

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

2020

- 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.

2019

- 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.

2018

- 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*).

2017

- 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.

2016

- 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.

2015 and earlier

- 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.