

# Understanding the bacterial population present during the progression of Ovine footrot.

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## Introduction

Ovine footrot is a major welfare concern for sheep farmers worldwide. Untreated footrot impacts negatively on the health and productivity of affected animals leading to reduced body condition, resulting in loss of income.

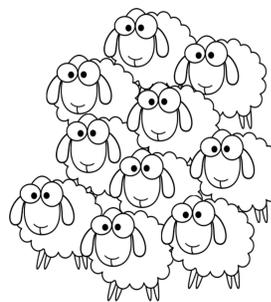
There are two distinct stages to developing footrot. Initial physical damage to the interdigital skin allows for colonisation of multiple bacterial species leading to interdigital dermatitis (ID). The progression of ID to footrot is caused by *Dichelobacter nodosus* (*D. nodosus*) prompting separation of the hoof horn from the underlining tissue. The role of a second bacterium, *Fusobacterium necrophorum* (*F. necrophorum*), is less clear, thought to be involved in establishing ID and/or to exacerbate the severity and prolong the persistence on the of footrot.

There are, however, multiple other bacterial species present at each stage of the disease, which could exacerbate the infection or alter conditions to favour pathogenic bacteria.

## Aim

Understanding the diversity of what bacteria are present during disease progression, to allow for an informed decision to be made on future effective vaccine development.

## Methods

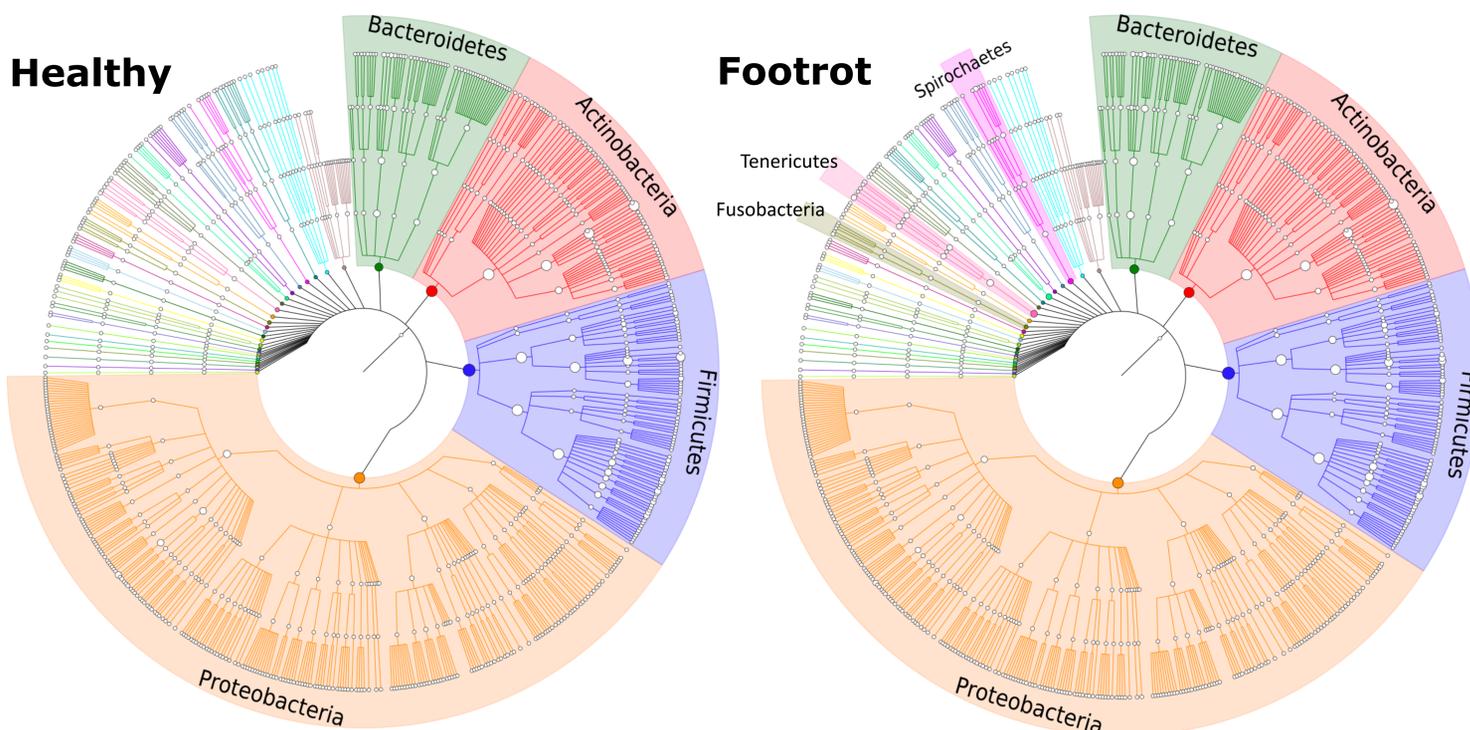


The interdigital space from healthy sheep and sheep with interdigital dermatitis or footrot were swabbed.



Whole bacterial DNA was extracted from swabs to sequence the microbiome (16SrRNA, MiSeq)

## Preliminary Results: Microbiome Diversity



- Ovine interdigital microbiota has a diverse population of bacteria.
- The main bacterial phyla are well represented in both, healthy and footrot feet.
- Spirochetes, *Fusobacteria* and Tenericutes were found in higher proportion within the footrot samples. These bacteria are also linked to bovine dermatitis.

The sequence data was analysed to identify the bacterial genera within the microbiome

## Future work

Collection of more samples will help identify if the species identified are more widely found, and if there are any geographical variance. Samples collected from healthy feet will also show if these different bacteria are normal microbiota. Speciation of the bacteria could elucidate any subtle proportion changes during infection progression.