

Master Theses and State Examinations (Prof. Dr. S. Sommer, first supervisor theses only)

- Katherina Miller (2025) Assessing the impact of oil palm monocultures on fusariosis infection prevalence and the egg microbiome of the yellow-spotted Amazon river turtle (*Podocnemis unifilis*) during embryonic development.
- Amelie Dorothee Nolzen (2025) Exploring the gut microbiome of the Yellow Mongoose (*Cynictis penicillata*).
- Jessica Hieber (2025) Ecological drivers of hatching success in the European Pond Turtle (*Emys orbicularis*): Influence of nest microbiomes and fungal metabolites.
- Corbinian Kümmerle (2025) Influence of Astrovirus infection on the gut microbiome of two frugivorous bat species (*Carollia perspicillata* and *Artibeus jamaicensis*) in the Panama Canal region.
- Sabrina Pia Geiger (2025) Impact of anthropogenic landscape disturbance on the gut microbiome of neotropical bats.
- Sebastian Sander (2025) The impact of *Fusarium* on the microbiome of autumn-emerging European pond turtle (*Emys orbicularis*) clutches.
- Vanessa Riegel (2024) Investigating shifts in Major Histocompatibility Complex (MHC) haplotype diversity and abundance in wild meerkats (*Suricata suricatta*) affected by tuberculosis using high-throughput sequencing.
- Johannes Fähnle (2023) Characterization and temporal dynamics of the trace amine-associated receptors in a wild meerkat population.
- Vanessa Riegel (2023) Investigating shifts in Major Histocompatibility Complex (MHC) haplotype diversity and abundance in wild meerkats (*Suricata suricatta*) affected by tuberculosis using high-throughput sequencing.
- Tatiana Tilley (2021) MHC class II diversity in lineages of an African bat species complex susceptible to coronavirus infection.
- Thomas Link-Hessing (2021) MHC class II diversity in a Coronavirus-infected African bat species complex.
- Akbal Ahu (2020) High throughput genotyping of MHC class II loci in South African meerkats suffering from tuberculosis.
- Ana Sofia Carranco Narvaez (2020) Unveiling the effects of the new fungal disease Fusariosis on the microbiome of the yellow-spotted Amazon river turtle.
- Andrea Vallejo Vargas (2020) Maintenance of adaptive genetic diversity in a small primate population and its implication for conservation.
- Fleischer Ramona (2019) The gut microbiome and correlations with MHC supertype occurrence of four endemic mockingbird species on the Galápagos islands.

- Gunzenhäuser Ruben (2019) Einfluss von Umweltveränderungen und intrinsischen Faktoren auf die Ektoparasitenbelastung von Kleinsäugetern im Tieflandregenwald Panamas.
- Schmitt Andreas (2019) Einfluss von Umweltveränderungen auf das Darmmikrobiom einer neotropischen Nagerart im Tieflandregenwald Panamas.
- Eibner Georg (2018) *Trypanosoma cruzi* infection in small mammals inhabiting neotropical landscapes with various degrees of anthropogenic environmental change.
- Grudzus Kara (2018) Validating a MHC next-generation sequencing workflow using an experimental set-up from a known model system.
- Männer Lisa (2018) Characterization of the MHC class II loci in meerkats, *Suricata suricatta*.
- Schumacher Julia (2018) Effects of Habitat Modification on *Bartonella* and *Helicobacter* Infections in Wildlife - Case Studies in Jamaican Fruit Bats (*Artibeus jamaicensis*) and Grey-brown Mouse Lemurs (*Microcebus griseorufus*).
- Kolar Miriam (2017) Characterization of Major Histocompatibility Complex class I genes of raccoons (*Procyon lotor*) using a next generation sequencing approach.
- Okeke Nnamdi Johnmary (2017) Genotyping a large number of Greater Flamingos (*Phoenicopterus roseus*) for MHC class II: A NGS barcoding method.
- Haque Shahi (2016) A preliminary study on the association between Mhc diversity and juvenile survival in wild population of Greater Flamingos using a next generation sequencing approach.
- Heni Alexander (2016) Genetic diversity of Toll-like receptor (TLR4, TLR7) genes in a neotropical rodent in landscapes differing in anthropogenic disturbance.
- Meier Matthias (2014) Studying the gut-associated microbial community of the black-backed jackal (*Canis mesomelas*) inhabiting the central Namibian cattle-ranching area: a next generation sequencing approach.