

North Wyke Farm Platform

Case study no. 26

Does antimicrobial resistance (AMR) selection in cattle differ between grazing systems common to the UK?

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Antimicrobial Resistance (AMR) arises when the microorganisms that cause infection survive exposure to a medicine that would normally kill them or stop their growth. Without effective antibiotics, even minor surgery and routine operations could become high risk procedures if serious infections can't be treated. Antibiotics excreted in faeces of farmed livestock could be a source of AMR in the environment.

UK beef farmers and their veterinary surgeons strive to maximise animal health and welfare within an effective low input production system. The organisation of the UK beef industry ensures a reduced reliance on antimicrobial interventions by effecting a reduction in disease incidence by widespread implementation of proactive management strategies. Therefore, AMR should be reduced in these systems.

Hypothesis: AMR SELECTION IN CATTLE DIFFERS BETWEEN GRAZING SYSTEMS COMMON TO THE UK (Fig. 1)

- H1 DIET - Forage type differentially promotes AMR in the faecal microbiome of beef cattle
- H2 SEASON - AMR increases in the faeces of winter-housed versus summer out-grazed cattle
- H3 ENVIRONMENT - Differential forage management affects antibiotic resistance gene (ARG) and FIO (faecal indicator organism) abundance in run-off from grazed fields

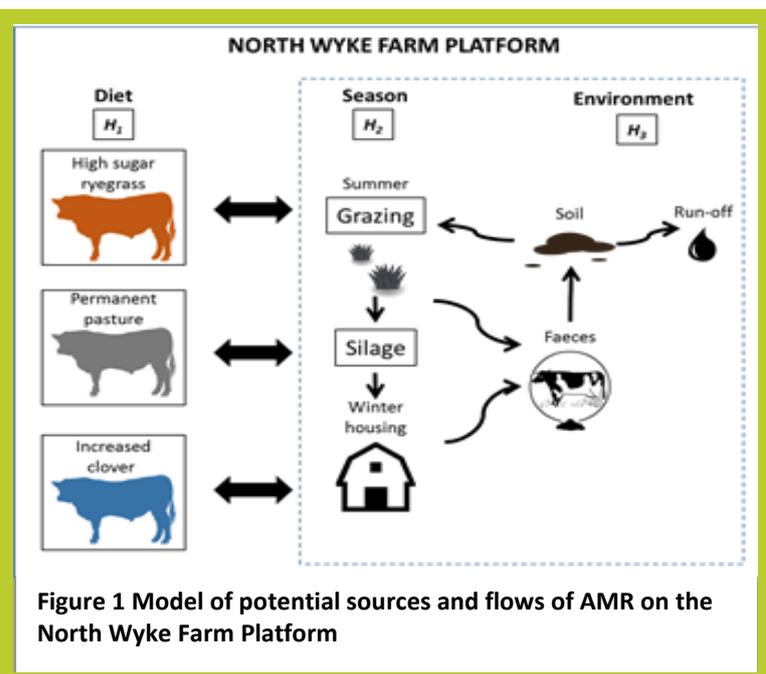


Figure 1 Model of potential sources and flows of AMR on the North Wyke Farm Platform



Figure 2 Resistance for commonly used veterinary antibiotics will be analyzed in dung and water.

EXPERIMENTAL APPROACHES (Fig. 2)

30 beef cattle were randomly selected from NW Farm suckler herd and divided into 3 x 10 cattle allocated to cohort of 30 on each NWFP farmlet. Faeces are collected monthly until slaughter

Veterinary-prescribed antibiotic treatments to cattle on the farm platform were recorded from the start of the experiment.

We are constructing metagenomic libraries of faeces collected from cattle before and after allocation to each of 3 farmlets, and applying disk diffusion analysis of *E. coli* from faecal samples of winter-housed and summer grazing cattle, and amplicon sequencing for ARGs in faeces and water flowing from grazed fields in summer and winter.

The outputs of this project will provide a baseline quantification of AMR in typical beef cattle systems, determine how prevalence of key ARGs varies in the microbiomes of cattle and is affected by management (specifically diet and housing), and establish prevalence of ARGs and AMR in FIOs that are co-transported to waterways adjacent to grazed and manured fields.

Ultimately the work will provide new evidence upon which to base recommendations to industry and policy makers on how to better manage cattle husbandry, the risk of contamination of watercourses with AMR from farming in the UK, reducing the risk of exposure and transmission of AMR to humans.