

**Brief Background**

- The use of antibiotics should be limited to cases where they are necessary. This means that the use of antibiotics should only be used to treat confirmed bacterial infections, and not as a preventative measure or for growth promotion.
- In addition, proper disposal of unused antibiotics should be practiced to reduce the chances of antibiotic-resistant bacteria spreading to the environment.
- Research and development of new antibiotics should be encouraged to create new options for treating bacterial infections.
- Previous studies on the diversity and abundance of drug-resistant genes in animal intestinal bacterial communities show that it will be very difficult for human to prevent and control animal bacterial diseases if the ARGs are transferred to and become prevalent in bacteria, which can become human pathogen.

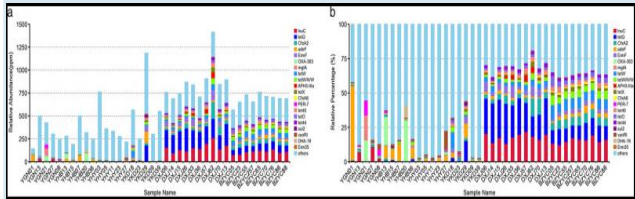


Fig1. Relative abundance of ARGs in each sample, and the unit PPM is the result of amplifying the original relative abundance data by 106 times; **a** Relative abundance of top 20 ARGs in all ARGs, and others represent the total relative abundance of non-top 20 ARGs

**Aim**

To understand the antibiotic resistance genes in bovine gut by metagenomic approach.

**Hypothesis**

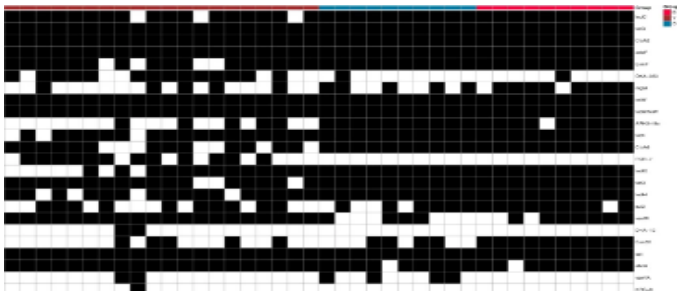
- The overuse of antibiotics in animal feed has been driven by the need to raise animals quickly in industrial farming operations, where animals are kept in close quarters and a single infection can quickly spread.

**Approach & Findings 1**

- The metagenomic library was constructed for evaluating ARGs reservoir in the gut of yak, beef, and dairy cattle.
- For beef cattle, it is 39% vs. 32%, 34% vs. 15%, 2% vs. 6% to *Firmicutes*, *Bacteroidetes*, and *Proteobacteria*, respectively. For dairy cattle, it is 34% vs. 28%, 41% vs. 16% to *Firmicutes*, *Bacteroidetes*, respectively. These asymmetric relationships suggest that *Firmicutes* are more likely to carry resistant genes in bovine fecal samples.

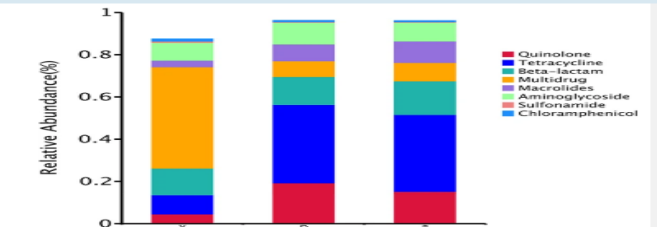
**Approach & Findings 2**

- Approximately 85–99% of microbes cannot be cultivated in the laboratory, which limits our understanding of microbes including those with ARGs therefore, the metagenomic approach was used to investigate the distribution and diversity of drug resistance genes in the intestinal tract of Bovine species.
- Fig 2. The heatmap of top 30 ARG distribution, the horizontal axis is the sample name, and the right vertical axis is the ARG name of resistance gene type.



**Approach & Findings 3**

Fig 3. The relative abundance of shared ARGs types assigned to each major antibiotic class among the group of yak, beef, and dairy cattle



- These findings suggest that antibiotic resistance in yak is driven by the presence of multidrug resistance genes, with two major antibiotic classes - tetracyclines and  $\beta$ -lactams - accounting for the majority of the total antibiotic resistance genes.
- This highlights the importance of controlling the use of antibiotics in yak, as well as in beef and dairy cattle, in order to reduce the spread of antibiotic resistance.

**Outlook**

- Antibiotic resistance genes such as tetracycline, quinolone, and  $\beta$ -lactam in the group of beef and dairy cattle via metagenomic approaches has been identified.
- The presence of these resistance genes in the environment suggests that there is potential for the spread of antimicrobial resistance between cattle, other animals, and humans. Therefore, further research is necessary to understand the sources and mechanisms of transmission of ARGs in livestock.