

## Martin Helmkamp

### Contact Information

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### Research Interests

Genomics and genome evolution  
Phylogenetics and evolutionary history  
Population and conservation genetics  
Gene regulation in complex systems  
Genetic basis of speciation and adaptive traits

### Academic Positions

- since 2020     **Senior Scientist**  
Leibniz Centre for Tropical Marine Research (ZMT), Bremen, Germany  
Fish Ecology and Evolution group, Prof. Oscar Puebla
- 2015 – 2019     **Research Associate**  
University of Hawai'i at Hilo, United States  
Tropical Conservation Biology and Environmental Science, Prof. Misaki Takabayashi, et al.
- 2014             **Guest Scientist** (4 months)  
Okinawa Institute of Science and Technology, Onna, Japan  
Ecology and Evolution group, Prof. Alexander Mikheyev
- 2012 – 2014     **Assistant Research Scientist**  
Arizona State University, Tempe, United States  
Social Insect Research Group, Prof. Jennifer Fewell
- 2009 – 2011     **Postdoctoral Researcher**  
Arizona State University, Tempe, United States  
Social Insect Research Group, Prof. Jürgen Gadau

### Education

- 2005 – 2009     **Doktor der Naturwissenschaften** (equivalent to PhD, summa cum laude)  
University of Hamburg, Germany | advisors: Dr. Bernhard Hausdorf and Dr. Iris Bruchhaus  
Thesis: “Molecular phylogenetic analysis of Bryozoa, Brachiopoda, and Phoronida”
- 1999 – 2005     **Diplom Biologie** (equivalent to Master's degree of Biology)  
University of Würzburg, Germany | advisor: Dr. Jürgen Gadau  
Thesis: “Phylogeography and spatio-temporal population dynamics of the leaf-cutter ant *Atta colombica* in the Barro Colorado Nature Monument, Panama”

## Technical Skills and Qualifications

- [Next-generation sequencing](#) (Illumina, PacBio, 10x Genomics) of genomes, transcriptomes, and reduced representation genomes (e.g. RAD-seq)
- [Bioinformatic applications](#) and workflows required for the processing, annotation and analysis of genome-scale datasets
- [Programming](#) (R, Perl, Python), shell scripting, high-performance/parallel computing, database management (e.g. SQL)
- Analysis of [phylogenetic relationships](#), selection signatures, population structure, and phylogeography using genetic markers at all scales (i.e. microsatellites to genome-wide SNP and gene sets)
- Basic and advanced [laboratory techniques](#), including RNA and DNA isolation, standard and qPCR, library preparation, and microsatellite genotyping
- [Lab management](#), logistics of tissue sample collection and related field work; Open Water Diver certificate (PADI), German motorboat license for inland waters (SBF Binnen)

## Selected Publications

30 peer-reviewed publications total, total citations > 2050, *h*-index = 17

[Helmkampf M.](#), Bellinger R., Scott G., Sim S., Takabayashi M. 2019. Draft genome of the rice coral *Montipora capitata* obtained from linked-read sequencing. *Genome Biology and Evolution* 11: 2045–2054.

[Helmkampf M.](#), Bellinger R., Frazier M., Takabayashi M. 2018. Symbiont type and environmental factors affect transcriptome-wide gene expression in the coral *Montipora capitata*. *Ecology and Evolution* 9: 378–392.

Sutton J., [Helmkampf M.](#), Steiner C., Bellinger R., Korlach J., Hall R., Baybayan P., Muehling J., Gu J., Kingan S., Masuda B., Ryder O. 2018. A high-quality, long-read de novo genome assembly to aid conservation of Hawaii's last remaining crow species. *Genes* 9: 393.

[Helmkampf M.](#), Wolfgruber T., Bellinger R., Paudel R., Kantar M., Miyasaka S., Kimball H., Brown A., Veillet A., Read A., Shintaku M. 2017. Phylogenetic relationships, breeding implications, and cultivation history of Hawaiian taro (*Colocasia esculenta*) through genome-wide SNP genotyping. *Journal of Heredity*: esx070.

[Helmkampf M.\\*](#), Mikheyev A.S.\*, Kang Y., Fewell J., Gadau J. (\* shared first-authorship). 2016. Gene expression and variation in social aggression by queens of the harvester ant *Pogonomyrmex californicus*. *Molecular Ecology* 15: 3716–3730.

[Helmkampf M.\\*](#), Cash E.\*, Gadau J. (\* shared first-authorship). 2015. The evolution of the desaturase gene family in insects with an emphasis on social Hymenoptera. *Molecular Biology and Evolution* 32: 456–471.

Simola D., Wissler L., Donahue G., Waterhouse R., [Helmkampf M. \(5<sup>th</sup> of 38 authors\)](#), et al. 2013. Social insect genomes exhibit dramatic evolution in gene composition and regulation while preserving regulatory features linked to sociality. *Genome Research* 23: 1235–1247.

Smith C. R., Smith C. D., Robertson H., [Helmkamp M. \(4<sup>th</sup> of 45 authors\)](#), et al. 2011. Draft genome of the red harvester ant *Pogonomyrmex barbatus*. Proceedings of the National Academy of Sciences of the United States of America 108: 5667–5672.

[Helmkamp M.](#), Bruchhaus I. and Hausdorf B. 2008. Phylogenomic analyses of lophophorates (brachiopods, phoronids and bryozoans) confirm the Lophotrochozoa concept. Proceedings of the Royal Society B 275: 1927–1933.

[Helmkamp M.](#), Bruchhaus I. and Hausdorf B. 2008. Multigene analysis of lophophorate and chaetognath phylogenetic relationships. Molecular Phylogenetics and Evolution 46: 206–214.

#### Academic Service, Teaching and Mentorship

- [Editorial Board Member](#) of Scientific Reports, Nature Publishing Group (since 2015)
- [Reviewer](#) for Molecular Ecology, Molecular Biology and Evolution, Genome Biology and Evolution, BMC Genomics, BMC Evolutionary Biology, Marine Pollution Bulletin, Frontiers in Zoology, Journal for Tropical Biology and Conservation, BMC Research Notes, PeerJ, Communications Biology
- [Instructor](#) for Organic Evolution (BIO 345) at Arizona State University (35 hours, 2014), guest lecturer for phylogenetic analysis at Arizona State University (2010) and University of Hawai'i (2015, 2016)
- [Mentor](#) of several PhD and Master's students, resulting in co-authorships of several research articles (e.g. with Monika Frazier, Elizabeth Cash, Rick Overson, and Josh Gibson), supervision and training of more than 20 undergraduate researchers in laboratory and field work