Table S1: Results of the Generalised Linear Mixed Model for the detection of *D. nodosus* by microbiological culture. Lesion score, lesion type, and lesion contamination were accounted for in the fixed model, and farm of origin was accounted for in the random model.

*Odds of a category testing positive for *D. nodosus* by culture compared with the reference category

Variable	P-value	Std Error	Category	Parameter Estimate	Odds Ratio*	95% Confidence Intervals[#]	
						Lower	Upper
Lesion score	0.021	0.58	Score 1	0	…	…	…
			Score 2	0.55	1.72	0.55	5.40
			Score 3	1.99	7.32	2.34	22.93
			Score 4	0.64	1.90	0.61	5.96
Lesion type	0.027	0.61	Active	0	…	…	…
			Inactive	-1.35	0.26	0.08	0.85
Lesion contamination	<0.001	0.49	High	0	...	...	…
			Moderate	1.61	4.99	1.90	13.07
			Low	2.42	11.21	4.28	29.39
Random (Farm)	…	0.71	…	1.04	…	…	…

[#]Where the 95% confidence intervals contain the value 1.00, there is no significant difference between the respective category and the reference category

Table S2: Results of the Generalised Linear Mixed Model for detection of the *D. nodosus* 16S rRNA gene using DNA prepared from swabs collected into mSTM. Lesion score, lesion type, and lesion contamination were accounted for in the fixed model and farm of origin was accounted for in the random model.

Variable	P-value	Std Error	Category	Parameter Estimate	Odds Ratio*	95% Confidence Intervals[#]	
						Lower	Upper
Lesion score	<0.001	0.86	Score 1	0	…	…	…
			Score 2	3.69	40.13	7.47	215.57
			Score 3	3.23	25.25	4.70	135.68
			Score 4	2.55	12.74	2.37	68.46
Lesion type	<0.001	0.56	Active	0	…	…	…
			Inactive	-2.41	0.09	0.03	0.27
Lesion contamination	<0.001	0.57	High	0	…	…	…
			Moderate	2.66	14.32	4.72	43.47
			Low	3.23	25.15	8.29	76.34
Random (Farm)	…	3.90	…	5.96	…	…	…

*Odds of a category testing positive for *D. nodosus* by PCR testing of DNA prepared from swabs collected into mSTM compared with the reference category

[#]Where the 95% confidence intervals contain the value 1.00, there is no significant difference between the respective category and the reference category

Table S3: Results of the Generalised Linear Mixed Model for detection of *D. nodosus* 16S rRNA gene using DNA prepared from swabs collected into LB. Lesion score, lesion type, and lesion contamination were accounted for in the fixed model, and farm of origin was accounted for in the random model. Categories in which there were fewer than five observations were collapsed.

Variable	P-value	Std Error	Category	Parameter Estimate	Odds Ratio*	95% Confidence Intervals[#]	
						Lower	Upper
Lesion score	0.422	0.57	Score 1/2	0	…	…	…
			Score 3/4	0.57	…	…	…
Lesion type	0.008	0.87	Active	0	…	…	…
			Inactive	-2.28	0.10	0.02	0.56
Lesion contamination	0.007	0.79	High	0	…	…	…
			Low/Moderate	2.14	8.50	1.81	39.92
Random (Farm)	…	1.57	…	2.00	…	…	…

*Odds of a category testing positive for *D. nodosus* by PCR testing of DNA prepared from swabs collected into LB compared with the reference category

[#]Where the 95% confidence intervals contain the value 1.00, there is no significant difference between the respective category and the reference category