INFECTIOUS DISEASES

Retrospective study of the relative frequency of cattle respiratory disease pathogens from clinical laboratory samples submitted by UK veterinary practices

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INTRODUCTION

Respiratory disease is a welfare concern as it is a leading cause of morbidity and mortality in cattle. It leads to substantial economic losses for farmers, attributable to treatment costs, and reduced growth, fertility and milk production. In addition, it has wider implications for human and environmental health (for example antimicrobial resistance) therefore, a greater understanding of its aetiology would be beneficial.

OBJECTIVE

To explore the relative frequency and seasonality of bovine respiratory pathogens in the UK (based on clinical case submission for laboratory PCR). The hypothesis was that season and age of cattle would be significantly associated with the relative frequency of respiratory pathogens.

MATERIALS AND METHODS

Retrospective data generated by a central Scotland laboratory from 407 clinical BRD samples (dairy and beef farms) were collected by 95 veterinary practices located throughout the UK between November 2020 and September 2022. Nasal swabs comprised 373 (91.6%) of the samples and 24 (5.9%) of the samples were lung tissue from postmortem examination, with the remainder of samples being unlabelled. Samples underwent RT-PCR testing for bacterial genetic material (Mannheimia haemolytica, Pasteurella multocida, Histophilus somni and Mycoplasma bovis) and viral genetic material (BHV-1, PI3, BCoV and RSV). Extracted nucleic acid was tested for the presence of viral and bacterial sequences using the VetMAX™ Ruminant Respiratory Screening Kit and VetMAX™ IBR/BHV-1 Reagents.

The majority of clinical bovine respiratory disease samples in the UK are multipathogenic. Bovine coronavirus has generally not been considered a significant contributing pathogen in the BRD complex in the UK (despite a growing body of evidence worldwide demonstrating both its presence and clinical importance in the syndrome). Warmer months and increasing age (in weeks) were significantly associated with a lower number of total pathogens identified from clinical bovine respiratory disease samples.

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RESULTS

- 316/407 (77.6%) of samples had more than one different bacterium detected and 72/407 (17.7%) had multiple viruses detected.
- In comparison with the colder months of autumn and winter (September to February), the warmer months (March to August) were associated with a significantly lower odds of respiratory disease for certain individual pathogens (RSV, PI3 BCoV and *Histophlius somni*), but not others (*Bovine herpesvirus 1, Mannheimia haemolytica, Mycoplasma bovis* and *Pasteurella multocida*) (5,6)
- For every increase in age of 1 week the odds of *Mannheimia haemolytica* and BCoV were lower (OR=0.98 and 0.94, p<0.01

FIGURE 1. Choropleth point map showing the distribution of veterinary practices (a) total bacteria (b) and total viruses (c) Identified from 407 clinical bovine respiratory disease pathogens submitted from 95 UK veterinary practices between November 2020 and September 2022. Deeper colours indicate a higher relative frequency of total bacteria from individual submissions.

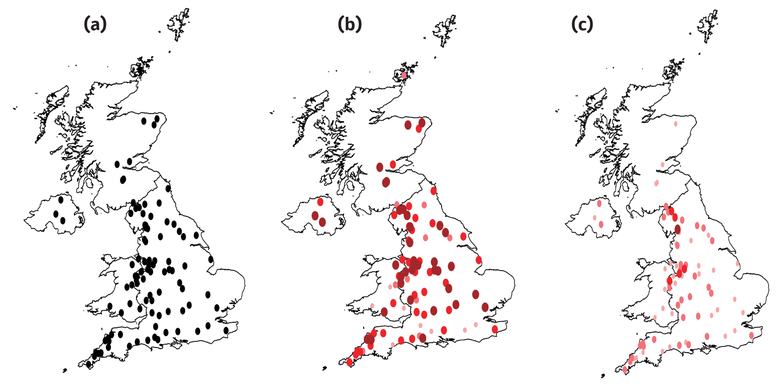

TABLE 1. Proportion and frequency of respiratory pathogens from 407 PCR samples submitted from 95 UK veterinary practices between November 2020 and September 2022.

	Pathogen							
PCR measurement	Bovine coronavirus % (n)	Infectious bovine rhinotracheitis % (n)	Histophilus somni % (n)	Mannheimia haemolytica % (n)	Mycoplasma bovis % (n)	Parainfluenza virus 3 % (n)	Pasteurella multocida % (n)	Respiratory syncytial virus % (n)
-	61.4 (250)	94.8 (386)	58.7 (239)	38.3 (156)	60.9 (248)	88.5 (360)	6.6 (27)	78.4 (319)
+	15.7 (64)	3.9 (16)	17.9 (73)	27.0 (110)	14.0 (57)	8.6 (35)	32.2 (131)	11.3 (46)
++	21.6 (88)	0 (0)	21.4 (87)	33.9 (138)	20.4 (83)	2.5 (10)	43.0 (175)	8.6 (35)
+++	1.2 (5)	1.2 (5)	2.0 (8)	0.7 (3)	4.7 (19)	0.5 (2)	18.2 (74)	1.7 (7)
Cumulative proportion positive (%)	38.6	5.2	41.3	61.7	39.1	11.5	93.4	21.6

Footnote: for some pathogens the proportion presented adds up to more than 100% as many samples identified multiple pathogens.

FIGURE 2. Percentage positive pooled samples for individual respiratory disease pathogens by season for 407 clinical bovine respiratory disease submissions from 95 UK veterinary practices between November 2020 and September 2022.

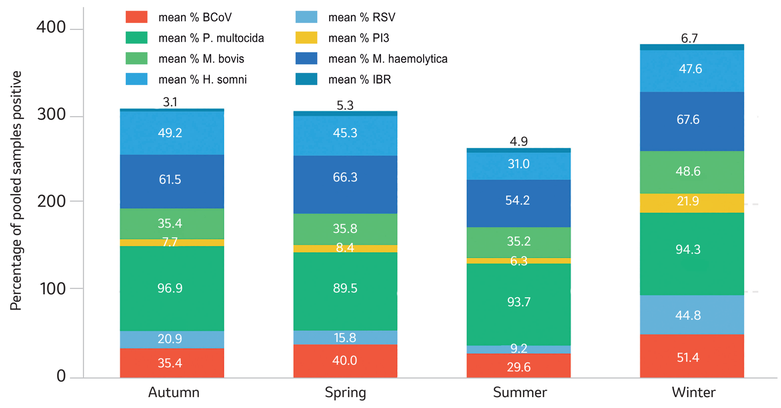

TABLE 2. Results of chi squared analysis showing the p-values for relationships between individual respiratory disease pathogens for 407 clinical respiratory disease samples submitted by 95 UK veterinary practices to a Scottish laboratory. Statistically significant (Bonferonni adjusted to account for multiple comparison) relationships are highlighted in bold text and each pathogen was considered individually with significance declared at p=0.007.

Pathogen	PI-3	*P. multocida*	RSV	BCoV	*H. somni*	IBR	*M. haemolytica*	M. bovis
PI-3	N/A	*0.21*	0.38	**<0.01**	0.29	*0.58*	0.47	0.25
P. multocida	*0.21*	N/A	*0.27*	0.07	0.09	*0.04*	**<0.01**	***<0.01***
RSV	0.38	*0.27*	N/A	0.61	0.72	*0.51*	0.95	0.15
BCoV	**<0.01**	0.07	0.61	N/A	0.32	0.96	<0.01	0.01
H. somni	0.29	0.09	0.72	0.32	N/A	0.90	0.04	**<0.01**
IBR	*0.58*	*0.04*	*0.51*	0.96	0.90	N/A	0.63	0.08
M. haemolytica	0.47	**<0.01**	0.95	**<0.01**	0.04	0.63	N/A	**<0.01**
M. bovis	0.25	***<0.01***	0.15	0.01	**<0.01**	0.08	**<0.01**	N/A

Footnote: PI-3= Parainfluenza virus 3; P. multocida= Pasteurella multocida; RSV= Respiratory syncytial virus; BCoV= Bovine coronavirus; H. somni= Histophilus somni; IBR= infectious bovine rhinotracheitis; M. haemolytica= Mycoplasma haemolytica; M. bovis= Mycoplasma bovis Where number of samples in each category was ≤5 samples, Fischer's exact test was then used in place of chi squared analysis and the p value is reported in italics.

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