Supplementary information

Table S1. GAM model output for number of new cases by calendar month and rainfall year. For each pathogen, a global model was fit for the number of cases per month ~ s(calendar month) + s(rainfall year) + sample number. We selected the final model by choosing the model with the lowest AICc.

MH, deviance explained = 56.90%				
parametric terms	Estimate	SE	z-value	p-value
(Intercept)	-0.18	0.23	-0.82	0.44
sample.number	0.04	0.01	5.00	<0.001
nonparametric terms		edf	chi squared	p-value
s(month)		1.75	6.95	0.009
MB, deviance explained = 65.40%				
parametric terms	Estimate	SE	z-value	p-value
(Intercept)	0.37	0.16	2.39	0.02
sample.number	0.04	0.00	8.41	<0.001
nonparametric terms		edf	chi squared	p-value
s(month)		1.92	8.47	0.005
Pi-3, deviance explained = 60.40%				
parametric terms	Estimate	SE	z-value	p-value
(Intercept)	-0.30	0.20	-1.28	0.20
sample.number	0.04	0.01	6.51	<0.001
nonparametric terms		edf	chi squared	p-value
s(month)		3.34	26.27	<0.001
AD-3, deviance explained = 59.40%				
parametric terms	Estimate	SE	z-value	p-value

(Intercept)	0.17	0.19	0.88	0.38
sample.number	0.03	0.01	5.11	<0.001
nonparametric terms		edf	chi squared	p-value
s(month)		2.00	14.28	<0.001
s(year)		1.46	5.56	0.03

BRSV, deviance explained = 74.80%

parametric terms	Estimate	SE	z-value	p-value
(Intercept)	-1.45	0.43	-3.37	<0.001
sample.number	0.06	0.01	4.39	<0.001
nonparametric terms		edf	chi squared	p-value
s(month)		7.96	20.69	<0.006
s(year)		1.88	40.68	<0.001

BHV, deviance explained = 48.60%

parametric terms	Estimate	SE	z-value	p-value
intercept	-0.36	0.23	-1.55	0.12
sample number	0.04	0.01	5.47	<0.001
nonparametric terms		edf	chi squared	p-value
s(year)		2.94	17.54	<0.001

Table S2. CRF Regression coefficients for each pathogen's occurrence probability. Coefficients are interpreted identically to logistic regression.

Pathogen	Predictor	coefficient (95% CI)
Pi-3	AD-3 occurrence	0.68 (0.64 - 0.72)
	BHV occurrence	0.63 (0.60 - 0.66)
	$season_{RL=dry}$ X BHV occurrence	0.17 (0.17 - 0.18)
	pregnant x AD-3 exposure	0.03 (0.04 - 0.03)
BHV	Pi-3 occurrence	0.63 (0.60 - 0.66)
	AD-3 occurrence	0.23 (0.17 - 0.27)
	$season_{RL=dry}$ X Pi-3 occurrence	0.17 (0.17 - 0.18)
	$lactating_{RL=non\text{-}lactating}$ X AD-3 occurrence	0.17 (0.08 - 0.21)
	$herd_{RL=Croc\ Bridge}$ X Pi-3 occurrence	0.09 (0.08 - 0.10)
	age X AD-3 occurrence	0.06 (0.07 - 0.06)
AD-3	Pi-3 occurrence	0.68 (0.64 - 0.72)
	$pregnant_{RL=non\text{-}pregnant}$ X bTB infection	-0.44 (-0.54 - -0.36)
	BHV occurrence	0.23 (0.17 - 0.27)
	$season_{RL=dry}$	0.21 (0.15 - 0.26)
	$lactating_{RL=non\text{-}lactating}$ X BHV occurrence	0.17 (0.08 - 0.21)
	bTB infection	0.03 (0.05 - 0.003)
	age	0.04 (0.07 - 0.01)
	pregnant x Pi-3 exposure	0.03 (0.04 - 0.03)
	lactating x bTB infection	0.05 (0.06 - 0.02)
	age X BHV occurrence	0.06 (0.07 - 0.06)
BRSV	$season_{RL=dry}$	0.2 (0.18 - 0.24)
	age	0.08 (0.07 - 0.09)
bTB infection	age	2.14 (1.92 - 2.40)
	$lactating_{RL=non\text{-}lactating}$	0.59 (0.51 - 0.69)
	$season_{RL=dry}$	0.45 (0.40 - 0.53)
	$pregnant_{RL=non\text{-}pregnant}$ X AD-3 occurrence	-0.44 (-0.54 - -0.36)
	horn width - age residuals	0.38 (0.27 - 0.53)
	AD-3 occurrence	0.03 (0.05 - 0.003))
	pregnant	0.12 (0.16 - 0.10)
	condition	-0.13 (-0.13 - -0.14)
	lactating x AD-3 occurrence	0.05 (0.06 - 0.02)
MB*	$season_{RL=dry}$	0.11 (0.01 - 0.19)
MH*	*no significant predictors*	---

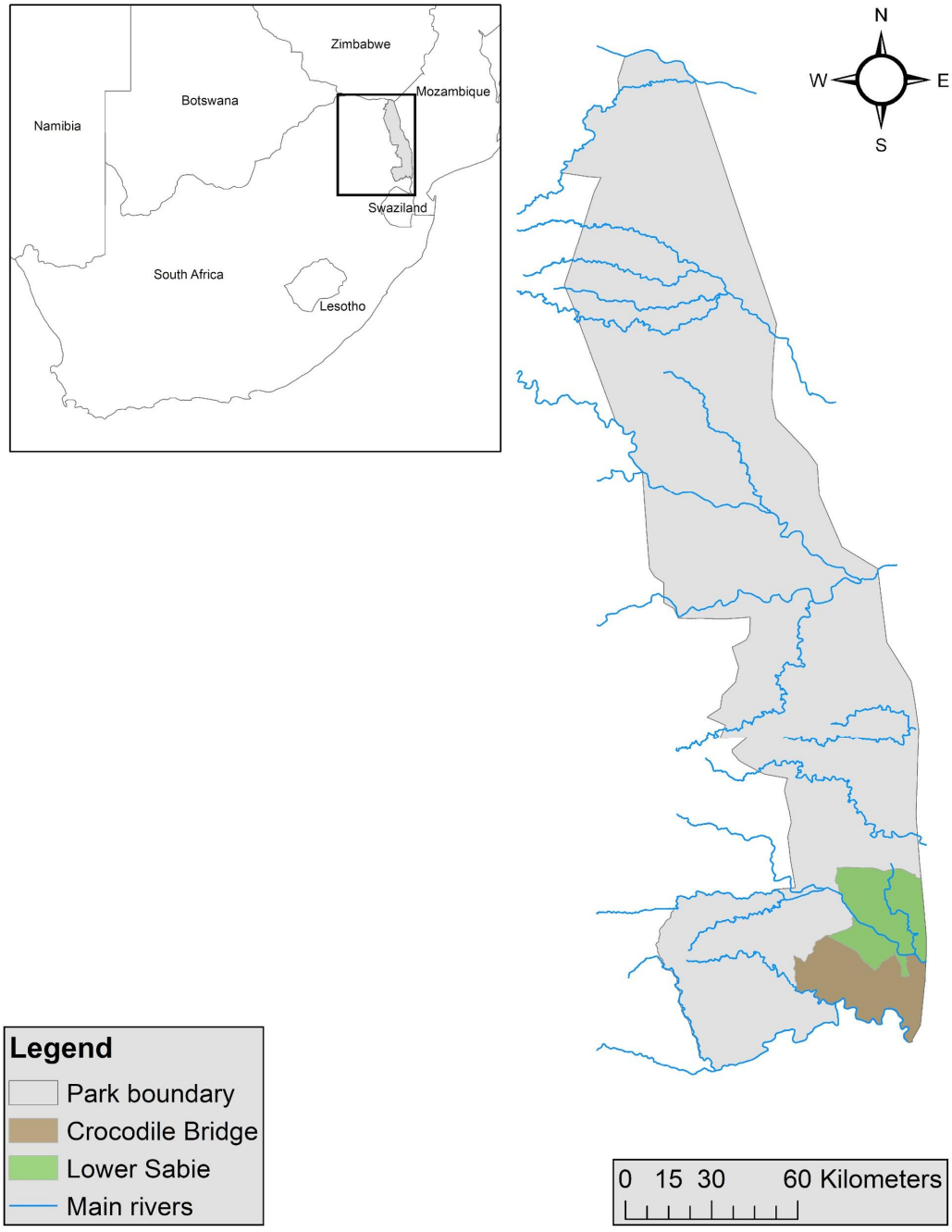

Figure S1. Map of LS & CB herd locations. Map courtesy of Rob S. Spaan.

Appendix S1. Detecting signatures of priority effects on occurrence of respiratory bacterial pathogens.

Priority effects may occur where *Mannheimia haemolytica* and *Mycoplasma bovis* proliferate following respiratory tract damage from viral infection (Rice et al., 2007; Srikumaran, Kelling & Ambagala 2007). Thus, we tested for signatures of priority effects by running an additional analysis that included MH and MB observations at one leading time step (t_{x+1}). We included occurrence of the four respiratory viruses (Bovine Adenovirus-3, Parainfluenza-3, Bovine Herpesvirus-1, Bovine Respiratory Syncytial Virus) at the current time step (t_x). Additionally, we included bTB status at t_x and host traits at both t_x and t_{x+1}. We ran the analysis and estimated parameters identically to methods outlined in the main text. Due to including time-lagged variables, we used 515 samples from 151 animals. We did not find any evidence for a priority effect (Table 1).

Table 1. CRF Regression coefficients for t_{x+1} occurrence probability of opportunistic bacteria. Coefficients are interpreted identically to logistic regression.

Pathogen	Predictor	coefficient (95% CI)
MB*	$season_{RL=dry}$	0.06 (0.001 - 0.13)
MH*	*no significant predictors*	---

Literature cited

Rice, J., Carrasco-Medina, L., Hodgins, D. & Shewen, P. (2007). Mannheimia haemolytica and bovine respiratory disease. *Animal Health Research Reviews,* 8, 117-128.

Srikumaran, S., Kelling, C.L. & Ambagala, A. (2007), Immune evasion by pathogens of bovine respiratory disease complex. *Animal Health Research Reviews,* 8, 215-229.