**Gene-environment interactions in a long-lived seabird: how do immune genes and pollution interact to affect the microbiome and fitness components of common terns?**

The way individuals look, behave and perform partly depends on the genes they inherited from their ancestors, and partly on the environment that they encounter. It's the interaction between the two that underlies the process of evolution by natural selection. Evolutionary ecologists therefore aim to understand which genetic variation lead to differences in performance between individuals, and which environmental factors are responsible for this, or affect it.

The environment has always been variable, but human activities currently cause major and extremely rapid global change. Among the many things that are changing, are the pathogens that individuals encounter (think of covid-19) and the level of pollution that they face. What these two environmental changes have in common, is that they may affect the reproductive performance as well as survival of individuals via effects on immune system functioning.

The microbiome is the collection of all microbiota that live on or within an individual's tissues. Over recent years, the gut microbiome in particular has been linked to a large number of human diseases and conditions. Moreover, recent work suggests that the microbiome is affected both by the variation in genes coding for molecules involved in the immune response, and by environmental pollution. The microbiome may therefore be one of the main mediators linking genetic variation to performance in interaction with the environment. At the moment, however, this link can only be

suggested based on results from separate lines of scientific work; a holistic study of all components is lacking.
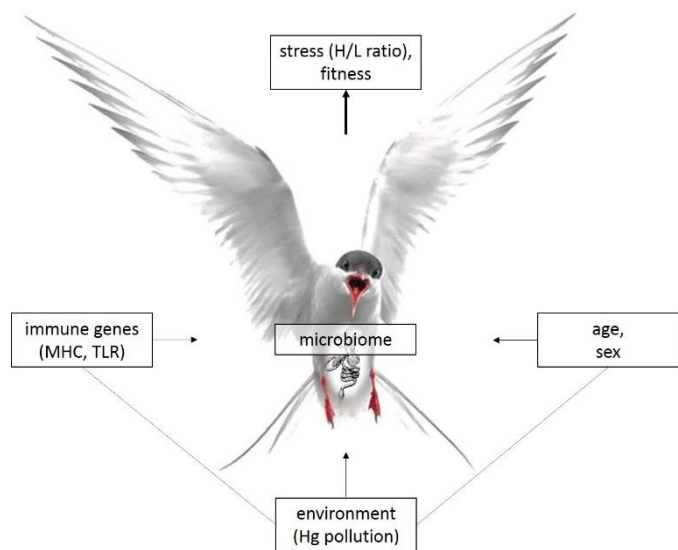
The main objective of the project we propose here therefore is to show how immune gene diversity and pollution interact to affect the microbiome and performance of individuals. We propose to do so by repeatedly sampling free-living common terns (*Sterna hirundo*) from a long-term individual-based study population from northern Germany. Specifically, we propose to collect blood and faecal samples from individually marked terns of known sex, age and ancestry to assess their immune genotype, as well as to repeatedly assess their contamination and composition of the microbiome. Moreover, we will monitor the environment (e.g. breeding density, food availability), as well as reproductive performance and survival of these birds.

Doing so will allow us to assess (i) within-individual changes in mercury contamination and the microbiome, (ii) the links between such changes and variation in the environment, and (iii) whether any effects on fitness components depend on immune genotype. As such, the project will give us insight into the process of natural selection with respect to environmental changes that are current and dramatic, and therefore provide us with knowledge that we can hopefully use to then inform conservation measures.