Developing a unified computational framework to evaluate biological, environmental and veterinary performances of livestock farms

Supervisory team:
Main supervisor: Dr Taro Takahashi (University of Bristol)
Second supervisor: Dr Kristen Reyher (University of Bristol)
Non-academic (CASE) supervisor: Dr Elisabeth King (Agriculture & Horticulture Development Board)
Prof David Barrett (University of Bristol)

Collaborators: Dr Graham McAuliffe (Rothamsted Research), Dr Debbie McConnell (Agri-Food and Biosciences Institute (NI))

Host institution: University of Bristol
CASE partner: Agriculture & Horticulture Development Board

Project description:
Livestock is the largest source of protein for humans and its existence is widely considered to be indispensable for various ecosystem services. For many smallholding farmers, livestock also provides multifunctional benefits, including an enhanced level of 'soil health' for arable enterprises through manure applications. At the same time, the sector is estimated to generate 7.1 Gt CO2e/year or 14.5% of human induced greenhouse gases (GHG) globally and, equally importantly, its reliance of antimicrobials has been associated with antimicrobial resistance (AMR) patterns observed amongst the human population.

Our research team has been tackling these two grand challenges of livestock agriculture for many years, albeit somewhat separately. For GHG, we have recently developed novel computational methods of life cycle assessment (LCA) which can address inter-animal differences in productivity and pollution propensity as well as heterogenous nutrient transfers attributable to different farming strategies. For AMR, we have devised and implemented the concept of antimicrobic footprinting to visualise AMR hotspots and also demonstrated that ceasing the use of highest priority critically important antimicrobials (HP-CIA) does not adversely affect production, health or welfare of animals.

Notably, our recent research has also discovered that, overall, environmentally more sustainable livestock production systems are also economically more profitable, even in the short run. This finding challenges the oft-cited notion of economic-environmental trade-offs within the realistic boundary of modern commercial agriculture, leading us instead to a hypothesis that carefully designed farming systems ('good farming') are likely to be able to achieve high animal production efficiency, low climate impacts and low antimicrobial use at the same time.

Motivated by this observation, this project will design a unified computational framework to evaluate biological, environmental and veterinary performances of livestock farms, with the ultimate view to compile a list of target variables that can assist commercial farmers' decision making. As part of this process, we will extend the method of antimicrobic footprinting to other antimicrobials, establish a feedback mechanism between antimicrobial use and other system variables, integrate it into the animal-by-animal LCA model to eliminate the 'weakest-link' bias, and then apply the framework to data collected at Wyndhurst Farm (University of Bristol, Somerset), North Wyke Farm Platform (Rothamsted Research, Devon) and a network of commercial farms identified by our industrial sponsor, Agriculture & Horticulture Development Board (AHDB).