Developing dairy-specific molecular screening tools to quantify the within-herd dynamics of antimicrobial resistance

Jolinda Pollock[1]*, Nadejda Lupolova[1], Fiona Burns[2], David L. Gally[1], Alexander Corbishley[1], Adrian Muwonge[1] & Michael R. Hutchings[2]

[1]*The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Edinburgh, UK;*
[2]*Animal and Veterinary Sciences, Scotland's Rural College (SRUC), Edinburgh, UK*
Corresponding author: Jolinda Pollock jolinda.pollock@roslin.ed.ac.uk

The widespread blanket usage of antibiotics at the end of lactation in dairy cattle is under increasing scrutiny, due to concerns about antimicrobial resistance (AMR). Although there is a view that blanket antibiotic administration will lead to selection of antibiotic-resistant bacteria, there is still little scientific and clinical evidence to support this in the context of bovine mastitis. Specifically, it is important that data is obtained to explore the relationship between antibiotic usage and the prevalence of antibiotic-resistant bacteria. In this paper, the development of dairy-specific molecular tools will be described, which will be used to analyse milk samples (n = 58) collected during a previously run experiment at Langhill Dairy Farm (Edinburgh, UK), where cows were assigned to one of three treatment groups at dry-off (Figure 1). Firstly, quantitative PCR assays will be designed to measure AMR gene abundances of specific relevance to the dairy sector. Secondly, AMR gene diversity and phenotypic resistance profiles of key mastitis-linked bacterial isolates will be elucidated using whole-genome sequencing and antimicrobial sensitivity testing, respectively. Finally, these data will be used to test the hypothesis that antibiotic usage at dry-off is linked to an increase in antibiotic-resistant bacteria in the milk microbiome.
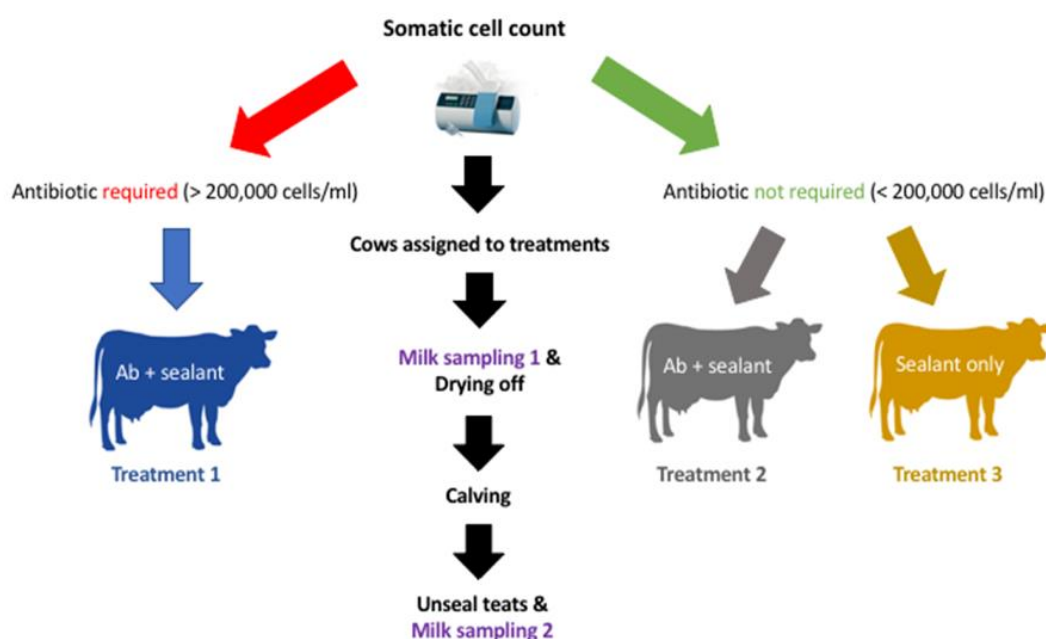
Figure 1: Flow diagram describing the assignment of cows to one of three treatment groups.