

Climate Changes and Emerging Wildlife-Borne Viruses in Norway

– a follow up report on major knowledge gaps
and research needs



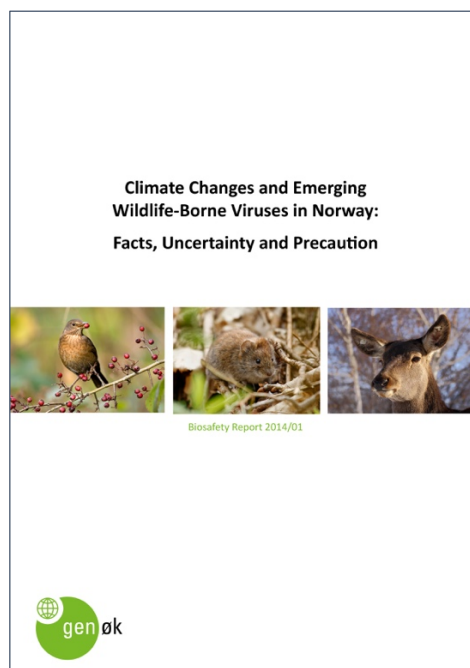
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Climate Changes and Emerging Wildlife-Borne Viruses in Norway

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The original report is available at genok.no/radgiving/rapporter/

Introduction

Most serious virus diseases affecting wildlife, domesticated animals and humans are caused by viruses with host and reservoir in small rodents, migratory birds, bats, mosquitoes, ticks and midges. Human Ebola virus disease, Zika virus and West Nile virus infections are timely but fatal reminder that viruses can emerge from reservoir species, jump hosts and spread to humans and animals. Until now, Northern Europe, including Norway, seem to be protected from emerging viruses and their hosts due to sub-optimal temperatures. This natural barrier may be eroded due to global warming with attendant tropical or sub-tropical temperatures in Norway, close interaction between reservoirs, virus vectors and vertebrate hosts as well as air travel and commerce. Thus, viruses and their reservoir hosts previously restricted to tropical and sub-tropical regions may find new ecological niche in Norway and Fennoscandia.

Biosafety Report 2014/01 by Prof Terje Traavik have explored the relationships between climate change and emerging wild-life borne viruses in Norway with the purpose of;

- i) describing the complexity of vector-borne virus life cycles,*
- ii) explore the influence of climate on these systems,*
- iii) explore the capacity to assess potential impact of perturbation in climate to these systems,*
- iv) place the issue of climate in the broader context of environmental change,*
- v) outline the kinds of information that will be necessary for more accurate prediction of future climate or environmental effects on vector-borne disease systems, and recommend research, surveillance and monitoring initiatives that may make the society able to act precautionary with respect to the described changes (Biosafety 2014/01, page 15).*

A major finding of the report is the paucity of research data concerning the occurrence, distribution and evolution of vector borne viruses in Norway, their reservoir and vertebrate hosts and the influence of climate and other anthropogenic factors on the vector-borne virus episystem. Without, empirical data, it is impossible to make scientifically valid recommendations to authorities on ways to pre-empt, predict and prevent the emergence or re-emergence of viruses from the wild in the context of global warming and other interacting anthropogenic factors. Thus, the goal of this follow up report will be to highlight the major knowledge gaps reported in Biosafety Report 2014/01 and briefly propose a research based methodological approach that will fill in the knowledge gaps in the short, medium and long term.

Specific objectives

- To identify major knowledge gaps reported in the Biosafety Report 2014/01.
- To propose credible and relevant research for the purpose of determining the occurrence, distribution and evolution of vector-borne virus episystem in Norway.

Core hypothesis

- Global warming, pollution, changes in the bio-distribution/phylogeography of virus-vectors and their wild life reservoir hosts, and the increasing interaction between humans, virus-vectors and their wildlife hosts will lead to increased virus outbreaks, emergence and re-emergence.

Core strategy

- Pre-emptive, precautionary based science through mapping of viromes before the emerge to cause diseases is a better model than responding to already emerged virus outbreaks.

Knowledge gaps

Ecology, competence, phylogeography of mosquitoes and mosquito vectored viruses in Norway

The indigenous mosquito species in Norway and their ecological spread was sampled over 30 years ago (Biosafety Report 2014/01, page 47). Paucity of data and knowledge gaps exists with respect to:

- Current status of indigenous mosquitoes species in different climatic zones of Norway.
- Occurrence and distribution of foreign aggressive mosquito's species in Norway.
- Occurrence, distribution and cell tropism of mosquito-vectored viruses in Norway.
- Competence of indigenous Norwegian mosquitoes to serve as reservoir hosts for non-indigenous viruses like Zika virus, West Nile virus, Dengue virus, Usutu virus, etc.
- Effect of climate warming on the biodiversity of mosquitoes and mosquito borne viruses.
- The effect of the interaction between global warming and anthropogenic factors on the evolution/co-evolution of mosquitoes and mosquito borne viruses and the implication for virus host range, virulence and resistance to antivirals. Of particular relevance is the effect of climate warming and pollution on the physiology of the virus and its reservoir hosts (Biosafety Report 2014/01, pp15-88).

Occurrence, distribution, competence and maintenance of ticks and tick borne viruses in Norway

Although many studies intended to map the distribution of ticks and tick borne viruses in Norway have been carried out or ongoing, key knowledge gaps remain as outlined below:

- Paucity of data on the distribution of ticks across all regions and climatic zones of Norway.
- Metagenomic analysis of tick borne viruses in Norway is lacking.
- Missing information concerning the spatial distribution of hosts, predators and species influencing tick populations and distribution of tick borne viruses.
- Information on non-resident tick species and their phylogeography is unknown.
- The role of co-infection, superinfection on the evolution and virulence of tick borne viruses in Norway is unexplored.
- The effect of the interaction between global warming and anthropogenic factors on the evolution/co-evolution of ticks and tick borne viruses and the implication for virus host range, virulence and resistance to antivirals. Of particular relevance is the effect of climate warming and pollution on the physiology of ticks and tick borne viruses (Biosafety Report 2014/01, pp15-88).

Occurrence, distribution and infection biology of midget born viruses in Norway

Biting midguts are vectors for two virus pathogens that cause diseases in ruminants, namely the blue tongue virus (BTV) and Schmallenberg virus (SBV). Norway was declared BTV-free since 2011 but SBV is prevalent in Southern Norway. Main knowledge gaps are outlined below:

- Metagenomic analysis of midget born viruses in Norway is lacking. Norway cannot be declared free of BTV without metagenomics analysis of midguts and cells/tissues of ruminants collected across different regions, climatic zones and seasons in Norway.
- SBV is believed to be a non-resident Norwegian virus that was spread to Norway from Denmark or Sweden but little is known if this virus have become endemic in Norwegian wild life and domestic ruminants.
- How climate warming and pollution either singly or in concert influence the spatial distribution of midguts, transmission, spread and maintenance of midget born viruses in Norwegian ecosystem is unknown (Biosafety Report 2014/01, pp15-88).

Vertebrate vector born viruses and non-vectored viruses with reservoirs in wildlife animals

Most serious virus diseases affecting wildlife, domesticated animals and humans are caused by viruses with hosts and reservoirs in small rodents, bats and migratory birds. Biosafety Report 2014/01 have provided insight into the reservoir host- virus interaction in Norway and this included (i) rodent borne viruses like Hantavirus and orthopoxviruses, (ii) bat borne viruses like Lloviu virus and European lyssaviruses, and (iii) viruses of different families borne by migratory birds. However, the studies of vertebrate vectored and non-vectored viruses carried out in Norway have not addressed key components of the reservoir host-virus epistystem. Some of the omitted research/knowledge gaps is outlined below:

- Sampling along routes and transit sites of migratory birds and subsequent metagenomics analysis of collected samples have not be done.
- Metagenomic analysis of rodent borne and bat borne viruses in Norway have not been done.
- Data on the interacting effects of climate change and chemical pollution on virus physiology and the host responses is unknown. Especially relevant is the role of multiple stressors (climate change and chemical pollution) on the host range, evolution transmissibility and virulence of the virus as well as its effect on the permissiveness of the host to virus infection.
- Effect of intra and inter mixed infection on the infection biology of the virus as well as the host is unexplored.
- The effect of food-web interaction (prey-predator) on the infection biology of the virus remain unknown (Biosafety Report 2014/01, pp84-103).

Resurrection of ancient viruses trapped in permafrost

Although this was not mentioned in Biosafety Report 2014/01, viruses trapped in permafrost may become alive with global warming. Present human and animal population may not have been exposed to these ancient viruses and thus may not have immunity against them. These ancient viruses which are hidden in permafrost for >30000 years may have the potential to cause serious infection in humans, animals and wild life. The melting ice on Spitsbergen may hide such viruses. The permafrost in Spitsbergen can give a snap shot of virus evolution across time and climate. The absence of research or data on the viromes buried in Spitsbergen is a major omitted research especially in the Norwegian/Arctic context.

Brief outline of follow-up research to Biosafety Report 2014/01

We have outlined key knowledge gaps and omitted research that were identified by the Biosafety Report 2014/01. While some of the omitted research can be addressed through large-scale pan-European projects (for example climate simulations), there are a number of credible, small scale, pilot projects that can fill in the knowledge gaps. GenØk has the capacity and competence to investigate two key areas namely:

- Metagenomic analysis of viruses/viromes from environmental samples.
- Response of vector borne viruses to multiple stressors (climate warming, chemical pollution, etc) either singly or in combination.

Metagenomic analysis of viruses /viromes in environmental samples

Objective:

To map the viromes in permafrost in Spitsbergen, mosquitoes in Norway airports and road tunnels, small rodents, small carnivores and migratory birds.

Methodological approach:

Present technologies used in rapid and sensitive detection of viruses are limited because they are designed to detect specific viruses or the fittest viruses. Thus, unknown and less fit viruses will go undetected even though some of them may emerge later as dangerous pathogens due to perturbation in virus-host interactions. *Deep genome sequencing of direct environmental samples without a priori selection pressure offer the possibility of mapping the entire virome including unknown viruses and virus quasi species. Thus, our core methodological strategy will be to use metagenomics to map the viromes present in permafrost, invertebrate reservoir hosts like mosquitoes and vertebrate reservoir/incidental hosts like rodents, migratory birds and small carnivores including wild and domestic cats.* Total DNA and RNA will be isolated from these reservoir/incidental hosts and subjected to metagenomics analysis. Analysis of the nature and distribution of viromes and their reservoir/incidental host across Norway ecological regions (north and southern Norway), seasons (winter, summer, autumn and spring), human activities (airports, road tunnels, urban and rural) will provide a good indicator of the effect of climate change on viruses in Norway.

Response of viruses to multiple stressors

Objective:

To map the effect of multiple stressors especially simulated temperature warming and chemical pollutants on the virus genome, transcriptome and proteome.

Methodological approach:

Selected viruses will be exposed to different temperatures and different concentrations of chemical pollutants singly and in combination. Total DNA, RNA and protein will be obtained for each treatment/treatment combinations. The response of the virus genome and transcriptome to the treatments will be obtained by deep genome sequencing and transcriptome analysis using Illumina and SolidTM platforms respectively. Proteomic profiling will be by Stable Isotope Labelling of Amino Acids in Cell Cultures (SILAC) combined with Q-exactive mass spectrometry.

Contribution and conclusion

We are willing to submit a full proposal of the outlined pilot project proposal if requested by the Agency. *If funded, the data that will be generated from this project will be essential to forecasting of future transmission risks, prediction of future outbreaks, development of vaccines, antivirals and diagnostic methods a priori to virus outbreaks as well as contribute to our understanding of virus evolution and the role of anthropogenic factors in virus emergence. To predict future virus outbreaks is the holy grail of public health prevention.* This proposed project (if funded) with its pre-emptive, precautionary and risk-based approach to virus emergence and re-emergence will be a credible but natural follow-up to Biosafety Report 2014/01.

Relevant Literature

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