M, Entian KD, Fischbach MA, Gerwick L, Gerwick WH, Gross H, Gust B, Hertweck C, Hofte M, Jensen SE, Ju J, Katz L, Kaysser L, Klassen JL, Keller NP, Kormanec J, Kuipers OP, Kuzuyama T, Kyrpides NC, Kwon HJ, Lautru S, Lavigne R, Lee CY, Linquan B, Liu X, Liu W, Luzhetskyy A, Mahmud T, Mast Y, Mendez C, Metsa-Ketela M, Micklefield J, Mitchell DA, Moore BS, Moreira LM, Muller R, Neilan BA, Nett M, Nielsen J, O'Gara F, Oikawa H, Osbourn A, Osburne MS, Ostash B, Payne SM, Pernodet JL, Petricek M, Piel J, Ploux O, Raaijmakers JM, Salas JA, Schmitt EK, Scott B, Seipke RF, Shen B, Sherman DH, Sivonen K, Smanski MJ, Sosio M, Stegmann E, Sussmuth RD, Tahlan K, Thomas CM, Tang Y, Truman AW, Viaud M, Walton JD, Walsh CT, Weber T, van Wezel GP, Wilkinson B, Willey JM, Wohlleben W, Wright GD, Ziemert N, Zhang C, Zotchev SB, Breitling R, Takano E, Glockner FO (2015) **Minimum Information about a Biosynthetic Gene cluster.** *Nature chemical biology* **11**(9): 625-631

12. Gao W, Monk I, Tobias NJ, Galdman S, Seemann T, Stinear TP, Howden BP, 2015. **Large tandem chromosome duplications facilitate niche adaptation during persistent infection with drug-resistant *Staphylococcus aureus*.** *MGen* **1**(2) DOI: 10.1099/mgen.0.000026.
11. Ablordey AS, Vandelannoote K, Frimpong IA, Amissah NA, Eddyani M, Durnez L, Portaels F, De Jonge B, Leirs H, Porter JL, Mangas K, Lam M, Buultjens A, Seemann T, Tobias NJ, Stinear TP, 2015. **Spread of a Nigerian clone of *Mycobacterium ulcerans* in a Buruli ulcer endemic region of Ghana.** *PLoS Negl Trop Dis* **9**(3):e0003681.
10. Tobias NJ, Mishra B, Gupta DK, Phan Ke L, Thines M, Bode HB, 2015. **Draft genome sequence of *Ochrobactrum anthropi* strain ML7 isolated from soil samples in the Vinhphuc province, Vietnam.** *Genome Announcements* **3**(2):e00218-15.
9. Dreyer A, Röltgen K, Dangy JP, Ruf MT, Scherr N, Bolz M, Tobias NJ, Moes C, Vettiger A, Stinear TP, Pluschke G, 2015. **Identification of *Mycobacterium ulcerans* Protein MUL_3720 as a promising target for the development of a diagnostic test for Buruli ulcer.** *PLoS Negl Trop Dis* **9**(2):e0003477.
8. Amissah NA, Gryseels S, Tobias NJ, Ravadgar B, Suzuki M, Vandelannoote K, Durnez L, Leirs H, Stinear TP, Portaels F, Ablordey A, Eddyani M, 2014. **Investigating the role of free-living amoebae as a reservoir for *Mycobacterium ulcerans*.** *PLoS Negl Trop Dis* **8**(9):e3148.
7. Lam MMC, Seemann T, Tobias NJ, Chen H, Haring V, Moore RJ, Ballard S, Grayson ML, Johnson PDR, Howden BP, Stinear TP, 2013. **Fitter and faster: Insights from the complete genome sequence of an epidemic hospital ST203 clone of vancomycin-resistant *Enterococcus faecium*.** *BMC Genomics* **14**:595.
6. Porter JP, Tobias NJ, Pidot SJ, Falgner S, Tuck KL, Hong H, Leadley PF, Stinear TP, 2013. **The membrane-associated mycolactone polyketide synthases are necessary but not sufficient for mycolactone biosynthesis.** *PLoS One* **8**(7):e70520.

5. Tobias NJ, Doig KD, Medema MH, Chen H, Haring V, Moore R, Seemann T, Stinear TP, 2013. **Complete genome sequence of the frog pathogen *Mycobacterium ulcerans* ecovar Liflandii**. *J Bacteriol* **195:**556-564.
4. Pidot SJ, Porter JL, Tobias NJ, Anderson J, Catmull D, Seemann T, Kidd S, Davies JK, Reynolds E, Dashper S, Stinear TP 2010. **Regulation of the 18 kDa heat shock protein in *Mycobacterium ulcerans*: an alpha-crystallin orthologue that promotes biofilm formation**. *Mol Microbiol* **78**(5):1216-1231.
3. Tobias NJ, Seemann T, Pidot SJ, Porter JL, Marsollier L, Marion E, Letournel F, Zakir T, Azuolas J, Wallace JR, Hong H, Davies JK, Howden BP, Johnson PD, Jenkin GA, Stinear TP, 2009. **Mycolactone gene expression is controlled by strong SigA-like promoters with utility in studies of *Mycobacterium ulcerans* and Buruli ulcer**. *PLoS Negl Trop Dis* **3**(11):e553.
2. Porter JL, Tobias NJ, Hong H, Tuck KL, Jenkin GA, Stinear TP, 2009 **Transfer, stable maintenance and expression of the mycolactone polyketide megasynthase *mls* genes in a recombination-impaired *Mycobacterium marinum***. *Microbiology* **155**(6):1923-1933.
1. Pidot S, Tobias NJ, Stinear T: **The pMUM Megaplasmid of *Mycobacterium ulcerans* and Closely Related Mycobacteria: A Blueprint for the Synthesis of Mycolactones**. In: *Microbial Megaplasmids.* Edited by Schwartz E, vol. 11: Springer Berlin / Heidelberg; 2009: 283-296.

Invited Presentations

- **University of Electronic Science and Technology of China,** School of Life Sciences, Chengdu, China – November 2017
- **University of Copenhagen,** Department of Biology, Copenhagen, Denmark – November 2016
- **Cambridge University,** Department of Biochemistry, Cambridge, UK – April 2013
- **Swiss Tropical and Public Health Institute,** Basel, Switzerland – May 2013
- **Goethe University,** Institute for Molecular Bioscience, Frankfurt am Main, Germany – June 2013
- **University of Melbourne,** Department of Microbiology and Immunology, Melbourne, Australia – July 2013

Presentations

- **Annual Conference of the Association for General and Applied Microbiology (VAAM), Mainz Germany:** Machine learning to decipher metabolic differences between *Photorhabdus* and *Xenorhabdus* 2019
- **American Society for Pharmacognosy Annual Meeting, Lexington, USA:** Natural product diversity associated with the nematode symbionts *Photorhabdus* and *Xenorhabdus* 2018
- **Canadian Society of Microbiology Annual Meeting, Toronto, Canada:** *Photorhabdus*-nematode symbiosis is dependent on Hfq-mediated regulation of secondary metabolites. 2016
- **Research in Computational Molecular Biology Conference**, **Frankfurt, Germany** Understanding entomopathogenic bacterial lifestyles through genome sequencing. 2015
- **6th European Conference on Prokaryotic and Fungal Genomics, Göttingen, Germany** Understanding entomopathogenic bacterial lifestyles through genome sequencing, 2015
- **World Health Organization Meeting on Buruli ulcer, Geneva, Switzerland**: Research meeting summary to all attendees. 2013
- **World Health Organization Meeting on Buruli ulcer, Geneva, Switzerland:** *Mycobacterium ulcerans* pathogenesis: a cell wall phenomenon. 2013
- **Victorian Infection & Immunity Network, Young Investigators Symposium, Melbourne, Australia**: Functional analysis of Hsp18: an immunodominant antigen expressed by *Mycobacterium ulcerans*. 2011
- **Bacterial Pathogenesis: BacPath10, Barossa Valley, South Australia:** Promoters involved in mycolactone gene expression and their application to studies of the pathogenesis and ecology of *Mycobacterium ulcerans*. 2009
- **Victorian Infection & Immunity Network, Young Investigators Symposium, Melbourne, Australia**: Discovery of promoters involved in mycolactone gene expression. 2009

Awards and Funding

- **TBG sequencing call:** Successful in 2018 (€15,000) and 2019 (US$ 24,150)for metagenomic sequencing of triatomines 2018-2019
- **Goethe Focus program Line A/B:** Small research grant of €5000 awarded on a competitive basis to generate preliminary data for future grant applications. 2016

- **Humboldt Fellowship:** Provided by the Alexander von Humboldt Foundation to outstanding early career researchers. 2014
- **CSL Award for best PhD thesis:** Awarded annually by the Commonwealth Serum Laboratories to the top-ranking thesis in the Department of Microbiology at Monash University. 2013
- **Victoria Fellowship:** A highly prestigious award ($18,000 AUD) from the State Government of Victoria, Australia to travel to an overseas institution for three months. 2012
- **Commercialization Training Scheme (CTS) award, Commonwealth Government:** to develop skills and knowledge involved in commercializing research and moving basic scientific results to marketable products. 2010
- **Faculty Postgraduate Research Scholarship, Monash University:** for funding to complete a PhD. 2007-2010

Teaching Experience

- **PhD student co-supervisor, Goethe University** 2017-present
  Three students: one completed, two ongoing
- **Lecturer in Master's Chemical Biology course, Goethe University** 2017-2019
  Lecturing to students on sequencing technologies and their applications
- **Master's student supervisor, Goethe University** 2014-present
  Five completed
- **Honours and Master's student supervisor, University of Melbourne** 2012-2013
  One Master's completed, three Honour's completed
- **Undergraduate research project co-ordinator, University of Melbourne** 2011
  Designed and supervised a research project for 12 students to perform in their 3rd year to utilize molecular biology concepts in the study of a bacterial infectious disease (*Mycobacterium ulcerans*)
- **Lead demonstrator for Molecular Biology Techniques Course, Micromon, Monash University** 2009
  Supervised a team of five demonstrators with 60 participants from various professional and postgraduate backgrounds in recombinant DNA technologies.
- **Demonstrator for Molecular Biology Techniques Course, Micromon, Monash University** 2007-2008
- **Undergraduate student demonstrator, Monash University** 2007-2009
  Supervised the practical component and organized tutorials of undergraduate courses including biology (1st and 2nd year; BIO1011, BIO2011), medicine (1st year; MED1011), molecular biology (2nd year; MOL2011, MOL2022), microbiology (2nd and 3rd year; MIC2011, MIC2022, MIC3011, MIC3990, MIC3032), virology (3rd year; MIC3022) and medical microbiology (3rd year; MIC3041).

Expertise

Microbiology, molecular biology, (meta)genome assembly and annotation, transcriptomics, chemical biology, linking genomics to metabolomics, analysis of large datasets.

References

Prof. Dr. Helge Bode

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Planned Research Priorities

My major research interest is in discovering links between microbes and the compounds that they produce in a given ecology. Specifically, my overall aim is to understand the contribution of natural products derived from insect microbiomes during various antagonistic interactions. By generating complementary datasets (metabolomic and (meta)genomic/transcriptomic) I believe we can develop a much deeper understanding of the contributions of individual traits (from genes to microbes and single compounds to families of molecules) in a given environment. In order to do this, I incorporate aspects of machine learning to rank features with respect to available metadata in any given context. Ultimately, I aim to use these data to exploit natural systems, generating microbial blockages in the natural transmission pathways of human pathogens.

Experimental System

In my research, the insect vector of Chagas disease is investigated. Chagas disease (American trypanosomiasis) is a neglected tropical disease caused by the protozoan parasite, *Trypanosoma cruzi.* The parasite is transmitted by insects of the family Triatominae (life cycle in Figure 1). Treatment of Chagas disease is limited to only two clinical drugs, with increasing resistance becoming a major impediment to treating the approximately 7 million people affected worldwide. Here, we study the microbiome of triatomines, in order to search for natural products, or classes thereof, that have anti-trypanosomal activity in an environment naturally encountered by the target organism.

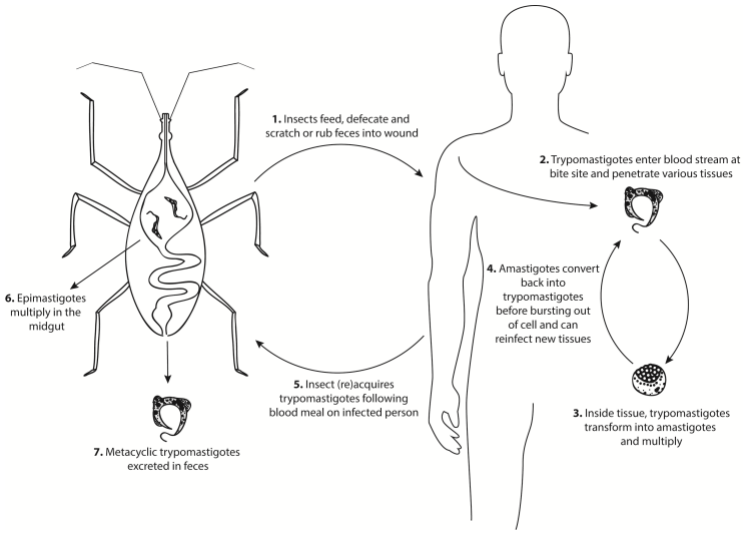

Figure 1. Life cycle of *Trypanosoma cruzi*. Insects colonized by *T. cruzi* take a blood meal before defecating. (**1**) *T. cruzi* trypomastigotes can enter the bloodstream if infected feces come into contact with the open wound. (**2,3**) Trypomastigotes can infect tissues where they convert to amastigotes and replicate. (**4**) Several rounds of replication may occur over extended periods leading to various health complications. (**5**) Uninfected insects can take up trypomastigotes when feeding on an infected individual where the trypomastigotes enter the mid-gut, (**6**) convert into epimastigotes and replicate. (**7**) Trypomastigotes are then found in the lower gut and excreted in feces.

High-throughput sequencing using Illumina is sufficient to assemble microbial natural product gene clusters, including polyketide synthases (PKSs) and non-ribosomal peptide synthetases

(NRPSs), which are of particular interest since several have demonstrated anti-trypanosomal properties. We additionally utilize high-resolution tandem mass spectrometry to identify metabolites produced at a given time-point and analyze these with a variety of software.

Linking metabolomics to genomics

High-quality, paired datasets from the same source, under the same conditions are essential to accurately analyze and pair natural product production to a given gene cluster. In this context, high-quality means sufficiently assembled (meta)genomes and high-resolution metabolomic data. Focusing on NRPS and PKS, the genomics information is used in discovery through heterologous expression in cases where the metabolite is unknown. Importantly, this can be matched back to metabolomic data and metatranscriptomic data in order to determine when a gene cluster is expressed as well as when the compound is detectable. Ultimately, matching natural products to gene clusters and expression profiles allows us to explore the underlying mechanistic pathways that lead to their production, thereby providing insights into their function(s).

High-throughput technologies inevitably create a bottleneck during analysis. Recently, we have begun to incorporate a ranking system into our analysis pipeline that aims to prioritize areas for further research using machine learning approaches. Since natural products, even in closed systems, are too numerous to study, our research aims to narrow down the field to those that are directly applicable to a given research question. In our research, this question is what compounds, gene clusters or microbes are important in combatting invasion of triatomine insects by *Trypanosoma*? How do we then link these individual compounds (or molecular families) with their cognate microbial gene cluster(s)?

Understanding the role of natural products in metagenomic systems

The purpose of natural products in complex environments can be properly understood once we have i) a gene cluster, ii) an expression profile, iii) a linked metabolite and iv) a bioactivity profile. With assembled gene clusters can be assembled, then techniques such as heterologous expression in an appropriate system can be used for identifying the produced metabolite. However, the genomic information collected is useful for constructing libraries (genetic or the organisms themselves) of bacteria and fungi that potentially produce bioactive metabolites. In terms of natural product discovery, this type of resource is unique in that it is isolated from an environment, few others have explored.

Exploitation of libraries containing these gene clusters are planned to be used in synthetic microbiome experiments, whereby different combinations of microbes are introduced into our triatomine system, which replaces the native microbiota. In this way, we can investigate synergism and antagonism of natural products in a very specific context in order to properly understand the roles of natural products in this niche.

Integration with TBG

Our model system is perfect for the above described analyses since we can generate testable hypotheses through exploring the underlying diversity and bioactivity of natural products. Future research will extend into other symbiotic systems to discover new natural products through metagenomics, in new ecological contexts. However, integration with the TBG will be extremely beneficial for these research ideas. Collaboration with AK Fürst for bioactivity testing, AK Bode for chemical structure elucidation and AK Janke for investigating the gene flow that led to speciation of triatomines capable of transmitting the disease (and those that are incapable) will all greatly advance the current proposal. This research will also complement that of AK Klimpel, by providing deeper insight into this hematophagous insect, with a clear path to extending the analysis to other insects. Additionally, the analysis pipeline can be both modified and extended to investigate natural products from microbiota present in soil (Lehmitz/Bálint) as well as other organisms.