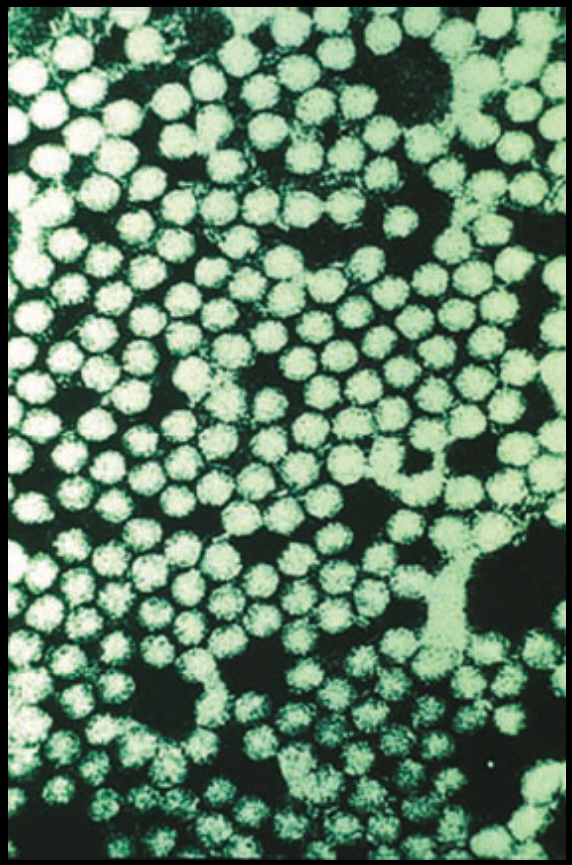
Introduction to mathematical modelling of foot-and-mouth disease in livestock

Julien Arino

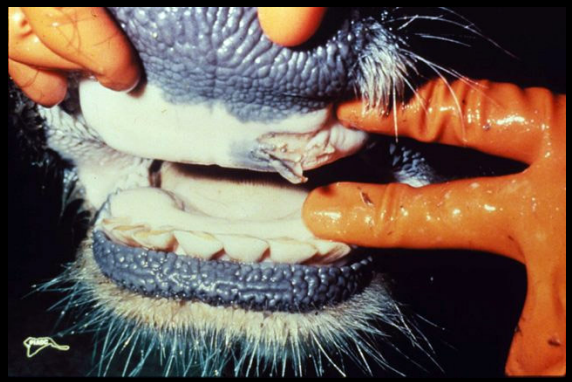
April 2023

- In these slides, I consider foot-and-mouth disease (FMD) in livestock
- FMD was also called hoof-and-mouth disease (HMD) in the UK, although FMD tends to be used globally now
- I only consider single population aspects here, spatial spread is a later lecture
- Most models are "spatial in some sense", so only three models reviewed here

Foot-and-mouth disease



- Severe, highly communicable **viral** disease of cattle and swine
- Also affects sheep, goats, deer and other cloven-hoofed ruminants. Horses not affected
- Elephants, hedgehogs and some rodents also susceptible but do not develop clinical signs of the disease



- Fever and blister-like sores on the tongue and lips, in the mouth, on the teats and between the hooves
- Many affected animals recover, but the disease leaves them weakened and debilitated

2001 United Kingdom HMD outbreak

- 2,000 cases of the disease in farms across most of the British countryside
- Over 6 million cows and sheep were killed to control the disease
- Ministry of Agriculture, Fisheries and Food (MAFF) adopted a policy of “contiguous cull” - all sheep within 3,000 metres of known cases slaughtered

Research in Veterinary Science 2002, **73**, *195–199*
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REVIEW

Foot and mouth disease

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SUMMARY

Foot and mouth disease (FMD) affects cloven-footed animals. It is caused by seven species (''types'') of Foot and Mouth virus (FMDV) in the genus aphthovirus, family Picornaviridae (ICTV 2000). FMDV is a single-stranded RNA virus, with a protein coat consisting of four capsid proteins enumerated as VP1, VP2, VP3, and VP4 (Garland and Donaldson 1990). © 2002 Elsevier Science Ltd. All rights reserved.

The disease is characterised by vesicular lesions on the coronary band of the hooves and in the mucosa of the mouth including the tongue and palate. The vesicles typically contain clear or straw-coloured fluid before they burst and heal. There is a rise in body temperature of some 3–4 °C. The lesions in sheep are often difficult to find and may be confused with other conditions (Ayers et al 2001).

The disease varies considerably in its severity. It may result in death or severe morbidity particularly in neonates but in areas where the infection is endemic the disease may be mild and the few vesicles that appear may heal without further damage.

HOST SPECIES

CATTLE, sheep, goats, and pigs are the main domesticated species infected. The Water Buffalo (*Bubalus bubalis*) can become infected and may also transmit infection to other species. Camelids, experimentally infected, contract the disease (Lubroth et al 1990) but there is no evidence of transmission to other domestic livestock and there seems to be some doubt as to whether they play any role in the epidemiology of the disease in domestic livestock (Fondevila et al 1995).

A wide range of wild cloven-footed animals contract FMD including deer and pigs. During the 2001 epidemic in the United Kingdom there was great concern that the various species of deer now abundant in the country might contract the disease and act as a persistent reservoir of infection. In the event, investigation of a number of cases of apparent disease failed to reveal the presence of FMD virus. The African Buffalo (*Syncercus caffer*) appears to be particularly susceptible to infection and may act as a reservoir host (see later).

Although FMD is known as a disease of cloven-footed animals it can occur naturally in other animals, e.g., the hedgehog (*Erinaceus* spp.) (McCauley 1963), and infection has been established experimentally in a number of other species. However, it is doubtful whether these animals play any part in the epidemiology of the disease (Snowdon 1968).

FMD is not considered zoonotic. Although clinical cases have been proven in human, these are extremely rare in relation to human exposure during outbreaks (Sellers et al 1970).

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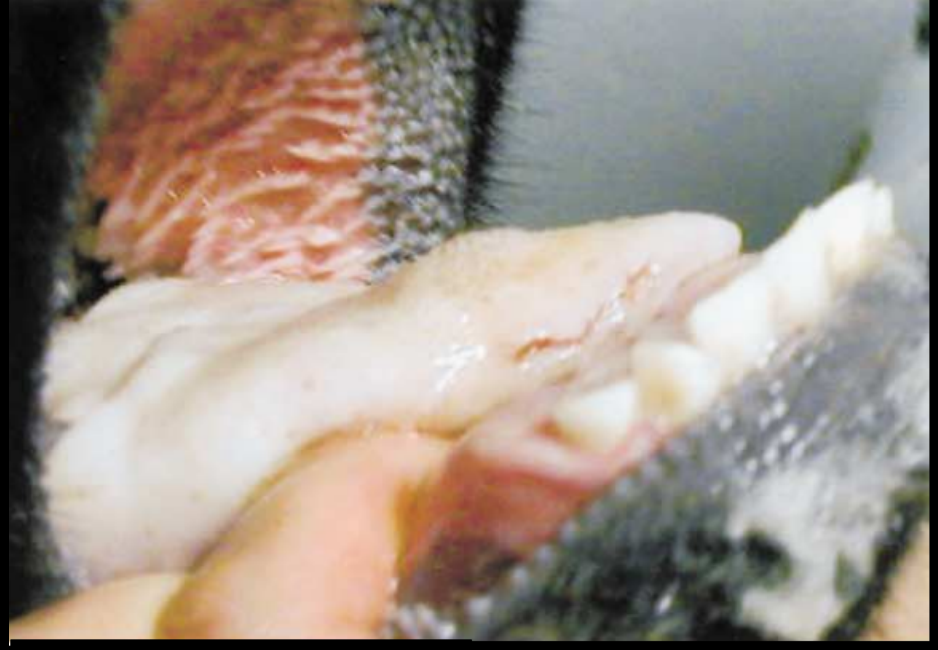
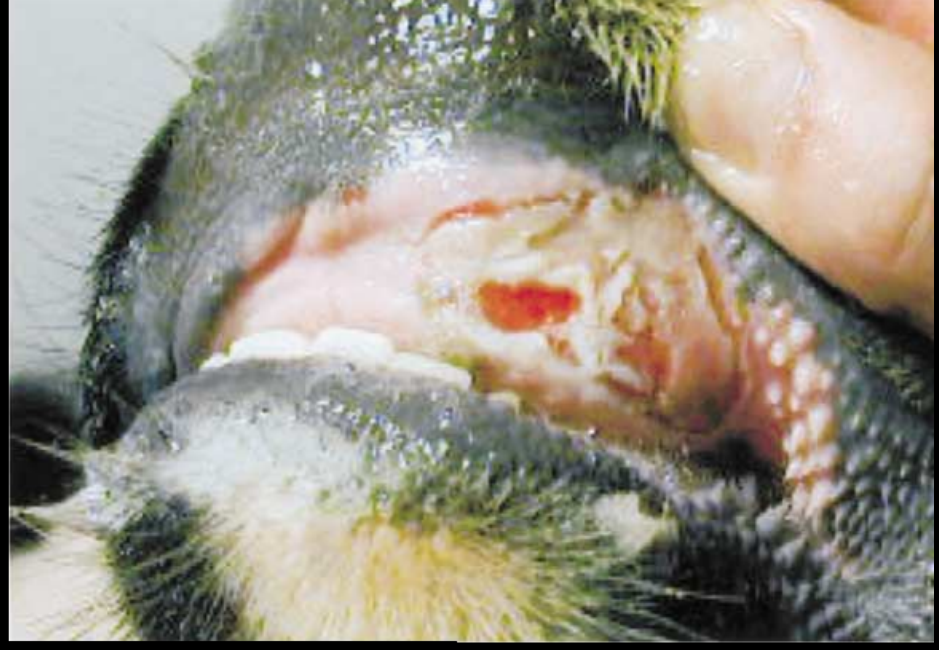
REVIEW

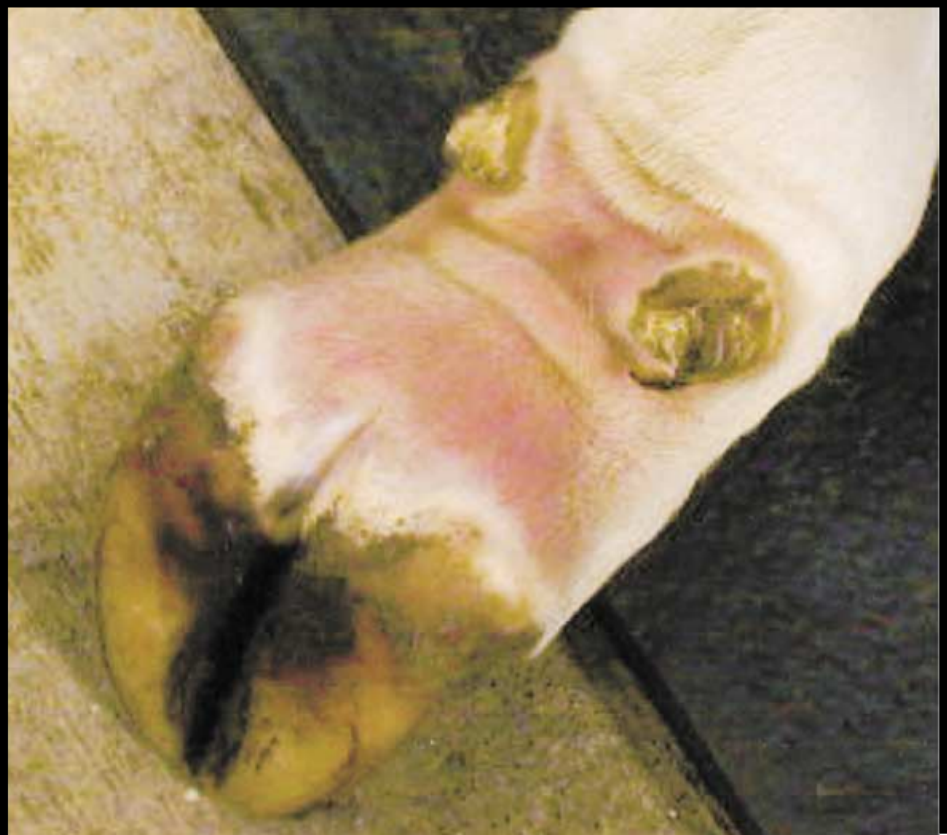
The Pathogenesis and Diagnosis of Foot-and-Mouth Disease

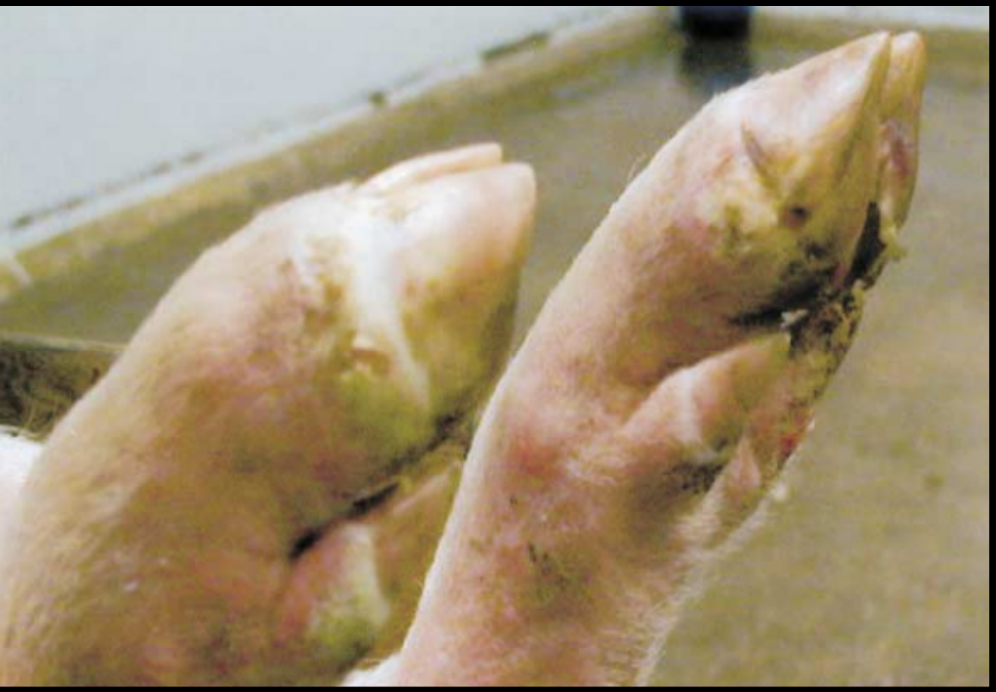
S. Alexandersen, Z. Zhang, A. I. Donaldson and A. J. M. Garland

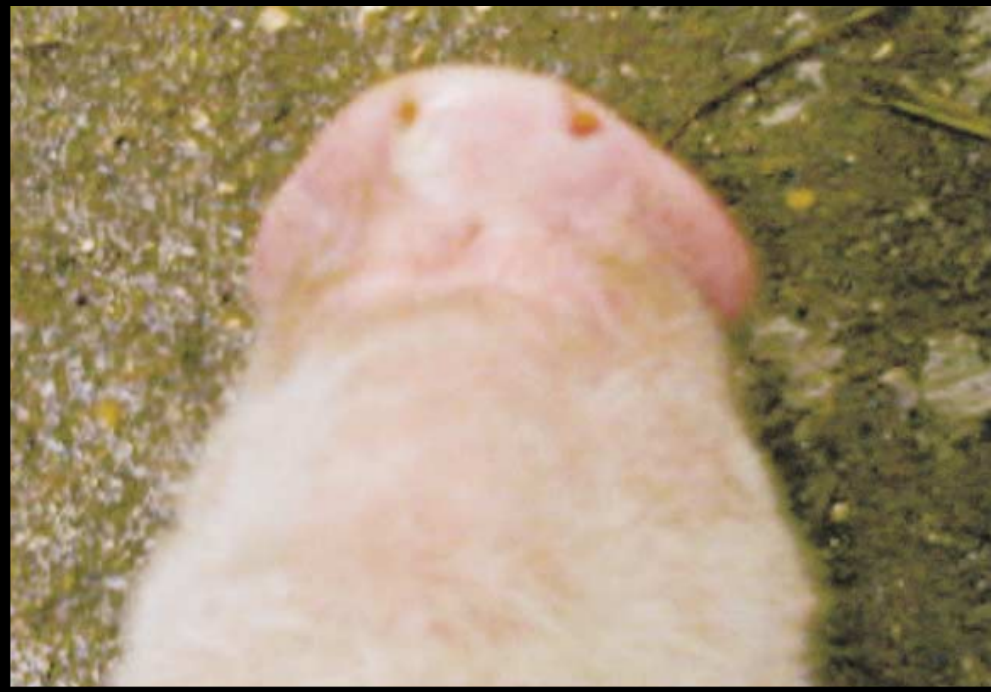
Pirbright Laboratory, Institute for Animal Health, Ash Road, Pirbright, Woking, Surrey GU24 ONF, UK Working,

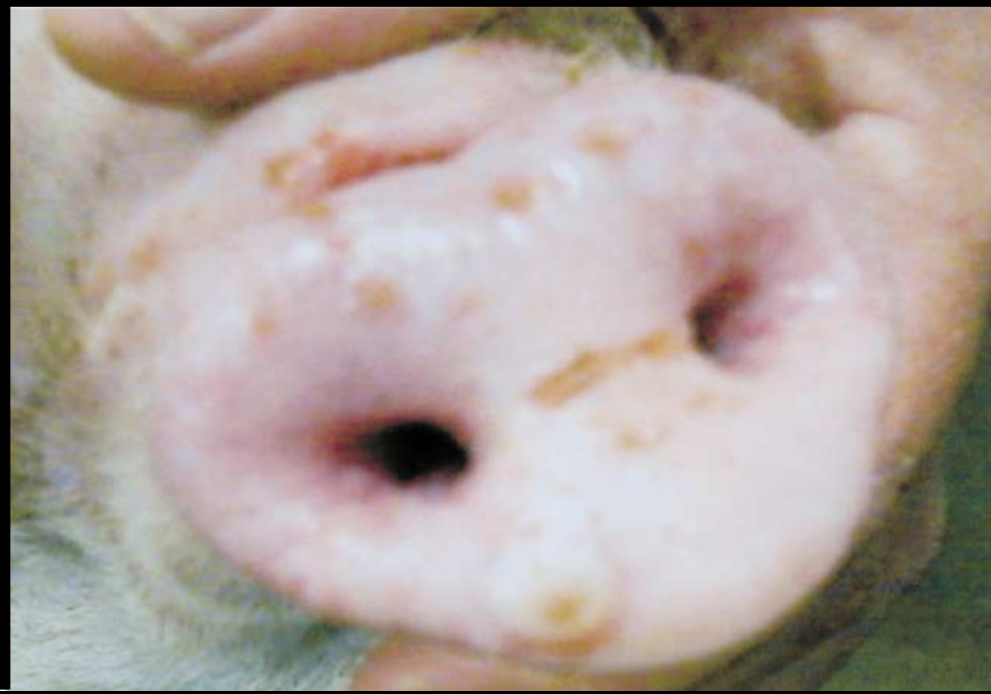












Jamal and Belsham *Veterinary Research* 2013, **44**:116
http://www.veterinaryresearch.org/content/44/1/116

VETERINARY RESEARCH

REVIEW Open Access

Foot-and-mouth disease: past, present and future

Syed M Jamal[1] and Graham J Belsham[2*]

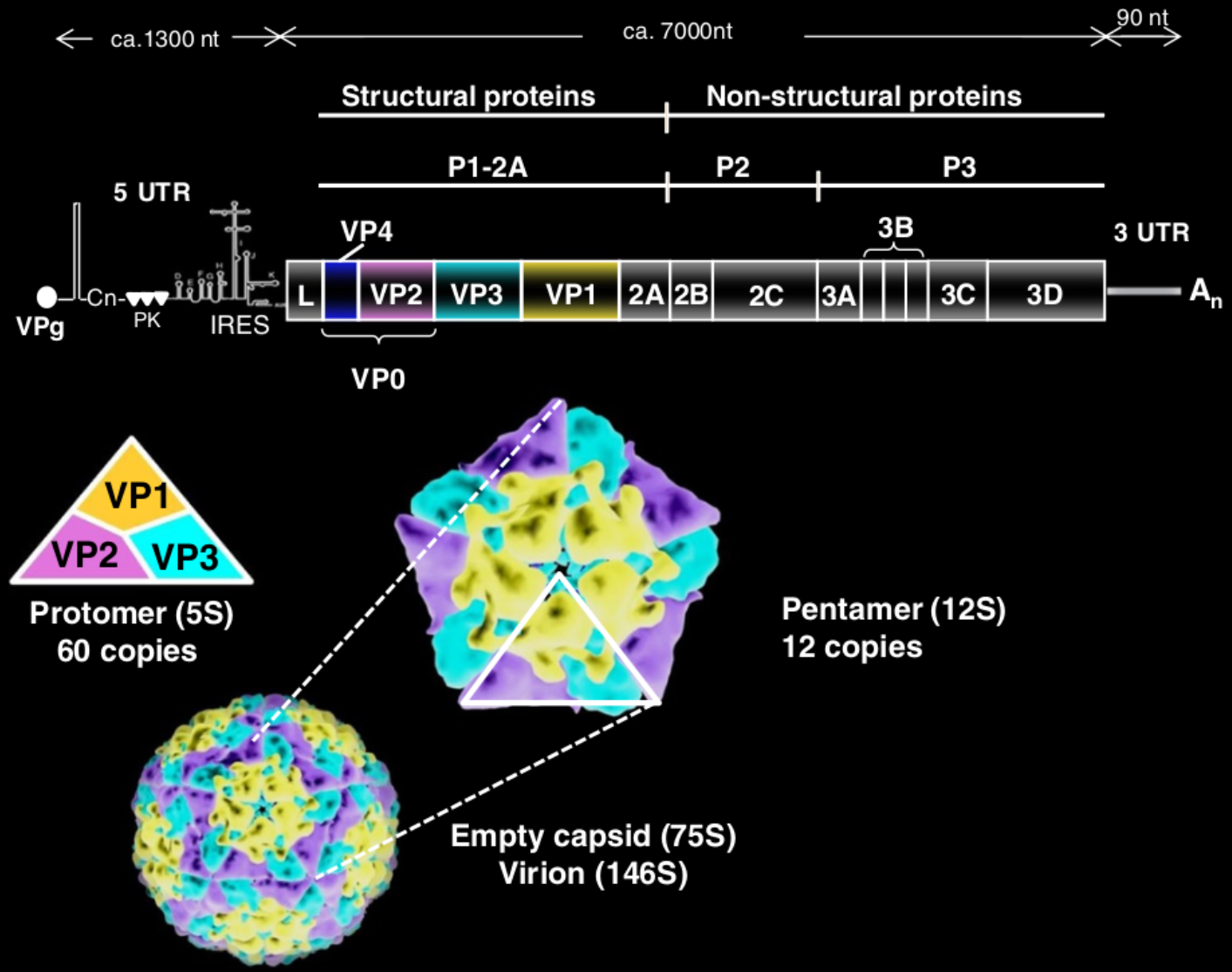


Figure 1 Genome organization of FMDV and the structure of virus. The FMDV genome includes a single large ORF, indicated by the shaded rectangle. The regions within the rectangle indicate the individual proteins. The 5′ UTR includes several distinct structural elements including: a poly(C) tract (Cn), 3 or 4 pseudoknots (PK) and the internal ribosome entry site (IRES). The VPg peptide is made in 3 different forms (encoded by the $3B_{1-3}$) and each acts as the primer for RNA synthesis so each RNA genome, when synthesized, is covalently linked to a VPg. The assembly of virus particles from protomeric and pentameric subunits is indicated. Assembled virus particles contain a single copy of the viral RNA and 60 copies of the 4 different capsid proteins (VP1-VP4). Self-assembly of empty capsid particles, lacking the RNA genome, can also occur. The VP4 protein is internal.

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PATHOGENESIS

The replication of the infectious particles is extremely rapid after entry through the upper respiratory tract or lung, with viraemia seeding infection into the epithelium where secondary virus multiplication results in vesicles and shedding from the udder in milk (Hyslop 1965, Sellars 1971). The incubation period, from infection to clinical signs, may be as short as 2/3 days or as long as 14 days (Garland and Donaldson 1990) and infected animals may become infectious before showing clinical signs (Burrows 1968a). The virus is excreted during viraemia for some days; thereafter as serum antibody develops viraemia decreases, and the animal ceases to be infectious as the lesions heal.

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Table 1
Selected estimated minimum doses* for various species and routes of exposure

Species	*Inhalation*	*Intradermal*	*Intramuscular*	*Nasal instillation*	*Oral*
Cattle	10	100	10^4	10^4–10^5	10^5–10^6
Sheep	10	100	10^4	10^4–10^5	10^5–10^6
Pigs	>800	100	10^4	Unknown	10^4–10^5

*The estimated minimum doses are those reported to cause *clinical* disease. It is emphasized that these are not absolute values but represent estimates based on different experiments that are not necessarily directly comparable. It is possible that even smaller doses might produce infection if large numbers of animals were exposed. Doses are given as TCID50 (bovine thyroid tissue culture 50% dose end-point estimates). For further information see the text and associated references. It should be noted that for intradermal and intramuscular inoculation, doses from 5 to 10 fold lower are cited in the literature, but without details of the assay systems used (Sellers, 1971).

Selected recorded maximum and calculated theoretical total infectivity titres of some secretions and excretions during the course of FMD in cattle

Secretion or excretion	Volume or weight*	Virus strain	Maximum recorded viral titre	Theoretical total viral content†	Reference
Blood or serum	30 litres	A119	$10^{5.8}$/ml	$10^{10.3}$	**A**
		O Canefa-9	$10^{5.6}$/ml	$10^{10.1}$	B
		Various	$10^{6.0}$/ml	$10^{10.5}$	C
		O BFS 1860	$10^{5.2}$/ml	$10^{9.7}$	E
		O Swiss 1/66	$10^{6.8}$ /ml	$10^{11.3}$	E
		A119	$10^{6.5}$/ml	$10^{11.0}$	E
		C Noville	$10^{7.8}$/ml	$10^{12.3}$	E
Lachrymal secretion	Unknown	O Canefa-2	$10^{7.0}$/sample	…	F
		O Swiss 1/66	$10^{6.3}$/sample	…	F
		C Noville	$10^{6.1}$/sample	…	F
Nasal secretion	Unknown	Various	$10^{7.7}$/g	…	C
		O BFS 1860	$10^{5.5}$/ml	…	E
		O Swiss 1/66	$10^{7.3}$/ml	…	E
		A119	$10^{6.0}$/ml	…	E
		C Noville	$10^{8.3}$/ml	…	E
Oral saliva	98–190 litres per day	Various	$10^{8.0}$/ml	$10^{13.3}$	C
		O Israel 1/63	$10^{8.5}$/ml	$10^{13.8}$	G
		O BFS 1860	$10^{6.7}$/ml	$10^{12.0}$	D
		O BFS 1860	$10^{6.0}$/ml	$10^{11.3}$	E
		O Swiss 1/66	$10^{7.8}$/ml	$10^{13.1}$	E
		A 119	$10^{7.0}$/ml	$10^{12.3}$	E
		C Noville	$10^{8.8}$/ml	$10^{14.1}$	E
Pharyngeal fluid (probang samples)	Probably as for saliva, (98–190 litres per day)	O BFS 1860	$10^{7.4}$/ml	$10^{12.7}$	D
		O BFS 1860	$10^{7.0}$/ml	$10^{12.3}$	E
		O Swiss 1/66	$10^{7.8}$/ml	$10^{13.1}$	E
		A 119	$10^{7.3}$/ml	$10^{12.6}$	E
		C Noville	$10^{8.3}$/ml	$10^{13.6}$	E
Faeces	14–45 kg per day	O Canefa-2	$10^{4.1}$/g	$10^{8.7}$	F
		O BFS 1860	$10^{2.0}$/g	$10^{6.7}$	D
		O Swiss 1/66	$10^{3.0}$/g	$10^{7.7}$	E
		A 119	$10^{2.0}$/g	$10^{6.7}$	E
		C Noville	$10^{3.3}$/g	$10^{8.0}$	E
Urine	8.8–22 litres per day	A119	$10^{4.9}$/ml	$10^{9.2}$	H
		O M11	$10^{4.6}$/ml	$10^{8.9}$	H
		O BFS 1860	$10^{2.5}$/ml	$10^{6.8}$	E
		O Swiss 1/66	$10^{5.5}$ /ml	$10^{9.8}$	E
		A 119	$10^{2.5}$/ml	$10^{6.8}$	E
		C Noville	$10^{3.3}$ /ml	$10^{7.6}$	**E**

A: From Cottral and Bachrach (1968). Titre in mouse ID50 /ml or g. Cattle infected by tongue inoculation. Report gives details of types and strains not listed in Table 4. B: From Cottral (1969).Titre in mouse ID50 /ml. Cattle infected by tongue inoculation. C: From Scott *et al.* (1966). Titre in calf kidney tissue culture as plaque-forming units (p.f.u.)/ml or /g. Cattle infected by tongue inoculation. Results obtained with seven types and strains of FMD, but the report gives collective values only. D: From Sellers *et al.* (1969). Titre in IB-RS-2 tissue culture p.f.u./ml or /g. Cattle infected by indirect contact with infected pigs. E: From Garland (1974). Titre in bovine thyroid tissue culture ID 50/ml or /g. Cattle infected by indirect contact with infected pigs. F: From Sutmoller and McVicar (1973). Titre in calf kidney tissue culture p.f.u./ml or /g or / sample. Cattle infected by intranasal instillation. G: From Hyslop (1965). Remarks as for A above. H: From Cottral *et al.* (1968). Remarks as for A above.

*Physiological data from Swenson (1970); Sellers (1971).

Transboundary and Emerging Diseases

Transboundary and Emerging Diseases

REVIEW

The Pathogenesis of Foot-and-Mouth Disease I: Viral Pathways in Cattle

J. Arzt[1], N. Juleff[2], Z. Zhang[2,*] and L. L. Rodriguez[1]

[1] Plum Island Animal Disease Center, Foreign Animal Disease Research Unit, Agricultural Research Service, United States Department of Agriculture, Orient, NY, USA

[2] Pirbright Laboratory, Institute for Animal Health, Woking, Surrey, UK

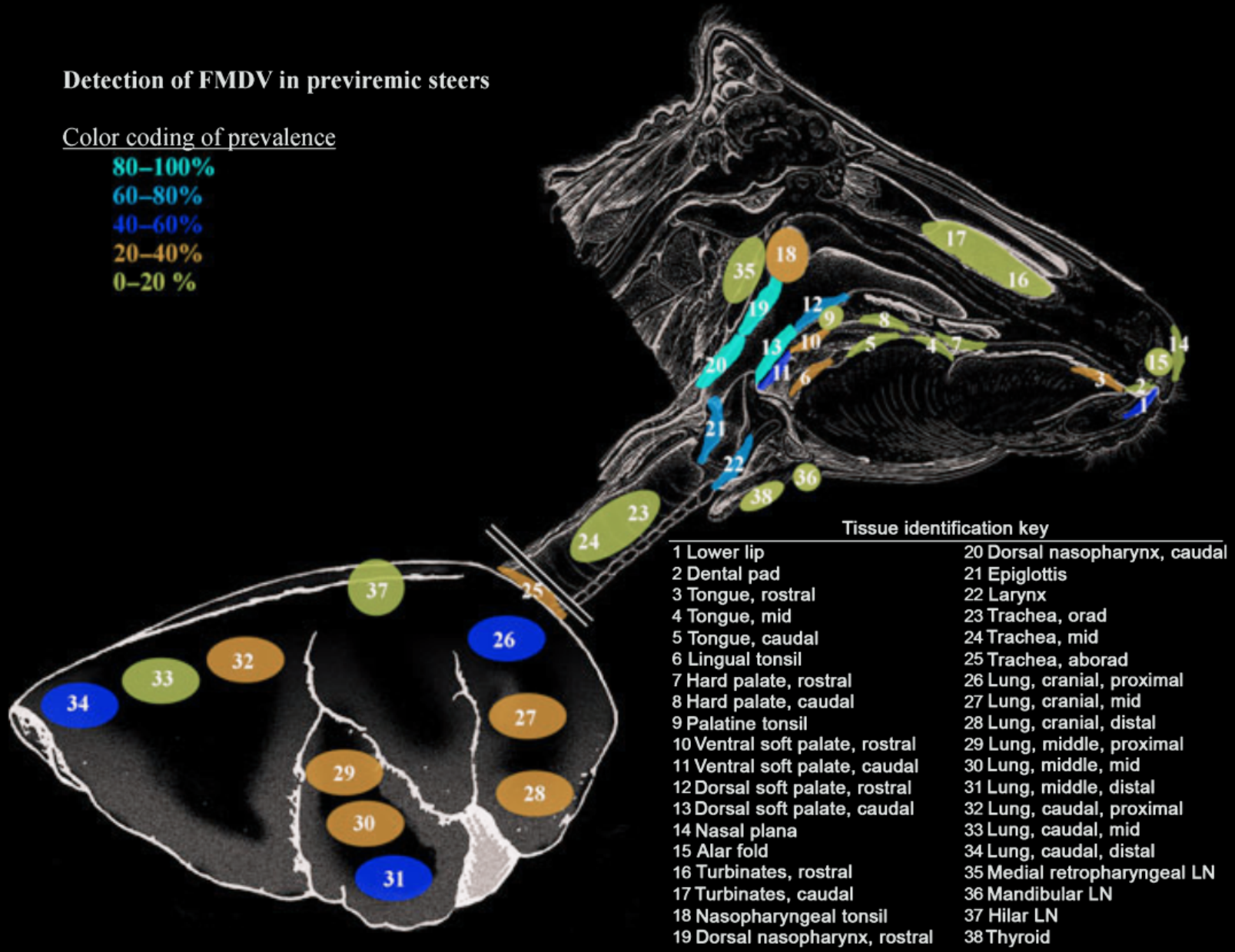

Fig. 1. Tissue-specific detection of foot-and-mouth disease virus (FMDV) or viral RNA by virus isolation (VI) or rRT-PCR in pre-viraemic steers inoculated via aerosol with 10^7 BID_{50} of FMDV-O1-Manisa 3–24 h prior. Only epithelia of the nasopharynx and larynx occupy the highest stratum of 80–100% indicating these tissues as the most consistent sites of primary infection. Prevalence values were calculated as number of animals in which a tissue was determined positive/number of animals in which that tissue was assayed. Inclusion criterion was negative VI on serum at the time of euthanasia. Data adapted from Arzt et al., Veterinary Pathology 2010.

Jamal and Belsham *Veterinary Research* 2013, **44**:116
http://www.veterinaryresearch.org/content/44/1/116

VETERINARY RESEARCH

REVIEW Open Access

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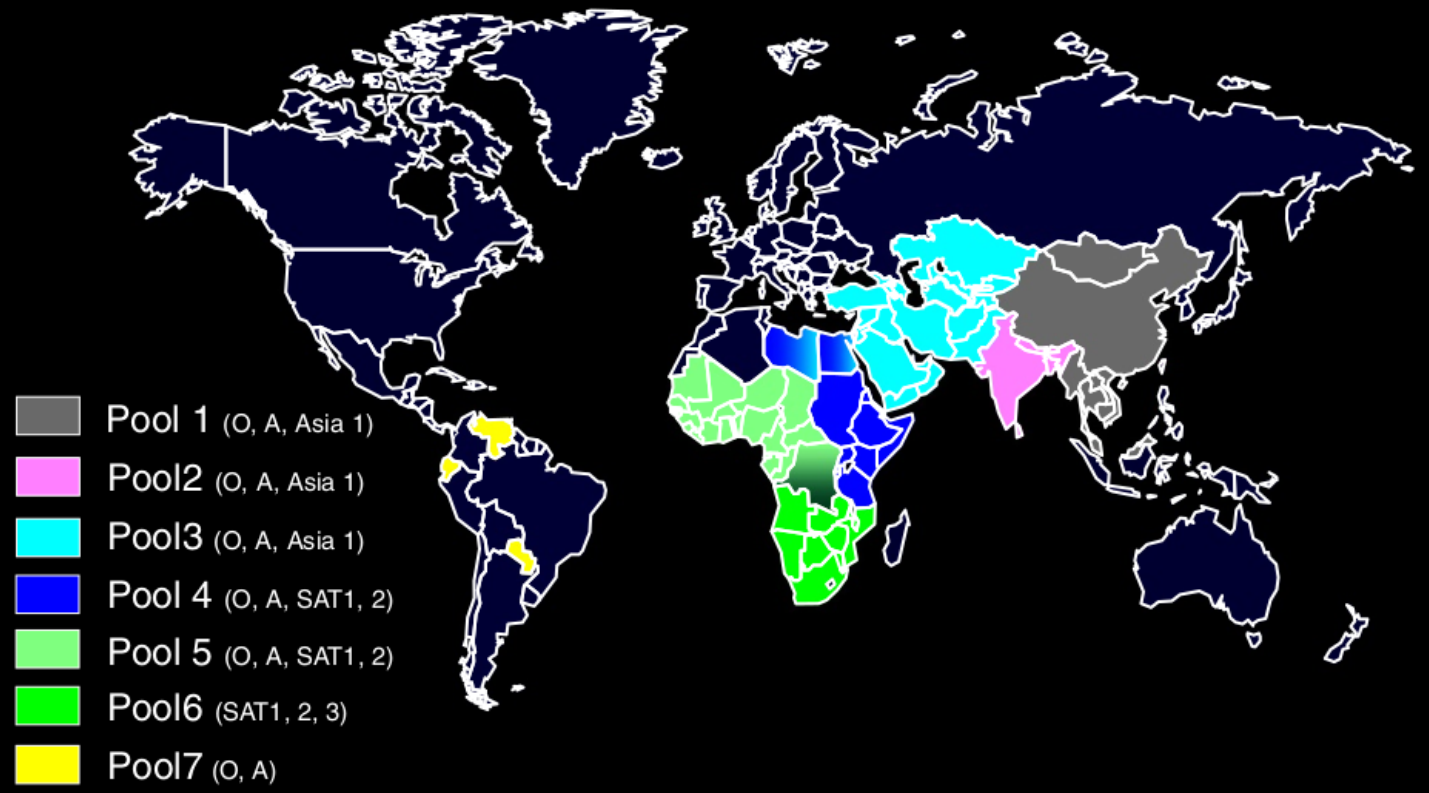

Figure 2 Geographical distribution of seven pools of foot-and mouth disease viruses. Serotype O FMDV is the most widely distributed serotype of the virus (in 6 of the 7 indicated virus pools) whereas, in contrast, SAT3 is only present in pool 6 (within southern Africa). The Asia-1, SAT1 and SAT2 serotypes also have quite limited geographical distribution. However, individual countries can have multiple serotypes in circulation at the same time and hence it is necessary to be able to determine which serotype is responsible for an outbreak if vaccination is to be used. Countries which are normally free of the disease (marked in yellow) can still suffer incursions of the virus which can have high economic costs.

CLINICAL MICROBIOLOGY REVIEWS, Apr. 2004, p. 465–493 Vol. 17, No. 2
0893-8512/04/$08.00+0 DOI: 10.1128/CMR.17.2.465–493.2004

Foot-and-Mouth Disease

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Available online at www.sciencedirect.com
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The Veterinary Journal 169 (2005) 197–209
The Veterinary Journal
www.elsevier.com/locate/tvjl

Review

A review of foot-and-mouth disease with special consideration for the clinical and epidemiological factors relevant to predictive modelling of the disease

R.P. Kitching [a], A.M. Hutber [b,*], M.V. Thrusfield [c]

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[b] *EpiVet, Reines House, Porlock, Somerset TA24 8QJ, UK*
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Accepted 7 June 2004

FMD characteristics

A few models

- Chis Ster, Dodd & Ferguson
- Mushayabasa, Posny & Wang
- Nur *et al*

Conclusion

PROCEEDINGS OF THE ROYAL SOCIETY B

Proc. R. Soc. B (2005) **272**, 1195–1202
doi:10.1098/rspb.2004.3046
Published online 15 June 2005

Review

Models of foot-and-mouth disease

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During the 2001 foot-and-mouth disease outbreak in the UK, three very different models were used in an attempt to predict the disease dynamics and inform control measures. This was one of the first times that models had been used during an epidemic to support the decision-making process. It is probable that models will play a pivotal role in any future livestock epidemics, and it is therefore important that decision makers, veterinarians and farmers understand the uses and limitations of models. This review describes the utility of models in general before focusing on the three foot-and-mouth disease models used in 2001. Finally, the future of modelling is discussed, analysing the advances needed if models are to be successfully applied during any subsequent epidemics.

Keywords: livestock disease; mathematical models; control

Most work on the 2001 UK epidemic is “spatial”

We come back to this in the lecture about spatial aspects

FMD characteristics

A few models

- Chis Ster, Dodd & Ferguson
- Mushayabasa, Posny & Wang
- Nur *et al*

Conclusion

Epidemics 4 (2012) 158–169

Contents lists available at SciVerse ScienceDirect

Epidemics

journal homepage: www.elsevier.com/locate/epidemics

Within-farm transmission dynamics of foot and mouth disease as revealed by the 2001 epidemic in Great Britain

Irina Chis Ster*, Peter J. Dodd, Neil M. Ferguson

MRC Centre for Outbreak Analysis and Modelling, Department of Infectious Disease Epidemiology, School of Public Health, Imperial College, London, United Kingdom

The model – Setup

- $S(t)$ number of animals on single species farm
- $n(t, j)$ number of infected animals on farm at time t infected at time j before t

Infectious load of farm at time t

$$P(t) = \sum_{j=0}^{t} \phi(j) n(t, j) \tag{1}$$

where $\phi(j)$ relative infectiousness of animal with infection age j

Initial condition

$$n(0,0) = I_0$$

$$n(0,j) = 0, \quad j > 0$$

$$S(0) = N - I_0$$

The model

$$S(t) = S(t-1)\max\left(1-\beta\frac{P(t)}{N},0\right), \quad t>0 \tag{2a}$$

$$n(t,j) = n(t-1,j-1), \quad t>0, j>0 \tag{2b}$$

with boundary condition

$$n(t,0) = S(t) - S(t-1), \quad t>0 \tag{2c}$$

Infectious profile

$$\phi(j) = \theta^2 j e^{-\theta j} \tag{3}$$

In case of two species farm, two cases

- $\theta^{-1} = 4$ days for cattle and $\theta^{-1} = 5$ days for sheep (TS1)
- $\theta^{-1} = 3$ days for cattle and $\theta^{-1} = 4$ days for sheep (TS2)

Model for two species

Infectious weight of mixed farm

$$F(t) = R_I P_C(t) + P_S(t) \tag{4}$$

where R_I is infectiousness of cattle relative to sheep

If mixing is asssortative between species

$$\begin{pmatrix} F_C(t) \\ F_S(t) \end{pmatrix} = \begin{pmatrix} 1 & \rho \\ \rho & 1 \end{pmatrix} \begin{pmatrix} P_C(t) \\ P_S(t) \end{pmatrix} \tag{5}$$

(mixing homogeneous when $\rho = 1$)

Infection times are unknown

Infection times are unknown and some infections may be hidden, so define the cumulative infectiousness by day t post infection for each species

$$Y_X(t) = \sum_{j=1}^{t} P_X(j), \quad X = \{S, C\}$$

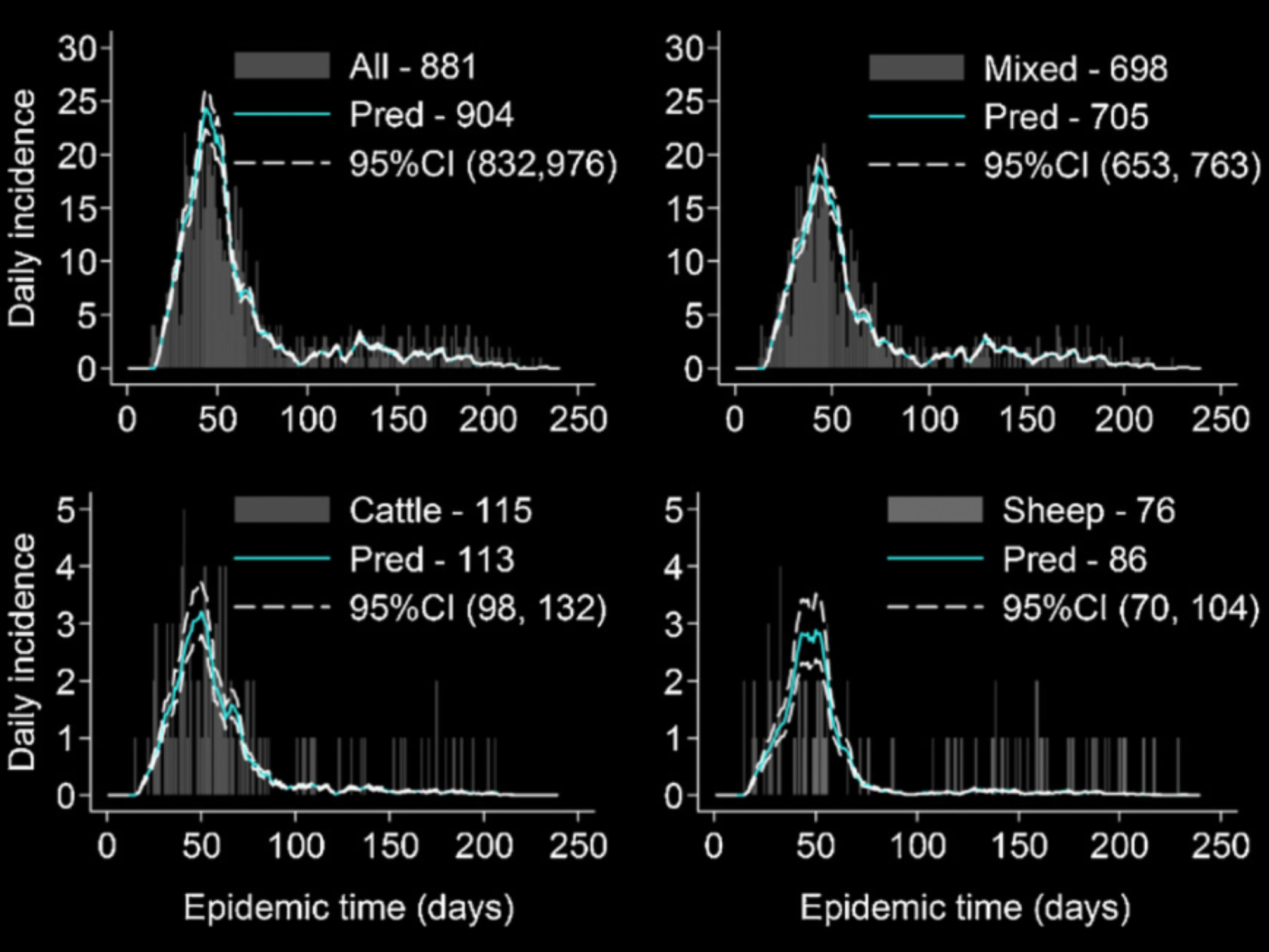
Hazard for surviving detection on day t

$$h(t) = 1 - \exp\left(-\frac{Y_C(t)}{\alpha_C N_C} - \frac{Y_S(t)}{\alpha_S N_S}\right)$$

where α_X detection threshold parameter (quantifies when saturation of detection hazard occurs)

They also look at a hybrid-farm model (HFM) and a between-farm model (BFM), additionally to this within-farm model (WFM)

		Within farm model			
		TS1		TS2	
		$C=0$ $S=0$	$C=1$ $S=1$	$C=0$ $S=0$	$C=1$ $S=1$
	Log likelihood	−7826 (−7964, −7724)	−7861 (−7988, −7755)	−7886 (−8007, −7781)	−7896 (−8010, −7798)
	DIC	17,057	17,180	17,176	17,196
	No of hidden infections	100 (81, 121)	104 (87, 126)	109 (91, 130)	105 (88, 126)
Within farm parameters	R_0R_0 cattle	21 (16, 25)	19 (15, 23)	15 (13, 18)	12 (10, 15)
	R_0 sheep	14 (10, 19)	13 (10, 16)	9 (7, 12)	8 (6.6, 10)
	Initial prop cattle (%)	7 (6.2, 8.1)	7.8 (6.8, 8.4)	7 (6.7, 7.5)	7 (6.8, 7.6)
	Initial prop sheep (%)	5.4 (5.1, 6.3)	5.2 (5.1, 6.4)	6.3 (6.1, 6.7)	6.9 (6.6, 7.2)
	α_C – cattle detection threshold	11 (9, 13)	11 (9, 13)	14 (5, 18)	11 (9, 13)
	α_S – sheep detection threshold	27 (19, 34)	28 (19, 27)	33 (23, 42)	28 (19, 27)
	Prop Q – cattle	41%	40%	53%	47%
	Prop Q – sheep	67%	68%	78%	76%
	Prop Q – mixed	33%	33%	45%	41%
	β_0Baseline β_0	7 (2, 13)	20.1 (2, 41)	3.7 (2.8, 6.8)	14 (5, 18)
	RS – farm level susc. ratio	3.1 (2.6, 3.8)	2.97 (2.5, 3.6)	3.15 (2.8, 3.7)	3.12 (2.6, 3.7)
Between farms					


All - 881
Pred - 904
95%CI (832,976)
Mixed - 698
Pred - 705
95%CI (653, 763)
Cattle - 115
Pred - 113
95%CI (98, 132)
Sheep - 76
Pred - 86
95%CI (70, 104)
Daily incidence
Epidemic time (days)

FMD characteristics

A few models

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- Nur *et al*

Conclusion

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MODELING THE INTRINSIC DYNAMICS OF FOOT-AND-MOUTH DISEASE

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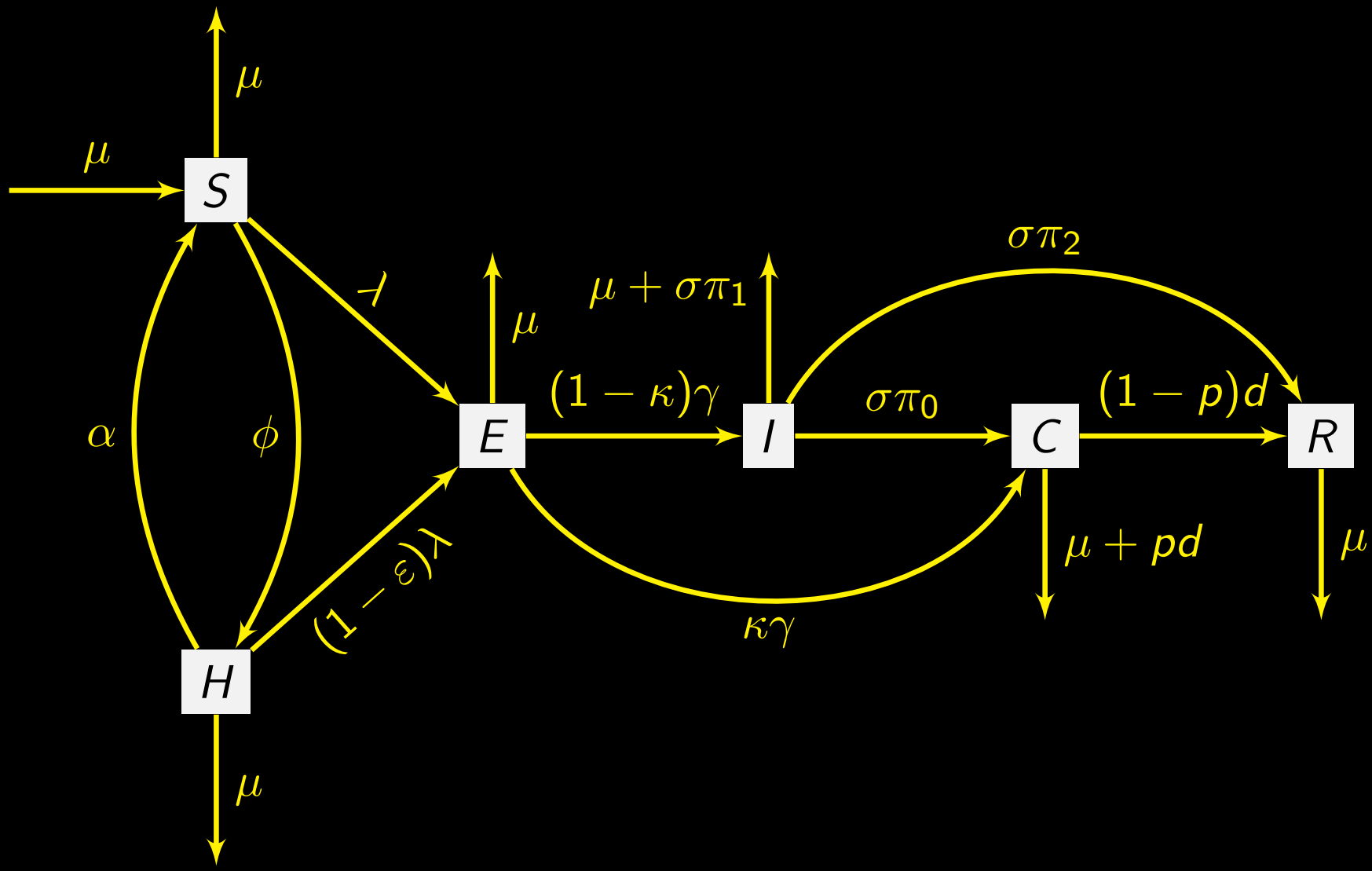
(Communicated by Jia Li)

State variables

- S susceptible
- H vaccinated
- E exposed
- I infected
- C carrier
- R recovered

$$N(t) = S(t) + H(t) + E(t) + I(t) + C(t) + R(t)$$


μ
μ
S
λ
μ
$\mu + \sigma\pi_1$
$\sigma\pi_2$
$(1-\kappa)\gamma$
$\sigma\pi_0$
$(1-p)d$
α
ϕ
E
I
C
R
$\mu + pd$
μ
$(1-\varepsilon)\lambda$
$\kappa\gamma$
H
μ

Parameter Definition	Symbol	Baseline value	Units
Exit rate	μ	0.001	day^{-1}
Vaccination rate	ϕ	0.006	day^{-1}
Incubation period	γ^{-1}	4	days
Vaccine waning rate	α	0.0056	day^{-1}
Average carrier period	d^{-1}	3.5	years
FMD transmission rate	β	0.6	day^{-1}
Average infectious period	σ^{-1}	7	days
Vaccine efficacy	ϵ	0.89 (0.5-0.89)	-
Proportion of infectious animals which progress to carrier population	π_0	0.35 (0.15-0.5)	-
Proportion of infectious animals which succumb to FMD-induced death	π_1	0 (0.0-0.05)	-
Proportion of infectious animals which recover from FMD	π_2	0.65 (0.45-0.85)	-
Proportion of exposed animals which become FMD carriers	κ	0.5 (0.15-0.5)	-
Proportion of FMD carriers which succumb to disease related death	p	0 (0.0-0.05)	-

TABLE 1. Model parameters and their interpretations.

Results

$$\mathcal{R}_c = \frac{\beta\gamma(1-\kappa)(\alpha+\mu+(1-\varepsilon)\phi)}{(\mu+\gamma)(\mu+\sigma)(\mu+\alpha+\phi)} \tag{6}$$

Theorem 1

When $\mathcal{R}_c \leq 1$, the FMD-free EP is GAS in

$$\Omega = \{S \leq S^0, H \leq H^0, N = 1\}$$

When $\mathcal{R}_c > 1$, $\exists$ unique EE EP that is LAS when $\mathcal{R}_c$ close to 1

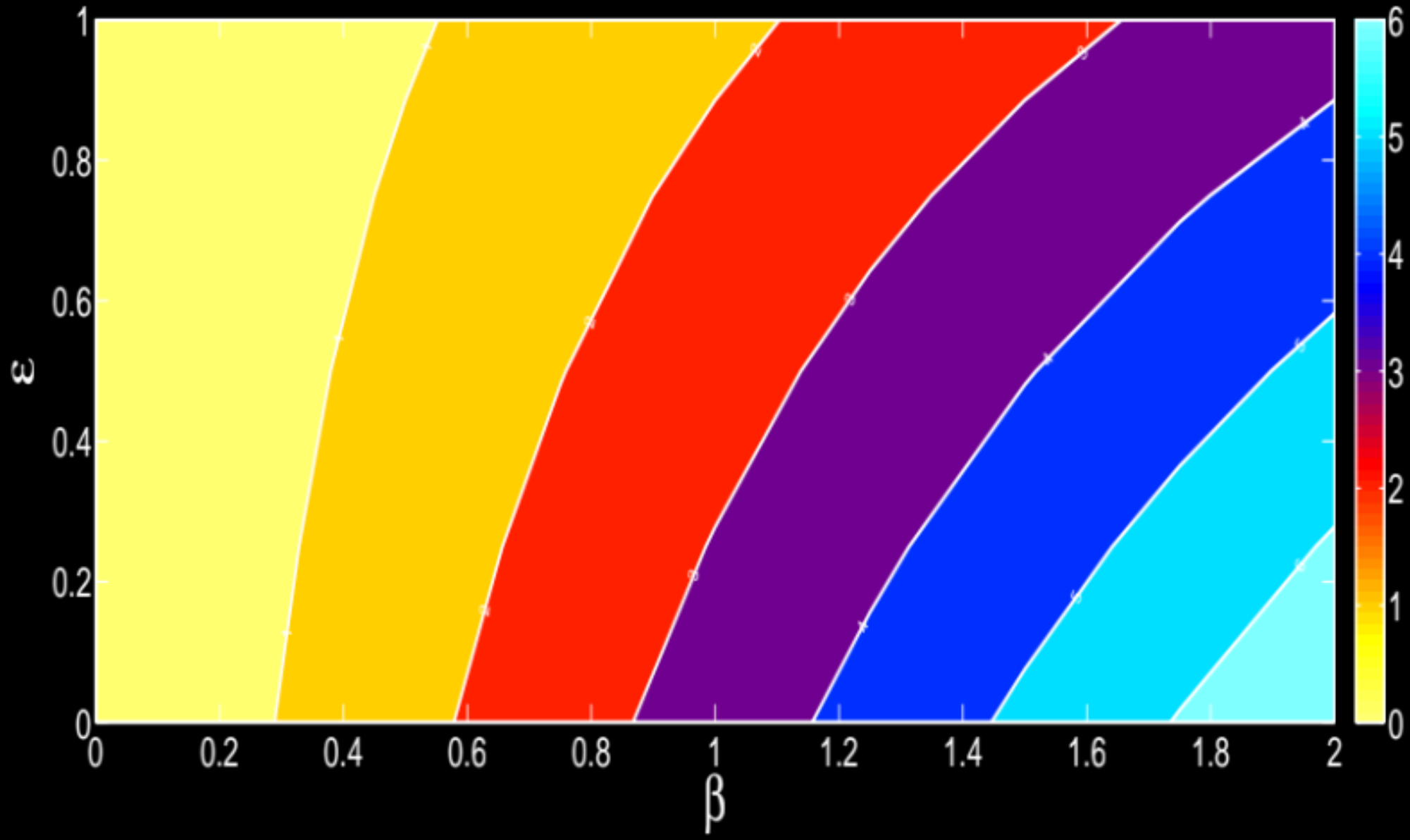


FIGURE 2. Contour plot of $\mathcal{R}_e$ as a function of β (FMD transmission rate) and ϵ (FMD vaccine protective factor). Other parameters are fixed and their values are provided in Table 1.

Periodic case

Then consider

$$\beta(t) = \beta_0 \left[1 + a \sin\left(\frac{2\pi}{365} t + \varphi\right)\right]$$

Compute $\mathcal{R}_0$ using the method for periodic systems (Bacaer, Wang & Zhao, Thieme)

In order to analyze the threshold dynamics of epidemiological models in periodic environments, Wang and Zhao [22] extended the framework in [21] by introducing the next infection operator

$$(L\phi)(t) = \int_0^\infty Y(t, t-s)F(t-s)\phi(t-s)ds\,, \tag{19}$$

where $Y(t,s)$, $t \geq s$, is the evolution operator of the linear ω-periodic system $\frac{dy}{dt} = -V(t)y$ and $\phi(t)$, the initial distribution of infectious animals, is ω-periodic and always positive. The effective reproductive number for a periodic model is then defined as the spectral radius of the next infection operator,

$$\mathcal{R}_0 = \rho(L). \tag{20}$$

The evolution operator $Y(t,s)$, for system (18) is

$$Y(t,s) = \begin{pmatrix} e^{-(\mu+\gamma)(t-s)} & 0 \\ \frac{(1-\kappa)\gamma}{\sigma-\gamma}\left[e^{-(\mu+\gamma)(t-s)} - e^{-(\mu+\sigma)(t-s)}\right] & e^{-(\mu+\sigma)(t-s)} \end{pmatrix}. \tag{21}$$

The next infection operator can be numerically evaluated by (see [17,18] for details)

$$(L\phi)(t) = \int_0^\infty Y(t, t-s)F(t-s)\phi(t-s)ds = \int_0^\omega G(t,s)\phi(t-s)ds,$$

where

$$\begin{aligned} G(t,s) &\approx \sum_{k=0}^{M} Y(t, t-s-k\omega)F(t-s-k\omega) \\ &\approx \frac{\alpha+\mu+(1-\epsilon)\phi}{\alpha+\mu+\phi}\,\beta(t-s)\sum_{k=0}^{M}\begin{bmatrix} 0 & e^{-(\mu+\gamma)(s+k\omega)} \\ 0 & \frac{(1-\kappa)\gamma}{\sigma-\gamma}\left[e^{-(\mu+\gamma)(s+k\omega)} - e^{-(\mu+\gamma)(s+k\omega)}\right] \end{bmatrix} \end{aligned} \tag{22}$$

Theorem 2

If $\mathcal{R}_0 < 1$, the FMD-free EP is GAS in Ω. If $\mathcal{R}_0 > 1$, then solutions to the system are uniformly persistent and the system admits at least one positive periodic solution

FMD characteristics

A few models

- Chis Ster, Dodd & Ferguson
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MATHEMATICAL MODEL OF FOOT AND MOUTH DISEASE CONSIDERING VACCINATION DISINFECTION AND EARLY QUARANTINE

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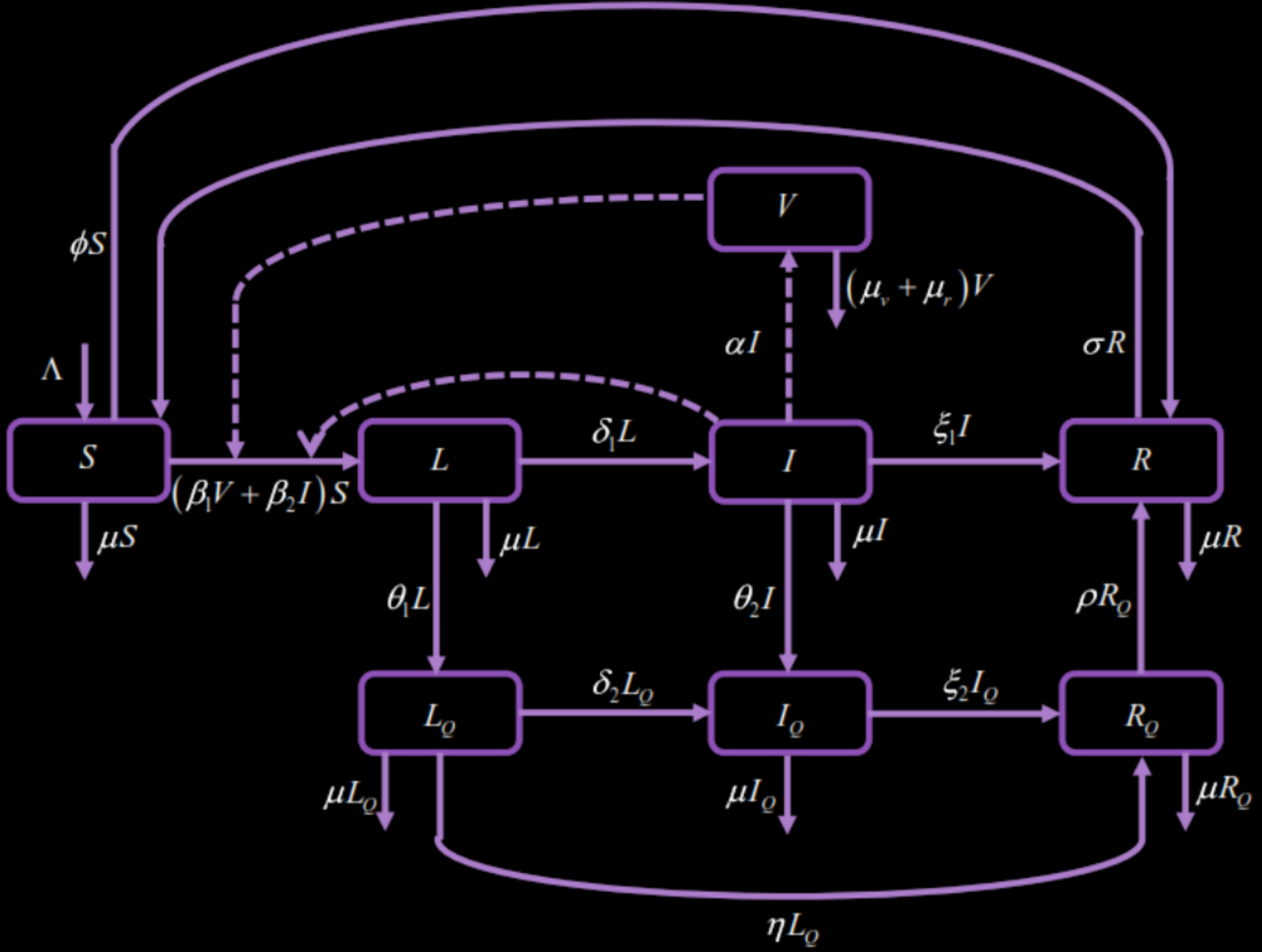
V
ϕS
$(\mu_v + \mu_r)V$
αI
σR
Λ
S
L
$\delta_1 L$
I
$\xi_1 I$
R
$(\beta_1 V + \beta_2 I)S$
μS
μL
μI
μR
$\theta_1 L$
$\theta_2 I$
ρR_Q
L_Q
$\delta_2 L_Q$
I_Q
$\xi_2 I_Q$
R_Q
μL_Q
μI_Q
μR_Q
ηL_Q

FMD characteristics

A few models

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Use and abuse of mathematical models: an illustration from the 2001 foot and mouth disease epidemic in the United Kingdom

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Appropriate use of models in the context of epidemiological knowledge and data quality (47, 93, 96)

Epidemiological knowledge	Data quality and quantity	
	Poor	**Good**
Poor	Exploration of hypotheses	Hypothesis testing
Good	Simplified representation of past events, and guarded use for prediction of future events	Detailed representation of past events, and prediction of future events