

Reference: 11/CW

**Project Title: DNA sequencing of historic and novel viral samples held within the NVRL**

**Supervisors:** [Dr Caroline Wright](#), [Dr Simon King](#)

**Research group:** [Non Vesicular Reference Laboratory](#)

**Project Summary:** The primary purpose of the Non-Vesicular Reference Laboratory (NVRL) is to provide both a national and international diagnostic service and to characterise outbreaks of livestock diseases caused by Bluetongue virus (BTV), African horse sickness virus, African swine fever virus, Peste des Petits Ruminants virus, and Capripox viruses. The NVRL is a World Organisation for Animal Health (OIE) Reference Laboratory for the diseases caused by these viruses and therefore provides a critical resource for developing countries to prevent and control exotic diseases of livestock.

As well as performing diagnostic tests on samples by using polymerase chain reaction (PCR) to test for the genetic material of the virus, genome sequencing can be used to determine further details such as the serotype or lineage of the isolate. Full genome or individual gene sequence data can also be used for the epidemiological tracing and/or phylogenetic analysis of these exotic viruses. As part of the applied research conducted by the group, such sequence data analysis can help define the evolutionary dynamics of the virus during an outbreak and contribute to the knowledge and understanding from which to base future outbreak control strategies.

This project will involve individual gene or full genome (where appropriate) sequencing, utilising the state-of-the-art sequencing platforms available at The Pirbright Institute, e.g. conventional Sanger as well as next-generation, high throughput Illumina sequencing. This sequencing will be performed on biological material, historic or contemporary, infected with any one of the viruses covered by the NVRL.

The placement will include training in selected molecular methods, including nucleic acid extraction, PCR and DNA sequencing, as well as a range of tools for the bioinformatic analysis of DNA sequence data. The successful student will be expected to work independently in the molecular suite after having obtained the relevant training. In addition, the student will support the NVRL in routine duties such as housekeeping, consumable management, sample reception and other duties as required.

As well as providing the successful student with practical experience of a range of topical scientific techniques, this predominantly sequencing based project offers the flexibility for the student to both contribute to the wider remit of the group and to develop their own research questions through the interpretation of sequencing data, in real-time. This placement will also provide a unique opportunity to work in an ISO/IEC 17025-accredited Reference Laboratory within a high containment facility.

**References for Suggested Reading:**

Flannery, J., King, S., Rajko-Nenow, P., Popova, Z., Krstevski, K., Dzadzovski, D., & Batten, C. (2021) Re-emergence of BTV serotype 4 in North Macedonia, July 2020. *Transbound Emerg Dis.* 68: 220– 223

King, S., Rajko-Nenow, P., Ashby, M., Frost, L., Carpenter, S., & Batten, C. (2020) Outbreak of African horse sickness in Thailand, 2020. *Transbound Emerg Dis.* 67: 1764– 1767

Rajko-Nenow, P., Brown-Joseph, T., Tennakoon, C., Flannery, J., Oura, C., & Batten, C. (2019) Detection of a novel reassortant epizootic hemorrhagic disease virus serotype 6 in cattle in Trinidad, West Indies, containing nine RNA segments derived from exotic EHDV strains with an Australian origin. *Infection, Genetics and Evolution.* 74: 103931

**To Apply:**

Please email your CV (no more than two sides of A4) and a covering letter, detailing why you would like to undertake the placement and the knowledge and skills that you will bring to the Institute, to [studentship@pirbright.ac.uk](mailto:studentship@pirbright.ac.uk).

**Closing date to apply: 09.00, 7th February 2022**