# **Dichelobacter nodosus metapopulations and the** epidemiology of footrot in an endemically infected flock

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## nterdigital dermatitis & severe footrot

### Interdigital dermatitis (ID)

... inflammation and/or lesions of the interdigital skin

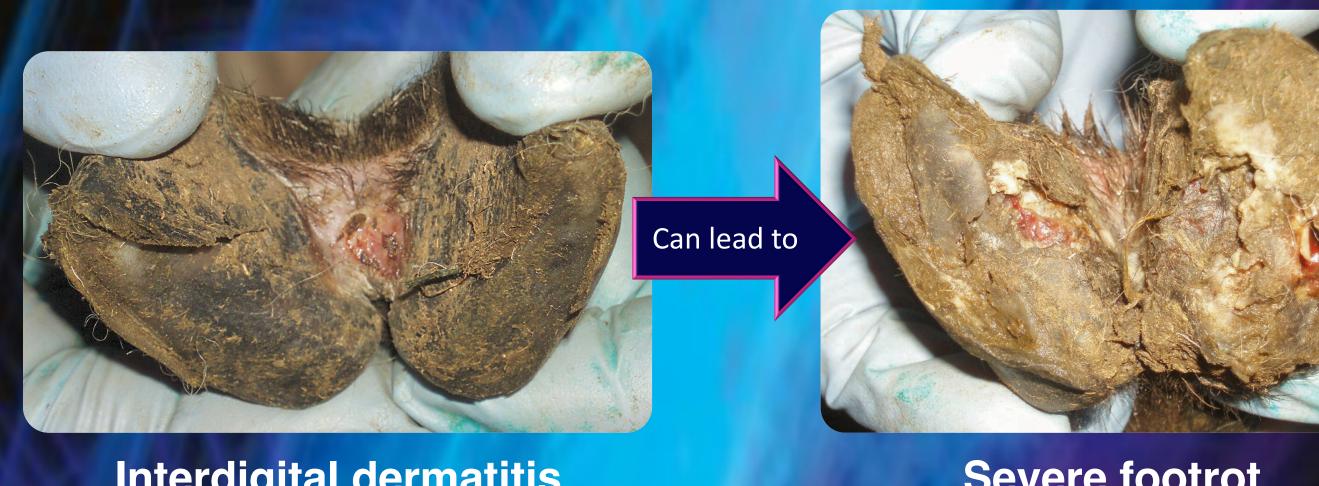
#### Severe footrot (SFR)

... separation of the hoof horn from underlying tissue

ID and SFR account for ~70% of foot lesions in UK sheep.

Dichelobacter nodosus





**Interdigital dermatitis** 

**Severe footrot** 



... the main causal agent of ID and severe footrot

Costs the industry between **£24** and £80 million per annum.

Virulence factors of *D. nodosus* include fimbriae, serogroups and proteases. These have been investigated but not in relation to disease severity. In addition, their role in the *D. nodosus* strain community remains unclear.

## Aims

To investigate strain types of *Dichelobacter nodosus* on feet:

- One/several dominant strains?
- Are strains in the same serogroup or different serogroups?
- Do certain *D. nodosus* strain communities explain disease severity?

To identify virulence factors of *Dichelobacter nodosus* and to determine what the association is between these and the severity of ID and SFR.



The *D. nodosus* strain community and virulence factors are being investigated in 25 ewes from one farm studied previously (Smith *et al.*, 2016 *Vet J*).

Ewes' feet were swabbed and scored in 4x 4-week sampling periods over 10 months plus outside those periods if a locomotion score >2was recorded.

# Results from D. nodosus load data

DNA has been extracted from all 923 swabs and run through quantitative PCR to detect and quantify D. nodosus.



**68%** of interdigital swabs were positive for *D. nodosus* (*rpoD* gene)

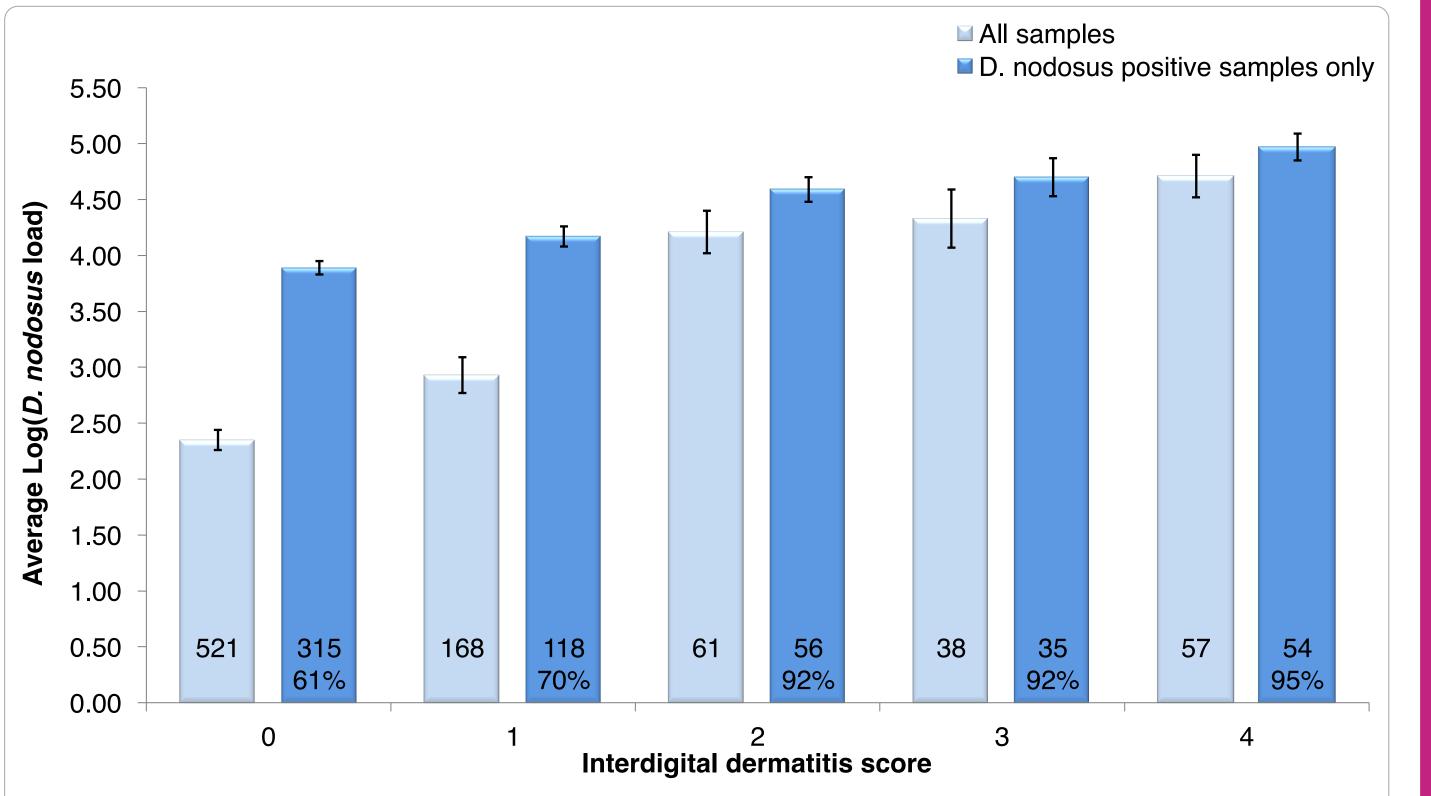
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 Oct Nov Dec Feb Mar May Jun Jan Jul Aug Apr 2010 2011 

On any occasion where a locomotion score >2 was recorded, treatment was given as per their allocated treatment group; either foot trim and antibiotic spray or antibiotic injection and antibiotic spray.

For each swab Log(*D. nodosus* load) per swab was calculated.

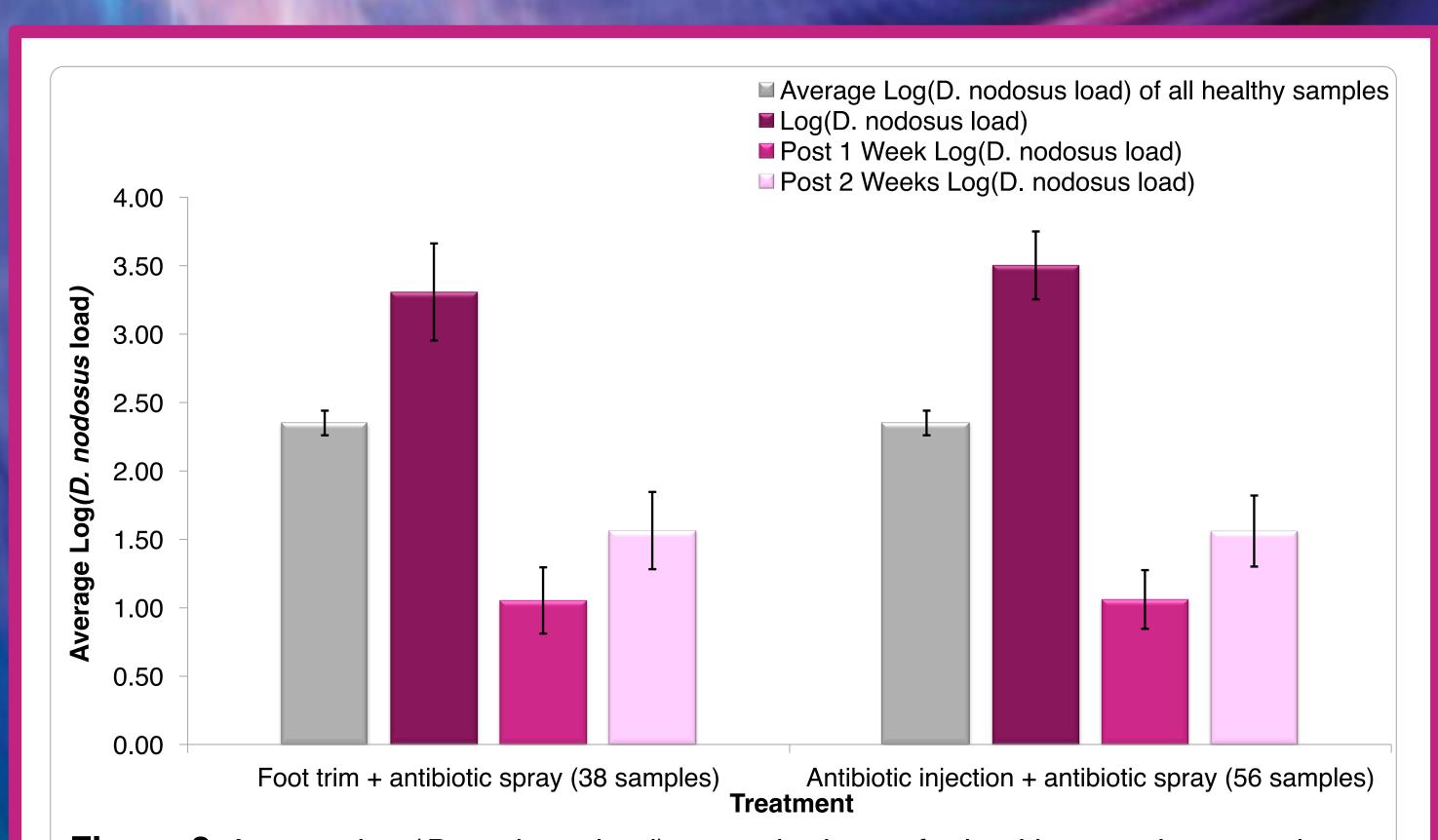
Log(D. nodosus load) significantly increased (p < 0.01) with each ID score (**Figure 1**). However, there was no significant difference in Log(*D. nodosus* load) between SFR 0 and 1.

Both treatment methods significantly reduced the external load of *D. nodosus* (**Figure 2**).



**Figure 1**: Number of samples, % of positive samples and average  $Log(D. nodosus load) \pm 1$ standard error per interdigital dermatitis score.

Samples from two feet of each sheep from Oct 2010 to Aug 2011 were selected for analysis – in total **923** samples; 845 interdigital skin samples and 78 non-interdigital lesion samples.



**Figure 2**: Average  $Log(D. nodosus load) \pm standard error for healthy samples, samples on$ the day a treatment was given and one and two weeks post treatment being given.

Samples with a higher load were more likely to be culturable (**Table 1**). This indicates that isolates are not from foot samples that are randomly representative.

(2%) just *D. nodosus* positive samples with isolates (all of which were 1/47 *D. nodosus* positive) with <1450 *rpoD* gene copies/sample 109/531 (21%) just *D. nodosus* positive samples without isolates (67% were *D. nodosus* positive) with <1450 *rpoD* gene copies/sample



Quantitative PCR is able to detect *D. nodosus* at lower loads

**Table 1**: Number and % of samples and average  $Log(D. nodosus load) \pm standard error$ for samples with isolates obtained from culture that were positive for *D. nodosus* (100%) and for samples **without** isolates obtained that were positive for *D. nodosus* (67%).

Samples with isolates		Samples without isolates	
No. (%) of samples	Average ± standard error Log( <i>D. nodosus</i> load)	No. (%) of samples	Average ± standard error Log( <i>D. nodosus</i> load)
47 (8)	$\textbf{4.63} \pm \textbf{0.11}$	531 (92)	$\textbf{4.12} \pm \textbf{0.05}$

#### Next...

PCR and isolate results (collected previously) will be compared with disease development.

A sub group of samples will be selected for MLVA (strain profile) and virulence factor analysis.

