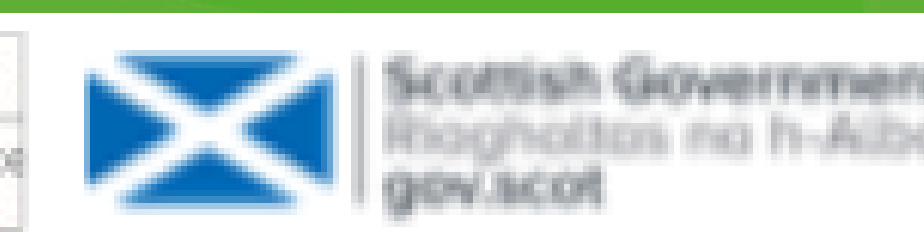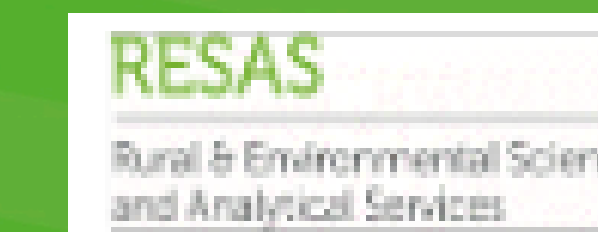# Surveillance for Antimicrobial Resistance in Livestock Units and the Surrounding Environment

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SEFARI — LEADING IDEAS FOR BETTER LIVES

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What is antimicrobial resistance (AMR)?

AMR occurs when bacteria, fungi, viruses and parasites adapt and stop responding to antimicrobials.

Why do we care?

Globally recognised as one of the major One Health issues affecting the world today (WHO, 2014).

AMR threatens our access to effective antimicrobials.

Human deaths from antibiotic resistant infections projected to increase 43% from 2014 – 2050 (He et al.,2020).

What is the problem?

The UK currently **does not have** a national surveillance strategy for the environment.

Key knowledge gap in the role **livestock play** in the transmission of AMR to humans and the shared environment.

This study i**nvestigates the AMR pollution risk** from **livestock units** to the **surrounding environment.**
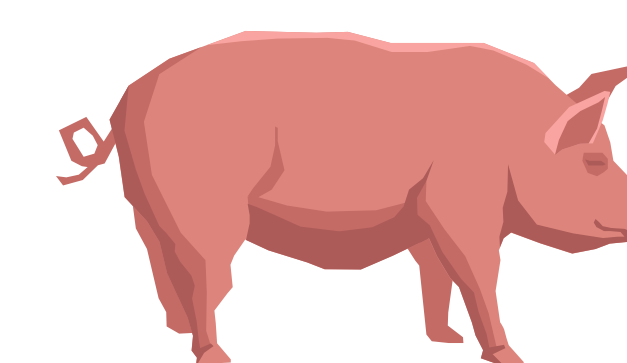
What did we do?

Carried out surveillance for AMR in the environment linked to livestock usage.
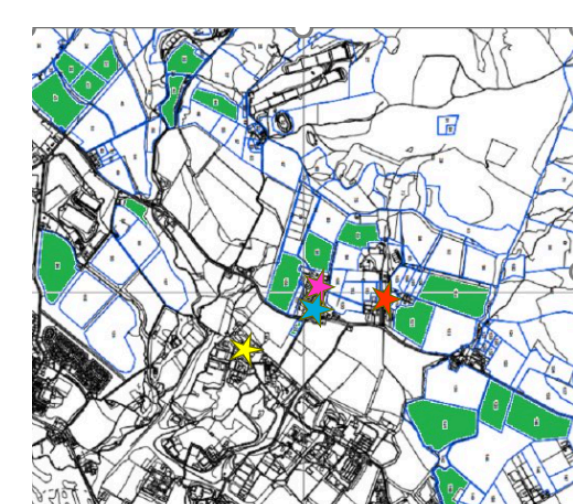
A study site was chosen with four closely co-located livestock units (pigs, cattle,sheep and chickens).

Fields were selected based on manure application and grazing history, giving four field categories

Livestock Units (pigs and cattle), samples of faeces (pen floor), slurry and manure, mice (faeces from colon).

Environment, samples of soil and vegetation, mice (faeces from colon)

Shotgun metagenomics were performed to investigate the AMR gene profile in all of the samples

Results

AMR gene count in **pigs** is considerably **higher** than in **cattle, soil and mice** (Fig1) .

Of the **475 genes** identified, **30% were found to be shared** between the **mice and pigs** (Fig 2).

With **8% of the genes being found in all four sample types** (Fig 2)

Outcome

This work will **enhance** our **understanding** of AMR across **livestock systems and their linked environments**, supporting **Scotland's contribution to the UK's national action plan on AMR.**
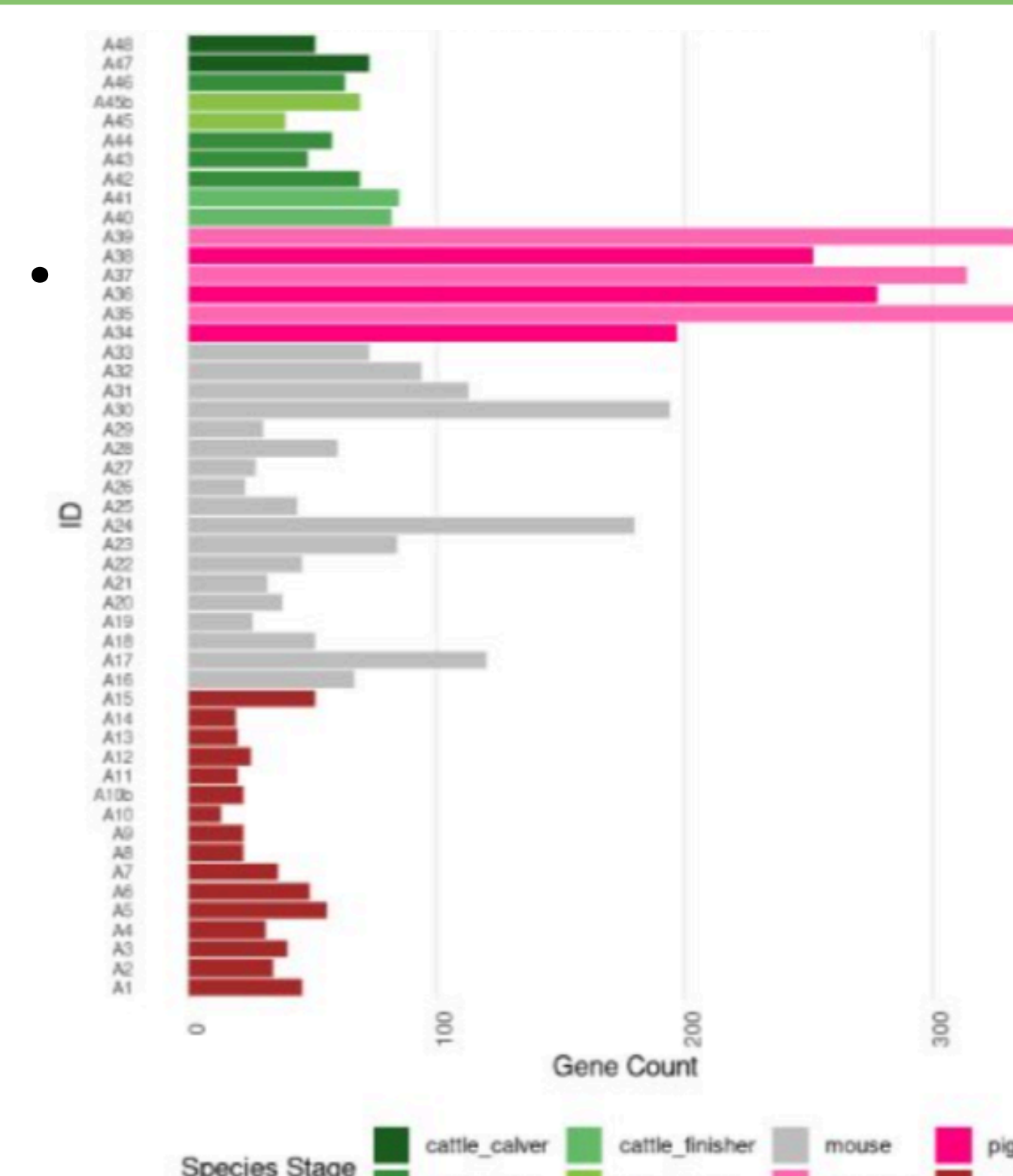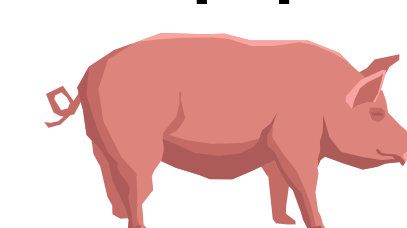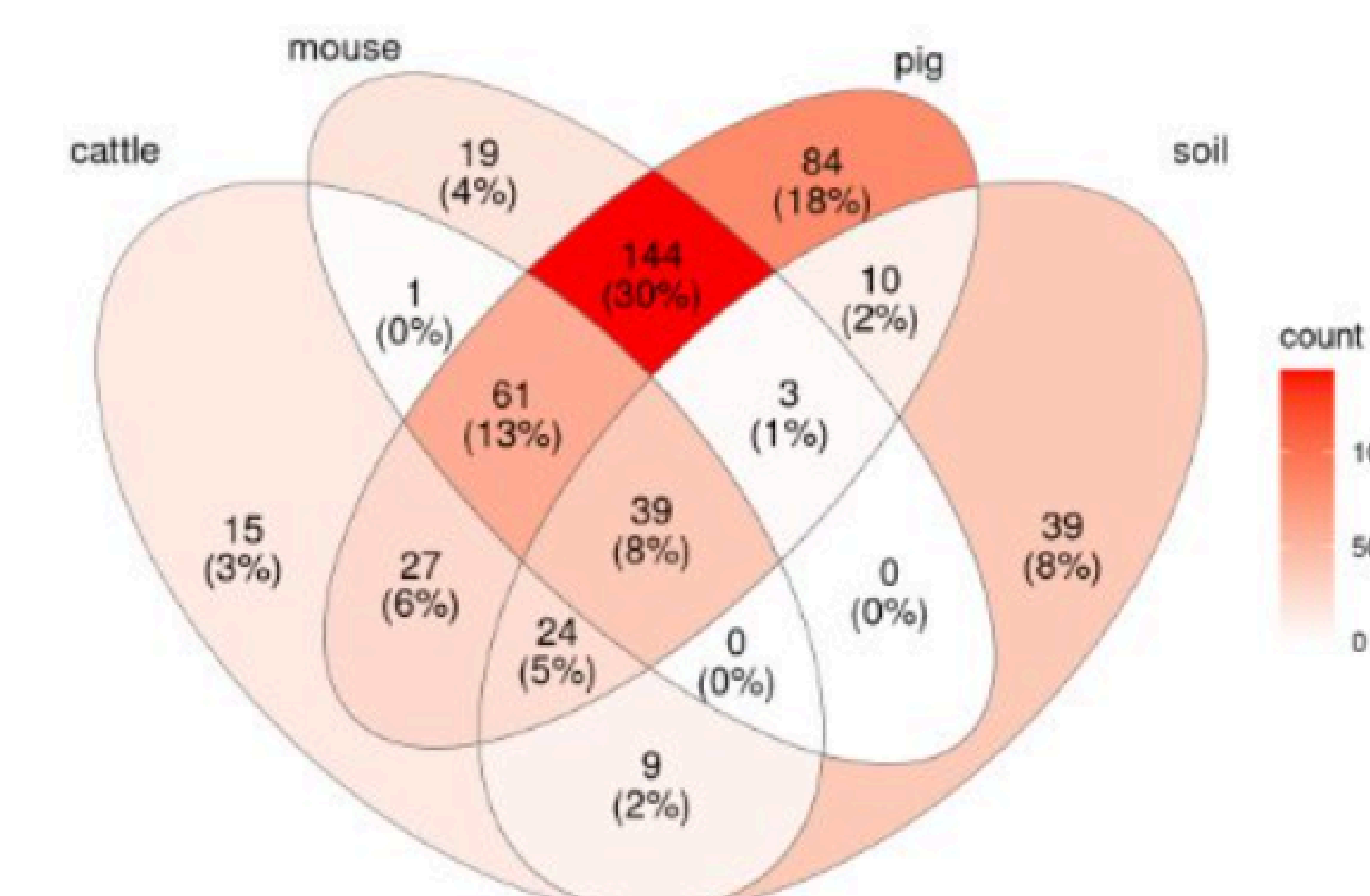

Figure 1 AMR gene count by sample type (n=48)

Figure 2 Count of AMR genes shared between each sample type (n=48)

References,He, et al 2020 https://doi.org/10.1038/s41545-020-0051-0 ,World Health Organization, 2014. ISBN: 978 92 4 156474