2020 Abstract Award Winners

Abdulsalam Adegoke (PhD student)

<u>Title</u>: Tick-borne bacterial and protozoan animal pathogens shape the native microbiome within *Hyalomma anatolicum anatolicum* and *Rhipicephalus microplus* tick vectors

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Ticks vector several bacterial, viral and protozoan pathogens of public and veterinary health significance. They also harbor a diverse community of microbes linked with success in their biological processes like hematophagy, hence vector competence. The interactions between bacterial and/or protozoan pathogens and their tick vector microbiome are yet to be investigated. For this study, we screened 320 *H. anatolicum* and *R. microplus* ticks for protozoan (*Theileria* species) and bacterial (*Anaplasma marginale*) pathogens using a PCR based assay. Subsequently, selected PCR positive and negative ticks were sequenced for their microbiome composition by analyzing the highly conserved V1-V3 region of the 16S rRNA bacterial gene using the MiSeq Illumina platform. Sequenced reads were analyzed using the QIIME 2 bioinformatics pipeline and microbial richness and abundance was estimated.

Our results revealed that the microbiome of female *H. anatolicum anatolicum* ticks was dominated by the endosymbiont *Candidatus Midichloria mitochondrii* (CMM) and *Francisella*-like endosymbiont (FLE), and their relative abundance remains constant with or without pathogen infection. *A. marginale* infected Male *H. anatolicum anatolicum* ticks were also co-infected with *Ehrlichia* species. Uninfected and *A. marginale* infected *R. microplus* ticks showed similar abundances of bacterial at the species level, while *Theileria* species infected *R. microplus* were completely dominated by three *Bacillus* namely *B. pumilus*, *B. carboniphilus* and *Bacillus* species, suggesting a pathogen induced bacterial dysbiosis. In support of the reduced abundances, both microbial diversity and richness were also observed to be significantly reduced in *Theileria* infected *R. microplus* ticks when compared to *Theileria* infected *H. anatolicum anatolicum* anatolicum.

Carlos Barreto (PhD student)

<u>Title</u>: Addition of polypropylene and polyester in soil shows no effects on microarthropod communities, but affects decomposition rates

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Microplastics are usually defined as plastic particles <5mm. They are manufactured in products for human consumption, thus beneficial to humans, although they have become an environmental threat

with potential negative interactions with organisms. As microplastics are highly abundant in soil, this study focused on soil-dwelling mites and collembolans because of their high potential for microplastic interactions and their importance role in ecosystem services. The effects of polypropylene and polyester microfibers of two different lengths (2–3mm and 5–6mm) on microarthropod communities and decomposition rates were addressed. Microplastic addition showed no effects on soil microarthropod communities (abundance and species richness) for the groups Oribatida, Prostigmata, Astigmata and Mesostigmata, Collembola, nor other invertebrates present in the soil samples. The addition of microplastics in the soil did affect litter decomposition rates for litterbags on the soil surface; higher mass loss (i.e. decomposition) was found in polyester treatments compared to control and polypropylene treatments, regardless of the length of the fibers. However, no significant differences were found on decomposition rates in the soil profile, measured by lamina bait sticks. Microarthropod community analysis using non-metric multidimensional scaling analysis (NMDS) found that communities were less similar in polypropylene addition treatments compared to polyester addition and control treatments, although PERMANOVA results were not significant. This study is the first to test the effects of microplastics on soil microarthropod communities, and no direct negative effects of microplastic addition were detected.