**Topics for summer internship 2023 at ENVT**

1. **Virology (VIRéMIE team)**

Our team of virology is part of the joint research unit of the National Veterinary School of Toulouse (ENVT) and the National Research Institute for Agriculture, Food and Environment (INRAe) Interactions Host-Pathogens. This year we are 8 permanent staff members (including scientists and research technicians), 4 PhD students and 2 master students. DVM and undergraduate students also join the team for their theses or short internships. Our group investigates the mechanisms of host-virus dialogue, using both *in vitro* an *in vivo* approaches.

**Contact: mariette.ducatez@envt.fr**

1. **Emergence of highly pathogenic avian influenza**

This project will use state-of-the art molecular virology to assess how the nucleotide sequence of the hemagglutinin gene segment modulates the genetic evolution from low pathogenic avian influenza to highly pathogenic avian influenza viruses.

Supervisor: Romain Volmer, DVM, PhD – Laboratory of virology – Ecole nationale vétérinaire de Toulouse - France

**Contact: romain.volmer@envt.fr**

<https://interactionshotesagentspathogenes.weebly.com/>

1. **Molecular epidemiology of avian influenza viruses**

Only two avian viruses are able by themselves to cause 100% mortality in chicken flocks: highly pathogenic influenza virus and velogenic Newcastle disease virus (NDV). Several other avian viruses cause severe losses in poultry flocks when associated with co-infecting pathogens. In Africa, very little is known on avian viruses, their circulation, evolution and spread. We have strong collaborations with Northern (Morocco), Western (Benin, Togo, Côte d’Ivoire, Mali), and Eastern (Uganda) Africa and are conducting molecular epidemiology studies mainly on respiratory viruses on the continent to be able to understand putative virus exchanges between wild and domestic birds and between geographic areas. We will work on African field samples, screen them for avian viruses by (RT-)PCR, take care of the virus isolation in embryonnated eggs, and carry out a molecular characterization of the strains (partial or full genome sequencing, phylogenetic analyses).

The internship will be co-supervised by Idrissa Sanogo (PhD student).

**Keywords:** avian and bovine respiratory viruses, Africa, molecular epidemiology

1. **Detection and characterization of influenza D virus**

Recent studies in the USA, in China, and our preliminary work in France have identified a new genus of the *Orthomyxoviridae* family, named Influenza D virus (IDV). This novel virus was shown to infect farm animals including swine and cattle, and to efficiently replicate and transmit in ferrets, the animal model of choice for transmission of influenza A virus (IAV), a well-known other Orthomyxovirus, to humans. IAV is well known to infect poultry and wild birds, with huge economic consequences for the food industry. In addition, IAV is also a major concern for human health; once this virus crosses the species barrier it might even adapt to its new host, becoming highly infectious and gaining the ability to spread from man to man and cause pandemics.

In contrast to IAV, there is only very scarce information on Influenza D and its risks for animal and human health. The virus seems to be circulating at a global level in farm animals, as antibodies against IDV has been detected in cattle in America (USA, Canada, Mexico, and Argentina), Asia (China and Japan), Africa (Benin, Togo, Morocco and Kenya), but also in France, Italy, Ireland, Luxembourg and Turkey. In addition, it has been shown that IDV can be isolated from sick cattle, while it might be associated in a complex of pathogens, which might hamper early detection.

The main scope of the internship is to generate highly needed knowledge for better risk assessment of IDV. We will work towards the evaluation of diagnostic tools and assessing the virus genetic and antigenic properties. The project is part of a European Union funded project with partners from Sweden, Belgium, Italy, Luxembourg and Ireland.

The internship will be co-supervised by Prof. Gilles Meyer.

**Keywords:** influenza D virus, molecular biology, serology, evolution, phylogeny, diagnostics.

**References:**

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Flynn, O., et al., Influenza D Virus in Cattle, Ireland. Emerg Infect Dis, 2018. 24(2): p. 389-391.

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O'Donovan, T., et al., Seroprevalence of influenza D virus in selected sample groups of Irish cattle, sheep and pigs. Ir Vet J, 2019. 72: p. 11.

Snoeck, C.J., et al., Influenza D Virus Circulation in Cattle and Swine, Luxembourg, 2012-2016. Emerg Infect Dis, 2018. 24(7): p. 1388-1389.

1. **Myxoma virus evolution from the 1960s to now**

Myxomatosis in Europe is the result of the release of a South America strain of myxoma virus in 1952. Several attenuated strains with origins in South America or California have since been used as vaccines in the rabbit industry. Using our archive virus collection (with samples from 1960s to now), we will aim at understanding the evolution and molecular clock of European myxoma viruses. Techniques to be used here: DNA extraction, PCR reactions for targeted genome regions, Sanger sequencing, phylogeny and molecular clock analyses.

The internship will be co-supervised by Pr. Stéphane Bertagnoli.

**Keywords:** myxoma virus, molecular biology, evolution, phylogeny, molecular clock

**References:**

Camus-Bouclainville et al, Genome sequence of SG33 strain and recombination between wild-type and vaccine myxoma viruses. Emerging Infectious Diseases 2011

Bertagnoli and Marchandeau. Myxomatosis. Rev Sci Tech. 2015