

KEYNOTE: Integrating evolution, biogeography, and host associations of feather lice across time and space

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The geographic distributions of organisms often change over time. Incorporating the evolutionary history of a group of organisms is crucial for understanding the biotic and abiotic factors responsible for driving these changes in distributions. For parasitic organisms, it is also important to include information about their hosts' evolution and biogeographic history. In addition to helping clarify patterns of parasite distributions, combining information from parasites and their hosts can provide insights into processes of host-parasite coevolution and the origin of parasite biodiversity. My presentation will focus on integrating evolutionary history and distributions of parasitic feather lice and their avian hosts. Lice are an ideal system for addressing broader questions about parasite evolution because they tend to be host-specific and are obligately associated with their hosts. I will present results from multiple studies that assess the evolutionary history of different groups of lice over multiple geographic and time scales. First, I will discuss the evolutionary history and historical biogeography of a globally-distributed clade of lice from pigeons and doves. Next, I will focus on the phylogeography of lice from specific geographic regions. Finally, I will present how genomic information from an individual louse can provide information on the historical distributions of both the louse species and its host species.



KEYNOTE: Of Lice and Men: global declines of Phthiraptera and other parasites in the Anthropocene

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Lice are species rich, cosmopolitan, and often host-specific. This has made them incredibly vulnerable to co-extinction when their host species decline. Yet despite this, conservation efforts directed at co-threatened lice remain largely unrealised. Dr. Hopkins and Dr. Kwak co-chair the newly established IUCN parasite specialist group which aims to support and expand efforts to assess and conserve the planet's parasites, including lice. Dr. Kwak will open with an examination of modern louse extinctions (and recoveries) and an overview of the present state of louse conservation biology. Dr. Hopkins will then detail the pair's recent efforts to assess the extinction risk of lice and other ectoparasites in the Antarctic region and to understand the drivers of louse declines in the region. They will then close with an overview of the short and long-term goals of the IUCN parasite specialist group, which aims to conserve lice and all other metazoan parasites of vertebrates.



KEYNOTE: Aqualice: the extraordinary marine insects

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Insects are considered the most ecologically and evolutionarily successful group of animals, surpassing all others in biomass, diversity, and ability to colonize almost any environment. However, while these statements are true for terrestrial environments, insects are virtually absent from the oceans, the largest habitat on Earth. Remarkably, a group of sucking lice are ectoparasites of amphibious hosts, such as pinnipeds (seals, sea lions, and the walrus) and the northern river otter. During the evolutionary transition of pinnipeds from land to sea, sucking lice had to manage the amphibian biology of their hosts, some of which can spend more than 80% of their time submerged and perform extreme dives to over 2000 m below the surface. These obligate and permanent ectoparasites have adapted to tolerate hypoxia, high salinity, low temperature and extremely high hydrostatic pressure. A major question that has been debated for decades is how seal lice survive during the long diving excursions of their hosts in the open ocean. For most of the year, lice are exposed to daily dives that in some cases can exceed depths of 2000 meters. In addition, they are unable to breathe atmospheric air during feeding periods that can last for months. In this talk I will discuss the major ecological, behavioral and physiological adaptations of seal lice to these conditions and how they are able to survive where no other insect can, in the depths of the ocean.



ROUNDTABLE: Effect of COVID-19 on head louse infestation and policy

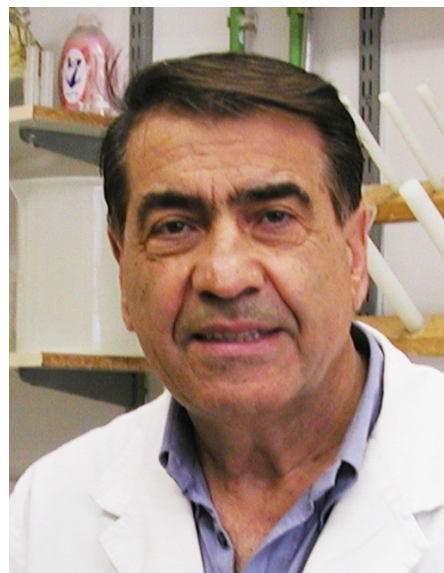
Chair: Ariel C. Toloza

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In March 2020, the World Health Organization (WHO) declared the COVID-19 outbreak as a pandemic. COVID-19 is caused by SARS-CoV-2, a variant of the coronavirus. Therefore, in March 2020, the Argentinean and Israeli governments established mandatory isolation for an indefinite period. This obligatory isolation interrupted regular classes avoiding direct contact between children, thus affecting the dispersal route of individuals and the evolution of head louse populations. Here, we show the results obtained through an online survey or sales of pediculicides of how confinement affected the prevalence of lice during lockdown compared to the situation prior to confinement. These works highlight the impact of social distance in the population dynamics of head lice and how it could affect the control strategies in the future.



ROUNDTABLE: Lice as human evolution markers

Chair: Ariel C. Toloza

Participants: Marina Ascunce¹, Niyomi House², Alejandra Perotti³

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Head lice have co-evolved with humans for millennia and can be used to study human history and evolution. From the analysis of the genetic variation in human lice by using both nuclear microsatellite loci and female-inherited mitochondrial DNA sequences, head lice populations can be divided into two major genetic clusters named I and II. Cluster I was found to be more common in Africa, while Cluster II was found to be more common in Europe and the Americas. Then, high-quality DNA from 1,500-2,000-year-old nits from ancient Argentinian human remains revealed that the mummies' ancestors had migrated from northwest Amazonia to the Andes of central-west Argentina. The cement also preserved ancient environmental DNA, including the earliest recorded case of Merkel cell polyomavirus. Animal-lice nits found on the hair of ~5000-year-old human remains support a very close interaction with camelids and foxes, proposing early events of animal domestication. Finally, whole genome sequences of human head lice from 43 countries showed that head lice populations are highly structured geographically, with five major genetic clusters corresponding to the five major continents with the highest genetic diversity detected in sub-Saharan Africa.



Insecticide resistance on human head louse populations

Chair: Ariel C. Toloza

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Insecticide resistance on human head louse populations is a growing problem worldwide and makes it more difficult to treat head lice that can lead to an increase in the number of head lice infestations. This is due to the excessive use of insecticides, which has led to the development of resistance in head lice. Here, we discuss the resistance levels, consequences and most frequently used actives of several regions like Africa, Asia, Oceania, Europe and the Americas. Finally, population genetic pathways are undergoing strong selection pressure exerted by the use of pediculicides by its host, identified by several signatures of positive selection. Also, genetic variants found on VSSC revealed a unique origin of *kdr*-type mutations.

