

1. FINAL PUBLISHABLE SUMMARY REPORT

The emergence of infectious diseases is often attributed to the adaptation of parasitic organisms to new hosts. In the case of vector-borne disease, pathogen transmission, and thus access to novel host types, will be strongly constrained by host use of the vector. In this way, host-associated specialisations in the vector organism can be a major factor mediating the evolution of the pathogens they transmit. The principal goal of this project was to investigate mechanisms of host specialisation in vectors and understand how it affects pathogen transmission, disease epidemiology and, ultimately, parasite evolution. To do this, we considered two parallel seabird-tick systems, *Ixodes uriae* and the species complex *Ornithodoros capensis*. Both ticks use a diverse range of colonial seabird species as hosts and both can transmit bacteria of the genus *Borrelia*. As these bacteria are responsible for diseases such as Lyme disease and Relapsing fever in humans, an understanding of their epidemiology, and in particular the role of seabirds in their large scale spread, is essential.

Following the discovery of repeated patterns of host-associated divergence in the polar seabird tick, *Ixodes uriae*, we first investigated the phylogeography of the tropical seabird tick complex *Ornithodoros capensis*. More than 150 *O. capensis* ticks from around the globe were typed and analyzed at one mitochondrial (16S rRNA) and one nuclear gene (18S rRNA). We found a much higher genetic diversity than expected according to previous morphological identifications and several cryptic species could be identified within a single geographic location (ie, presence of cryptic species in sympatry). At a large spatial scale, geographic distance clearly plays an important role in determining the spatial structure of these ticks. At a more local scale, tick populations structured by host species, suggesting that host specialization has also likely played a major role in the diversification of the complex. With the help of a Master student (S. ORTUN FLAMENT) we have started to develop additional nuclear genetic markers (microsatellite markers) to further understand patterns of local population structure and gene flow in these ticks. This on-going work will continue as a collaborative project during the return-phase of the fellow to Barcelona, Spain. In order to fully consider the consequences of population structure and host use for disease epidemiology, we carried out a literature review of what is known about seabird ticks, their dispersal patterns and the pathogens they carry (Dietrich et al. 2010). Clearly, seabird tick systems may harbour an important diversity of pathogens that can interact with terrestrial systems.

As previously mentioned, the *Ixodes uriae* system has shown repeated patterns of host-associated population structure, even when the host seabirds are under sympatric conditions. In this part of the project, we aimed to use this information to characterise patterns of prevalence and infection intensity of *Borrelia* bacteria among these host races in several geographic locations. By combining novel statistical methods (ie, site-occupancy modelling) and a quantitative PCR approach, we showed the existence of strong biases in the probability of detecting Lyme disease bacteria in the different tick host races. These biases can lead to a significant underestimation of *Borrelia* prevalence in the vector ticks and are due to differences in the intensity of infection of *Borrelia* bacteria among *I. uriae* host races (see Figure 1). From this data, it is clear that certain seabird species – tick race combinations are more important than others for the large scale circulation of the pathogen. This work also suggests that similar patterns may be present in other vector-borne disease systems and that host specialisation in the vector

requires more explicit consideration in these systems. This study has been recently published in *Evolutionary Applications* (Gómez-Díaz et al. 2010).

Finally, we investigated patterns of genetic diversity and population structure of marine *Borrelia* bacteria in different seabird-host races and multiple geographic locations with the aim of understanding the diversity, evolution and interaction with terrestrial disease systems. Initial studies indicated the presence of several *Borrelia* species in marine polar systems, but that most seabird colonies were dominated by the species *Borrelia garinii* (Duneau et al. 2008, Dietrich et al. 2008). We then performed multilocus sequence analyses in collaboration with the Pasteur Institute (Paris) on more than 60 marine isolates and 10 terrestrial isolates of *Borrelia garinii*. Results show that *B. garinii* spirochetes circulating in the marine system are highly diverse. Microevolution in marine in this bacterium seems to be mainly clonal, but genetic structure and selection analyses suggest that adaptive evolution may act as a diversifying mechanism in this system. However, selection by the seabird host seems to be more evident than that by different tick races. Results also show evidence of recombination between marine and terrestrial strains, thus confirming that Lyme disease bacteria are exchanged between these two enzootic cycles and highlighting the importance of considering the marine system when modelling Lyme disease epidemiology. The results of this work are currently being prepared for publication.

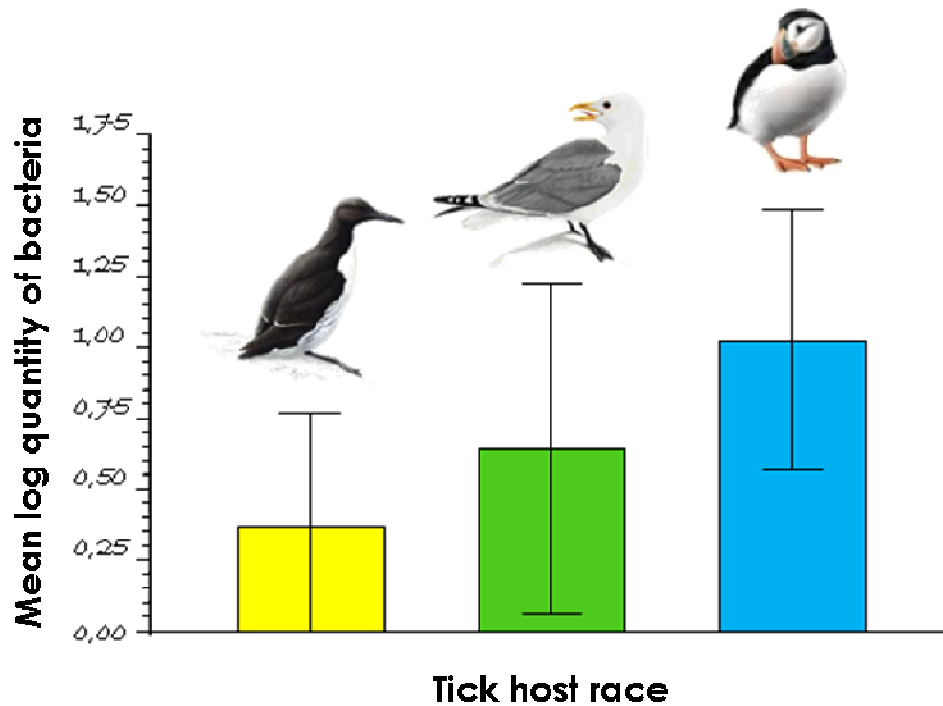
In addition to intensive field and laboratory work, this Marie Curie grant provided the opportunity for the fellow to develop and refine her knowledge on different technological advances and their application to the study of parasite ecology and evolution. Indeed, during her 24 months at the GEMI laboratory, Dr. Gómez-Díaz published two articles on these issues (Gómez-Díaz 2009, Gómez-Díaz & Figuerola 2010).

List of keywords

Vector-borne diseases- Ixodes uriae – Ornithodoros capensis – Borrelia –host-associated divergence- genetic population structure- selection- recombination

Websites where additional information may be found:

http://gemi.mpl.ird.fr/IPA/Equipe/Gomez/index_EG.htm



*Figure 1. Using quantitative PCR methods, we have shown variation in infection by Lyme borreliosis bacteria (*Borrelia burgdorferi* s.l.) among host-associated races of *Ixodes uriae*. This graph illustrates the relative number of bacteria per tick (infection intensity \pm 95% CI) in three host races : ticks from common guillemots (*Uria aalge*), black-legged kittiwakes (*Rissa tridactyla*) and Atlantic puffins (*Fraterecula arctica*). The difference among tick races in bacterial intensity indicates that the “puffin-tick” system may be more competent for *Borrelia* than the others. This variation among races may have important consequences for the circulation of this pathogen at different spatial scales.(after Gomez-Diaz et al. 2010)*