UNIVERSITY OF COPENHAGEN
DEPARTMENT OF VETERINARY AND ANIMAL SCIENCES

Thesis projects for BSc and MSc students

The Veterinary and Zoonotic Virology Group

Who we are: Our research group is located at the beautiful Frederiksberg Campus, University of Copenhagen. We are a social and ambitious group, consisting of 2 laboratory technicians, 4 PhD students, 6 postdocs, 3 academic employees and 1 professor. We enjoy each other's company and value social gatherings within the group, such as the daily lunch, a weekly breakfast, cake club, and sporadic team building events.

Our research focuses on viruses in Danish animal production. We strive to increase the current knowledge of new and existing viral pathogens and to bridge the understanding of animal and human health. Selected focus areas include research on the mechanisms underlying viral disease within the natural host animal, host-pathogen interactions, and virus evolution and adaptation.

Read more about the group here:

https://ivh.ku.dk/english/research/bacteria_and_viruses/veterinary-and-zoonotic-virology/

Available Projects:

- Establishment of an influenza D virus antibody test
- Influenza D virus in Danish Pigs
- Prevalence and characterization of Porcine Respirovirus and Orthopneumovirus in Danish pigs
- Molecular characterization of recently circulating influenza A and D viruses from cattle
- Culturing of Porcine Rotavirus A and cross neutralization test against the most frequently detected RVA genotypes
- Diversity in tropism among influenza A virus strains and characterization of receptor distribution in ferrets
- Ecology and evolution of parvoviruses in wildlife and at the interface between domestic and wild animals [WiPP – Wildlife Parvovirus Patrol]
- Discovery and characterization of novel arboviruses in ticks [ARBO-WATCH]
- GenBank spring cleaning one virus family at the time: *Parvoviridae*
- Prevalence of feline viruses in shelter cats

Establishment of an influenza D virus antibody test

Project Description: Influenza D virus is a relatively newly discovered virus belonging to the same virus family as influenza A virus, which is known for causing respiratory disorders in humans and a wide range of animal species. Recently, influenza D virus was detected for the first time in Denmark in connection with a large calves project, where 100 Danish cattle herds were examined. Serum samples were collected from calves in these herds, and the samples will be analyzed for the presence of antibodies specific for influenza D virus in order to determine the serum prevalence of this virus in Danish calves. The aim of this project is to establish an antibody analysis (ELISA test), which is specific for antibodies against influenza D virus.

What we are looking for: We are seeking curious and motivated Bachelor's or Master's students who want to learn how to establish and implement a new analysis, which can be applied to many other research fields. Students of any natural science background are welcome to apply.

Contact us: Assistant Professor Nicole B. Goecke (nbgo@sund.ku.dk)

Influenza D virus in Danish pigs

Project Description: This project will investigate how widespread influenza D virus is in Danish pigs and cattle. Influenza D virus is a relatively newly discovered virus belonging to the same virus family as influenza A virus, which is known for causing respiratory disorders in humans and a wide range of animal species. Influenza D virus was recently detected in Denmark for the first time in connection with a calves project, where 100 Danish cattle herds were examined. The virus was found to be present in 12 out of 100 herds. In other countries, in addition to calves, influenza D virus has been detected in animal species like pigs, horses, sheep and goats. Therefore, it could be of interest to examine the occurrence of influenza D virus in Danish pigs in order to get an idea of how widespread the virus is within this animal group. The project will include methods like RNA extraction, PCR, preparation for next generation sequencing and bioinformatics.

What we are looking for: We are looking for curious and motivated Bachelor's or Master's students who want to learn different molecular methods, which can be applied to many other research fields. Students of any natural science background are welcome to apply.

Contact us: Assistant Professor Nicole B. Goecke (nbgo@sund.ku.dk)

Prevalence and characterization of Porcine Respirovirus and Orthopneumovirus in Danish pigs

Project Description: Porcine Respirovirus and Orthopneumovirus are both novel recognized pathogens in the swine production causing symptoms related to respiratory disease. However, the prevalence of both viruses in Danish swine is currently unknown. In this project, swine influenza negative samples submitted to the Danish swine influenza surveillance will be analyzed to determine if Porcine Respirovirus and/or Orthopneumovirus can be detected in these samples originating from pigs with respiratory disease. Positive samples will be selected for further characterization using next generation sequencing, and phylogenetic analysis will subsequently be performed.

What we are looking for: We are looking for curious and motivated Bachelor's and Master's students to join this project. Students of any natural science background are welcome to apply.

Contact us: Associate Professor Pia Ryt-Hansen (piarh@sund.ku.dk)

Molecular characterization of recently circulating influenza A and D viruses from cattle

Project Description: In 2024, highly pathogenic influenza A viruses (IAVs) of the H5N1 subtype were detected in dairy cattle for the first time. Within a year, these viruses spread through dairy farms in the US affecting at least 943 farms in 16 different states, and they continue to circulate in cattle populations. Additionally, more than 40 humans with previous contact to cattle were infected. Since cattle have previously been neglected as hosts of IAVs, these novel viruses need to be studied to understand their viral characteristics to gauge their zoonotic potential.

A different genus of *Orthomyxoviridae*, influenza D viruses (IDVs), occur naturally in cattle and will also be analyzed on the molecular level. While these viruses predominantly circulate in livestock, high seroprevalence in humans with frequent contact to cattle hints at zoonotic potential.

The aim of this project is to analyze the mutations arising in these bovine-derived viruses. Techniques will include, but are not limited to, molecular cloning, mutational analysis, cell culture, and reporter assays.

What we are looking for: We are looking for curious and motivated Master's students who want to study why certain viruses cause zoonotic infections and learn techniques used in molecular biology. Students of any natural science background are welcome to apply. Previous lab experience is required.

Contact us: Postdoc Philipp P. Petric (ppp@sund.ku.dk)

“Culturing of Porcine Rotavirus A and cross neutralization test against the most frequently detected RVA genotypes”

Project Description: This project is centered on some of the most common virology techniques. There is a need to investigate the level of cross protection provided by the Rotavirus A virus (RVA) vaccine strain towards commonly found RVA genotypes from Danish pigs. The student must formulate a laboratory protocol for replication and isolation of RVA and following start a cell line to replicate some of the most found RVA genotypes in Denmark. Monospecific polyclonal serum will subsequently be isolated, purified and tested in in vitro neutralization assays against the panel of genetic diverse RVA isolates. Thus, possible vaccine disabilities can ultimately be assessed.

What we are looking for: We are looking for curious Master’s veterinary students to join this project. Students must be motivated to participate in the virology group and driven to investigate the topic where the outcome of the project also should be in focus.

Contact us: PhD-student Kasper Pedersen (kasper.pedersen@sund.ku.dk)

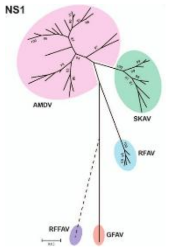
“Diversity in tropism among influenza A virus strains and characterization of receptor distribution in ferrets”

Project Description: Influenza A virus (IAV) causes respiratory disease in a variety of animal species and humans. Some strains of IAV can transmit between humans and pigs while others cannot. The reason for this is still unknown. The ferret transmission model is often used to study the pandemic potential of IAVs as human seasonal IAVs transmit very well between the ferrets and avian and swine IAVs are poorly transmitted. IAV enters the host cell by receptor-mediated endocytosis. The IAV host receptors are sialic acids (SA) linked to a galactose (gal) in either an α2,3 or α2,6 linkage (SA-Gal-α2,3 or SA-Gal-α2,6). Avian IAVs prefer the SA-Gal-α2,3 receptors whereas human and swine generally prefer SA-Gal-α2,6 receptors. These IAV receptors can be visualized within host tissues through lectin histochemistry. The objective of this master's thesis project is to comprehensively analyze tissue samples obtained from ferrets infected with diverse IAV strains, including ones adapted to pigs and humans. This analysis will primarily involve lectin histochemistry to map the distribution of IAV receptors and IAV immunohistochemistry to determine the tissue tropism of the virus. The project is part of a PhD project and you will work in close cooperation with PhD student, Charlotte Kristensen.

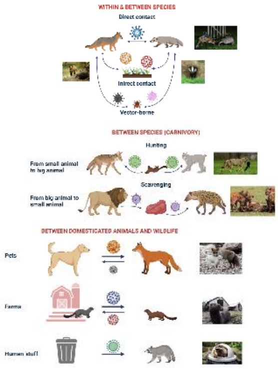
What we are looking for: We are looking for curious and motivated Master’s veterinary students to join this project.

Contact us: Postdoc Charlotte Kristensen (chark@sund.ku.dk)

“Ecology and evolution of parvoviruses in wildlife and at the interface between domestic and wild animals [WiPP – Wildlife Parvovirus Patrol]”



Parvoviruses are among the smallest known viruses, yet they possess significant pathogenic and emergence potential. These viruses are found across the entire animal kingdom, in vertebrates and invertebrates, on land and in marine environments. We apply epidemiogenetics, parvogenomics, and phylogenetic modelling to study the ecology and evolution of parvoviruses in wildlife, with a particular focus on carnivorans.



Our primary interests include elucidating cross-species transmission dynamics and assessing the impact of human-associated viruses (such as canine parvovirus 2 and Aleutian mink disease virus) on wildlife populations. We use broad-spectrum PCRs and metagenomics to identify and obtain the full genome sequences of known and novel parvoviruses and then perform phylogenetic analysis. This work is conducted in close collaboration with the Section of Parasitology and Pathobiology, the Globe Institute, and several international partners.

We have samples from many different animals (fox, marten, badger, wolf, mink, seals, dogs…) and multiple countries (Spain, Denmark, Poland, and expecting more from Canada, Italy, UK). We investigate many different viruses, animals, and environments, so there is the possibility of deciding the project direction.

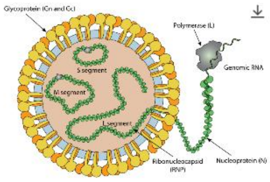
Check our latest paper: https://www.mdpi.com/2076-0817/14/8/734

Contact us: (marta.canuti@sund.ku.dk)

Discovery and characterization of novel arboviruses in ticks [ARBO-WATCH]

Climate change, through warmer temperatures, altered rainfall patterns, and increased anthropogenic disturbance of natural habitats, is driving large-scale shifts in animal behaviour, ecology, and dispersal. Arthropods are moving or expanding their ecological ranges, and microbial equilibria are being disrupted, leading to changes in pathogen distribution and transmission dynamics. Arthropod-borne pathogenic microorganisms (arbopathogens) are spilling over into previously unaffected territories, including areas at higher latitudes and elevations, and their geographic ranges are expected to continue expanding.

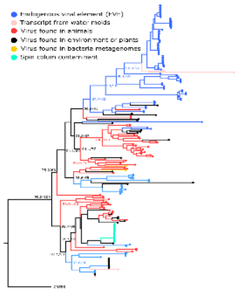
We focus on identifying and monitoring novel or unexpected vector-borne pathogens before they become health threats. We coordinate this project in collaboration with the Section for Parasitology and Pathology, the Globe Institute, the University of Milan, the University of Warsaw, and the University of Naples.



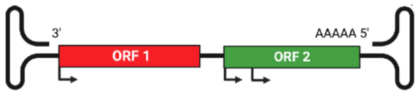
We are currently investigating ticks from Europe and Africa and performing virus discovery through metagenomics. We are also focusing more specifically on two bunyaviral genera (*Orthonairovirus* and *Bandavirus*) and a flaviviral genus (*Orthoflavivirus*) through pan-genus PCRs. Once identified viruses are fully genetically characterized and their host and geographic distributions assessed through epidemiogenetics.

Contact us: (marta.canuti@sund.ku.dk)

GenBank spring cleaning one virus family at the time: Parvoviridae



The advent of metagenomics made virus discovery within everyone’s reach, both technically and financially. While this has created great research opportunities and our knowledge of the ecology and evolution of viruses has vastly improved, the exponential increase in sequence data was accompanied by an exponential increase in mistakes in sequence databases. This created a lot of issues because automated sequence analyses pipelines rely on these databases, generating an unstoppable vicious cycle of wrong annotations.



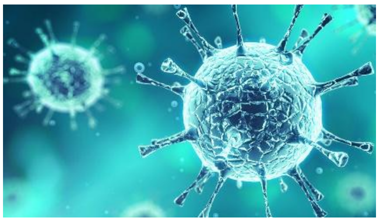
Our main research focus is virus discovery, and this GenBank chaos is creating a lot of problems for us. Furthermore, as members of the International Committee for Taxonomy of Viruses (ICVT) *Parvoviridae* study group, it is our task to keep the taxonomy of parvoviruses up-to-date. However, GenBank is polluted with sequences that are wrongly labelled as parvoviruses. By carefully analyzing these sequences, we already created 2 brand new virus families and a new virus realm. This is a bioinformatic project that will exclusively involve computer work and include fishing databases for viruses and performing highly challenging phylogenetic analysis to study virus evolution and create a curated parvovirus sequence database.

This project is done in collaboration with the Globe institute and collaborators from the ICTV, particularly Judit Penzes from the Texas A&M University.

Contact us: (marta.canuti@sund.ku.dk)

Prevalence of feline viruses in shelter cats

In cat shelters the prevalence of viruses is normally higher than in private homes, and sometimes viral outbreaks occur due to the high number of cats in a small space. This project will aim at establishing real-time quantitative PCR assays to detect feline viruses such as Feline Coronavirus (FCoV), Feline Herpesvirus (FHV-1), Feline Calicivirus (FCV), Feline Panleukopenia Virus (FPV), Feline Leukemia Virus (FeLV) and Feline Immunodeficiency Virus (FIV) and determining the prevalence of these viruses in samples obtained from cat shelters. At the same time clinical registrations will be collected to determine the significance of these viruses. Selected positive samples will undergo genome sequencing to provide an insight into which strains are circulating in Denmark.



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