Ciência Rural, Santa Maria, v. 23, n. 3, p. 325 - 328, 1993.
Recebido p/ publicação em 21/10/92. Aprov. p/ publicação em 07/04/93.

MARKOV CHAIN MODELING OF ENDEMIC CATTLE DISEASES IN THE TROPICS OF MEXICO.

USO DA CADEIA DE MARKOV COMO MODELO PARA DOENÇAS ENDÊMICAS DE BOVINOS NOS TRÓPICOS DO MÉXICO.

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SUMMARY

Endemic diseases measured by prevalence of IgG antibodies by ELISA all showed remarkably stable overall prevalences over a study period of 3 years. This however does not mean that incidence is low or absent. Observed transition from the state of being positive for a disease to the state of being negative and vice versa suggested fairly high incidence rates (and rates of waning antibodies) for all 19 disease agents tested for. In spite of this dynamic situation Markov Chain simulations indicate that a steady prevalence is reached in a fairly short time. Markov Chain simulations may also be useful in elucidating seasonal changes in prevalence.

Key words: prevalence, Markov Chain, ELISA, México.

RESUMO

Doenças endêmicas medidas pela prevalência de anticorpos IgG pelo ELISA mostraram prevalências totais notavelmente estáveis num período de estudo de 3 anos. Isto entretanto, não significa que a incidência é baixa ou ausente. A transição observada entre o estado de positivo para uma doença para o estado negativo e vice-versa sugeriu taxas de incidência razoavelmente altas (e perda de anticorpos) para os 19 agentes infecciosos testados. Apesar desta situação dinâmica, simulações da Cadeia de Markov indicam que uma prevalência fixa é alcançada num período de tempo razoavelmente curto. A Cadeia de Markov como modelo pode também ser útil para a elucidação das alterações sazonais na prevalência.

Palavras-chave: prevalência, Cadeia de Markov, ELISA, México.

INTRODUCTION

Studies of IgG antibody levels to a number of infectious disease agents of cattle in the tropics of Mexico showed remarkable fluctuations (Barajas-Rojas et al, 1993a, 1993b, 1993c). Some of the fluctuations could be related to state of pregnancy and seasonal variation. In spite of the fluctuations the overall prevalence of positive tests remained remarkably stable over a 3 year period.

In this paper we examine the possibility that fluctuations in antibody levels are caused by waning of antibodies followed by reinfections.

MATERIAL AND METHODS

Based on recorded ELISA reversals, from negative to positive and vice versa and total prevalence in 1988-1989 overall transition probabilities on a bimonthly basis were calculated.

Selected diseases were modelled using the Markov Chain approach to illustrate how quickly endemic disease with different incidence levels may reach an overall stable prevalence. A simulation of seasonal variation of prevalence of bluetongue antibodies was also carried out. The choice of the Markov Chain seems logical since the system we deal with can be described by two states (positive and negative) and the animals move between these two states with given probabilities. Furthermore the Markov Chain approach assumes that the present state of an individual does not depend on earlier states; this agrees with the assumption that infection of individual animals is a random process. Finally Markov Chain models with fixed transition probabilities tend to stabilize after relatively few iterations which seem to agree with the observed overall stable prevalences for the entire study period (1986, 1988, 1989).

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The study area, its animal population and the method of ELISA has been described in an earlier publication (BARAJAS-ROJAS et al, 1993a).

RESULTS

The observed transition rates from positive to negative and from negative to positive during bimonthly ELISA tests of 181 producing cows are shown in table I.

Table I
Observed rates of transmission (from positive to negative and vice versa) during bimonthly testing of 181 producing cows from the tropics of Mexico, 1988, 1989.

AGENT	Overall Seroprevalence	Observed rates of transitions of consecutive tests	
		positive to negative	negative to positive
BTV	87.7	0.09	0.60
AM	59.7	0.27	0.47
SD	38.0	0.50	0.32
LH	41.0	0.35	0.25
MB	59.0	0.16	0.38
ST	47.3	0.25	0.28
TG	40.0	0.46	0.33
PM	36.0	0.37	0.22
BRSV	60.3	0.28	0.46
CF	41.0	0.40	0.33
RV	54.0	0.41	0.39
LM	37.3	0.51	0.31
CB	34.3	0.39	0.25
CL	34.3	0.39	0.23
HS	20.3	0.52	0.14
BLV	17.3	0.42	0.09
PI3	37.3	0.52	0.31
BVD	10.0	0.27	0.08
IBR	2.67	0.78	0.02

Codes for antigens:
BTV = *Bluetongue virus*
AM = *Anaplasma marginale*
SD = *Salmonella dublin*
LH = *Leptospira interrogans serovar hardjo*
MB = *Mycoplasma bovis*
ST = *Salmonella typhimurium*
TG = *Toxoplasma gondii*
PM = *Pasteurella multocida*
BRSV= *Bovine Respiratory Syncytial Virus*
CF = *Campylobacter fetus*
RV = *Rotavirus*
LM = *Listeria monocytogenes*
CB = *Coxiella burnetii*
CL = *Chlamydia psittaci-trachomatis*
HS = *Haemophilus somnus*
BLV = *Bovine Leukemia Virus*
PI3 = *Parainfluenza 3 Virus*
BVD = *Bovine Viral Diarrhea virus*
IBR = *Infectious Bovine Rhinotracheitis Virus*

From this data Markov Chain transition matrices were constructed for three disease agents: Bovine Viral Diarrhea virus, low overall prevalence (10%); **Leptospira interrogans serovar hardjo**, medium overall prevalence (41%) and Bluetongue virus, high overall prevalence (87. 7%). Markov Chain simulations were carried out and the results are shown in Tables II, III and IV. The herd size is fixed at 100 and it is assumed that at the beginning one cow is positive. The same results would be obtained if it was assumed that all cows were negative at the beginning, the source of infection being the environment or other animal populations. When the simulated prevalences reach steady state they correspond closely to the observed prevalences: 9.88% versus 10.00, 41.66 versus 41.00 and 86.95 versus 87.7. This is not surprising since observed and simulated prevalences are based on the same data set.

The simulated steady states are reached in a

Table II
Development of a steady state of prevalence of antibodies to *Bovine Viral Diarrhea Virus* in producing cows of the tropics of Mexico, 1988, 1989. Markov Chain simulation based on observed transition probabilities.
Herd size arbitrarily fixed at 100 cows.

Transition matrix

TRANSITION PROBABILITIES

	POSITIVE	NEGATIVE	
POSITIVE	0.27	0.73	1.00
NEGATIVE	0.08	0.92	1.00

Calculated prevalence, bimonthly:

MONTH	POSITIVE COWS	NEGATIVE COWS
0	1	99
2	8.19	91.81
4	9.56	90.44
6	9.82	90.18
8	9.87	90.13
10	9.88	90.12
12	9.88	90.12

Table III

Development of a steady state of prevalence of antibodies to *Leptospira interrogans serovar hardjo* in producing cows in the tropics of Mexico,1988, 1989. Markov Chain simulation based on observed transition probabilities. herd size arbitrarily fixed at 100 cows.

Transition matrix

TRANSITION PROBABILITIES

	POSITIVE	NEGATIVE	
POSITIVE	0.65	0.35	1.00
NEGATIVE	0.25	0.75	1.00

Calculated prevalence, bimonthly:

MONTH	POSITIVE COWS	NEGATIVE COWS
0	1	99
2	25 40	91.81
4	35.16	90.44
6	39.06	90.18
8	40.62	90.13
10	41.25	90.12
12	41.50	90.12
14	41.60	58.40
16	41.64	58.36
18	41.66	58.34
20	41.66	58.34

Table IV

Development of a steady state of prevalence of antibodies to *Bluetongue virus* in producing cows in the tropics of Mexico, 1988, 1989. Markov Chain simulation based on observed transition probabilities, herd size arbitrarily fixed at 100 cows.

Transition matrix

TRANSITION PROBABILITIES

	POSITIVE	NEGATIVE	
POSITIVE	0.91	0.09	1.00
NEGATIVE	0.60	0.40	1.00

Calculated prevalence, bimonthly:

MONTH	POSITIVE COWS	NEGATIVE COWS
0	1	99
2	60.31	39.69
4	78.70	21.30
6	84.40	15.60
8	86.16	13.84
10	86.71	13.29
12	86.88	13.12
14	86.93	13.12
16	86.95	13.05
18	86.95	13.05
20	86.95	13.05

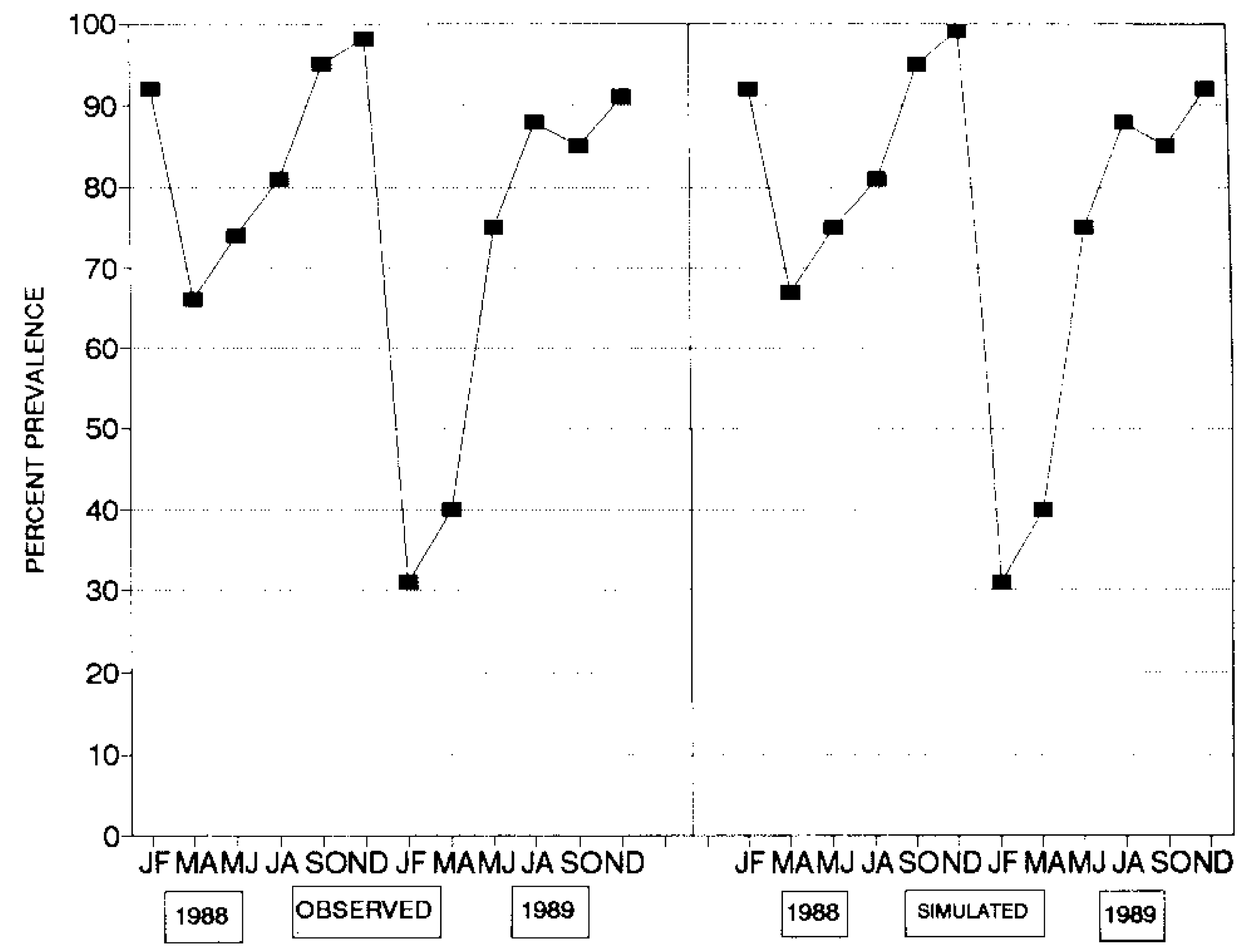

FIGURE 1. Observed and simulated seasonal changes in prevalence of antibodies to **Bluetongue virus** in producing cows in the tropics of Mexico 1988, 1989.

period of 1 - 1.5 years; this is a rather short period and in agreement with the fact that overall observed prevalences were almost the same over the total 3 years study period.

For diseases with pronounced seasonal variation simulation using overall transition probabilities misses interesting aspects of the disease. Antibodies to Bluetongue virus show strong seasonal variation (Figure 1). The decrease in prevalence is assumed to result from decreased vector activity that will reduce the number of animals remaining positive because re-infection occurs less frequently and also reduce the transition probability from negative to positive. Increasing prevalence is caused by the opposite situation. Table V and Figure 1 show the result of a simulation with transition probabilities varying with season. The same simulation can be obtained with other, different combinations of transition probabilities; here it was chosen to keep the probabilities of positive animals remaining positive fairly high because of longevity of antibodies and because these animals may be the most attractive for the vector. The transition negative to positive was allowed to fluctuate tenfold over seasons.

DISCUSSION

Although endemic diseases may show a very stable prevalence over years this does not mean that

Table V
Observed and simulated seasonal (bimonthly) prevalences of antibodies to *Bluetongue virus* in producing cows in the tropics of Mexico, 1988, 1989.

Markov Chain simulations with variable transition probabilities. Size of herd arbitrarily fixed at 100.

YEAR	MONTH	Positive cows observed	Positive cows simulated	ASSUMED TRANSITION PROBABILITIES Positive to positive	Negative to negative
1988	JF	92	92	0.36	0.06
	MA	66	67	1.00	0.24
	MJ	74	75	1.00	0.24
	JA	81	81	1.00	0.72
	SO	95	95	1.00	0.72
	ND	98	99	0.31	0.06
1989	JF	31	31	0.90	0.18
	MA	40	40	1.00	0.58
	MJ	75	75	1.00	0.52
	JA	88	88	0.90	0.52
	SO	85	85	0.95	0.72
	ND	91	92		

active disease transmission is absent. In this study of a cattle population of the tropics of Mexico there are indications that a disease as Bovine viral Diarrhea with a long term prevalence of 10% actually has a 8% bimonthly incidence rate; for **Leptospira interrogans serovar hardjo** with a steady prevalence of 41% the bimonthly incidence rate may actually be 25% and for Bluetongue virus with a steady prevalence of 87.7% the overall bimonthly incidence rate may be 60%. The latter show strong seasonal variations that may be illustrated by means of Markov Chain modeling.

ACKNOWLEDGEMENTS

We appreciate the assistance in sample and data collections of Dr. Eusebio García Neria and Dr. Rebeca Acosta and personnel of the Centro de Investigación Enseñanza y Extension en Ganadería Tropical-CIEEGT of the Faculty of Veterinary Medicine. National Autonomous University of Mexico. Mexico City.

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