NERC PROJECT SUMMARY – Dr. Ben Longdon

A major source of emerging infectious diseases are viruses moving into new host species. Such 'host shifts' or 'jumps' are well-documented in the case of human pathogens such as HIV, Ebola-virus, and SARS-CoV-2. To understand the emergence of new viruses, we need to identify factors that predict which viruses infect which host species. However, we have much to learn about how the environment, evolutionary relatedness, and recent species history determine which species share viruses.

Here we will use a 'snapshot' of the UK moths (Lepidoptera) and their viruses to tease apart the relative importance of the different factors that shape the virus community. Thanks to systematic sampling by the National Moth Recording Scheme and the Rothamsted Insect Survey, the British moths are arguably the most closely studied and best characterised group of invertebrates in the world. We will combine this unique dataset on moth ecology with the genomic sequencing of viruses from more than 200 species of moth.

Our first goal is to understand what viruses infect UK moths, how they are related to each other and to other viruses, and how many host species they infect. We will test how often these viruses have jumped between hosts, and whether they preferentially jump between closely related hosts, or hosts in the same environment.

Our second goal is to understand how host ecology and environment determine which hosts are infected by which viruses. For example, we will test whether more abundant host species have a greater number and diversity of viruses, and whether species with overlapping environments share more viruses. We will also test whether more generalist species, larger species, or species in certain environmental conditions are infected by a more diverse range of viruses.

Our third goal is to examine the effect of host and virus evolutionary relatedness, and how these factors interact to predict virus sharing. For example, we will test whether closely related host species have similar viruses, and whether closely related viruses infect similar sets of hosts.

Finally, we will examine whether species that have recently arrived in the UK and/or those with expanding ranges, have fewer viruses or viruses that are more likely to infect a broad range of hosts.

This work will help to determine the relative importance of ecology and the environment, evolution, or species history in determining the distribution and abundance of viruses across host species, and will provide fundamental insights to help conceptualise a framework for understanding future disease emergence.

While a focus on high-profile pathogens that infect humans is clearly essential from a public health perspective, such focus limits our ability to test the fundamental rules that underly pathogen emergence. Moreover, invertebrates are keystone species in many food webs and so are fundamental to life on earth, but at the same time act as pests and vector pathogens. Therefore, this work will also have important outcomes for both our fundamental understanding of disease biology, and also applied insect-science, biocontrol and applied virology.