# Assessing disease risks in changing environments: Greylag geese as an



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## exemplar study

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#### Background



### Wildlife genotyping

- Climate-driven environmental changes can significantly affect the levels and distribution of microbial pathogens and the hosts that carry them.
- To better understand these risks, robust, sensitive methods for pathogen detection and accessible approaches to sample wildlife carriers and ecosystems are required.



- Populations of Greylag geese (*Anser anser*) in Scotland (migratory and resident) have rapidly increased in size over the last 30 years
- In Orkney, an estimated 20,000 geese are "resident" and a further 40,000 geese arrive from Iceland during the winter months.
- This significant change in **biodiversity** is thought to be driven by **climate change**.
- Due to the resultant widespread faecal contamination of pastures and water, we are investigating microbial risks associated with goose faecal material (MRI-D4-2).

- Faeces provide a **non-invasive** source of DNA as samples can be collected from the ground.
- We have developed genotyping methods using  $\bullet$ goose faecal samples targeting mitochondrial & MHC diversity.
- This may enable different goose species / ulletpopulations / family groups to be identified and potentially enable discrimination of migratory from resident geese (analysis is on-going).

		*	860	*	880	*	900	*	920	*	940	*	960
OrkGLAllele3	:	ACTTTGACAGC	GACGTGGGGCA	GTATGTGGCTG	ACACGGAGCTG	GGCAAGCCTA	CAGCTGACTAC	TGGAACAGT	CAGCCTGAAGI	FACTGGAGAA	TGCAAAGACI	GCAGTAGA	CACGTTCT
MRIEmbden	:		A		T		r		.gc	G.	AG		
ChineseSG1	:		A		T		rc.		.gc	G.	AG		
ChineseSG2	:			T		GZ	AG.AGA.GAG.			G.	G		G
ChineseSG3	:						r		.gc				A
OrkGLAllele1	:			.c			r		cc.	c.	GAG.CG.G	.A	
OrkGLAllele2	:	т				GZ	АТ		cc.	c.	GAG.CG.G	AA	A.A
OrkGLAllele4	:			T		GA	AT.AGA.G		c				
OrkGL142Allele5	:			A		GZ	AT.AGA.G			c.	GACG	.A	G
OrkGL142Allele6	:			A		GZ	AT.AGA.G			c.	GACG	.A	G
OrkGL77Allele7	:												
OrkGL77Allele8	:												
ICEGL71Allele9	:		A	T		GZ	AG.AGC.G		c	G.	G	т	A

MHC class II Diversity in Wild Orcadian and Icelandic Greylag Geese compared with the domesticated Embden and Chinese Swan Goose



Greylag geese in Orkney



Greylag geese in Iceland

Results will be compared with microbial data to investigate correlations of pathogen carriage with specific goose cohorts.

**One Health** approaches are key to understanding the spread and emergence of zoonotic pathogens and antimicrobial resistant bacteria within different environments.

This requires a range of methodologies to be used in combination to investigate microbial, host and environmental factors.

![](_page_0_Figure_31.jpeg)

Orkney goose

Management Group

Food Safety

Water Safety

Communities

Public Health

#### **Ecosystem sampling**

- Ecosystem sampling enables transmission routes and  $\bullet$ reservoirs, as well as persistence of viable pathogens in the environment to be identified and investigated.
- We are investigating water, soil and sediment samples from farmed and wild ecosystems in Orkney and Iceland.

![](_page_0_Picture_35.jpeg)

For **migratory birds**, pathogen carriage in breeding and migratory sites must be considered.

**Engagement with a wide stakeholder group** is key for appropriate experimental design, data interpretation and impact.

#### **Detection of pathogens and antimicrobial resistance**

We are investigating the transmission of microbial pathogens between geese, cattle and calves.

![](_page_0_Picture_40.jpeg)

• *Cryptosporidium* is a gastrointestinal parasite responsible for causing diarrhoeal disease in neonatal calves, lambs, and humans.

![](_page_0_Picture_42.jpeg)

• *Campylobacter* is the biggest bacterial cause of human gastrointestinal disease in the UK and an important foodborne pathogen.

For water samples, in-field filtration methods were  $\bullet$ developed to support bacteria culture and DNA analysis from remote sites.

#### New technologies

• We are trialling the use of a **cutting-edge sequencing technology** (Nanopore sequencing) for disease surveillance in wildlife and the environment

![](_page_0_Picture_47.jpeg)

Long reads of sequenced DNA can be used to identify which bacterial species carry which AMR genes.

#### Outcomes

- Results will be used to assess the **risk of goose faecal contamination** to livestock and public health and the development of strategies for disease control.
- This project will provide a **road map to support further studies** where engagement with a range of stakeholder groups is necessary and whose interests should be fairly represented.

![](_page_0_Picture_52.jpeg)

![](_page_0_Picture_53.jpeg)

![](_page_0_Picture_54.jpeg)

• Antimicrobial resistance (AMR) is a critical global health issue and it is vital that we better understand transmission of resistant bacteria within farmed and natural ecosystems.

Results reveal carriage of *Cryptosporidium* and *Campylobacter* by geese. DNA sequencing will be used to compare pathogen types obtained from geese, cattle and calves and look for evidence of transmission. Methods to extract bacterial DNA have been optimized for AMR gene profiling.

• Methods will support additional **One Health studies** and **conservation efforts** related to wildlife diseases in changing environments.

![](_page_0_Figure_58.jpeg)

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