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APPLIED STATISTICS

AN AUTOREGRESSIVE MULTIVARIATE MODEL FOR FASCIOLOSIS

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Empirical mathematical models have an important role to play in the representation of many physical and biological processes and have been in use for many years (Draper and Smith, 1966). The advent of modern computing technology has led to their increasing use in the agricultural industry (Whittemore, 1981) in an attempt to find strategies for optimal production (Goodall & Agnew, 1988). These models may be broadly divided into two main categories, deterministic and stochastic. The former assume that input values and parameters are known with complete certainty, while the latter include a component of random variation. Since most epidemiological processes cannot be defined with certainty, stochastic models are likely to provide greater practical benefit in this key area.

The construction of empirical stochastic models has generally involved the fitting of regression equations to a set of discrete observed data points corresponding to some physical or biological process. Such equations postulate the existence of dependent and independent variables. Particular care must be taken when the observed independent variables are measured over time. In this situation more complex and sophisticated time series analysis is necessary. The objectives of such time series analysis may be classified into three areas, description, explanation and prediction.

The description of a time series usually involves graphically plotting the observed data and assessing whether a trend and a seasonality pattern is present. Some series are dominated by these obvious features and a simple model may be adequate to describe the variation in the time series. However, it is frequently necessary to construct a model for the more complicated stochastic component of any time series.

The explanation of a time series may be possible if the variation in one time series may be associated with the variation in another time series. This may lead to a deeper understanding of the mechanism which generated any given time series. Multiple regression models are generally of use in this explanation process (Chatfield, 1980).

The prediction of the future values of a time series involves the investigation and formulation of the most suitable mathematical model for forecasting purposes. Such prediction is often very closely related to the problem of control. For example, in the mathematical modelling of disease processes, it is particularly important to be able to predict whether the expected risk of disease will exceed certain levels.

This latter objective of modelling a time series is especially relevant in the control of fasciolosis (liver fluke). This is a serious economic disease of cattle and sheep with a worldwide distribution. Although heavily

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infected animals may die, very many more, which are less severely affected, suffer a substantial reduction of growth and production. Additionally, when affected animals are presented for slaughter, the valuable liver is invariably condemned due to the presence of characteristic pathological lesions. Detailed records of liver condemnations due to such lesions can therefore accurately reflect the annual prevalence of this important disease (Dargie, 1987).

Fasciolosis can be controlled by a number of methods, the most important and widespread in operation throughout the world being the strategic use of modern flukicidal drugs. However, the frequency and most effective timing of their use must be dependent on the estimated annual risk of the disease.

It has been established and accepted for many years that the annual prevalence of fasciolosis is dependent on previous prevailing climatic conditions (Ollerenshaw and Rowlands, 1959). This enabled the formation of primitive forecasting models to estimate the annual risk from this important disease and thus provide the basis for specific veterinary advice on necessary control measures

This paper describes the formulation of a mathematical forecasting model which accurately predicts the annual prevalence of fasciolosis in the cattle and sheep populations of Northern Ireland. The paper details the interrogation, using a comprehensive computer system, of an integrated database of relevant abattoir and meteorological variables. The paper also records how the model was first used in 1987 to warn producers in Northern Ireland of the high risk of the disease and highlights the extreme precision achieved.

DATABASE

The specific type and location of pathological changes causing condemnations in all cattle, sheep and pigs slaughtered throughout Northern Ireland is recorded on a centralised database. Data is available from 1969 and is dynamically updated on a monthly basis. This database is analysed using a computerised data analysis system which was established in 1986 (McIlroy et al 1987). The system has been used to investigate the epidemiology of economically important diseases in the cattle, sheep and pig populations of Northern Ireland (McIlroy et al., 1988).

The monthly prevalence of liver condemnations due to fasciolosis in sheep was used in the formulation of the model. Over 90% of sheep slaughtered in abattoirs are aged 12 months or less and therefore condemnations will generally reflect the occurrence of disease within the previous year (Simmons and Cuthbertson, 1985). This facilitated the investigation of the cross-correlation between the time series of the annual prevalence of liver condemnations due to fasciolosis and the corresponding time series of concurrent prevailing weather conditions. The prevalence of liver condemnations due to fasciolosis was computed as a percentage of the total number of sheep slaughtered on a monthly basis and a distinct seasonality pattern was found which was consistent from year to year. The average monthly prevalence of fasciolosis (with corresponding standard errors) in sheep in Northern Ireland from 1970 to 1986 is demonstrated in Fig. 1. The minimum prevalence was invariably recorded in July and August with the maximum levels being achieved throughout the winter period. In view of the consistent and distinct seasonal pattern in the prevalence of this disease and the known dependence for its development on previously occurring

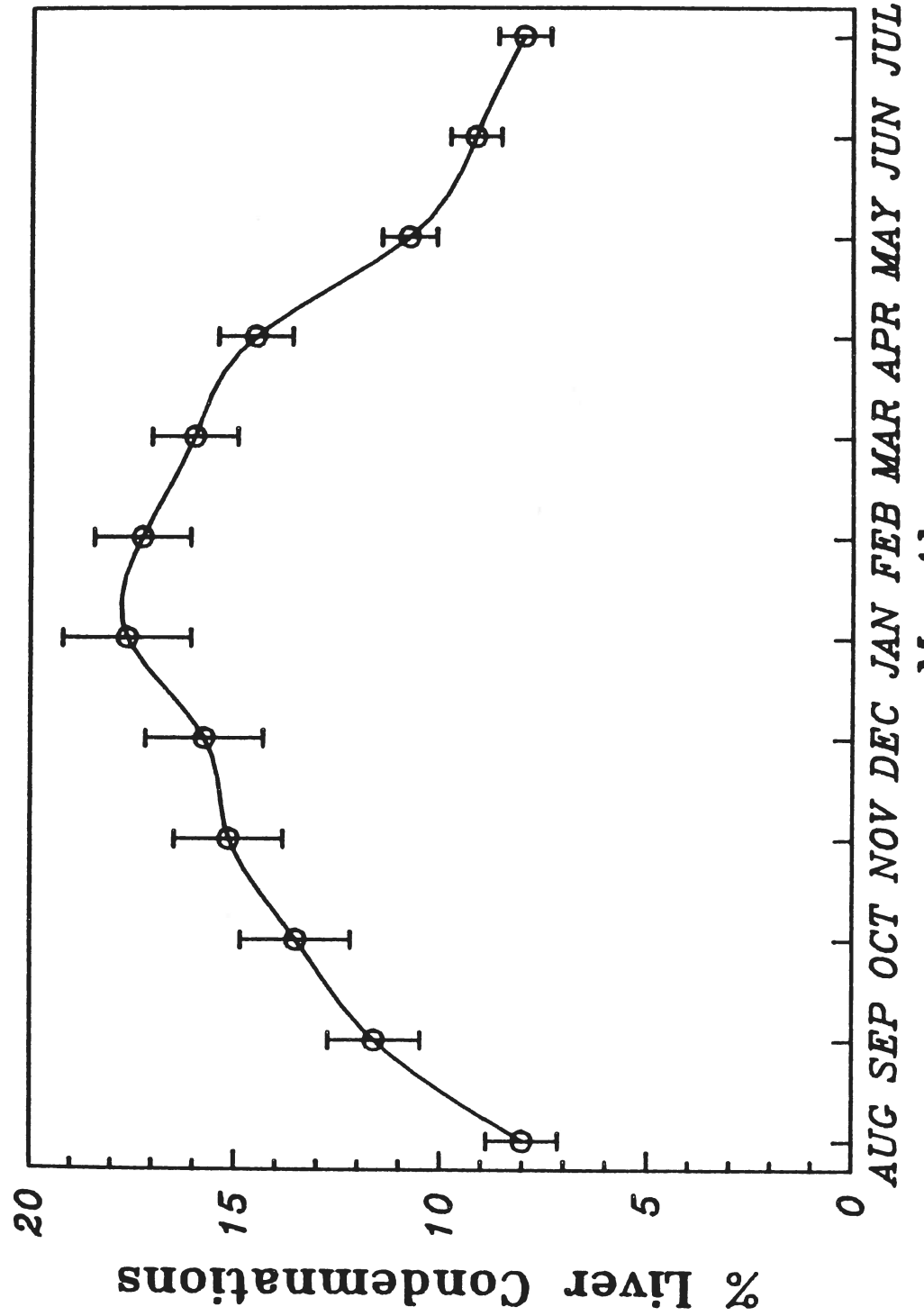

Fig. 1: The average monthly prevalence of liver condemnations due to fasciolosis in sheep

favourable weather conditions, a meaningful fasciolosis year was defined. Each fasciolosis year was defined as commencing in August and terminating in the following July. The average prevalence for each fasciolosis year available from the abattoir pathology database was computed and are demonstrated in Fig. 2.

UNIVARIATE MODEL

A wide variety of autoregressive integrated moving average (ARIMA) processes were fitted to the new time series of the annual prevalence of fasciolosis. Such ARIMA processes were investigated using the methodology described by Box and Jenkins (1968). Using this methodology, a process is defined to be autoregressive of order p if;

$$X_t = \alpha_1 X_{t-1} + \ldots + \alpha_p X_{t-p} + Z_t \quad \ldots (1)$$

where (Z_t) is a purely random process with mean zero and variance σ^2_z, and (α_i) are constants. This is statistically similar to a multiple regression model. However, in this procedure X_t is regressed not on independent variables but on retrospective values of X_t. Such a procedure is hence termed autoregressive and the resulting process of order p abbreviated to an AR (p) process. Additionally, Z_t can be defined as a moving average process of order q if defined as;

$$Z_t = \beta_1 Z_{t-1} + \ldots + \beta_q Z_{t-q} \quad \ldots (2)$$

where (β_i) are constants. This is defined to be an MA (q) process. The mixed autoregressive moving average process containing p AR terms and q MA terms is abbreviated as an ARMA (p, q) process. The ARMA (p, q) process is given by;

$$X_t = \alpha_1 X_{t-1} + \ldots + \alpha_p X_{t-p} + \beta_1 Z_{t-1} + \ldots + \beta_q Z_{t-q} \quad \ldots (3)$$

Furthermore, where non-stationary time series exist, it may be necessary to difference the series, a technique widely used in econometrics (Chatfield, 1980).

If X_t is replaced by $\nabla^d X_t$ in equation 3, then such a model is called an "integrated" model because the stationary model which is fitted to the differenced data has to be summed or integrated to provide a model for non-stationary data. Writing, $W_t = \nabla^d X_t$, the general autoregressive integrated moving average process is of the form;

$$W_t = \alpha_1 W_{t-1} + \ldots + \alpha_p W_{t-p} + \beta_1 Z_{t-1} + \ldots + \beta_q Z_{t-q} \quad \ldots (4)$$

This process is referred to as an ARIMA (p, d, q) process since the original time series has been differenced d times. In practice, the value of d is often taken to be one.

A correlogram of the autocorrelation coefficients for the univariate time series of the annual prevalence of fasciolosis as computed for each fasciolosis year is demonstrated in Fig. 3. This correlogram clearly highlights a very highly significant ($p < 0.001$) lag 1 autocorrelation coefficient of 0.8 and clearly indicates the non-stationary nature of the

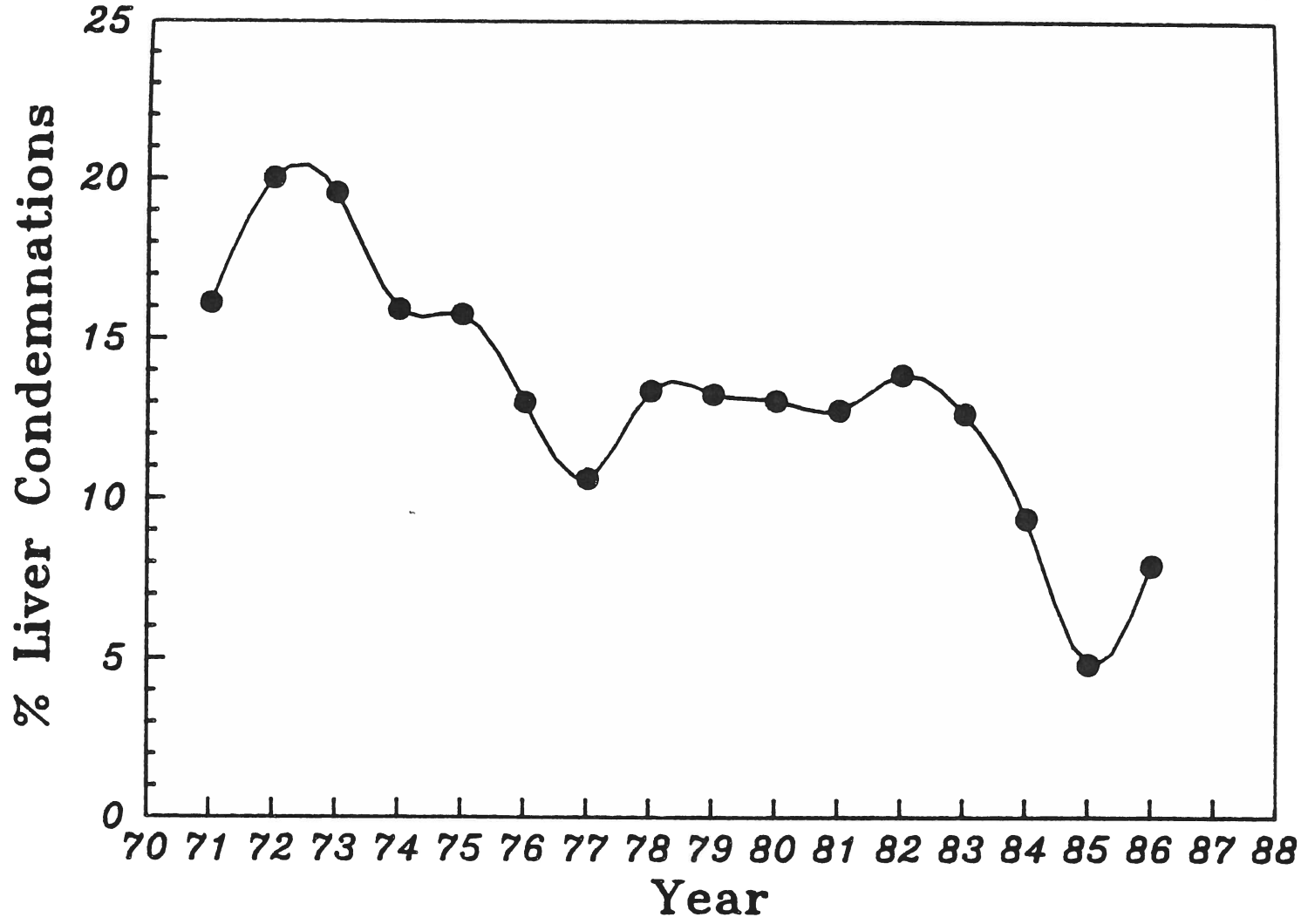

Fig. 2: The average annual prevalence of fasciolosis in sheep

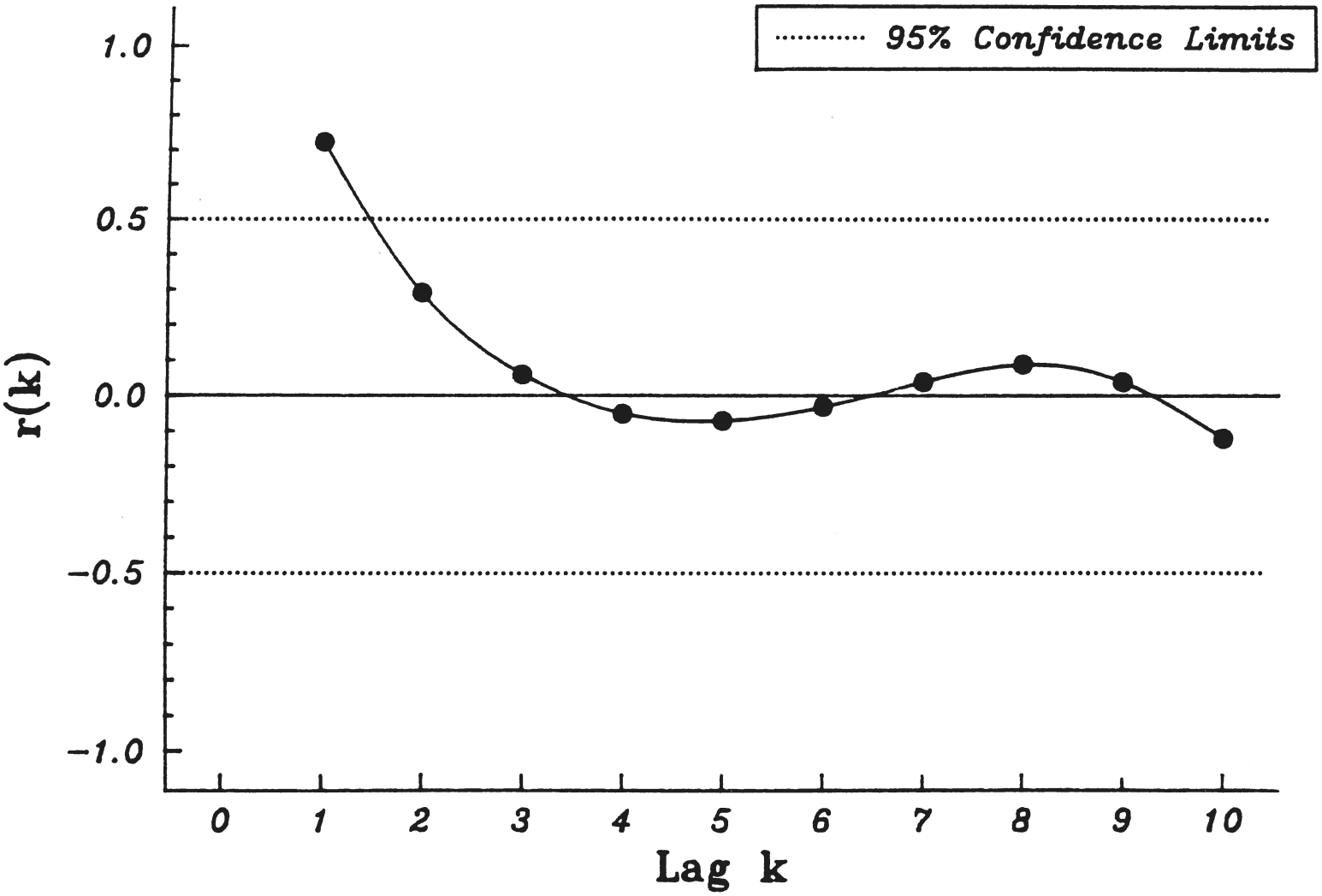

Fig. 3: The correlogram for the univariate time series of condemnations due to fasciolosis in sheep

time series and substantiates the use of the statistical techniques defined above.

The criterion of Akaike (1978) was used to determine the ARIMA process most suitable for the time series. This was found to be a first order Markov process (Feller, 1957). This was defined to be;

$$X_t = \alpha X_{t-1} + Z_t \quad \ldots \quad (5)$$

where X_t is the annual level of fasciolosis and Z_t is a random term.

A least squares fit value of 0.8 was obtained for α and the proportion of variation accounted for was 67%. The correlogram for the residuals of the first order Markov process is shown in Fig. 4. This correlogram clearly indicates the creation of a stationary time series. Notably, no demonstrable effect on the annual prevalence of fasciolosis was found from the level of the disease recorded 2 or more years previously. These findings substantiate important epidemiological determinants associated with fasciolosis which suggest that infective stages of the parasite do not normally survive on grazing pasture from year to year.

MULTIVARIATE MODEL

The analysis of the univariate time series determined for the first time that the previous year's prevalence of fasciolosis accounts for 67% of the variation recorded in the time series. However, the sole use of this finding would have a very limited practical value as an applied forecasting model.

In view of the established dependency of this disease on prevailing weather conditions at certain key periods of the year, the input which such climatic conditions had on the remaining variation in the time series was rigorously examined. The original univariate time series was analysed by ranking fasciolosis years into ascending order depending on the level of all possible weather conditions prevailing. This process involved computing the average monthly value of all individual weather variables and all possible linear combinations of such monthly values over the entire time series. The 18 fasciolosis years were then categorised into 2 groups, high and low, depending on the weather conditions being above or below the median value of the entire time series. The average monthly prevalences of liver condemnations for the years within each group were computed. The computed values were subjected to the arcsine root transformation and a paired t-test used to compare the mean values for each of the above categories. Using this procedure 5 weather variables were associated with very highly significant differences ($p<0.001$) in the annual prevalences of fasciolosis as determined by specific liver condemnations. These 5 weather variables were mean temperature, wind, rain for the months June, July, August (summer) and mean temperature, wind for the months March, April, May (spring). The time series for all these weather variables were also investigated as ARIMA (p, d, q) processes as previously described for the univariate time series of fasciolosis. All of these 5 weather time series were found to be stationary. Using the forward elimination procedures defined by Draper and Smith (1966) the residual fasciolosis series was regressed as a dependent variable against the independent 5 weather variables. The slopes of the regression equations obtained for mean summer temperature, wind and rain were found to be very highly significant ($p<0.001$). The corresponding slopes for the mean spring values for temperature and wind were found to be

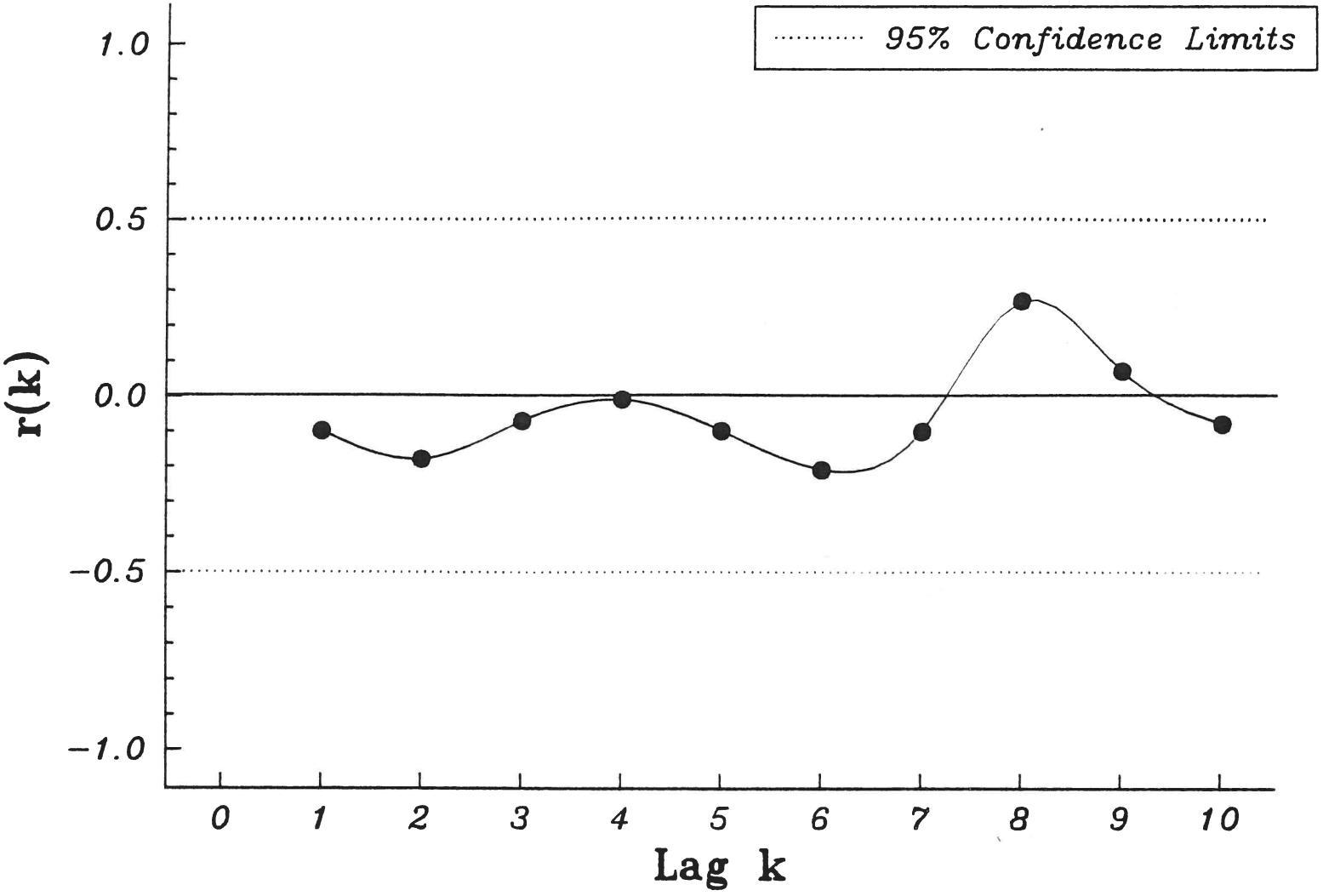

Fig. 4: The correlogram for the residual time series of condemnations due to fasciolosis in sheep

significant ($p<0.05$). The inclusion of all 5 weather variables in a multiple regression model yielded a very highly significant multiple correlation coefficient of 0.95 (R^2 = 90%). The equation obtained was;

$$Z_t = 38.4 - 2.6W_1 + 1.6W_2 - 2.5W_3 + 0.5W_4 + 1.8W_5 \quad . \; . \; . \; (6)$$

where W_1 = mean summer windspeed (knots), W_2 = mean summer rainfall (mm), W_3 = mean summer temperature (°C), W_4 = mean spring windspeed (knots), W_5 = mean spring temperature (°C).

PRECISION OF MODEL

The fitted values from this new model and the observed values for individual fasciolosis years are shown in Fig. 5 and clearly indicate the establishment of an accurate system for determining the annual prevalence of this economically important disease. The precision of this new autoregressive, multivariate model was now assessed against existing forecasting models for the annual prevalence of fasciolosis using the database of specific liver condemnations. The principal models in use are those formulated by Ollerenshaw and Rowlands (1959) and Ross (1970). The former consists of the calculation of a monthly M_t index for the months May to October inclusive. Such an index describes the potential development of the parasite and is calculated by;

$$M_t = N\,(R - P + 5). \quad . \; . \; . \; (7)$$

where R is the rainfall, P is the potential transpiration and N is the number of days with more than 0.2 mm of rain. In May and October the computed M_t value is divided by 2. The latter forecasting model described by Ross (1970) is based on an index of the total number of "wet days" occurring between June and August inclusive. A meteorological "wet day" is a 24 hour period with more than 1 mm of rain.

Using the annual prevalence of fasciolosis as the dependent variable and the M_t index as the independent variable, a regression equation was calculated. The R^2 value obtained was 0.5% and the slope of the equation was not statistically significant. The same process was carried out using the "wet day" index as the independent variable. An R^2 value of 1.8% was obtained and the slope of the equation was again not significant. These analyses clearly demonstrate that meteorological data alone cannot form the basis of an accurate forecasting model for fasciolosis. Furthermore, the analyses would suggest that the methods of establishing the annual prevalence of the disease, which relied solely on the recorded prevalence of acute fatal fasciolosis in sheep, were inaccurate. Additionally, in the formulation of both these models, research workers neglected to consider the profound and serious impact of the previous year's prevalence on the subsequent annual prevalence of the disease. These findings highlight the necessity of performing comprehensive time series analyses when variables are being recorded and compared retrospectively in time. The use of simple regression techniques may lead to incorrect interpretations of the results obtained, even when recorded data accurately reflects the dependent variable.

FORECASTING

In view of the very high proportion of variation in the fasciolosis time series accounted for by the new autoregressive, multivariate model

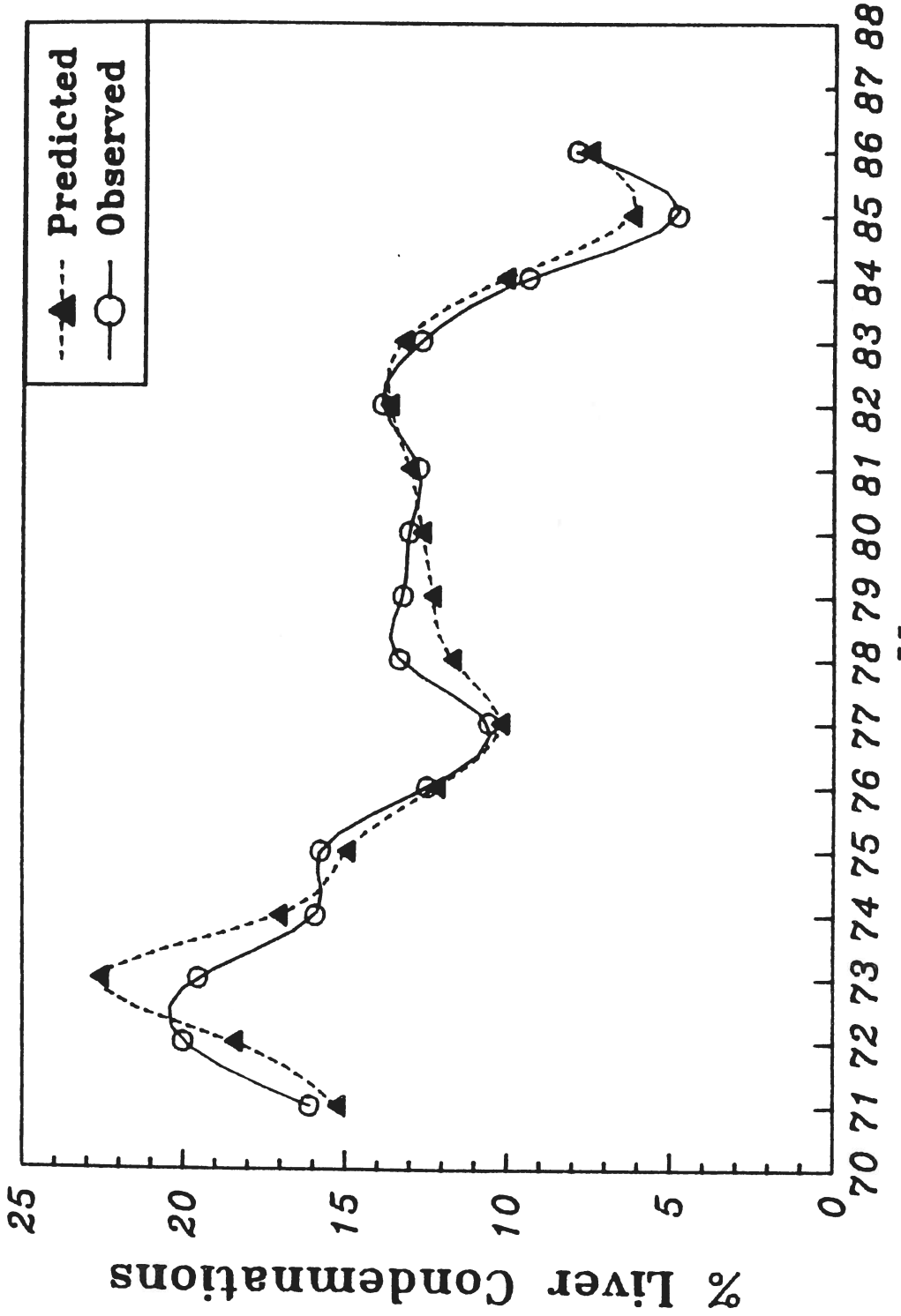

Fig. 5: The observed and predicted annual prevalence of fasciolosis in sheep

(R^2 = 90%), a detailed investigation was undertaken to assess the forecasting capacity of the model. This was achieved by fitting the model to the time series between 1969 and 1984 and using the fitted model to predict the expected prevalence of the disease in the subsequent fasciolosis year. This involved inserting the prevalence of the disease observed in the fasciolosis year of 1984 and the relevant recorded spring and summer meteorological data into the fitted model. The deviation between the actual observed prevalence of fasciolosis and the value predicted by the model was less than 0.5%. This analytical procedure was repeated by fitting the model up to 1985 and predicting the following year's prevalence of disease. This again was compared with the actual observed prevalence for that year and again the difference found to be less than 0.5%.

These highly successful investigations confirmed that the new model could be used, with a very high degree of confidence, to forecast the annual prevalence of fasciolosis and thus form the basis of specific advice on the effective use of strategic control measures. The model was first used, on a live basis, in early September 1987 to forecast the expected prevalence of fasciolosis in the following year. The model included the previous year's prevalence and all relevant meteorological variables up to and including August 1987. The model thus included all necessary information required to give a totally accurate prediction, at a time when effective control procedures could practically be implemented by producers. The model predicted a very substantial increase in the prevalence of this important disease in Northern Ireland and the media were used to highlight the extreme degree of risk. The model predicted that the prevalence of fasciolosis would increase by a factor of 1.4 from the level of disease experienced in the previous year. In the summer of 1988, when condemnation data from all abattoirs in Northern Ireland was collated and the database fully updated, the actual observed prevalence of fasciolosis was found to differ from the value predicted by the model by 0.3%.

CONCLUSIONS

A new autoregressive, multivariate model has been formulated. The model can accurately predict the expected prevalence and thus risk of fasciolosis in any year. The model contains components which are available at a time of the year when effective control measures can be implemented to prevent economic losses from the disease. The model was established using comprehensive statistical time series analysis of an extensive database of abattoir pathology and meteorological data. Notably, the abattoir pathology database accurately reflects the true prevalence of the disease in the cattle and sheep populations.

The model will be used at the beginning of every September as the basis of Government advisory campaigns on the frequency and use of strategic control measures against the disease. The model can be used to forecast the annual risk of fasciolosis in any region of the world where information on both the previous year's disease prevalence, as determined by specific abattoir condemnation data, and the relevant temporal meteorological conditions are available.

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THE STATISTICAL ANALYSIS OF A FIELD STUDY OF THE REPRODUCTIVE PERFORMANCE OF DAIRY HERDS

S.V.MORANT*

One of the most difficult aspects of managing a dairy herd is controlling its calving pattern. A commonly accepted target for individual cows is an interval between successive calvings of 365 days. On many farms an annual block calving pattern has practical advantages, although the strictness with which policies designed to maintain a tight seasonal calving pattern are pursued varies considerably between herds.

The most common measure of an individual cow's reproductive performance is her calving interval. It is a measure that gives appropriate weighting to all the factors that determine reproductive performance (e.g. interval from calving to the first ovulation post partum, ovulation detection rate, pregancy rate, embryo loss rate), yet it is easy to get and easy to understand.

The reproductive performance of a herd, or any group of animals, is often characterised by the average calving interval of the individual animals. This measure has 2 major flaws. The first is that it necessarily excludes cows that never calve again. Second, it is likely to be 'untypical' of the majority of cows that do calve again. Fig. 1 shows the distribution of intervals between first and second calvings for more than 170,000 Friesian cows (Gnanasakthy and Morant, 1988). The mean calving interval is 384 days. But nearly 2 cows out of 3 had calving intervals less than this, and the most common calving interval was between 350 and 360 days.

These difficulties of interpretation arising from the statistical properties of calving intervals can be avoided, and some of the techniques used in a field study of reproductive performance in dairy herds will be described. The stochastic processes that generate these properties will also be outlined.

DESCRIPTIVE STATISTICS

In the example above nearly two thirds of calving intervals were less than the mean, 384 days, and this is the basis for claiming that it does not characterise the distribution well. One possibility is to find the interval that is exceeded by exactly half the cows. This point is called the median and it is at 372 days. Half the cows have calving intervals greater

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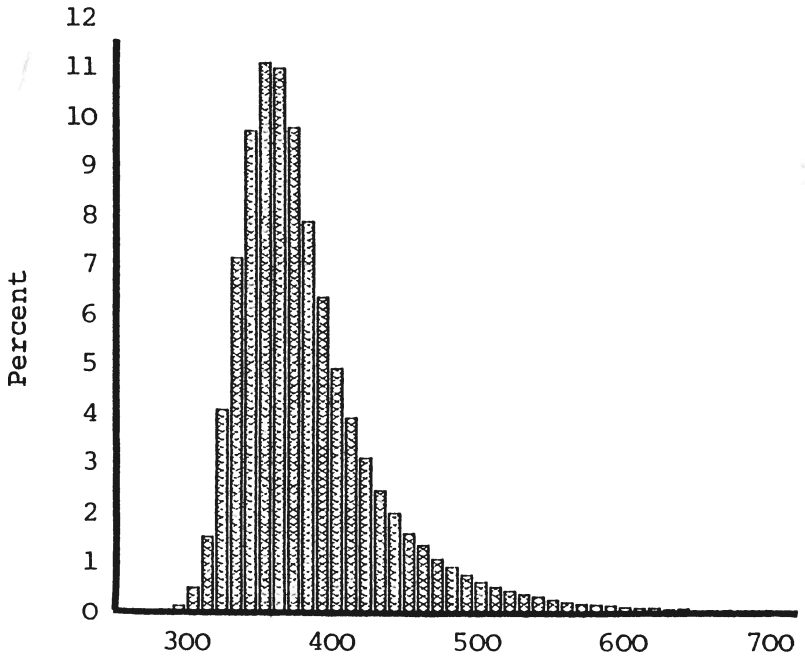

Fig. 1 The distribution of calving intervals for 170,000 second lactation Friesian cows

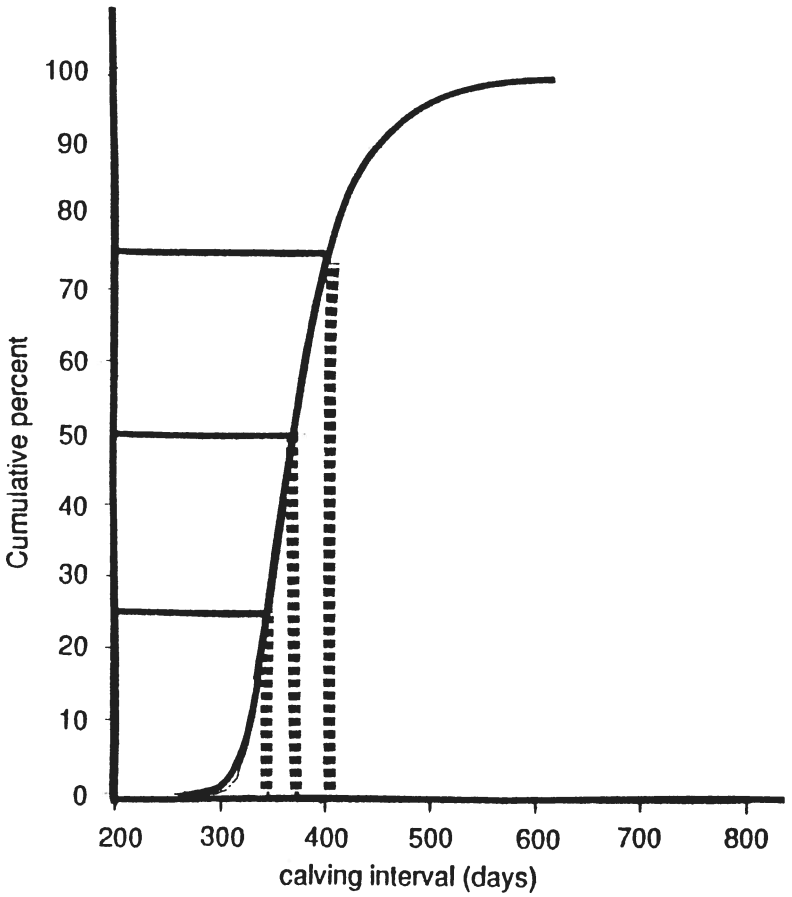

Fig. 2 The cumulative distribution of calving intervals for 170,000 second lactation Friesian cows, showing the median and lower and upper quartiles of the distribution.

than 372 days and half have intervals less than 372 days. For distributions that are likely to be asymmetrical the median has a better claim than the mean to being a 'representative' figure.

The idea of looking for the interval before which 50% of animals have calved can be extended to other proportions. We could find the interval before which, say, 25% of cows calved again, or before which 75% calved again. This leads to the idea of cumulative distributions, which summarise the whole distribution in terms of the proportions above or below any given value. Fig. 2 is the cumulative distribution for the data in Fig. 1. The median and 2 other commonly used measures, the upper and lower quartiles, are marked on the diagram. 25% of the cows will have calving intervals below the lower quartile, and 25% above the upper quartile. The upper and lower quartiles therefore span the 'middle' half of the distribution, and can be a useful measure of its spread. Several distributions could be summarised concisely either graphically or in a table (Table 1).

Table 1. Percentiles of the distribution of calving intervals of British Friesian cows of different parity

	Percentile										
Parity	10	20	25	30	40	50	60	70	75	80	90
2	355	346	350	355	363	372	382	395	403	414	448
3	333	343	348	352	360	368	377	389	396	406	438
4	333	343	347	351	359	367	376	388	396	406	437
5	332	342	347	351	359	367	376	388	396	405	437
6	333	343	347	352	359	367	377	389	397	407	439
7	333	343	348	352	360	368	378	391	399	410	442
8+	334	345	349	353	361	370	380	394	403	414	450

Cumulative distributions have another advantage. It is not necessary to exclude cows that never calve again. Fig. 3 shows the cumulative curve for the calving to conception interval in one of the herds in the field study (Bloomfield et al., 1986). It never reaches 100%. Less than 70% of the animals were pregnant again 200 days after calving and most of the remaining cows were culled as barren, but their presence does influence the position of the median. Had the barren cows been excluded the median calving interval would have been about 100 instead of 133 days, giving a very misleading impression of the reproductive performance in this herd.

The other cumulative curves in Fig 3 give an indication of the relative importance of some of the major components of this herd's reproductive performance. Although half the cows had resumed ovarian cycles within 23 days of calving, and by 46 days at least one heat had been recorded in half the animals, it was more than 73 days before half the herd was served for the first time. Only half the cows were pregnant again within 118 days of calving, but the lag in establishing successful pregnancies due

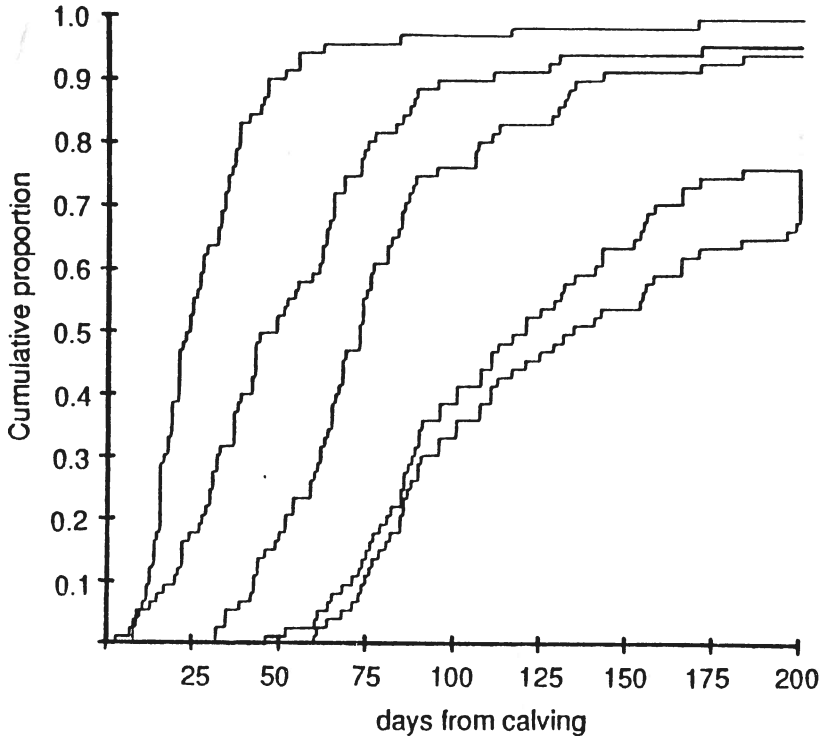

Fig. 3 Cumulative distributions of the intervals from calving to first ovulation, first recorded heat, first insemination, first pregnancy and successful pregnancy in a herd of 75 cows.

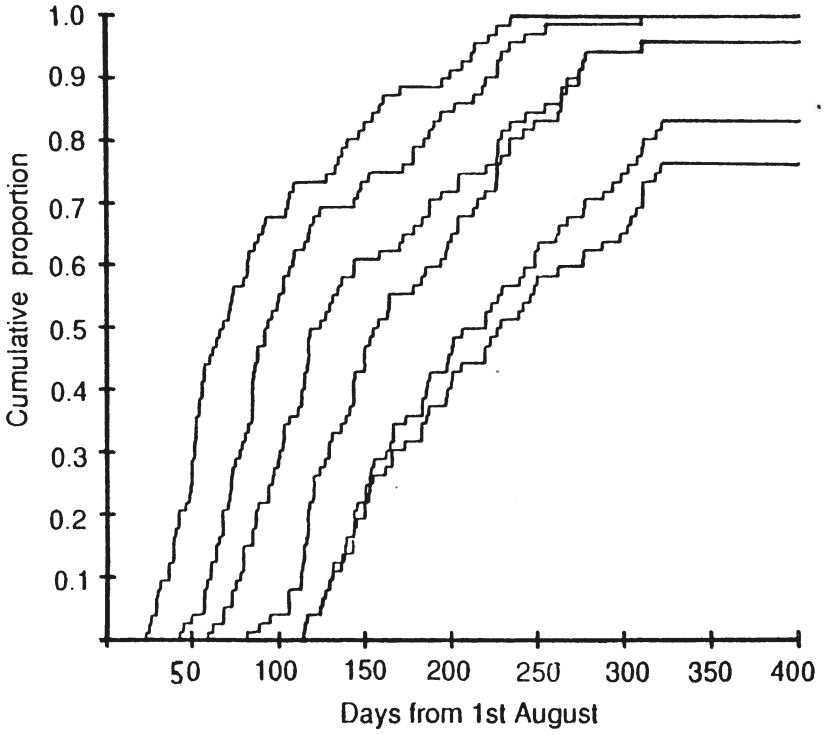

Fig. 4 Cumulative distribution of dates calving, first ovulation, first recorded heat, first insemination, first pregnancy and successful pregnancy in a herd of 75 cows.

to embryo loss was another 15 days. Although more than 95% of the cows in this herd were served at least once, almost all of them within 135 days of calving, little more than 50% of the herd was pregnant by this time.

Calving patterns can be summarised by cumulative distributions in the same way as calving intervals. The time axis is a calender date rather than an interval of time measured from calving for each cow, and Fig. 4 displays the data from Fig. 3 in this way. The curve on the extreme left is an additional one, showing the initial calving pattern. Calvings started in late August, half the herd had calved by 6th October (66 days from 1st August), and less than 10% were still to calve by 12th February (194 days). The 'middle' half of the herd calved between 19th September (49 days) and 8th December (129 days), a spread of 80 days. In the following season (the curve on the extreme right shifted further to the right by approximately 281 days by the gestation period) half the herd had calved by 22nd December (pregnant by day 227), and the middle half of the herd calved between 9th October and 24th March of the next year, a span of 166 days. The median calving date therefore drifted by 77 days, and the spread in the calving pattern, as measured by the interquartile range, increased by 86 days.

These two measures provide a means of comparing the overall performance of several herds. Fig. 5 shows the drift in the median calving date and the increase in the spread of the calving pattern from one year to the next in the 22 herds in the field study. Only three herds brought their median calving date forward, and in most herds it slipped back by between 15 and 45 days. Only one herd had a tighter calving pattern in the second year than in the first and the variation between the other herds was very large. In four herds more than 25% of the cows failed to calve again, and the interquartile range for these herds is therefore infinite.

ANALYTICAL STATISTICS

The statistics described so far do not have very great analytical power. They describe what has happened without revealing why it has happened. A cow will reproduce only if she ovulates and she is inseminated at an appropriate time and she conceives and she does not subsequently lose the embryo. The purpose of our field study was to quantify the effects of failure in each of the areas on calving patterns. It was therefore necessary to identify when cows had ovulated, whether oestrous behaviour had been observed in association with each ovulation, whether a properly timed insemination had been given, whether the cow became pregnant to it, and whether the embryo survived to term. It was also necessary to describe mathematically how the uncertainty associated with each of these events governs the uncertainty in the behaviour of a calving pattern, and limits a herdsman's control over it.

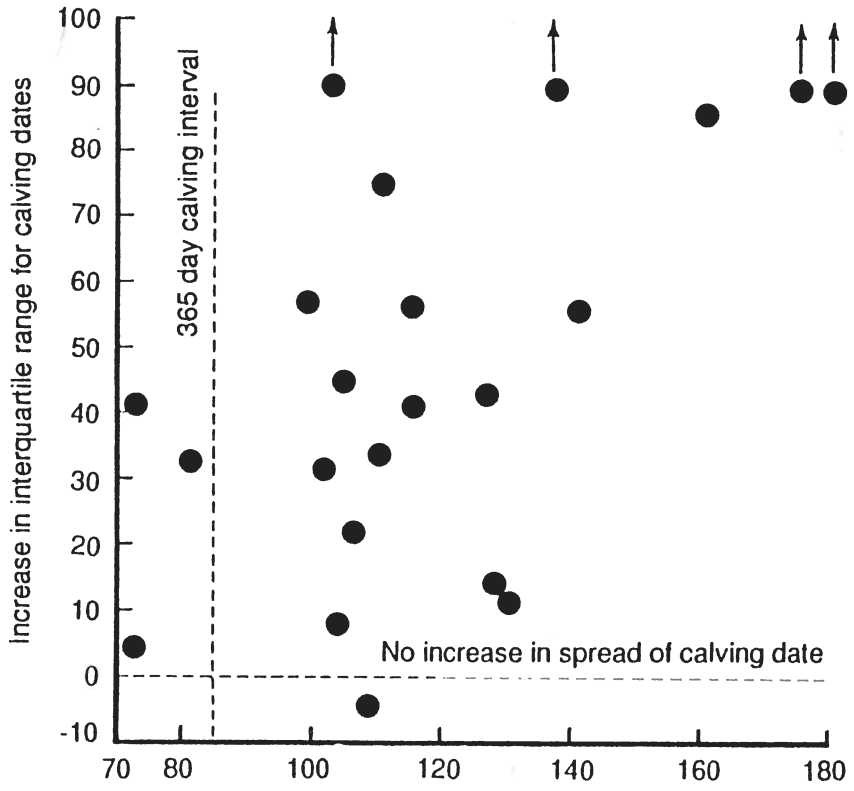

Fig. 5 Intervals from median calving date to median pregnancy date and increases in the interquartile range of calving dates (excluding replacement animals) in 22 herds.

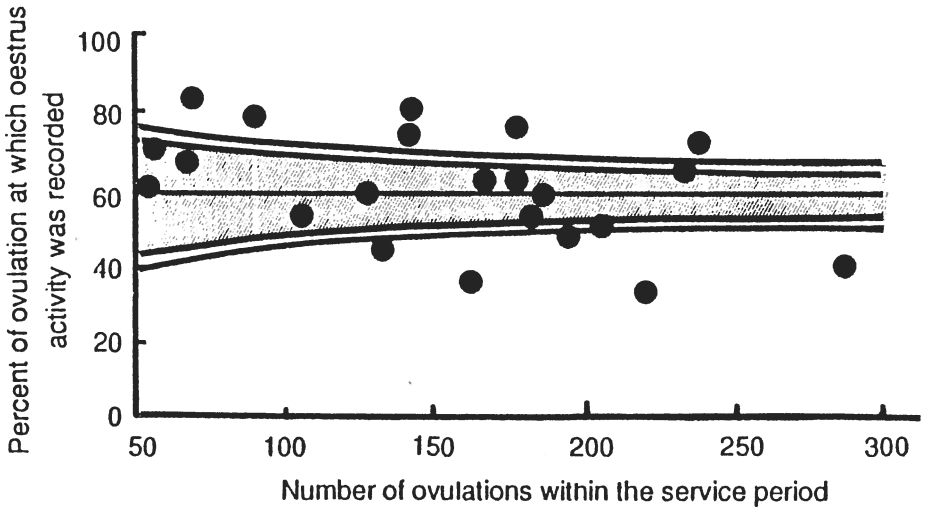

Fig. 6 Percent of ovulations within the service period accompanied by recorded oestrous activity in 22 herds.

Ovulations were detected by constructing progesterone profiles from concentrations of the hormone measured in milk samples collected 3 times per week. Numerical rules were devised to locate each ovulation within the profile, and in this way any subjective interpretation of the patterns in the hormone concentrations was avoided.

The intervals post partum to the onset of the first normal cycle are easily obtained from these profiles. The distributions within each herd were highly skewed, and the medians ranged from 18 days in one herd to 40 days in another (Table 2). In 16 of the 22 herds more than 75% of the animals had cycled by 42 days post partum and more than 90% had cycled by 63 days in 18 herds. In the majority of herds, therefore, most cows ovulated before the start of the service period. Very few had not cycled by 85 days, the minimum calving to conception interval needed for a calving interval of 365 days or less.

Table 2. Percentiles and interquartile ranges of the distribution of intervals (days) from calving to first ovulation in 21 herds.

Herd	Percentile 10	25	50	75	90	Range
1	14	18	26	41	56	23
2	13	17	24	34	46	17
3	15	29	39	59	70	30
4	13	17	26	37	49	20
5	14	17	26	31	55	14
6	11	14	21	31	44	17
7	16	20	29	42	53	22
8	12	17	24	33	47	16
9*	25	32	39	51	61	19
10	13	17	25	37	50	20
11	10	13	28	39	61	26
12	13	17	23	36	58	19
13	14	16	22	30	41	14
14	13	17	32	52	66	35
15	13	19	26	36	54	17
16	18	28	40	69	97	41
17	14	18	28	43	64	25
18	11	14	21	28	44	14
19	12	16	23	35	46	19
20	12	15	26	43	53	28
21	15	18	25	34	54	16
22	11	13	18	25	32	12

*Sampling started late in this herd and some ovulations may have occurred before the first samples were taken.

The proportions of ovulations at which oestrus was detected by the herdsmen can also be derived from the progesterone profiles, in conjunction with the herdsmen's own records. Fig. 6 shows these proportions for each herd. Since each proportion is based on a different number of ovulations, each is subject to a different amount of statistical variation. The inner pair of lines in Fig. 6 show the 95% confidence intervals for proportions based on between 50 and 300 ovulations, and the outer pair show the 99% intervals, assuming a simple binomial process is operating with a 'success' rate of 57%, the overall ovulation detection rate in the 22 herds. The observed proportions in each herd are plotted against their denominators. There is clearly a large amount of extra-binomial variation in these proportions, and there is substantial variation in ovulation detection rates from one herd to another, additional to the random variation that would be expected within herds.

Pregancy rates to 'properly timed' inseminations in each herd are shown in Fig. 7. Two herds lie outside the 99% confidence region, and another 4 lie outside the 95% region, but the extra variation between herds in pregnancy rates is very much less than in ovulation detection rates. A similar analysis of embryo loss rates suggests very little differences between herds, other than by chance.

THE MATHEMATICAL STRUCTURE OF CALVING PATTERNS

If inseminations may be given as soon as a cow begins to cycle, if they continue until the cow becomes pregnant, no matter how long it takes, and if there are no embryo losses, then the calving interval (C) can be split into three sections: the intervals from calving to the first ovulation (X), from first ovulation to pregnancy (Y) and the gestation period (G).

The second of these, from first ovulation to pregnancy, is zero if the first ovulation is detected (probability p) and the insemination is successful (probability q), i.e. the cow becomes pregnant at her first ovulation with probability pq. If she does not become pregnant at the first ovulation (probability 1-pq), she then has a chance of becoming pregnant at her second ovulation, again with probablility pq. The overall chance of becoming pregnant at the second ovulation is therefore (1-pq)pq. In general the chance of becoming pregnant at the n^{th} ovulation is $(1-pq)^{n-1}pq$. By elementary probability theory, the average number of ovulations needed to get a cow pregnant is (1-pq)/pq, and if we assume that the cow cycles regularly at 21 day intervals the average time taken to get a cow pregnant following her first ovulation is 21(1-pq)/pq days.

By very similar arguments the possibilty of embryo losses can be taken into account, although complications arise because they can occur at a variable stage of pregnancy. The expected calving interval can eventually be written

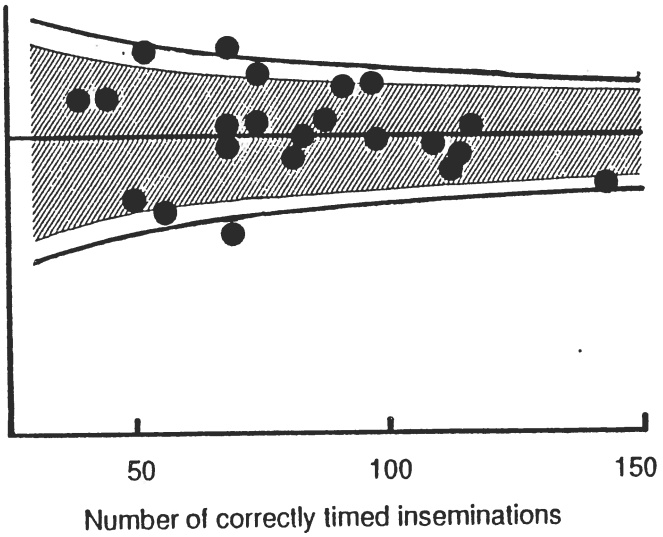

Fig. 7 Percent of correctly timed inseminations followed by at least 20 days of high progesterone concentrations in 22 herds.

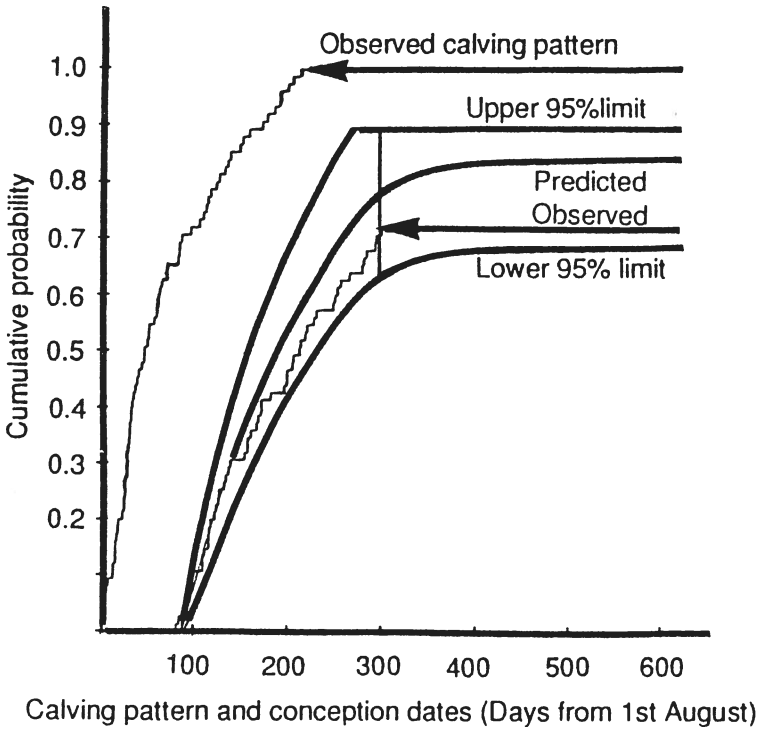

Fig. 8 The cumulative distribution for a calving pattern and the observed and predicted cumulative distribution of subsequent pregnancy dates.

$$C = X + Ze/(1-e) + 21(1-pq)/[pq(1-e)] + G$$

where e is the probability of an embryo loss and Z is the average time at which losses occur.

Although many unrealistic assumptions have been made to arrive at this equation, it does serve to illustrate the underlying stochastic processes governing the behaviour of calving intervals and patterns.

First, the two probabilities p and q always occur together as the product pq. In other words, calving patterns depend only on the probability of a cow conceiving at each ovulation, and it makes no difference whether you have an ovulation detection rate of 0.5 and a pregnancy rate of 0.8 or vice versa. However, this multiplication of the probabilities implies strong interactions between them in the calving intervals. A unit change in ovulation detection rate, for example, will have a different effect in calving intervals depending on the pregnancy rate in the herd.

Second, the equation is highly non-linear in all three probabilities p, q and e. Hence the rate of response in calving patterns to a change in any one of them depends not only on the value of the others, but also on its own initial value.

Although this equation gives mean calving intervals only it is possible to determine the entire distribution of calving intervals that would arise under given conditions, i.e. for given values of p, q and e and for given distributions of X and Z. By doing so we see why the distribution of calving intervals are skewed. The number of ovulations a cow has before becoming pregnant has a geometric distribution, and it is this that generates asymmetry in the interval from first ovulation to conception. It is exaggerated further by the distribution of intervals from calving to first ovulation, which is itself skewed, and by embryo losses when they occur.

Management policies limit the service period. Usually cows will not be inseminated before a certain date or earlier than a certain number of days post partum, or both. There will normally also be a limit on the amount of time that a cow can remain empty before being culled, and this will truncate or censor the data. Nevertheless it is possible to describe all these processes mathematically and to build a more realistic model from which to predict responses in calving patterns (Morant, 1985).

Because the model predicts the whole distribution of calving intervals we do not have to rely on measuring responses in terms of mean calving intervals. From the distributions of individual calving intervals we can estimate the likely distribution of dates of conception in a herd starting with any given calving pattern. We can calculate not only the most likely distribution, but also the range within which it is likely to lie, and

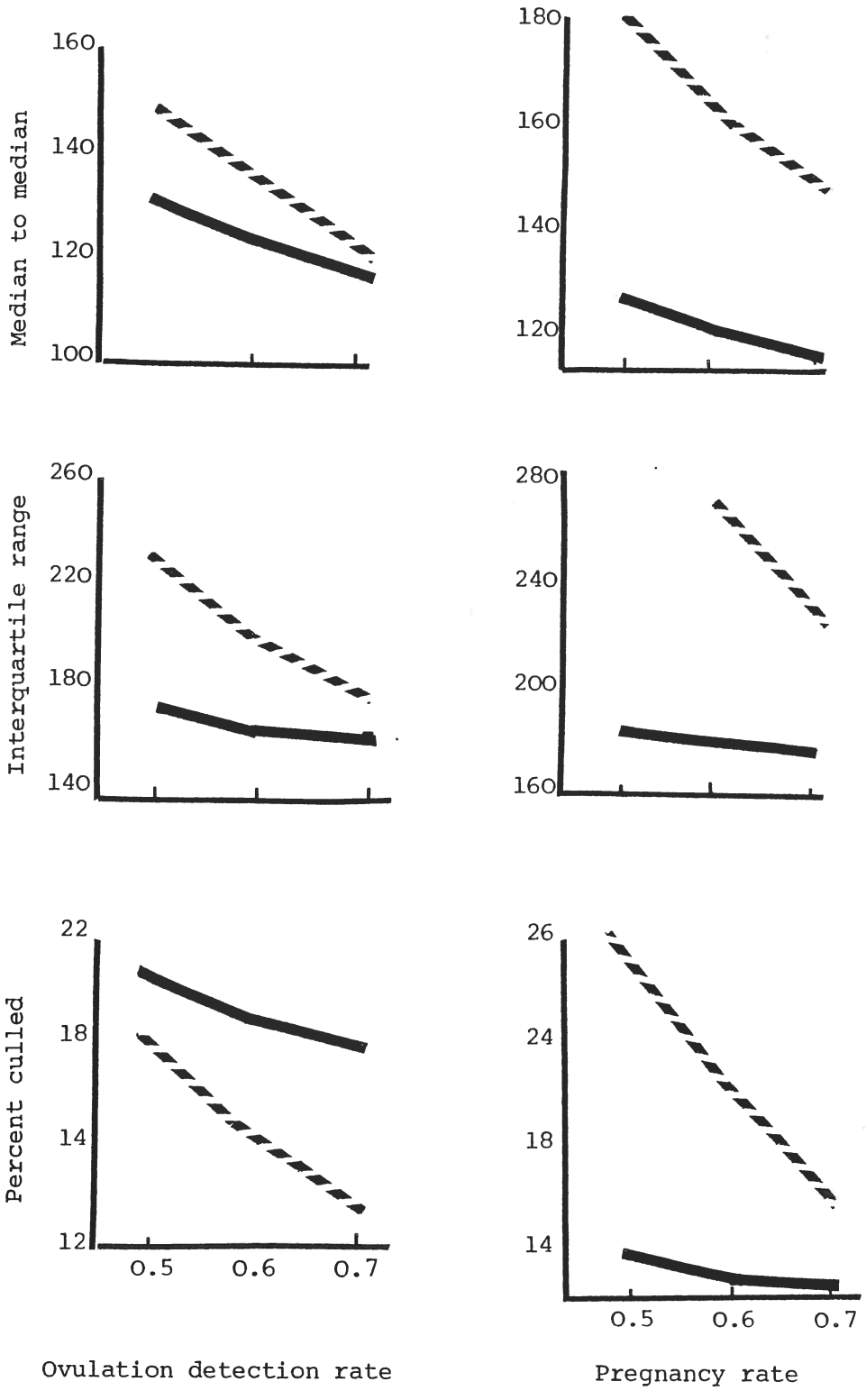

Fig. 9 Predicted responses in median calving date, the interquartile range of calving dates and the culling rate to changes in the ovulation detection rate and pregnancy rate in two herds. ▬▬ ▰▰▰

comparing this range with the observed pattern we can test the adequacy of the model (Fig. 8).

We can then go on to measure responses in calving intervals or calving patterns predicted by the model using the same techniques we used for the initial exploratory analysis. For example, we can predict the response we would expect in each herd to changes in the ovulation detection rate, or to the pregnancy rate (Fig. 9). The interval from median calving date to median conception date responds differently to the same change in ovulation detection rate in different herds. The range of responses to the same change in pregancy rate is even greater. The interquartile ranges are even more sensitive to the changes, and the interactions and non-linearity in them are even more apparent. The culling rate too is highly responsive, but not in a simple linear or additive way.

SUMMARY

Simple summary statistics have been used both for exploratory analysis of reproduction data and to convey the results of a sophisticated mathematical modelling exercise. They have a dual advantage. They do not make inappropriate assumptions about the statistical behaviour of such data, but they do describe its behaviour in terms that are readily understood and that have direct practical relevance.

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METHODS OF ANALYSIS OF DISEASE INCIDENCE DATA IN A SURVEY OF BOVINE CLINICAL MASTITIS.

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The usual method of analysis of disease incidence is to divide the individuals on the basis of the attribute under investigation and then to further subdivide them according to the presence or absence of disease. The data are then tabulated in the form of a 2-way contingency table and a χ^2 test used to assess the statistical significance of any differences in disease incidence between the levels of the attribute under investigation. The analysis of 3-way tables or tables of higher dimension is more complicated and until recently it has only been possible to use approximate methods. However, statistical software is now available to fit what are known as log-linear models to such data. This paper describes the use of log-linear models for the statistical analysis of disease incidence data in a survey of bovine clinical mastitis. Models are fitted to investigate the independent effects of herd, season and stage of lactation on mastitis incidence.

MATERIALS AND METHODS

Data

Forty eight dairy herds in Wiltshire, Somerset and Dorset using the Milk Marketing Board Mastitis Control Service were selected to study the benefit to farmers of regular collection and analysis of clinical cases of mastitis. Twenty four of the herds received a monthly computer analysis of their clinical mastitis incidence, the other 24 not. Full details of the methods of data collection and analysis are described by Rowlands and Booth (1988). The study began in September 1986 and after 12 months the average incidence in these two groups of herds was 34 and 38 cases per 100 cows respectively (Rowlands and Booth, 1988). However the range in incidence among herds was large (from 5 to 102 cases per 100 cows) and so the difference in mean incidence was not statistically significant ($P>0.05$).

For the purposes of this paper, which considers the first 12 months of the study from 1st September 1986 to 31st August 1987, the two groups have been combined. Average herd size was 124 (range 51 to 217 cows) with a total of 6,115 calvings occurring during the 12 months. There were 2,053 clinical cases of mastitis recorded during the 12 months in the 48 herds.

Sixty four of the cases occurred either during the dry period, after 400 days of lactation or in cows for which the date of calving was not known. These have been excluded for the purposes of this paper leaving a total of 1,989 cases between 0 and 400 days of lactation for consideration.

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Table 1. Numbers of cases of clinical mastitis, numbers of cow days at risk and probabilities of occurrence of mastitis grouped by month and stage of lactation.

Months	Stage of lactation (days)	Number of cases (n_{ij})	Number of cow days (N_{ij})	Probability of occurrence of mastitis ($p_{ij} = n_{ij}/N_{ij}$)
Sep-Oct	0-3	68	9924	.00685
	4-7	40	9824	.00407
	8-14	30	16533	.00182
	15-60	65	164471	.00040
	61-120	24	41918	.00057
	121-180	13	26778	.00048
	181-400	30	344929	.00009
Nov-Dec	0-3	50	6028	.00830
	4-7	32	6266	.00511
	8-19	25	11358	.00220
	15-60	151	180198	.00084
	61-120	197	219482	.00090
	121-180	33	41850	.00079
	181-400	47	156391	.00030
Jan-Feb	0-3	27	2912	.00927
	4-7	7	3093	.00226
	8-14	15	6033	.00249
	15-60	107	102569	.00104
	61-120	190	218390	.00087
	121-180	133	207034	.00064
	181-400	35	119154	.00029
Mar-Apr	0-3	16	1557	.01028
	4-7	19	1591	.01194
	8-14	8	2958	.00270
	15-60	40	50319	.00080
	61-120	91	129671	.00070
	121-180	105	221264	.00048
	181-400	68	453284	.00015
May-Jun	0-3	8	610	.01312
	4-7	6	629	.00954
	8-14	3	1141	.00263
	15-60	19	22875	.00083
	61-120	29	61190	.00047
	121-180	36	125116	.00029
	181-400	61	773554	.00008
Jul-Aug	0-3	29	3428	.00846
	4-7	8	2901	.00276
	8-14	11	4227	.00260
	15-60	17	27671	.00061
	61-120	8	27693	.00029
	121-180	18	59167	.00030
	181-400	70	600512	.00012

The incidence of clinical mastitis was tabulated in a 2-way table by month (September-October, November-December, ..., July-August) and stage of lactation (0-3, 4-7, 8-15, 16-60, 61-90, 91-120, 121-180 and 181-400 days after calving) to provide the subclasses shown in Table 1. The reasons for the choice of these levels are discussed later in the paper. At the same time the total number of days that fell within each stage of lactation and monthly period for all cows in the herds were summed to give the total numbers of days that cows were at risk in each subclass. The average probability of a single case occurring on any one day can then be calculated for any subclass as the number of cases divided by the total number of days at risk. These are given in Tables 1 and 2.

Table 2. Numbers of cases of clinical mastitis per day per 100 cows (p_{ij} x 100) by month and stage of lactation.

	Stage of lactation (days)							
Month	0-3	4-7	8-14	15-60	61-120	121-180	181-400	weighted mean
Sep-Oct	.685	.407	.182	.040	.057	.048	.009	.044
Nov-Dec	.830	.511	.220	.084	.090	.079	.030	.086
Jan-Feb	.927	.226	.249	.104	.087	.064	.029	.078
Mar-Apr	1.028	1.194	.270	.080	.070	.048	.015	.040
May-Jun	1.312	.954	.263	.083	.047	.029	.008	.016
Jul-Aug	.846	.276	.260	.061	.029	.030	.012	.022
weighted mean	.810	.461	.218	.073	.077	.050	.013	.0445

Model fitting

Before describing the methods of analysis for log-linear models it may be helpful to sketch the statistical methods used in fitting models to continuous data. The fitting of a model may be regarded as a way of replacing a set of data values y by a set of fitted values derived from the model. The fitted values, denoted by E(y), will not equal the y's exactly and there will be some discrepancy between them. We measure this discrepancy by calculating the sum of squares $\Sigma \{y-E(y)\}^2$, and from it the variance.

Suppose 3 dairy herds are divided to compare two treatments A and B. A model fitted to determine the effect on milk yield might be written:

milk yield = constant
+ effect due to herd
+ effect due to treatment
+ error

This type of model is known as an additive model in that terms describing each effect are added one to another. The lines in this model can be included one line at a time, and, after each step, the discrepancy between observed and fitted values calculated as illustrated in Table 3. We use analysis of variance to assess the reduction in discrepancy (or sums of squares) at each stage. Table 3 shows, on the left, the sequence of models and their discrepancies, and on the right, the analysis of variance table with its sums of squares calculated from the differences between successive discrepancies. As we shall see later, the log-linear method of analysis results in an analysis of deviance table similar in form to that of analysis of variance. The word deviance is defined as the discrepancy between observed and fitted values in the log-linear analysis, which is analogous to the sums of squares in analysis of variance. Differences in discrepancies between successive models are used to form an analysis of deviance table.

Table 3. An illustration of the method of fitting successive terms to the model: milk yield = constant + herd + treatment, showing the relationship between discrepancy and analysis of variance.

			Analysis of variance		
Model	d.f.*	Discrepancy+	Sums of squares	d.f.	Source of variation
Constant	5	1000			
			600	2	Herd ignoring treatment
Constant + herd	3	400			
			300	1	Treatment eliminating herd
Constant + herd + treatment	2	100			
			100	2	Residual

* assuming 3 herds and 2 treatments
\+ calculated as the residual sum of squares between observed and fitted values

Once the final model is determined, which makes the discrepancy as small as possible, standard errors can be calculated for the various parameters, and t tests used to determine the statistical significance of the different parameters in the model.

RESULTS

Table 2 shows that a case of clinical mastitis in our study is more likely to occur earlier than later in lactation. Indeed, the likelihood of a case occurring on the day of calving and up to 3 days afterwards was more that 10 times that between 15 and 120 days of lactation. Similarly, the incidence of clinical mastitis between November and February was twice that in the months of September and October, March and April and four times that in the other 4 months; these differences in seasonal incidence could, however, be influenced

by calving pattern. A proper study of these interrelationships between stage of lactation and season requires a more rigorous statistical analysis. For example, Table 2 indicates an interaction between season, stage of lactation and mastitis incidence in which the days immediately after calving had a higher incidence between March and June (1.2 cases/d/100 cows) than at other times (0.8). However, Table 1 shows a decline in numbers of cows in early lactation from September to June with few cows calving from March onwards.

Counted data are often the result of a Poisson or Poisson-like process, and the statistical analysis of such data has in recent times been based on what is known as a log-linear model. Such a model fitted to the data in Table 1 would be of the form:

log (number of cases) = constant
+ log (number of cow days at risk)
+ effect due to monthly period
+ effect due to stage of lactation
+ error

Mathematically this might be written

$$\log (n_{ij}) = a + \log (N_{ij}) + m_i + s_j + e_{ij} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots \text{(i)}$$

where n_{ij} and N_{ij} are the numbers of cases of mastitis and cow days at risk, respectively, for monthly period i (i = 1,..,6) and stage of lactation j (j = 1,..,7), and where a is a constant, m_i the effect due to month and s_j the effect due to stage of lactation. The term log (N_{ij}) is often referred to as the 'offset'.

The model is written in this logarithmic form to aid statistical analysis. However, if we take the antilogs of each of the terms we can show that equation (i) can also be expressed in the form:

$$E (n_{ij}) = a'm'_i s'_j N_{ij} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \text{(ii)}$$

where log a' = a, log $m'_i = m_i$ and log $s_j' = s_j$

This is the basic model and is different in form from that usually used in classical methods of analysis of variance, as described earlier, for which effects are assumed to be added one to another. The model assumes instead that the number of cases of mastitis is roughly proportional to the number of cow days at risk and that any effects due to month or stage of lactation are multiplied one to another. The idea of an effect behaving in a proportional or multiplicative way seems a reasonable one, especially in an example such as this where there is a considerable range in incidence (Table 2). Thus, for the analysis of disease incidence data a multiplicative model is often more plausible than an additive one.

The random variation in the model is assumed, as a first approximation, to be Poisson. The properties of Poisson distribution are that var(X) = E(X) = p, in other words the mean and variance are the same. Thus the variance can be estimated from the average value of p_{ij} in Table 2, namely 0.000445. The assumption of a Poisson distribution may not be always strictly valid in the sense that the data for analysis may be more widely dispersed than that predicted by the Poisson model. A slightly looser assumption is then made that the error variance = kp where k is known as the heterogeneity factor or index of dispersion. The value of k can be estimated in the analysis.

The mathematical theory of the analysis log-linear models is described by

M^{c}Cullagh and Nelder (1983) and the models can be fitted by statistical packages such as Genstat 5 (1987) or GLIM (1985). The analysis leads to what is known as an analysis of deviance which, as previously indicated, can be thought of as a generalisation of an analysis of variance. The deviance, which is analogous to a residual sum of squares in the analysis of variance, is a measure of discrepancy and is distributed approximately as χ^2. Mean deviance is the deviance divided by the corresponding degrees of freedom. The error mean deviance is a measure of the dispersion index k. Each deviance approximates to a χ^2 distribution and the ratio of mean deviances approximates to an F distribution, the same as that used in analysis of variance.

The interpretation of an analysis of deviance table is best illustrated by example. Before doing so values of N_{ij} in Table 1 can be divided by 100 without loss of generality. This reduces the number of decimal places in p_{ij}, and means that p_{ij} can be considered instead as the number of cases of clinical mastitis per day per 100 cows. Model (i) was fitted by Genstat (1987) to give the analysis of deviance shown in Table 4. The terms for month and stage of lactation represent individual contributions to the total source of variation when eliminating the effect for each other, and so they and the error deviance do not add up to the total. In other words model, (i) has been fitted twice with month and stage of lactation in turn the last term to be added. Respective deviances were then calculated to eliminate the effect due to the other, as illustrated in Table 3.

Table 4. Analysis of deviance for model $n_{ij} = a'm_i's_j'N_{ij}$

Source of variation	d.f.	Deviance	Mean deviance	F	P values
Month	5	121.06	24.21	8.35	<0.001
Stage of lactation	6	1705.26	284.21	98.00	<0.001
Residual	30	86.88	2.90		
Total	41	2449.93			

Statistical tests can be carried out as follows:

1. $\chi^2_{30} = 86.88$ (error deviance). This is highly significant (P<0.001) and implies k>1. In other words there is inter-subclass variation which exceeds that predicted by the Poisson distribution. k = 2.90, the value of the error mean deviance.

2. If the Poisson assumption is valid (in this case it is not), tables of percentage points for the χ^2 distribution can be looked up with $\chi^2_6 = 1705$ (stage of lactation) and $\chi^2_5 = 121$ (month).

3. If the Poisson assumption is invalid (k>1), χ^2 tests are not appropriate. Instead, mean deviances are divided by the residual mean deviance to give $F_{5,30}$ and $F_{6,30}$ values, which can be compared with percentage points in tables for

the F distribution. These are shown in Table 4 as being both significant ($P<0.001$).

We can summarise the conclusions so far as follows: both stage of lactation and month have significant effects on mastitis incidence with the major variation due to stage of lactation; however there is also evidence of inter subclass variability (in other words an interaction between month and stage of lactation).

Estimates and standard errors of the parameters in the log-linear model

$$E(\log(p_{ij})) = E(\log(n_{ij}/N_{ij})) = a + m_i + s_j \quad \text{(from (i))}$$

can also be calculated. Since the number of levels of each parameter is one more than the number of degrees of freedom, 5 and 6 respectively (Table 4), constraints need to be applied to ensure that only 5 or 6 independent parameter levels are estimated. For analysis of variance these constraints are usually written as $\Sigma m_i = 0$ and $\Sigma s_j = 0$. For example, in the earlier illustration involving treatments A and B, treatment means would be calculated as $a + t_1$ and $a + t_2$ in such a way that $t_1 + t_2 = 0$. Genstat and GLIM, however, set $m_1 = 0$ and $s_1 = 0$ and estimate the other levels as deviations from m_1 and s_1 respectively. Thus, in interpreting a Genstat or GLIM analysis, it should be noted that estimates of parameters displayed in the print-out represent deviations from the first level. Standard errors are also given which represent the standard errors of differences from the first level.

Table 5. Parameter estimates in log-linear model $\log p_{ij} = a + m_i + s_j$

Parameter		Estimate	s.e.	t
Constant		-0.494	-	-
Month (m_i)	Sep-Oct	0.000	-	-
	Nov-Dec	0.563	0.130	4.32
	Jan-Feb	0.611	0.136	4.50
	Mar-Apr	0.401	0.147	2.72
	May-Jun	-0.079	0.180	-0.44
	Jul-Aug	0.070	0.175	0.40
Stage of lactation (s_j)	0-3	0.000	-	-
	4-7	-0.574	0.201	-2.86
	8-14	-1.341	0.215	-6.24
	15-60	-2.499	0.149	-16.78
	61-120	-2.531	0.146	-17.29
	121-180	-2.885	0.161	-17.92
	181-400	-4.033	0.163	-24.75

This may become clearer from Table 5 which shows parameter estimates for both month and stage of lactation. Monthly estimates range from 0.401 to 0.611 between November and April. These represent the differences on a log scale from the value in September to October. Corresponding t values are significant for November to February ($P<0.001$) and for March to April ($P<0.05$). Estimates for May to August are practically zero and non-significant. The conclusion, therefore, is that the average incidence of clinical mastitis, adjusted for stage of lactation, is greater throughout winter than summer. Parameter

estimates for stage of lactation become increasingly negative as lactation advances and t values show a significant decline up to 15-60 days and then again after 180 days. The higher incidence of clinical mastitis in early lactation is clear.

The parameter m_i estimates the difference in log means between monthly periods i and 1. Using the dot notation to signify summation this can be written

$$E(\log p_{i.} - \log p_{1.}) = E(\log (p_{i.}/p_{1.}) = m_i$$
$$= \log m_i' \text{ (from (ii))}$$

Taking exponents of both sides the equation becomes

$$E(p_{i.}/p_{1.}) = m'_i$$

Similarly,

$$E(p_{.j}/p_{.1}) = s'_j$$

Thus, by taking exponents (or antilogs) of each of the parameter estimates in Table 5, we obtain estimates of the expected proportional changes on the original scale. Results of these calculations are shown in Table 6 for both month and stage of lactation. Expected proportional changes with respect to the first levels (Sep-Nov, and 0-3 days) are shown in the first column.

Table 6. Comparison of observed and expected incidences of clinical mastitis by month and stage of lactation.

Parameter		Expected* proportion of level 1	Observed+ incidence	Expected× incidence
Month	Sep-Oct	1.000	0.044	0.034
	Nov-Dec	1.756	0.086	0.059
	Jan-Feb	1.843	0.078	0.062
	Mar-Apr	1.493	0.040	0.050
	May-Jun	0.924	0.016	0.031
	Jul-Aug	1.073	0.022	0.036
	Weighted mean	1.320	0.0445	
Stage of lactation	0-3	1.000	0.810	0.856
	4-7	0.563	0.461	0.482
	8-15	0.262	0.218	0.224
	16-66	0.082	0.073	0.070
	61-120	0.080	0.077	0.068
	121-180	0.056	0.050	0.048
	181-400	0.018	0.013	0.015
	Weighted mean	0.0520	0.0445	

* Antilogs of estimates in Table 5.
\+ From weighted means in Table 2.
× The calculation of this column is described in the text.

The averages of these proportional changes, weighted by the numbers of days at risk (1.320 and 0.0520, Table 6), can be shown to be $E(p)/E(p_{1.})$ and $E(p)/E(p_{.1})$ respectively.

It follows that

$$1.320 = 0.0445/E(p_{1.})$$

and $$0.0520 = 0.0445/E(p_{.1})$$

where $E(p) = 0.0445$ from Table 2.

Hence $E(p_{i.}) = 0.034$ and $E(p_{.j}) = 0.856$ (see Table 6)

Expected values for other parameter levels can then be derived as given in the third column of Table 6. This column demonstrates the effect of adjustment for stage of lactation on seasonal differences. The first 3 values in column 2 overestimated the seasonal effect. Indeed, after adjusting for stage of lactation, the expected average incidence in September and October was similar to that between May and July. Average values for winter and summer months calculated from Table 6 were 0.057 and 0.034 respectively, representing an increase in incidence in winter when, cows were housed, of about two thirds. Stage of lactation effects dominated and so there were only slight adjustments to them due to season (Table 6).

Table 7. Analysis of deviance for model $n_{ijk} = a'm_i's_j'k_k'N_{ijk}$

Source of variation	d.f.	Deviance	Mean deviance	P values
Main effects				
Month (M)	5	46.9	9.38	<0.001
Stage of lactation(S)	6	795.3	132.55	<0.001
Herd (H)	11	65.4	5.95	<0.001
Interactions				
M X S	30	41.9	1.40	NS
M X H	55	87.7	1.59	<0.01
S X H	66	138.7	2.10	<0.001
Residual	302	338.8	1.12	
Total	475	1750.5		

As has already been shown there was significant inter-subclass variation. These subclasses are made up of cases of clinical mastitis taken from different herds and so the magnitude of k may be reflecting inter-herd variation. To investigate possible herd interactions the 12 herds which had most numbers of

cases of mastitis during the 12 months (averaging between 35 and 80 cases per 100 cows) were selected and the model extended to include an additional parameter for herd. Extra parameters were also included to describe interactions between stage of lactation and month, between herd stage of lactation and between herd and month. The analysis of deviance is shown in Table 7. The residual mean deviance is now only slightly greater than 1 and so the assumption of a Poisson distributed error is justified. The χ^2 test can therefore be used for determining the significance of main effects and interactions. Table 7 shows a significant herd x stage of lactation interaction, but not one for month x stage of lactation. This suggests that stage of lactation effects occur independently of season. There was also a small herd x month interaction.

DISCUSSION

The analysis of counts has recently given rise to a large literature, mainly based on the idea of the log-linear model. Such models have been used fairly widely in human medicine, but rarely in veterinary epidemiology. Other models such as logistic regression are also used; these are for proportions, say the proportion of cows affected per annum (r/n), which may be assumed to follow a binomial distribution that models the number of successes r out of n trials. The transformation used is log (r/(n-r)); the analytical approach is similar and also leads to an analysis of deviance. In some applications it may not be clear which model is appropriate. In such cases either model would probably lead to the same conclusion, especially if r is small relative to n, and so the log-linear model, having the simpler algebraic expression, might be preferred. Some examples of the use of the logit function have been published by one of the authors (e.g. Rowlands, Lucey and Russell, 1986; Rowlands, Russell and Williams, 1988).

The purpose of the present paper has been to demonstrate application of the log-linear model in the analysis of disease incidence data. The model is based on two concepts, firstly that systematic effects are multiplicative, and secondly that the error distribution is Poisson in nature. Statistical analysis is by analysis of deviance in which the residual mean deviance k measures the degree of dispersion of data beyond the assumption of a true Poisson model.

If $k>1$ then the analysis demonstrates additional inter-subclass variation superimposed on the Poisson distribution. We have seen how subdivision of the month x stage of lactation subclasses (Table 2) into smaller subclasses by herd has removed most of the inter-subclass variation. We can, therefore, assume that the error variation among herd x month x stage of lactation subclasses is Poisson. This may seem rather surprising when there are other known sources of variation that have not been taken into account in the model. The Poisson hypothesis assumes that the probability of a case of clinical mastitis occurring within a particular time span is independent of other cases and that all cows are equally susceptible. However, it is known that mastitis incidence increases with age and that a few cows have a large number of cases in a year (Booth & Rowlands, 1989). Further, mastitis infection may suddenly spread through a herd so that several cases of clinical mastitis develop over a short period of time. The sizes of the subclasses in Table 2, however, are fairly large, covering a period of 2 months and several days of lactation, and this may have had a dampening effect on small spikes in mastitis incidence.

The terms in an analysis of deviance all have approximate χ^2 distributions. These approximations are better for large than small numbers of observations and may be poor when there are several zeros. The analysis of deviance table should be regarded as a screening device for picking out important terms in the

model; whilst significance levels may be quoted, it should be born in mind that the fewer the data the more approximate these levels are. It is well known how a correction factor may be applied to the χ^2 test for a 2 x 2 contingency table with numbers below 5. A similar correction is not available for larger tables but it is generally understood that the occurrence of small numbers becomes less of a problem when the degrees of freedom of χ^2 increase. Nevertheless, the aim should always be to attempt to ensure that subclasses are defined in such a way that numbers are not too small. This has been done in this example. Before preparing Table 2 a preliminary, larger table was first formed in which months were kept separate and stage of lactation was divided into smaller intervals. Taking into account the numbers of observations in each subclass, and also the trends in incidence with month and stage of lactation in this preliminary table, a number of levels were combined to give the subclasses shown in Table 2.

Sometimes the error deviance reduces to a value less than 1 ($k<1$). This means that the data are underdispersed. This is impossible if the Poisson assumption is correct and probably means that too many parameters are being fitted. The appropriate model is the one which reduces the residual deviance to a value of k close to 1, and subsequent addition of further parameters which make $k<1$ should be ignored.

Both Genstat and GLIM fit effects in sequence. Therefore, each term in the analysis of deviance table describes the effect of inclusion of the latest term in the model eliminating the effects of other terms already fitted higher up the table. To determine the analysis of deviance tables shown in Tables 5 and 7, in which each effect was adjusted for each other, Genstat was run several times, each time changing the order in which the model was fitted.

In conclusion, the analyses of deviance show that cows were more susceptible to clinical mastitis both in early lactation and to a lesser extent also when they were housed in winter. The effect of stage of lactation was consistent throughout the year and, on the whole, seasonal patterns of incidence tended to be similar across herds. There was, however, an interaction between herd and stage of lactation. A comparison of the patterns between 2 herds (one showing no effect of stage of lactation on incidence) is given by Rowlands & Booth (1988). This interaction is worthy of further investigation. It may be that different herd patterns may be typical of the pathogens primarily involved as the major source of infection.

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STATISTICAL METHODS IN HUMAN EPIDEMIOLOGY

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The use of statistical methods in human epidemiology has a long history. At the time of the Great Plague, Graunt (1662) introduced the life table, a method for charting life expectancy. Lind (1753) used a controlled experiment on sailors to demonstrate the protective effects of citrus fruit against scurvy. Perhaps most famous of all is the work of Snow (1855), who used survey techniques to trace the source of cholera in the Golden Square area of London. More recent examples are the studies into the relationship between smoking and lung cancer by Doll and Hill (1950 and 1964). From such pioneering exploits the subject of statistical epidemiology, applied to human populations, has evolved. The application of such ideas in veterinary epidemiology seems to be less well developed. This paper will present the study methods that are now widely used in human epidemiology, showing the circumstances for which each method is most suitable. It is hoped that this will serve as a reference for those who can usefully apply these methods in animal populations.

PLANNING AN EPIDEMIOLOGICAL STUDY

Epidemiological investigations may involve the compilation of data for a variety of reasons including:

Background descriptions: to serve as a general background for further, more specific, studies or to describe a problem of current concern. An example is the national morbidity studies carried out by the Royal College of General Practitioners.

Planning: to assist in deciding how to allocate resources or services, for example, the use of information on road traffic accidents to plan the siting of ambulance stations.

Monitoring and evaluation: to keep a check on progress. For example, how has the elective admission (waiting) list size varied from year to year in a given health district?

Investigating causality: to find the cause of a disease or other health problem. For example, are leukaemia cases often associated with the proximity of nuclear power stations?

Testing new methodology: trying out new methods of care or treatment, such as tests of a new drug to treat AIDS victims.

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The reason behind the investigation will normally determine just what data should be collected and just what constitutes real information in the particular context (that is, how the data should be analysed). If, for instance, more cases of AIDS were recorded after the new drug was put into common use, this would not be valid evidence to reject the drug. There could be more new cases or, indeed, a more sensitive method of recording. The treatment would need to be tested using an experiment.

Steps in an epidemiological investigation

These are:

(1) Define the objectives.
(2) Design the study.
(3) Collect, organize and verify the data.
(4) Analyse the data.
(5) Present the results and make recommendations.

This paper will concentrate on step (2). Step (1) and, to some extent, step (3) are predominately the realm of the investigator. The remainder is the subject of many statistical textbooks such as Armitage and Berry (1987) and Woodward and Francis (1988). Thrusfield and Aitken (1985) discuss the use of statistical analysis in veterinary epidemiology.

TYPES OF EPIDEMIOLOGICAL STUDY

1. Secondary data: using data that are already available as raw data or synthesised in a published form. These include routine statistics such as birth and death notifications. For example, Anderson et al. (1985) used the routine records of general practitioners and hospitals to uncover an outbreak of legionnaires disease in Reading.

2. Cross-sectional surveys: a census or (more usually) a sample survey of individuals or institutions at a specific point in time. For example, the Scottish Heart Health Study (Smith et al., 1987) sampled individuals within sampled local government districts in order to describe inter-regional differences in the prevalence of cardiovascular disease and supposed risk factors.

3. Cohort studies: individuals are followed up over time. For example, the Scottish Heart Health Study monitors subsequent deaths from its selected subjects through death registrations. In this way it may be seen whether subjects with a certain risk factor, such as smoking, do indeed suffer higher mortality due to heart disease than do non-smokers.

4. Case-control studies: a group of people with a specified disease (the cases) and a group without (the controls) are compared to look for differences and thus possible causes. For example, after the Reading outbreak all cases of legionnaires disease were compared with a set of non-cases, similar in demographic characteristics, to discover whether those with legionnaires disease (13) had visited any areas of the town centre more frequently than those without (36). From Table 1 it seems that the Butts Centre is the most likely source of the legionella bacteria.

5. Clinical trials: experiments carried out on individuals to assess the efficacy of a treatment, method of care or prevention. For example, one group of patients who have experienced myocardial infarction could be treated with a beta-blocker and another group with a placebo. In order to evaluate the treatment each group would then be followed up to see how many deaths occur. Barber and Lewis (1982) describe a number of such trials.

Table 1. Number of visits to different areas of Reading.

Areas visited	Number of cases (13)	Number of controls (36)
Butts Centre area	12	21
Minister St., Broad St., Chain St. Triangle	9	21
Railway station area	3	9
Forbury Gardens area	3	6
Abbey Sq. area	9	19
South St. area	4	9

6. Community trials: experiments carried out on communities to assess the efficacy of a treatment, for example, health education initiatives to increase the public awareness of 'healthy living', typically as a means of reducing cardiovascular disease, such as the project in North Karelia, Finland (World Health Organisation, 1981).

Each of the six types of study will now be considered in more detail, listing both the advantages and disadvantages of each.

SECONDARY DATA

Advantages

* Cheap, quick, easy and authoritative.

Disadvantages

* may not be complete (e.g. when using hospital records to investigate morbidity, only the most serious cases are found).

* may not be entirely appropriate (e.g. where the definition of in-patient does not include day cases - that is people who do not occupy a bed overnight).

* may not be linked (e.g. two related, but distinct, periods of hospitalization
may not be identified as belonging to the same patient).

* may be out of date.

Secondary data, when they exist, should certainly not be ignored. Often, however, they can provide only a crude description of the epidemiological problem and suggest where more detailed research should be aimed. See Chapter 2 of Woodward and Francis (1988) for a more detailed discussion.

CROSS-SECTIONAL SURVEYS

Advantages

* collect just what is required.

* particularly useful for description.

Disadvantages

* less useful for exploring causality (since there is no control over the factors and no time sequence involved).

* can only accurately measure **prevalence** (number of existing cases) and not **incidence** (number of new cases); this can cause bias (e.g. where death quickly follows 'infection').

* can only accurately measure the current status of risk factors, not those that might have existed in the formative stages of the disease (e.g. people may change their habits as a consequence of contracting the disease).

* to get accurate results for the cross-section a large sample size may be necessary (e.g. when sampling individuals to discover what proportion have the symptoms associated with a disease that is moderately rare).

Sample surveys usually involve generalization from the sample results to results about the overall parent population. Such inferences can be made more precise by using random sampling to reduce bias and using stratification (i.e. sampling within distinct sub-groups) to reduce the variability of the results. Costs may be reduced by sampling clusters rather than individuals, such as chosing only patients registered with a limited number of practitioners rather than patients from all over the country. See Moser and Kalton (1971) for more details.

The restriction of having just one cross-section in time can be removed by repeated surveying. This is sometimes called x **trend analysis** For example, the WHO multi-national project to monitor trends and determinants in cardiovascular disease (MONICA, 1987) encompasses three cross-sectional surveys in each chosen geographical region over a ten year period. Each time the levels of the hypothesised risk factors are measured. Since this does not involve linking individuals between surveys, great difficulties in establishing causality remain.

COHORT (LONGITUDINAL, PROSPECTIVE) STUDIES

Advantages

* give information on sequence of events (necessary for demonstrating causality).

* can study many outcomes.

Disadvantages

* expensive and time consuming.

* not suitable for diseases with a long latency.

* may suffer from study effects (someone may act differently just because he is being studied).

* withdrawals (e.g. migrants) can be a problem.

* can study only one factor.

* exposure to factor may change.

Cohort studies are mainly used to investigate the causal effects on health of having a factor, such as being a heavy drinker, living in a deprived area or being discharged early from hospital. Causal effects of the factor are much more strongly demonstrated if a control group, that is a non-factor group, is used. Hence patients discharged home early after an operation are followed up alongside patients kept in hospital for the usual length of stay. Otherwise bias can occur. For example, observations may be so intensive that episodes of ill-health are found which would not normally be recorded on routine systems. See Mednick and Baert (1981) for examples of cohort studies.

CASE-CONTROL (RETROSPECTIVE) STUDIES

Advantages

* quicker and cheaper than cohort studies.

* can study many factors.

Disadvantages

* do not involve a time sequence.

* may suffer from bias because cases (more interesting!) are researched more thoroughly.

* can study only one outcome.

* cannot estimate risk of getting the outcome (although the relative risk can be approximated for rare diseases).

Case-control studies are more reliable if the controls are chosen so as to be as similar to the cases as possible (e.g. by age and sex) in all ways except the factor of interest. This can be achieved by matching a control, or controls, to each case. Controls would normally be drawn, within matching constraints, by random sampling. See Schlesselman (1982) for more details about case-control studies.

CLINICAL TRIALS

Advantage

* ideal for demonstrating causality (since the investigator controls allocation of treatment and the time sequence is present).

Disadvantages

* may be expensive and time consuming.

* may suffer from study effects.

* withdrawals can be a problem.

* may involve an element of risk, and so are sometimes considered unethical.

As with cohort studies a control group is essential to protect against changes in background conditions. The control group should match the 'active' group as closely as possible to avoid confounding effects. With chronic conditions this may be achieved exactly by the use of a cross-over study.

Allocation of patients to treatment should be made at random and with blindness to avoid bias. Pocock (1983) provides a clear account of the statistical methods used in clinical trials.

COMMUNITY TRIALS

Similar to clinical trials except that there is much less control, and consequently the evidence for causality is weaker.

SUMMARY

There are six basic study methods available to the epidemiologist. Since clinical and community trials essentially involve doing something to a patient or group they are called **intervention** studies; surveys, cohort and case-control studies are called **observational** studies. Another aspect which distinguishes the types of study is how data collection relates to time. This is illustrated by Fig. 1.

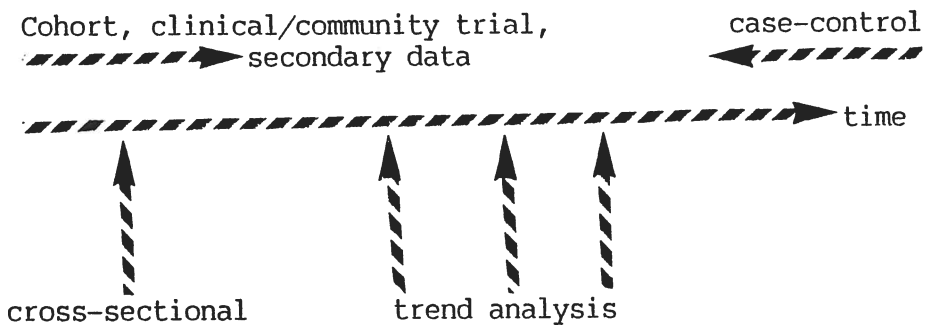

Fig. 1 Study designs related to time.

Clearly the 'correct' study design for any epidemiological problem, in humans or animals, will depend upon the aims of the study. Here a crucial distinction should be made between an objective of description and one of demonstrating causality. Inevitably the chosen design will also depend upon the resources available and the practical constraints imposed by working with living beings.

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ECONOMIC STUDIES

ASSESSING THE ECONOMIC EFFECTS OF MASTITIS AT THE HERD LEVEL USING FARM ACCOUNTS DATA

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Mastitis is widely quoted as being the most important disease affecting milk production in countries with modern intensive dairy sectors. The grounds upon which 'importance' is defined are usually left unspecified, but it can probably be taken to mean the frequency with which mastitis is encountered in dairy herds and the magnitude of the negative effects it creates. It would appear that up to one quarter of all cows may suffer the disease, with some 40 clinical cases per 100 cows (Booth, 1988); subclinical incidence adds significantly to these figures. Estimates of costs associated with mastitis show some variability, but all indicate that its economic impact is not trivial. Blowey (1986) attributed costs of £40 per case, while Wilesmith et al. (1986) estimated £50; Rowlands and Booth (1988) suggest the figure is likely to be even higher. To the individual farmer, this cost could represent a reduction of some 8 per cent in gross margin for each cow which suffers clinical mastitis. Taken together, herd-level estimates like these result in calculations of losses to the dairy sector as a whole of quite impressive magnitude. At the 1988 British Mastitis Conference the figure of £90m loss to the UK dairy sector was reported with the kind of certainty normally reserved for natural constants. The issue is seen with the same apparent clarity in the USA, where according to Lightner et al. (1988) "mastitis is the single most costly disease affecting the dairy industry.... accounting for about 26% of the total disease cost ($186.13 per cow per year)".

All this quoting of figures on the economic cost of mastitis may be interesting, but it is entirely pointless if the effects are unavoidable. However, clinical mastitis is eminently controllable by a mixture of drugs and management practices. The relevance of economic estimates, therefore, is to guide decisions about what sort of avoiding action it is worth taking, and how much. To pursue this question, the effects both of mastitis as a disease and of its control procedures have to be viewed within an explicitly economic - rather than a veterinary or epidemiological - framework.

INFORMATION FOR WHAT PURPOSE?

Much scientific enquiry has been justified on arguments about the intrinsic importance of knowledge and the fundamental curiosity of man. None of this sort of approach has any relevance to economic enquiry, however, which is a strictly pragmatic exercise. Along with all the other applied sciences it is concerned with identifying variables and relationships which best reflect the workings of some particular system, measuring relevant

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values and parameters, and then using that information to manipulate the system so as to achieve specified ends.

Thus there is no purpose in measuring the economic costs of a disease just to find out how 'big' or 'small' they are. Nor are loss estimates of any value unless they are accompanied also by information on (a) the disease control regime, if any, to which they relate, and (b) whether, and to what extent, those losses might be affected by increases and decreases in disease control expenditures. Further, there is no escaping the necessity for this information to reflect as accurately as possible actual or achievable positions, not simply notional situations. It may be impossible to achieve the kind of precision that is sought in engineering calculations, laboratory experimentation or technical science measurement. But that does not permit one to feel satisfied with just broad approximations. The ultimate value of information is to guide action, and wrong information inevitably leads to the wrong decisions being taken; hence it is as necessary to be careful in making economic measurements (or estimates) as in any other field.

To achieve this requires exercising care in two areas. First, we need a clear concept of what is being measured. The concept of 'loss' is a composite of both benefits foregone and additional costs incurred. Without careful definition of these components it is easy either to omit elements in one or other category, or conversely to commit errors of double counting. Second, we require appropriate techniques for measuring the economic quantities and for aggregating them together. This causes us to confront such questions as how to value output losses or additional labour inputs attributable to the presence of disease, and highlights the complex analytical issues in moving from herd-level figures to estimates at the national level.

In the light of this, it is not entirely clear how we should interpret figures which place the economic losses of mastitis at £50 per case or £100 million annually to the dairy sector. In particular, are these losses something that just have to be tolerated, like the negative economic effects of bad weather? Presumably not, in the case of mastitis. We need to know, therefore, how much of the loss is avoidable and at what cost in terms of additional veterinary and other expenditures. The essential quest is for some measure of the 'economically unnecessary loss' so that appropriate action can be taken to eliminate it. That in turn requires a clear definition of the baseline from which losses are measured. Is it zero levels of clinical mastitis, or some previous lower level, or some level technically specified as acceptable and achievable, or simply average levels of some sort? Associated with each of these situations will be entirely different management and disease control regimes, each of which represents a different cost component in the calculated 'loss' figure.

These questions can be posed in the context of either the individual herd or the national dairy herd. To the individual dairy farmer, the relevant information is the various revenue losses and extra expenditures that show up in his bank account; they are referred to properly as the 'financial' costs of the disease, since what they measure is simply the monetary impacts as perceived by that individual. Strictly speaking the term 'economic' costs of the disease should be restricted to the effects on the overall economy. This may require using values other than market prices in order to reflect the real values of output and inputs - for example where overall milk supplies are in surplus or prices are distorted by administrative support, subsidies or taxation. Estimates for the cost of mastitis at the national level will be an aggregation of all the direct effects manifested in the individual

affected herds, plus a diverse array of indirect effects experienced outside the population of dairy farmers. Included here, for example, are losses in sectors beyond the farm gate - because of the reduced suitability of mastitic milk in processing, the extra costs incurred in milk sampling and testing, and other expenditures in public sector programmes designed to control the disease and its effects.

Despite the diversity of the literature on mastitis it is not clear that an unambiguous conceptual definition of the losses, nor an appropriate framework for collecting and analysing relevant information, has been fully established and tested. Consequently, there remains much uncertainty surrounding the true economic effects of a disease which, although complex in bacteriological and physiological terms, is nominally more straightforward economically than many other conditions. Where the literature has turned to the economic aspects it has focussed primarily on simply measuring effects, rather than seeking to identify the treatment strategy for controlling the disease at its most economically acceptable level. In order to pursue this wider objective, it is necessary first to establish an appropriate conceptual basis upon which to assess the economic effects and options.

ESTIMATING ECONOMIC EFFECTS AT THE HERD LEVEL

The economic effects of mastitis are generally summarised in terms of a series of identifiable costs that it gives rise to. Jasper et al. (1982) classify these into the following categories:

A.	decreased milk production	reduced monetary receipts
B.	discarded milk	
C.	reduced sale value of cull cows	
D.	increased expenditure on replacing cows	increased monetary outlays
E.	increased expenditure on drugs	
F.	increased expenditure on veterinary services	
G.	increased labour time.	

The cost components in this list fall into two quite distinct groups. Items A, B and C are losses in the form of reduced revenue compared to a zero disease incidence. By contrast, items D, E, F and G represent costs in the form of increased outlays of resources in response to the occurrence of the disease. The presumption seems to be that if information on each of these items is collected for an individual herd and added up, the resulting figure will be the economic (i.e. financial) loss imposed on that particular farming business (over a year, or for a single case) due to the presence of mastitis. That may or may not be true. A second presumption, which is necessary in deriving estimates at the national level, is that similar information collected from a sample of herds will yield an 'average' loss figure which can be raised by the appropriate proportion to yield an aggregate estimate. That, as we shall see, is almost inevitably not true.

It is not even clear that the estimate derived from data for an individual herd is really a valid measure. This stems from the unspecified baseline implicit in studies that collect information under the above structure.* There is no relevance in a loss figure which uses a zero incidence of mastitis as the baseline unless the disease can be eliminated

*Only Beck and Dodd (1988) seem to have addressed directly this issue.

and the herd then kept free at no further cost. For sure, compared to some ideal world in which there was no mastitis its presence does cause extra expenditures and output losses. But that is rather like saying that, compared to an ideal world of perfect thermal efficiency, there are such-and-such heat losses from a particular home. Because a significant proportion of those losses are quite unavoidable, and so cannot be influenced by any decisions concerning house design or heating policy, information on their magnitude is of no relevance to anything. By the same token, once mastitis is an integral part of the dairy production environment the 'without disease' baseline has no relevance in identifying information to guide decisions. We now need to define some particular 'with mastitis' situation to represent the base from which all measurements relate. Then, as higher costs under categories E-G are incurred (which represent expenditures to control mastitis) one would expect lower losses under categories A-D. The relevant 'costs of mastitis' to the individual herd are then the revenue losses above this base level plus the additional control expenditures that are incurred.

This point can be explored in more detail using the stylised relationship shown in Figure 1. This reflects two general propositions: (a) increasing expenditures on mastitis treatment/control within a given herd (from left to right on the horizontal axis) lead to reduced incidence of the disease and hence lower output losses and (b) the effectiveness of disease control expenditures in lowering output losses progressively declines - i.e. it gets increasingly expensive to achieve successive incremental reductions in

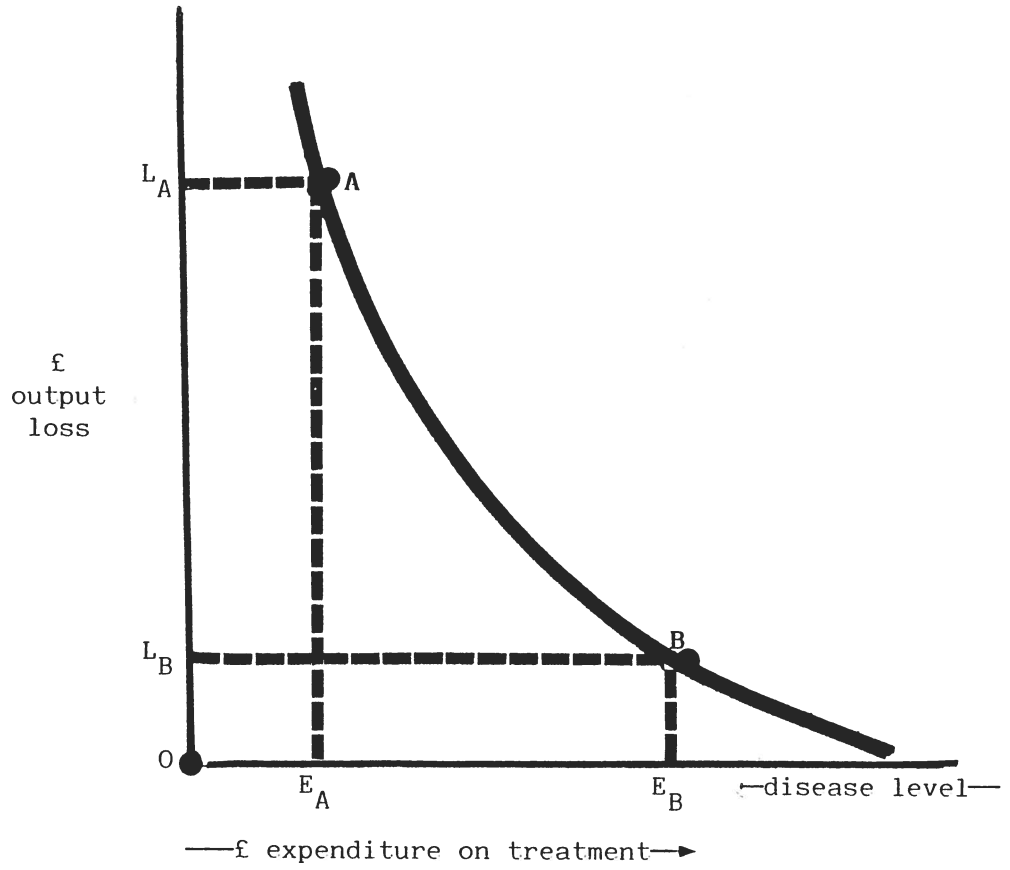

Fig. 1 The general relationship between treatment expenditures and output losses.

disease incidence.* Now, in an ideal world the dairy herd's position would be reflected by point O - no disease losses and no control expenditures because mastitis is gratuitously absent. However, once disease is in the system at some level of threat individual herds will find themselves at some point on the curve, such as at A or B. The economic costs they suffer will be the sum of the components represented on each axis. For example, Herd A spends E_A on mastitis treatment and therefore experiences an incidence level which incurs losses of output measured by L_A. Herd B has higher treatment costs E_B, but suffers markedly lower reductions in output value L_B as a result - and consequently lower losses in total.**

Since both axes of the diagram have identical units - units of money - it follows by simple mathematics that at point C on the curve (now shown in Figure 2) the total loss due to mastitis is the lowest attainable and is measured by $L_C + E_C$, which is equal to L_O. This is the point where the 'economically avoidable loss' referred to earlier is minimised. It is not possible to find a combination of treatment expenditure and associated output loss with a lower total monetary value. At point C the gradient of the curve is exactly (minus) 1. To the left of this point, £1 of treatment expenditure reduces output loss by more than £1; to the right of point C, £1 of treatment yields a saving of less than £1 in output losses. (The student of economics should recognise this point as another manifestation of the standard economic optimum position where the marginal cost equals the marginal gain.) For Herd A, therefore, the relevant economic quantity to measure is $(L_A - L_O)$ rather than L_A; this is its <u>avoidable</u> disease loss.

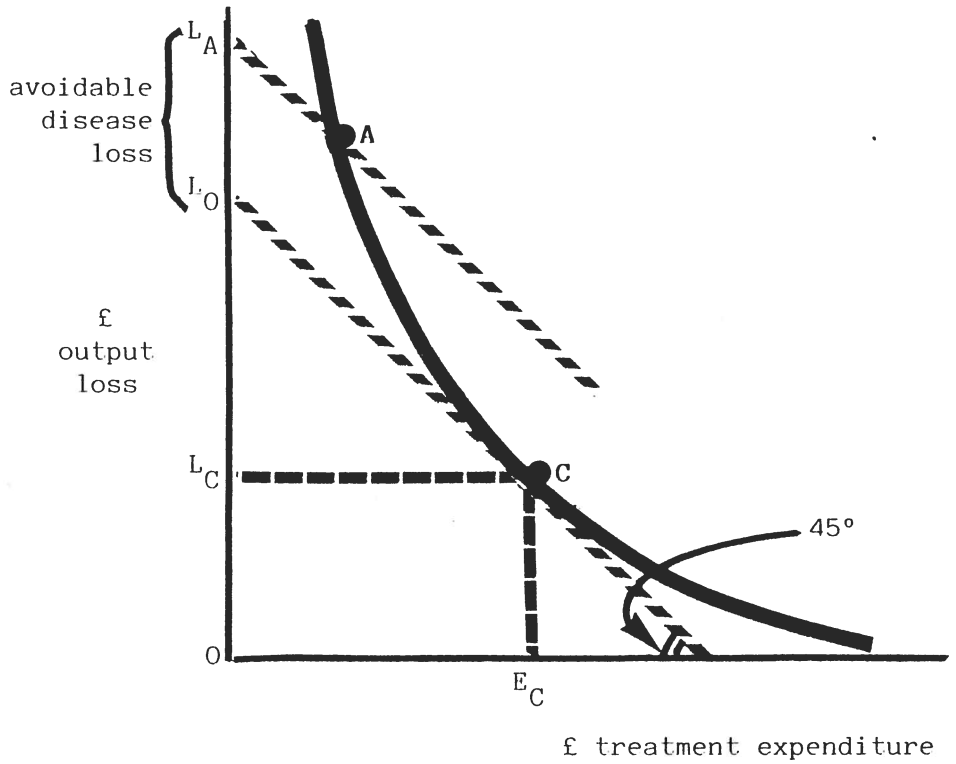

Fig 2. Defining the baseline for measuring the costs of disease.

*This statement reflects the phenomenon of 'diminishing marginal returns' commonly associated with economic input-output relationships.

**That is $(E_B + L_B) < (E_A + L_A)$.

A second major point highlighted by this conceptual framework is the liability to overestimation of loss figures derived by averaging data collected from a sample of herds. Assume the sample consisted of Herd A and Herd B, each having the different mastitis incidence and treatment regimes represented in Figure 3. The simple arithmetic means of the recorded output losses and of treatment expenditures for the two herds will be given by point X; these imply an average output loss of $\bar{L}$ is associated with treatment costs of $\bar{E}$.

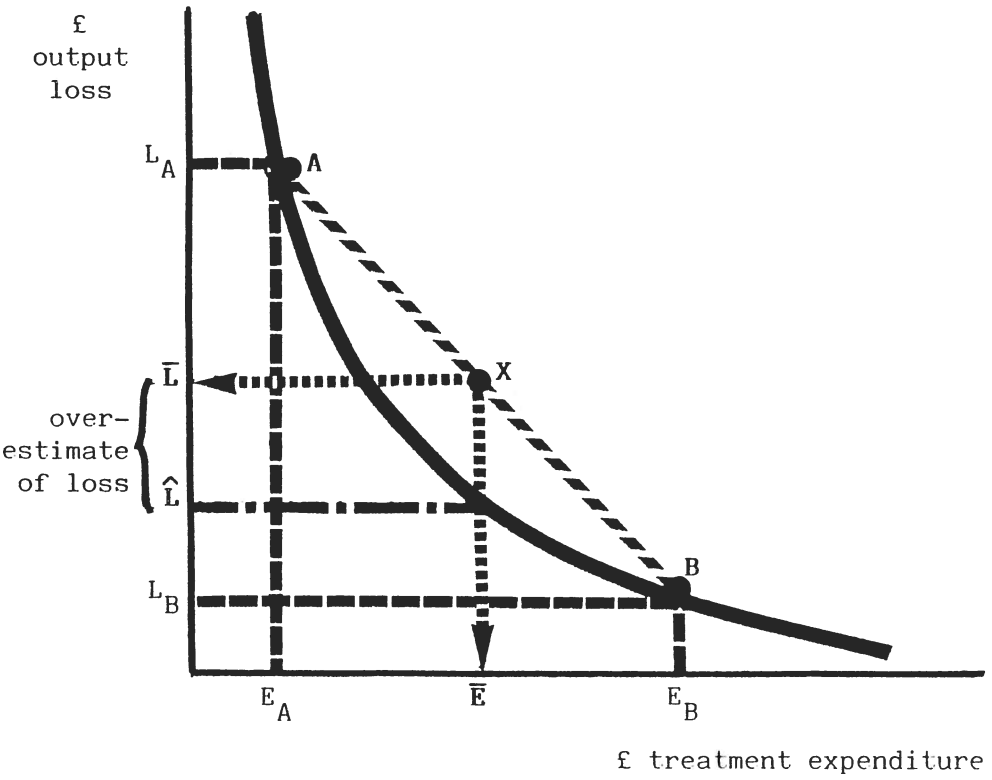

Fig. 3 Sample means lead to overestimates of output losses.

However, the true output loss for a treatment level of $\bar{E}$ is somewhat lower, at $\hat{L}$. This simple diagram highlights the fact that multiplying up to a national level the mean values derived from different samples of herds is liable to inject an upward bias into estimates of the economic costs due to mastitis (in addition to the magnification caused by using the 'zero' baseline). So is mastitis really the most important disease affecting milk production?

The major point emerging from this discussion is not the gross inaccuracies implicit in conventional figures of disease losses. Rather, it makes clear that it is information on the economic relationship in the disease control/output loss complex that is really needed, not point estimates of the 'costs'. The non-linear nature of the relationship shown in the diagrams above is hypothesised on the basis of standard economic principles. Until attempts are made to collect data in a way which allows this relationship to be established empirically there can be little further advance in using economic analysis to guide disease management decisions. Nevertheless, since the economic characteristics of mastitis, and of its control procedures, start first within the individual herd before spreading out to become of interest at the national level, then it is with the herd we must start to assemble information for economic analysis. The primary source of such information is the farm account.

FARM ACCOUNTS INFORMATION

The word 'account' has two distinct meanings which reflect the use of financial information about a farm business. As a verb, 'to account' for revenues and expenditures means to explain fully where they came from or went. This involves setting up a series of boxes (headings) and allocating every relevant financial quantity somewhere into this structure. It is essentially a process of decomposing totals into a pre-specified set of components - or alternatively, constructing those totals from the various constituent components. Such procedures are best labelled 'taxation accounts', since that is their typical use. Their intent is to enable the calculation of some 'net' figure (income, profit, rate of return, etc.) which summarises the overall performance of the business during a given period (usually a year). They occupy the interest of accountants, but have little to offer the economist. Rather like estimates of disease losses, they do not suggest anything about what decisions should be made since their focus is on totals, their orientation is backward looking, and their purpose explanatory.

By contrast, information for economic analysis needs to serve questions of the form "what would be the net effect of doing (a specified) something different?" The interest is not in accounting for the period just passed, but exploring the implications of some new situation that might be created. The focus, therefore, is on marginal quantities (i.e. changes from the current situation), the orientation forward looking, and the purpose exploratory. The relevant concept of 'account' here is as a noun, and it implies a structured array of information. The categories that make up this structure relate to particular cost variables whose values can be altered by management decision, and the revenue variables that will be altered in consequence. Such 'management accounts' thus play an entirely different role in the farm business, and generally emphasise different components of its financial structure.

One major characteristic of management accounts is their distinction of farm production inputs (i.e. costs) into 'fixed' and 'variable' components. Fixed costs, by definition, are those that will not change as a result of the decisions being contemplated. Thus, for example, the annual depreciation of buildings and machinery, the costs of the regular hired and family labour force, the rent of land, interest charges on capital borrowings, and a vast array of 'overheads' will not alter whether a mastitis control programme is undertaken or not, nor with the nature of that control scheme. Consequently, regardless of how they fascinate the accountant or the Inland Revenue, in these circumstances there is no need for any information at all on these 'cost' elements in any estimation of losses due to mastitis or the effects of treatment.

On the other hand 'variable costs' are, by definition, those components whose values will be affected by any management decisions that might be made (or, in the present context, are affected by the presence of disease in the livestock production system). Thus, expenditures for feed, grassland production, veterinary medicines and services, replacement animals etc. are all likely to vary with the disease management regime adopted, as will the revenues received from milk and calf output, cull cows, etc.

These distinctions are crucial if information is to be assembled which accurately reflects, not only the true economic (or financial) effects of disease, but also the relevant costs and benefits associated with alternative disease control strategies. It should be noted that the identification of what is a fixed cost and what a variable cost component is not unique.

Because the distinction is to serve the purposes of a particular decision, the implications of that decision have to be considered fully before it becomes clear which costs and revenue quantities will be affected - and therefore what information is needed. The structure of a typical management account for a dairy farm is portrayed in Figure 4.

HERD FINANCIAL MONITORING

The purpose of establishing a monitoring system is to exercise control so that any unfavourable deviation from planned performance can be identified and appropriate corrective action taken, to the extent that this is within the herd manager's power. It may be necessary to make adjustments to the overall plans, of course, under the influence of changing circumstances. As Kingston (1987) has rightly pointed out in the context of pig herds, the veterinary surgeon has a unique role in management motivation. In most cases he has frequent, if not (yet) regular, access to the production unit and its performance records, and his experience and specialist knowledge enable him to make sound, critical assessments of herd performance and managerial capability. However, since livestock production is in the end a commercial activity, it is the resulting financial progress and performance that has to be the ultimate focus of attention.

Amongst farm enterprises milk production is ideally suited to budgetary control but too few farms have such systems, since in most cases record keeping and accounting procedures tend to have evolved rather than to have been developed systematically to meet the needs of the business. On many farms record keeping is confined still to satisfying legal requirements (producing annual accounts for taxation, VAT returns and employee-related statements). On more progressive farms the availability of data is unlikely to handicap a herd health management programme because more detailed recording systems have usually been established - although there may be a need to improve the use to which the data is put (for monitoring purposes). However, the industry contains many farms, even those occupying the middle ground in efficiency terms, which cannot provide on demand the enterprise level information required.

Effective monitoring involves both selecting the right techniques and obtaining the necessary data; in agriculture it is usually the latter that provides the greater problems (Barnard and Nix, 1979). There are two alternative approaches to the herd monitoring process:

(i) Collect only the minimum of herd-specific data relating to technical aspects of herd performance and management (for example, TBC's, cell counts, calving index) and combine and compare these with broad estimates of the financial implications based on previous studies, commonly accepted standards and guesswork.

(ii) Establish or extend the individual herd monitoring programme to include the routine recording of associated financial measures which can be related directly to the data on technical performance and interpreted accordingly. Just as technically, so financially farms exhibit great variability in performance.

The former (comparative) approach using national or regional standards in farm business management is a long-established feature of the industry. Certainly, the techniques can give a broad indication of the overall position of the individual herd and various sources of both financial and technical

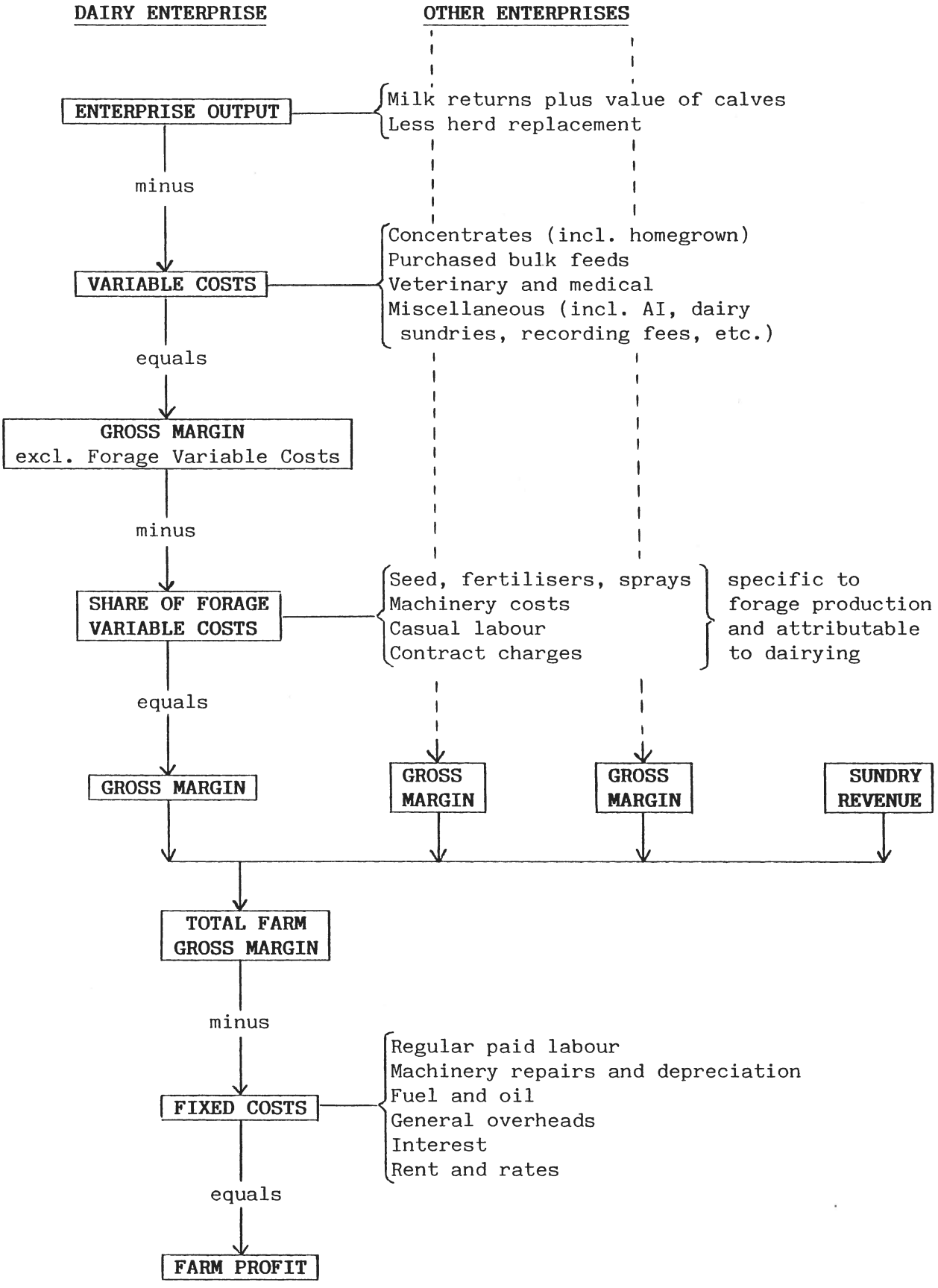

Fig. 4 Typical dairy farm account structured for management purposes.

standards are available. However, such comparative analysis has grave limitations both conceptually and practically. First the data depict average relationships, whereas for economic decision making it is what happens at the margin that is important. Second the differences between herds in both quantity and quality of resources, managerial potential and objectives of farmers, influence herd performance and results so much as to limit the applicability and relevance of inter-herd comparisons. It is argued that the more detailed (and diagnostic) the purposes to which the data are put, the more obvious (and serious) the limitations of a comparative analysis approach and the more speculative (and misleading) the conclusions drawn from the use of average or standard data.

The conclusion must be that, for the individual herd, the establishment of a comprehensive recording and monitoring scheme which includes simple financial as well as technical information is essential if it wishes to assess seriously disease incidence and its implications. It is inconceivable that technical data for the 'average herd' would be used as a basis for its decision-making; equally 'average' financial data must be regarded as inadequate for business monitoring purposes. Beck and Dodd (1988) recognise the unsuitability of reliance in loss estimates on the 'average' herd with 'average' levels of sub-clinical and clinical mastitis. However, while their work provides a useful starting point for initiating a monitoring programme its (necessary) broad assumptions invalidate its application to individual herds for diagnostic and management purposes.

HERD MONITORING: A CASE STUDY

The monitoring exercise reported here was undertaken as part of a project which aimed to evaluate the effects on profitability of 'improved herd management' This was defined at the outset as the adoption of intensive veterinary advice on mastitis control, herd breeding and fertility. This initially broad definition of herd management later became even more diffuse as the results of the monitoring programme caused attention to focus on a series of wider management aspects which required attention if the herd was to move closer to achieving its potential. The implications of this for the results of a single herd case study are considered later.

When monitoring commenced in September 1985 the herd comprised 85 cows with an average yield of 4035 litres. The herd also had an allocated milk quota some 12 per cent above the then current level of production, so there was both scope and ample opportunity to increase total production as well as improve individual cow performance and efficiency. For monitoring purposes milk hygienic quality was considered the most accessible indication of herd health status, although its limitations in this respect were fully acknowledged. A simple monthly recording system was established which required access to the farm's financial accounts. Since there were few detailed records of herd performance relating to the pre-project period it was necessary to analyse financial and other information for up to two years prior to the start date. It is never easy to construct retrospectively a comprehensive financial analysis of a single enterprise, but in this case it did prove possible - albeit with a few informed estimates - to establish a baseline from which future changes in herd performance could be assessed.

From its inception the project was "....aimed at showing how working more closely with the veterinary surgeon to improve herd management can increase efficiency and help offset the effect of milk quotas". Additionally the intention was to improve disease status with respect to mastitis, with the

implicit assumption that such changes would be manifest in the financial performance of the herd. In this way, it was hoped that the project might demonstrate the nature and scale of the likely benefits accruing to a 'typical' dairy farm following the introduction of a herd health programme based on regular fortnightly visits by the veterinary surgeon.

The value to the herd manager of a monitoring system was demonstrated vividly on several occasions throughout the study period and, in particular, several problems associated with feeding were identified. During the first winter a short term problem emerged as a result of feeding fodder beet heavily contaminated with soil, whilst in the second winter silage of indifferent quality depressed technical and financial performance and highlighted the need for improved practices in grassland conservation. At the end of the first year an unplanned and speculative change to the brand of teat cup liners resulted in spectacularly poor Total Bacterial Count (TBC) and Mastitis Cell Count (MCC) results, at 100 thousand bacteria/ml and 1310 thousand cells/ml respectively. The annual effects of this unexpected divergence from the downward trend of monthly results are shown in Figure 5.

It is beyond the scope of this paper to discuss in detail the study results, which are reported elsewhere. However, Table 1 summarises the changes in milk hygienic quality which occurred over the 30 months. Given the poor position from which the farm started it is hardly surprising that the rate of improvement was particularly rapid during the first year, with

Table 1. Milk hygienic quality changes

	Total bacterial count			Mastitis cell count		
	Rolling annual average	Change	% change	Rolling annual average	Change	% change
	'000 bacteria/ml			'000 cells/ml		
August 1985	24.5	-	-	1046	-	-
August 1986[a]	15.0	-9.5	-39	521	-525	-50
August 1987	10.0	-5.0	-33	391	-130	-25
February 1988	10.9	+0.9	+9	342	-49	-13

[a]Adjusted to exclude exceptional recordings in August 1986.

TBC falling 39 per cent and MCC 50 per cent. Further substantial gains occurred during the second year and MCC, in particular, was continuing to improve at an annual rate of about 27 per cent during the last six months of the study. When the project ended in February 1988 the herd's milk hygienic quality for the first time exceeded the national average although, clearly, much further improvement was still possible.

Some indication of the progress made both technically and financially can be gauged from Table 2. Average milk yield rose 24 per cent, concentrate use fell by 50 per cent, whilst margins increased by three quarters over the period. By comparison with regional standards, the herd moved from bottom third to top third level in terms of margin per cow. It is calculated that the overall herd margin (over concentrates and veterinary costs) rose £20411 on an annual basis, of which about two thirds could be attributed to the effect of the project.

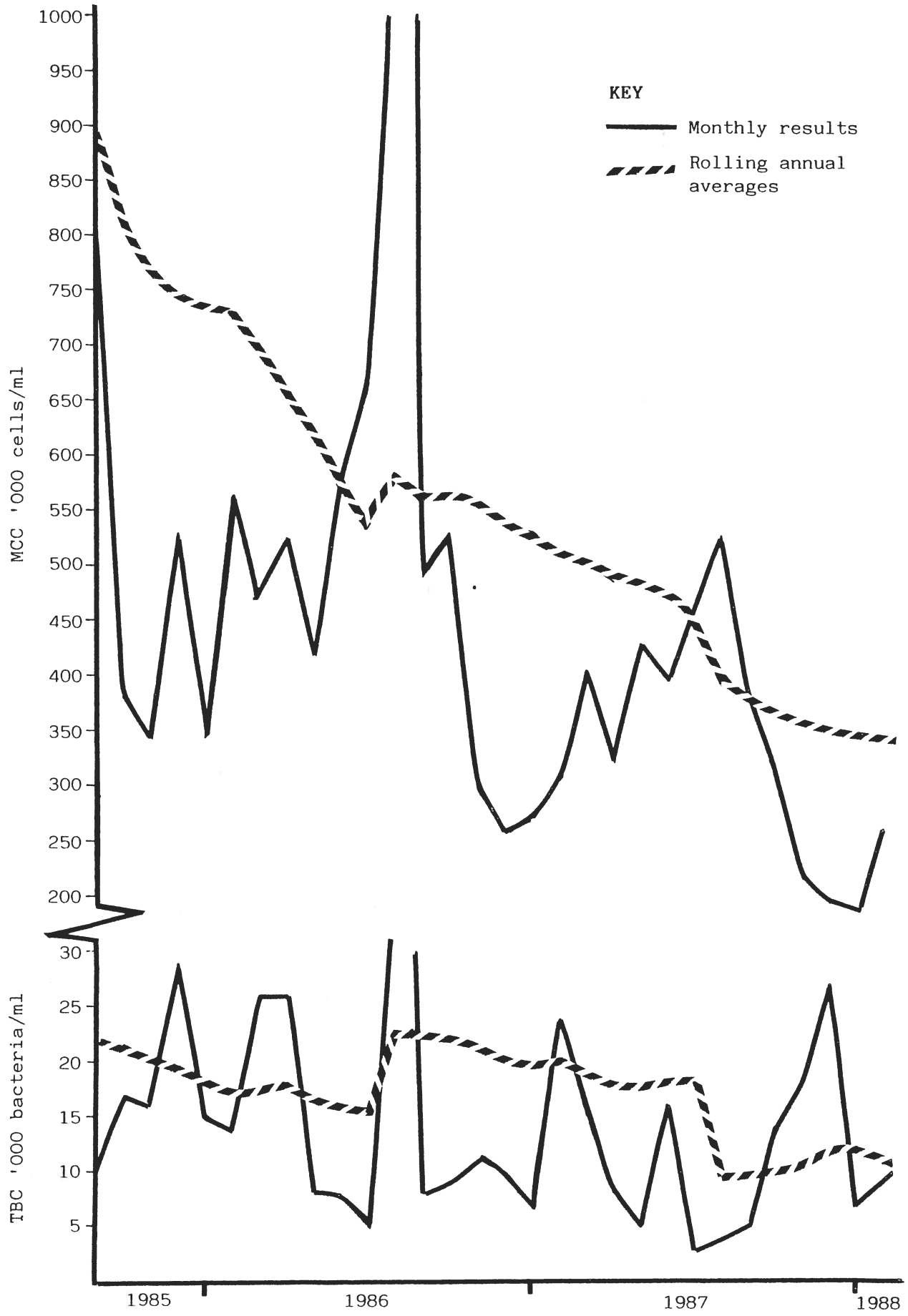

Fig. 5 Milk hygienic quality changes over the project period

Table 2. Changes in performance per cow

	Rolling twelve months to		Change	% change
	August 1985	February 1988		
Milk yield (litres/cow)	4035	5009	+974	+24%
Concentrates (kg/litre)	0.34	0.17	-0.17	-50%
		£ per cow		
Milk sales	597	824	+227	+38%
Margin over concentrates	414	717	+303	+73%
Margin over concentrates and veterinary costs	404	697	+293	+73%

The foregoing review points only to the overall success of the project when judged from the farm business standpoint of financial return and technical productivity. However, although the veterinary input, including advice and pharmacology, formed the core of the project several other changes in the general management of the study herd were made as a result of specialist advice throughout the course of the project.

In the context of the present paper the study provides several useful conclusions. First, in the practical realm of commercial milk production no farmer can afford to make one change in management and then refrain from further changes until the full effects of the first are evident. Any herd level monitoring exercise, however well designed and executed, could be expected to encounter similar problems. Any assessment of the financial, let alone economic, implications of mastitis at herd level will need to grapple with this reality.

Second, the study not only highlighted the potential contribution of the veterinary adviser but also illustrated clearly the integrated nature of the dairy enterprise. Successful herd management requires the effective operation of the complete milk production system rather than merely individual subsectors within that system. The veterinarian's role may be substantial but, nevertheless, is unlikely to be dominant; certainly, the specifically veterinary influence, even with a disease such as mastitis, may take no more than a supporting role within the overall disease management strategy.

Third, on even the least promising of farms it is possible to establish the discipline of a recording and monitoring system providing that, in such cases, regular support can be maintained by the veterinary adviser. At the beginning of the study the farm had few records other than those required by law, but the farmer adapted well to the routine of extracting and recording the essential data. Once accessible, the task of financial analysis and computation is straightforward and, as the case study showed, even quite basic records can be used to monitor progress and identify fundamental problems.

Finally, such a monitoring exercise can result in additional (indirect) costs which, on the case study farm, principally involved labour both manual (with the milking routine) and managerial, and including extra attention given to improving the herd breeding performance. Furthermore there is, of course, the indirect effect of such a project in that, as management emphasis increased, so performance improved simply because of the attention to detail stimulated by the existence of the project but independent of its real components. The value of this 'placebo effect' cannot be separately distinguished within the overall assessment. Clearly, whilst the productivity and efficiency of a dairy herd involves the successful management of a multiplicity of different factors any attempt to attribute directly cause and effect is dependent on the adjustment of only one aspect of managerial policy or practice at a time. In a biological production process, subject to various influences beyond the control of the manager, the conclusion must be that large scale replication is required.

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AN ECONOMIST'S VIEW OF VETERINARY EPIDEMIOLOGY

K.S. HOWE*

This paper is the outcome of reflection on the session 'Teaching Economics in the Veterinary Curriculum' held at the 1988 Conference of the Society for Veterinary Epidemiology and Preventive Medicine (SVEPM). At the time, discussion on the papers which were presented persuaded this author that there is very little purpose at all in teaching economics to students of veterinary epidemiology or, indeed, any other subject in the veterinary curriculum. However, the strength of this new and altogether unexpected conviction was subsequently challenged with some force by a number of veterinary scientists. Evidently, economics is regarded as indisputably useful by veterinarians in both private and public sector occupations. The 'pros and cons' of the debate will not be rehearsed here; the fact that veterinarians find economics useful is justification enough for teaching some elements of the discipline to veterinary students. However, careful consideration of the various arguments led to the conclusion that, as far as possible, economics should not be presented as an adjunct to subjects more conventionally regarded as the components of epidemiology, but as an integral part. For this to be a legitimate and workable possibility, it is essential that economics is found to share common ground with epidemiology. Clearly, links which do not exist cannot be invented, but a way to establish whether there are close relationships is to examine and interpret epidemiology from an economist's point of view.

It might seem at first that concern for integrating economics more closely with epidemiology is mainly practical. It means that students potentially can learn some economics more easily, and so in less time, if economics is seen to be concerned with perceptions about the world which are not substantially different from what is familiar to them from other aspects of epidemiology. However, thinking about the relationships between economics and veterinary epidemiology leads to conclusions which are of more fundamental consequence than mere teaching considerations. Some of the relevant arguments were introduced by the author elsewhere (Howe, 1988), and the present paper is to some extent a development of those earlier ideas.

THE NATURE AND SCOPE OF VETERINARY EPIDEMIOLOGY

Veterinary epidemiology has emerged only quite recently as a self-contained discipline. An important basic text was published by Schwabe et al. in 1977, but at the time when this Society was conceived in the early 1980's there was still much discussion as to the definition of the subject

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and the precise delineation of its boundaries. That earlier volume has since been followed by works from Thrusfield (1986) and Martin et al. (1987), while the more specialised text by Putt et al. (1987) also warrants mention as a source with a particularly strong economics orientation. It is these three most recent contributions which have been used as the main background references for this paper. They show certain striking characteristics which are of particular interest.

First, the presentation of the subject matter of epidemiology in these books is by no means identical although, as is to be expected if epidemiology is in any sense identifiable as a discipline, there are certain similarities. All begin with an outline of basic concepts and principles, but this is characteristically brief, and all discuss disease control. Taken as a whole, Thrusfield might perhaps claim to have produced the more carefully structured and comprehensive of the two more general texts. For example, separate chapters are devoted to determinants of disease, the transmission and maintenance of infection, and the ecology of disease. However, the single most remarkable feature of these basic texts is that overwhelmingly they are concerned with questions of measurement and data. This extends from the interpretation of what are essentially simple ratios (eg prevalence, incidence, morbidity and mortality rates) to basic statistics (eg frequency distribution, measures of association, hypothesis tests), data sources and manipulation (eg surveys, observational studies, field trials), sampling techniques and experimental design, and modelling, where modelling is explicitly taken to imply an exercise in quantification. Serological epidemiology, which is also discussed by Thrusfield, similarly concerns measurement. It is hardly surprising, therefore, to find that the economics of disease is treated as a particular kind of measurement framework in much the same way.

CONCEPTS, DATA AND INFORMATION

It must be stressed forthwith that measurement is obviously an indispensable part of epidemiological studies. Epidemiology has no ultimate purpose unless it deals with questions about the real world, and these require the use of data. However, any system which is intended to generate information about the world logically starts with a set of concepts. The literature on information systems reminds us that

> "Data are the result of measurement or counting, but when one sets out to quantify anything, the first question that must be answered is, "What is to be counted or measured?" If the configuration of data produced is to be internally consistent and have some correspondence with reality, the ideas quantified must bear a meaningful relationship to each other and to the reality of the world being described. In other words, there must be some concept of the reality of the world that is to be measured."
>
> (Bonnen, 1975 page 757)

The importance of concepts cannot be exaggerated* because

> "Reality is nearly infinite in its variation and configuration and must be simplified or categorized if man's mind is to handle it in a

*For further justification see, for example 'On Concepts', Chapter 3 of E.R. Emmet (1968)

> systematic way. Thus, in producing accurate data, one either implicitly or explicitly develops a set of concepts which in some significant degree is capable of portraying and reducing the nearly infinite complexity of the real world in a manner that can be grasped by the human mind. Data are a symbolic representation of those concepts."
>
> (Ibid.)

It is perhaps incumbent on an economist to conclude by observing that

> "If the concepts are not reasonably accurate reflections of that real world, then no amount of sophisticated statistical technique or dollars invested in data will produce useful numbers."
>
> (Ibid.)

The ultimate purpose of obtaining data, which reflect concepts about the nature of reality, is to generate an input for a decision-making process. The input is information, and it comes from the analysis and interpretation of data. It is a common error to suppose that data and information are synonymous, and this they most certainly are not. The relationship between concepts, data, and information are fundamental to understanding the nature of any information system, the elements of which are illustrated in Fig. 1.

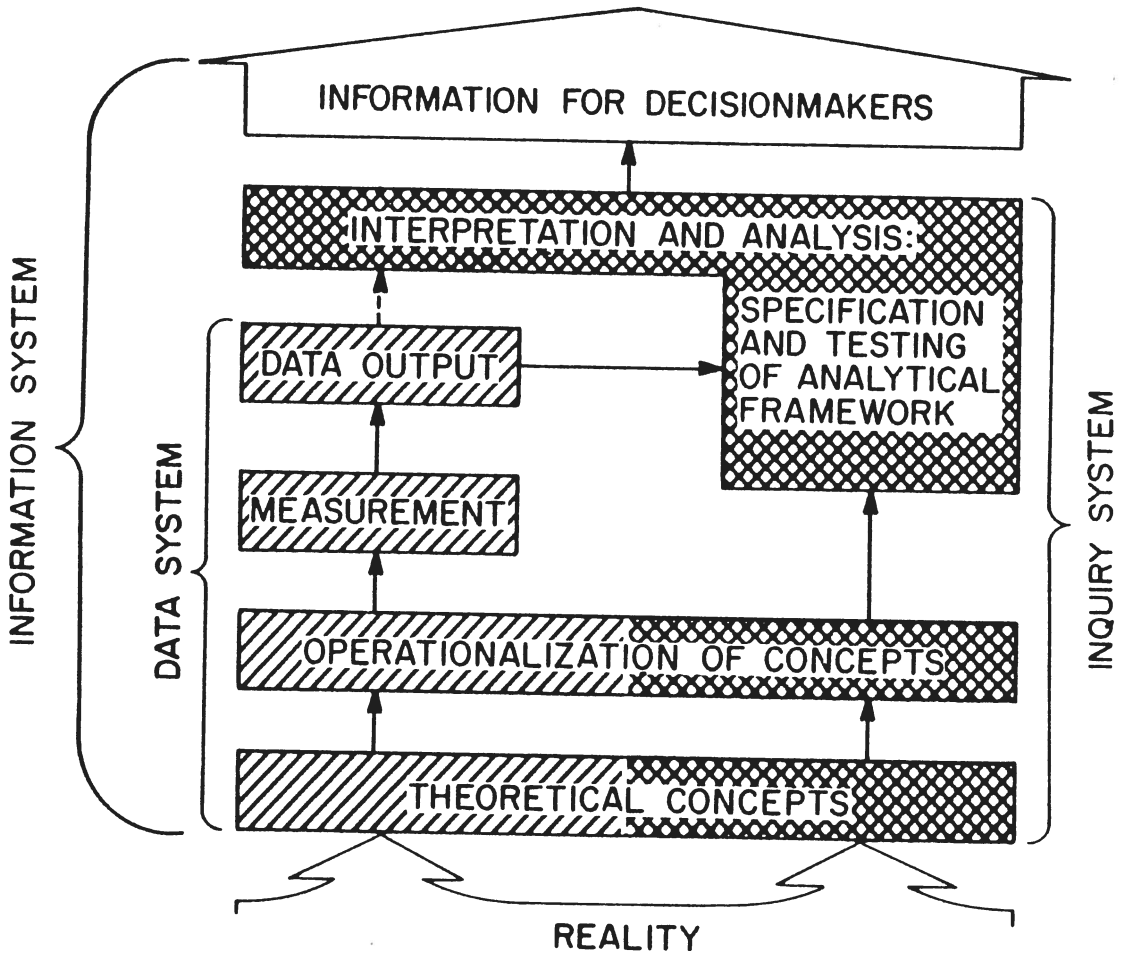

Fig. 1 An agricultural information system (Bonnen, 1975) applicable to epidemiology

While the context is mainly agricultural economic, the discussion in Bonnen (op. cit.) and Riemenschneider and Bonnen (1979), draws on a literature which emphasises that the relevant principles are widely applicable. The significance of this in the present context is that epidemiology is simply one example of an information system. What is disconcerting, at least initially, is to discover that the standard texts on veterinary epidemiology appear to stress data and measurement while they have relatively little to say about concepts.

The scope for closer integration of economics with epidemiology rests, first and formost, on the possibilities for discerning similarities from a conceptual point of view. There is no problem at all in finding common ground as regards the quantitative techniques which are used. Correlation coefficients, least-squares regression, chi-square tests, Markov chains, linear and dynamic programming, survey design, and all the rest, are to be found in any well-trained economist's 'tool-box' just as they might be for an epidemiologist. The important difference seems to be that economics is founded on a very extensive set of theoretical concepts about the nature of the world. The validity of these concepts constantly is tested and the characteristics of their interrelationship explored by applying equally general and rigorous analytical principles to data. But in marked contrast to epidemiology, a foundation text in economics commonly will not have a number in it. Concepts and relationships are presented using geometry and algebra, not to make life difficult for students (though invariably it does) but in emphasis of the point that what is being presented is a widely applicable framework of powerful simplicity. Numerous empirical problems can legitimately be addressed once certain critical ideas and theoretical models are mastered. Only after some minimum degree of competence has been achieved in the essential basics are data and measurement problems confronted. Economics courses in higher education tend to be structured to reflect the requirement that measurement should never be attempted without a thorough grounding in basic theory.

CONCEPTS IN VETERINARY EPIDEMIOLOGY

First impressions can be misleading, and perhaps epidemiology is not mainly about measurement and data. Logically, the best way to find out is to look more closely at what epidemiologists regard as their basic concepts. Each of the most recent texts contains a chapter which deals explicitly with concepts in epidemiology*. As a reminder, and paraphrasing Bonnen's words, the essence of a concept is that it is an idea or general notion which is an abstraction from the particular, and so helps to simplify and classify our observations about the real world. The complexity of the 'seamless whole' which constitutes reality is such that without the simplification and classification of phenomena our ability to interpret reality becomes unmanageable.

Naturally, each of the textbooks discusses concepts in different ways, but the objective here is not to review the texts in themselves. All that matters in the present context is what is included under the heading of concepts. With the one exception where it is introduced beforehand, epidemiology is defined, in so many words, as the study of disease in

*The specific references are to Martin et al. Chapter 1, Putt et al. Chapter 2, and Thrusfield Chapter 3.

populations. Clearly, the population is the fundamental concept in epidemiology which, for operational purposes, may be defined as, say, the population at risk, a herd, or an animal species. A disease determinant is another concept, which can be classified as extrinsic or intrinsic, and relates to hosts and agents. A host may be definitive or intermediate, and is distinguished from a vector which provides mechanical or biological transmission of infectious agents. The environment is also an important concept, although there are different views as to whether agents should be regarded as part of the environment or kept separate (Martin et al. page 11). Interestingly enough, disease itself is a concept which seems never to merit explicit discussion. What is 'disease'? Presumably it is taken for granted by veterinarians that everyone knows or else, as with the proverbial elephant, no one can define it but everybody knows one when they see it.

Of course, other refinements can be made to the classification of the main epidemiological concepts which has been summarised above. In general, however, the picture which emerges is of a set of conceptual entities (population, host, agent, environment) which, by virtue of their association, together contribute to the existence of disease. The population sets the context, and the environment the conditions, within which host and agent interact to produce disease.

All of this is relatively straightforward and reassuring; epidemiology does indeed have a broad conceptual basis which is special to itself. However, the fact remains that the standard texts do tend to overlap their explicit introduction of concepts with an outline of methods and definitions which have more to do with measurement*. For example, they variously introduce endemic, epidemic, and sporadic occurrence which are strictly quantitative statements about the frequency of disease. Infectivity, virulence and pathogenicity are other measures. However, perhaps most revealing is the definition by Martin et al. of epidemiology as the study of the frequency, distribution, and determinants of health and disease in populations. The references to frequency and distribution make explicit that epidemiology is to do with measurement. Also, the authors go on to note that to some people epidemiology is merely a set of methods, a viewpoint which tends to be reflected in the structure of their own text. A further sense that concepts are confused with other things is reinforced when the authors quote the "four principles or concepts about disease" of MacMahon and Pugh (1970). Here, concept is regarded as synonymous with principle, which it is not. In contrast to a concept, a principle in scientific discourse is a general theorem or 'law' about behaviour. In the context of Figure 1, principles are conjoined with data in specifying and testing the analytical framework to investigate whether the set of general concepts and principles are capable of leading to predictions consistent with particular observations about behaviour in the real world.

Discussion of epidemiological concepts in the texts also extends to such matters as the meaning of the terms 'variable', 'causation', and 'statistical association'. Of course, none of these is peculiar to epidemiology. It is true that apparently they are most applicable in the context of disciplines, such as epidemiology and economics, concerned with relationships which are

*It is worth stressing in the context of measurement, ie obtaining **quantities**, that as Emmet (op. cit. p74) points out, a concept stands for "an abstraction, a **quality**, something that cannot be pointed to and thus defined ostensively" (emphasis added).

inherently quantifiable. However, the basic logic is common to all analytical disciplines, inherently quantitative or not. For example, a historian must be as aware of the dangers of confusing causation with correlation as any epidemiologist.

A conclusion to be drawn from the foregoing is that there is, as yet, some uncertainty as to what distinguishes epidemiology from other disciplines and defines its own unique conceptual contribution. Perhaps this partly explains the fusion in the standard texts of discussion about truly conceptual matters and questions of investigative procedure and measurement. Yet it would be entirely misleading to imply that veterinary epidemiologists are unaware of the uncertainties regarding the novel contribution of the discipline. In asking the question "is epidemiology a science?", Thrusfield (op. cit. pp 17-19) gives a useful summary of perceptions about the nature and scope of the discipline. However, having set out here to examine the relationships between epidemiology and economics, the conclusion that epidemiology is less sure of its identity than economics is unhelpful. For all that, it turns out that even just consideration of the most basic concept in veterinary epidemiology, that of the population, is instructive when analysed from an economist's point of view.

ECONOMICS AND THE POPULATION CONCEPT

Epidemiology is the study of disease in animals not as individuals, but when they occur in populations. Examples of populations include all animals in a pen, a herd or flock on a farm, in a given locality, or nationally. Always, the common characteristic of a population is that it is an aggregate of individuals. In mathematical terms, it is all the elements in a set, and these elements may in turn be grouped into any number of subsets. A significant observation about the nature of subsets which are important in studying animal populations is brought out very effectively by Martin et al. They draw attention to the fact that populations are composed of a number of levels of **organization.**

> "For example, the levels of organization from smallest to largest may be conceptualized in the following manner: cells of similar structure or function form organs, organs form body systems, and individuals are composed of body systems. Litters, pens, or herds are composed of a number of individuals; a collection of herds in the swine or dairy industry. Each higher level of organization has characteristics beyond those of the lower levels. Individuals have more properties or characteristics than the sum of all the body systems; likewise, herds of animals have more properties than the individuals that compose them."
>
> (Martin et al. op. cit. page 6)

What is an economist to make of all this? First, animal populations are conceptualized as a hierarchy of systems, in which each level represents a higher level of organizational complexity than the one before. Although the context is different, there are interesting parallels here with the implications of Thrusfield's brief discussion of the relationship between epidemiology and other diagnostic disciplines (op. cit. page 18). The notion of a 'hierarchy is systems' is potentially a fruitful one to explore more generally in attempting to gain a more precise image of the scope of epidemiology. For present purposes, however, attention is confined to assessing the extent to which economic concepts map into the organizational hierarchy identified by Martin et al. This in itself is consistent with a

systems approach, because the aim is to discover in what areas economic considerations cannot be excluded if the characteristics of an animal population 'system' are to be properly understood for the purposes of epidemiological analysis. In the jargon, it could be said that this is an attempt to specify the limits which define 'organizational autonomy'*.

There is no doubt that the levels of organization below that of an individual animal - the cells, organs, and body systems - are of no intrinsic interest to economists. For that matter, neither are litters or pens of animals, except where these entities happen to be synonymous with a herd or flock. Herds and flocks are certainly of economic concern, and so is any aggregate of these which constitutes a larger animal industry. A clue to the reason for this is contained in the quotation from Martin et al. Note that higher (more aggregated) levels of organization are said to have properties which exceed the sum of those contained in the lower (less aggregated) levels of organization. Why this is so for, say, the relationship between cells and organs, is something for biological scientists to answer. But for individual herds and the larger animal industry, one reason for greater organizational complexity is the additional influence of human intervention. Animals are grouped into herds, and individual herds into a larger animal industry, because people (farmers, to be specific) choose how many individual animals are to be aggregated into single units. Their purpose in doing so is to obtain the products of those animals (which may at some time include the animals themselves) which have economic **value** because other people want those products for consumption. Not all entities from animals are 'products' of economic value. For example, people have no use for the cells and body systems of cattle as such**, but they do consume meat and milk. It is for this reason that meat, milk, and other animal products have prices. They are the entities to which people attach value, and it is these which are all that matter to an economist***. Dissimilar products have different prices because people attach different relative valuations to them. The greater the valuation of a given product, the higher the price and, other things being equal, the greater the incentive for a farmer to attempt to increase production. However, a beef cattle producer, shall we say, will know that he can keep only limited additional numbers of animals even if beef prices are sufficiently attractive for him to wish for more. Forage acreage may be limited, for example, as well as his managerial ability to cope with additional cattle numbers. These technical constraints are mirrored in changing costs of production, and it is common in economics to make reference to, say, the optimum size of a cattle enterprise, something which reflects the technical conditions of production but is defined with regard to the behaviour of costs.

In their observations about levels of organization in animal populations, Martin et. al. do not consider the factors which influence how lower levels of organization are transformed into higher levels. Sometimes the determinants will be predominantly biological, as with cells and organs, and sometimes economic, such as how many individual animals are kept in a typical

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*See Dent and Blackie, 1979, pp 4-5, von Bertalanffy (1962), and Ackoff (1971) for further background. These last two papers are reprinted in Beishon and Peters (1976).

**It is always possible to point out exceptions which confirm the general rule!

***In practice, not all objects of value have prices, but that need not detain us here.

herd. Remembering the context in which these issues are being discussed, it follows that both biology and economics are indispensable for fully understanding all of the processes by which simple animal cells at one extreme eventually become transformed and structured into a complex animal industry at the other. Moreover, both disciplines are essential for comprehending the origins, pathways, and consequences of disease, a malevolent influence which impedes efficiency at various points in the organizational hierarchy*. In brief, both biological sciences and economics are indispensable for understanding the different levels of organization discernible in animal populations. It follows that both disciplines have an intrinsic part to play in analysing the effects of disease in those populations; in other words, both economics and biology are indispensable to veterinary epidemiology.

SOME FURTHER OBSERVATIONS

It has been said that animals are grouped into units as an outcome of the exercise of human choice aimed at the production of commodities of economic value. Yet this is only a partial explanation of a more complex network of organizational entities concerning animal populations which are of economic significance, and these are discussed in relation to Fig. 2.

Economics distinguishes between the technical unit (an individual animal), the plant (a herd or flock), the economic unit** (a farm-firm), the household, and the environment. A firm or a plant comprises an ordered set of technical units devoted to production, selected and combined according to economic choice for reasons which have been described. In contrast, the household is a consumption unit while the environment, by definition, represents all those factors which are not susceptible to control. It is the firm and the household which require additional comment. The distinguishing feature of a firm is the presence of an 'entrepreneur', the person (or sometimes a board of directors) who makes decisions about what to produce, how much to produce, by what methods, and using which resources. The beef cattle farmer in the example above is one such example of an entrepreneur. In some circumstances, such as on a specialist pig or dairy farm, what happens in relation to the herd is effectively the same as what happens to the farm-firm, but in mixed farming this is not necessarily so. For example, a disease outbreak in livestock may have implications for resource use and efficiency in a farmer's arable crop production. Thus in asking questions about the consequences of disease in animal populations, sometimes it may be necessary to look beyond the direct economic effects on livestock production itself. Furthermore, when it occurs in any economic unit such as a herd, farm-firm or larger animal industry, animal disease is important not primarily for its impact on animals but on the human population affected, including consumers who may suffer in an economic rather than a medical sense.

A household is an entity regarded in economics as conceptually distinct from the production unit, or firm. In farming, firm-household interrelationships are frequently of considerable economic importance, but

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*The concept of a physical transformation process also has a place in this particular context (see Howe, 1988).

**Note that the term 'economic unit' is used in a less specific sense later in the text.

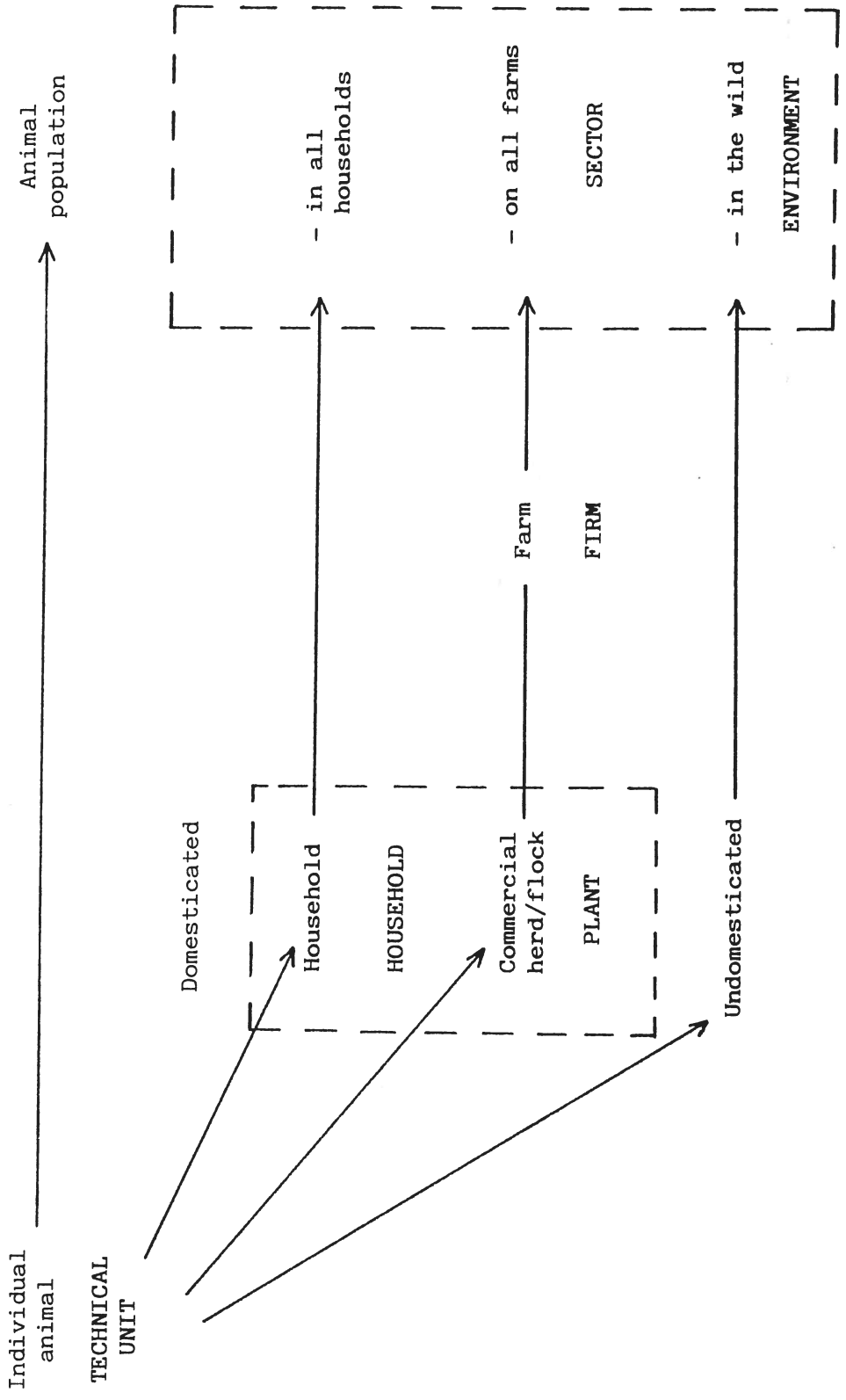

Fig. 2 The economic structure of animal populations

the distinction between production and consumption has to be retained for analytical purposes. Outside of farming and similar family-based economic activity, households are exclusively consumption units. In that capacity they 'consume' not only the products of farm livestock, but also the benefits they obtain from ownership of companion animals. It almost goes without saying, therefore, that the concept of a population also extends to groups of households which contain animals kept as pets. Again, it is recognised that the organizational complexity of animal populations is inextricably bound up with economic units. For many practical purposes, epidemiology functions within a framework which is essentially economic.

Finally, it is not without importance to recall that many animal species in the wild naturally associate in groups. Those that do so belong, conceptually, to the environment. Here they may act as reservoirs of infection which impinge on those animal populations which are structured by human intervention for economic ends. A case in point is the role of badgers in transmitting bovine tuberculosis to domesticated cattle in the UK. Efforts made to restrict infection by the control of badger populations represent an attempt to remove badgers from the environment and bring them, in conceptual terms, into the autonomous system which is controllable by human intervention and is influenced by the disease.

SUMMARY AND CONCLUSIONS

This paper started out as a response to the need to find more effective ways to integrate economics with the teaching of epidemiology. That deceptively simple task has led to a review of the scope and conceptual foundations of epidemiology, to an outline of information systems as a prelude to a general discussion of concepts, some reflections on the population as the fundamental concept of epidemiology, a return to systems but from a different perspective and, finally, to consideration of the relationship between economic and animal populations. Undoubtedly it will be necessary to return to a number of the areas which have been covered for more thorough exploration. However, one conviction which has grown with reflection on the issues raised is that the originators of SVEPM showed great wisdom when it was decided to exclude the word 'economics' from the Society's name. Economics is surely not a supplement to, but an intrinsic part of, the discipline of veterinary epidemiology.

It might be thought that all such matters are empty of any real importance, and that getting on with 'doing veterinary epidemiology' is what is useful, not wasting time and effort exploring abstract ideas. An answer to that point of view is contained in the arguments which have been presented in favour of clarifying concepts before becoming entangled with data - without concepts, there is no way of knowing that measurement makes sense. Since writing the greater part of this paper, two quotations have come to hand which support the contention that this paper has dealt with issues which needed to be addressed. Both come from contributors to the International Symposia on Veterinary Epidemiology and Economics, the first from Roger Morris in the opening paper in 1982, and the second quoted by Hans Riemann in his synoptic review at the close in 1988.

> "Finally we need to raise the quality of educational efforts with undergraduate students and professional personnel. Veterinary epidemiology and economics are areas of the curriculum which are exceptionally difficult to teach well, because the concepts and approaches are different in nature from other subjects, and students

> find it troublesome to adjust to them. I am convinced that the use of case studies is the best single way of overcoming the problem".
>
> (R.S. Morris, 1983, p12)

> "I have found less and less evidence of scientific creativity and more and more striking deficits in the understanding of biology and the other sciences that relate closely to epidemiology. The literature of epidemiology is becoming an archive of the results of information derived from mechanical application of multivariate analysis. Investigators are more interested in the mechanics of data analysis than in the substance of the issues being addressed".
>
> (Petitti, 1988)

It is possible to agree with Roger Morris that case studies are a useful aid in teaching because they 'bring alive' for students what otherwise might seem to be dull abstractions. But the danger is that each is by definition a special case, and students may find themselves in the situation with any subject which places excessive reliance on case studies that they view it as simply a collection of special cases. The power of any science lies with its ability to abstract that which is generally applicable from examples of the particular. To repeat the crucial point, without a basic foundation of concepts and principles, it cannot be known that what is being measured makes sense, and therefore that what purports to be information is not in fact misinformation. Against that background, Petitti's observations need no further comment. In their book, Martin et al. devote the eighth of twelve chapters to 'Theoretical Epidemiology; Systems Analysis and Modelling'. It happens, of course, to be mainly about quantitative techniques. Perhaps epidemiology will have come of age when an entire textbook is devoted to theoretical epidemiology - and like a textbook of theoretical economics, there isn't a number in it.

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PIG EPIDEMIOLOGY

EPIDEMIOLOGY AND CONTROL OF CLASSICAL SWINE FEVER

S. EDWARDS*

Hog cholera was first recognised in Ohio, USA in 1833. It was only later in the last century that a disease in Europe termed "swine fever" was recognised to be the same entity. The European nomenclature has in recent years acquired the prefix "classical" to distinguish it from African swine fever, although, as Liess (1981) pointed out, by no means all outbreaks follow the 'classical' picture of an acute febrile haemorrhagic syndrome with a high mortality. Historical precedent was followed in naming the causal agent officially as hog cholera virus (HCV) (Fenner, 1976). Classical swine fever (CSF) is still of major concern for global animal health. It has been eradicated from a number of countries which practise intensive pig production (including the British Isles, the Scandinavian countries, USA, Canada and Australasia). It is not a problem in predominantly Moslem countries, where few pigs are kept. It is still a problem in most countries in South America and in much of Asia. In continental Europe a major epizootic started in 1981-2, peaked in 1984, and extended briefly in 1986 into Britain (which had remained free for the previous 15 years). A further isolated case in 1987 did not spread, and we retain our officially swine fever free status.

PATTERNS OF SPREAD

The epidemiology of CSF has been fully described and reviewed by Terpstra (1988). Accordingly the present paper seeks only to highlight the major features and to relate these to the control measures in force as we approach the implementation of the European Community (EC) internal market at the end of 1992. In a study of the epidemiology and economics of swine fever in Europe, Ellis et al. (1977) found evidence for a 3-4 year periodicity of epizootics, which was related to the fluctuating fortunes of the pig industry and positively correlated with pig meat prices. On top of this there was a seasonal variation, with peaks of swine fever incidence in spring and autumn. Geographically, it was possible to identify certain high-risk areas in Belgium, France, Italy, Netherlands and West Germany. These coincided with areas with high pig population densities and large average pig herd sizes. As these areas also had a high proportion of breeding herds, it was concluded that they constituted enzootic foci of swine fever virus infection, from which epizootic flare-ups would occur when other factors favoured the spread of the virus.

From studies of the sources of infection in swine fever outbreaks, it is clear that the major factors responsible for spread of the virus are movements of live infected pigs, mechanical transmission on vehicles or personnel, and

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the feeding of contaminated waste food products. This was well illustrated by the series of 10 outbreaks of CSF in England in 1986 (Williams & Matthews, 1988) in which the three primary cases arose from the feeding of virus-contaminated waste foods to the pigs, in one case as household scraps (a procedure no longer permitted), in the second through unlicensed feeding of swill and failure to process it, and the third through inadvertent contamination of cooked swill by unprocessed material at a licensed premises. One of these primary outbreaks went unrecognised and was only identified through subsequent tracings. Infected pigs were sold through a market and led to a series of secondary outbreaks in which infection was attributed variously to (a) movement of infected pigs onto the farm (b) direct or indirect contact with the infected pigs at the market (c) contact by carriage on the same vehicle as the infected pigs (d) mechanical transmission at market (probably on boots). It is important to note that, although acutely affected pigs are obviously sick and are unlikely to be sold on or sent to market, infected pigs in the prodromal phase of the disease are potent shedders of the virus (Wood et al.,1988). Any pigs which do not die from the acute disease may also continue to carry and shed the virus for some time after clinical recovery.

A further complication which arises once the infection becomes established in a breeding population of pigs is the "carrier sow" syndrome (Huck & Aston, 1964), in which infection crosses the placenta and infects the litter, with a variety of consequences dependent on the gestational stage at infection. Effects seen may include embryonic death, mummification, still-births, weak livebirths, congenital defects (including neurological tremors), or apparently normal but persistently infected offspring (Liess, 1984). The latter are immunotolerant to the virus, develop no antibody response, and shed the virus throughout life, although most of them succumb to a progressive fatal illness within a year of birth (Van Oirschot, 1988). These persistently infected piglets are an important means by which infection can spread from infected breeding herds to fattening units. Some strains of HCV can also show chronic persistence following post natal infection of young pigs (Baker & Sheffy, 1960).

PRINCIPLES OF CONTROL

1. Recognition

In CSF-free countries in particular, a continuing publicity campaign is essential to maintain awareness of the disease among veterinarians and pig farmers. CSF should always be considered as a differential diagnosis for any acute febrile haemorrhagic syndrome in pigs. If swine fever is suspected, confirmation can only be given by specific laboratory tests. Tests must also be carried out for African swine fever, which is clinically indistinguishable from CSF although caused by a quite separate virus. Laboratory techniques are continually being improved and are unlikely to cause any problems in diagnosis provided that appropriate samples, in good condition, are submitted for examination (Harkness, 1985).

Not all strains of HCV cause the classical severe acute haemorrhagic syndrome as described in the textbooks. There is as yet no laboratory method of distinguishing high and low virulence strains. The picture is further complicated by considerable variation in the individual responses of pigs inoculated with any one strain. Indeed there was a certain variability in clinical expression among the 1986 outbreaks in England. Mild forms of CSF

are a major concern for controlling authorities, as the disease could go unsuspected for a considerable time. The clinical signs of low virulence strains seen in Europe have mainly been of a non-specific type of reproductive failure (Van Oirschot, 1988), which can easily be put down to other, more commonplace, causes.

2. Movement of live pigs

It is highly probable that, once swine fever is diagnosed in a herd, there will already have been movements of potentially infected animals off the premises. The ability to rapidly and accurately trace such movements is essential to prevent the establishment of further foci of infection. In England in 1986 a number of infected herds were identified through such tracings, and indeed it was by tracing back that the probable primary source of infected stock coming into the market was identified. The difficulty of carrying out such detailed tracing, combined with the lack of herd identifying marks on pigs, has been an important factor limiting the elimination of swine fever in some countries (Terpstra, 1988).

3. Waste food feeding

Pig movements are the main route of virus spread in infected countries and CSF-free countries such as UK maintain a strict control on import of live pigs. Although we do not import fresh pork from CSF-infected areas, it is known that the virus can survive many curing processes and it was concluded that the recent outbreaks originated from imported processed pig meat products (Williams & Matthews, 1988). The complexities of the meat trade did not permit exact identification of the source. Proper cooking of waste food fed to pigs and other animals has disease control benefits quite apart from swine fever, but it is essential to ensure that the regulations are strictly adhered to. Publicity material should be aimed at pig farmers so that they understand the dangers, not only of industrial scale waste food feeding but also the casual disposal to pigs of household scraps.

4. Intervention

Four levels of swine fever control can be identified:

Uncontrolled enzootic infection: Unrestricted vaccination is practised according to the requirements of individual herds.

Controlled vaccination: A number of European countries have employed compulsory vaccination of all pigs, or of nucleus breeding herds, in a defined infected area with the aim of reducing the weight of infection as a preliminary to a stamping out policy.

Stamping out: Vaccination is prohibited and maximum efforts are expended to identify and remove all foci of infection. All swill fed to pigs must be properly cooked.

Maintain freedom from CSF: Rigorous control of live pig imports must be maintained, together with import controls on potentially infected animal products and continued regulation of waste food feeding. Early recognition of outbreaks must be the aim, together with facilities for the accurate tracing of routes of spread in the event of an outbreak, and regulations to control pig movements in infected areas.

CONTROL OF CLASSICAL SWINE FEVER IN THE EUROPEAN COMMUNITY

Ellis et al. (1977) carried out an economic appraisal of three control policies for the EC: I. Maintaining the status quo, with a variety of national control policies. II. Permitting unrestricted intra-community trade in pigs, with the concomitant assumption that generalised vaccination would be required for the foreseeable future. III. An agreed community policy to eradicate CSF, with financial support from the community budget. Even on a pessimistic prediction for swine fever incidence, the third option produced the lowest economic losses over a 6 year period, with further savings to be made in subsequent years. An earlier analysis of the benefits of swine fever eradication in Britain (Ellis,1972) showed a net gain to the pig industry of between £20 million and £37.5 million from 1963-1975.

EC legislation was subsequently enacted, beginning in 1980 with Directive 80/217 introducing Community measures for the control of CSF. Details of the relevant legislation, and progress to date, are given by Bendixen (1988). The member states which could not be declared officially CSF-free were required to produce a five-year plan based on these key activities:
(a) systematic slaughter of all pigs in infected herds
(b) epidemiological investigations to identify sources of infection
(c) cessation of routine vaccination within two years.

The avowed intent was, and is, EC-wide eradication of CSF. Progress in the first five years was rather disappointing, being confounded by the recent epizootic centred on Belgium, Netherlands and West Germany, so some national plans have had to be extended. Recent entrants to the EC (Greece, Portugal and Spain) have instituted similar five year plans. As far as the UK is concerned we are obliged to comply with EC directives for CSF control but as these correspond closely with our existing national legislation this has caused no great difficulty.

Bendixen (1985), reflecting on the poor progress on the continent, considered that the main reason was that intensive production had developed too far without the necessary implementation of animal health control measures. He recommended the introduction of upper limits on area pig population density and herd size, physical/geographical barriers between herds to contain spread by contact, pig movements direct from farm to farm avoiding markets wherever possible, protective measures at individual farm level to prevent introduction of infection, and international collaboration especially to control spread at frontiers.

BEYOND 1992

The EC member states have agreed that by the end of 1992 an internal market will be established in which goods, persons, services and capital can move as freely between member states as they can within states (Marchant, 1988). The veterinary sector will not be exempted from the general principle of free movement, and it is the intention to establish a single European animal health policy. The generally high health status of UK livestock may seem to be threatened in some areas, yet it may give us trading advantages in others (Davies & Stevenson, 1988). Diseases will be classified in three groups: (1) notifiable epizootic and/or exotic diseases, including foot and mouth disease, African and classical swine fevers; (2) contagious diseases notifiable on a herd basis (e.g. tuberculosis, brucellosis); (3) diseases controllable on a voluntary health scheme basis.

For group 1 the aim is community-wide eradication, and on present progress CSF shows the greatest promise towards achieving that aim by 1992 (Table 1). Many member states are already officially CSF-free, and in others CSF-free regions have been declared. After 1992, if any pockets of infection remain, or new outbreaks arise, they will be dealt with as infected areas and appropriate control measures implemented. Community legislation for CSF is already in place and national boundaries will cease to have any significance as far as CSF-status is concerned.

Table 1. Classical swine fever outbreaks in the EC

Country	1984	1985	1986	1987	1988*
Belgium	9	64	80	83	2
Denmark	0	0	0	0	0
Eire	0	0	0	0	0
France	19	2	20	5	15
Germany (W)	1041	342	46	41	3
Greece	3	1	0	0	0
Italy	13	27	29	13	12
Luxembourg	0	0	0	1	0
Netherlands	176	36	1	1	0
Portugal	10	3	0	0	0
Spain	1	2	0	0	0
UK	0	0	10	1	0

*Provisional figures

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THE EPIDEMIOLOGY OF AFRICAN SWINE FEVER

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African swine fever (ASF) is an acute contagious disease of domestic pigs caused by a large icosahedral DNA virus which is the only known member of an un-named virus family. The virus is present in many areas of Africa where it persists in a natural transmission cycle between wart hogs and soft ticks (Ornithodoros moubata) which inhabit their burrows. Disease only occurs in domestic pigs and the acute form is characterised by fever and haemorrhages in the lymph nodes, kidneys and heart. The virus can be spread readily within the pig population by direct and indirect means without the requirement for the soft tick vector. Since its spread to Europe in 1957 the disease has become endemic in southern Europe, in Spain, Portugal and Sardinia. The disease is extremely expensive both to control and eradicate and may also produce severe financial losses as a result of the prohibition of international trade. There is no vaccine available and control and eradication are only possible by adopting a total slaughter policy.

AFRICA

ASF virus infects wart hogs in many countries of Africa (Wilkinson, 1981) and has also been isolated from a species of soft tick, Ornithodoros moubata, which lives in the burrows of these wild swine in east Africa (Plowright, 1984) and southern Africa (Thomson et al, 1983; Wilkinson et al, 1988). There is no evidence for either vertical or horizontal transmission of the virus between wart hogs and they become infected, probably soon after birth, following the bite of an infected tick. A transient, low level of viraemia is produced in the young wart hogs (Thomson et al, 1980) which is sufficient to infect those uninfected ticks which feed on them during this brief period of viraemia. Within the tick population virus is transmitted trans-ovarially, trans-stadially and from males to females during copulation (Plowright, 1977). This natural transmission cycle between soft ticks and wart hogs forms a reservoir of virus from which it is unlikely that it will ever be eliminated. The methods of virus spread from wild swine to domestic pigs are not well understood but domestic pigs can become infected by feeding on wart hog tissues containing virus or by the bites of infected ticks. There would appear to be little or no opportunity for contact between domestic pigs and wart hogs which live in areas remote from those inhabited by humans and their pigs. The most likely sources of virus for domestic pigs are infected ticks carried on wart hogs which have been shot and brought back to villages or farms where domestic pigs are kept or scraps of infected tissues from these animals.

Once domestic pigs become infected there is no further need for the soft tick as a virus vector, and the virus is readily transmitted directly from pig to pig through virus present in secretions and excretions or in blood. Virus may also be transmitted indirectly by infected pig meat or

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fomites or mechanically by biting flies such as Stomoxys calcitrans (Mellor et al, 1987).

Although ASF virus is widely distributed in O. moubata and wart hogs in Africa south of the Sahara the disease does not occur in domestic pigs in all these areas (Wilkinson, 1981). In some countries, where pig-keeping is mainly organised on a commercial basis, ASF has been very effectively controlled by preventing contact between the wild-life reservoirs of virus and domestic pigs by ensuring that all pigs are kept in fenced enclosures.

ASF is endemic in many parts of Africa in which local or 'indigenous' pigs are kept in villages where they are allowed unrestricted access in the village and surrounding area and forage for their food. This allows free movement and mixing of different groups of pigs which, together with the uncontrolled trade in pig meat, facilitates the spread of ASF. In some areas pigs are confined at night, and at certain times of the year, such as during the early part of the growing season, they may be confined during the day as well. The latter practice may give rise to the apparent seasonal incidence of the disease in some areas where outbreaks are reported to occur less frequently during the rainy season when the pigs are confined both day and night.

An investigation of some of the factors involved in the maintenance of ASF in such an endemic area has been carried out in Zambia. ASF virus has a widespread distribution in Zambia and has been isolated from O. moubata from wart hog burrows in Game Parks in the north, south and west central parts of the country but the disease has only ever been recorded in the Eastern Province (Wilkinson et al, 1988). This part of the country has a relatively large population of local village pigs and the disease has been endemic there for many years. The genomes of virus isolates collected from O. moubata inhabiting wart hog burrows in Game Parks in four separate areas of the country were compared by restriction enzyme site mapping (Dixon & Wilkinson, 1988). Virus isolates from these different areas showed considerable diversity and the regions of the genomes that differed were distributed throughout the genome. When the genomes of domestic pig isolates from the Eastern Province of Zambia and the adjoining endemic area of Malawi were examined it was found that they were closely related to each other and that the differences between genomes were mainly in variable regions located in both the left and right terminal parts of the genome. These differences have been used to subdivide the Zambian virus isolates into four provisional groups (Figures 1 and 2).

The close relationship between the virus isolates from domestic pigs, in contrast to the differences observed between the tick isolates, suggests that virus is persisting in this endemic region by circulating within the domestic pig population rather than by continual reintroduction of virus from the wild life reservoir. In addition the presence of antibodies to ASF virus in sera from some local pigs in this region indicates that some pigs recover from disease and suggests that recovered pigs may act as carriers of the virus.

The relationship between domestic pig isolates of ASF virus from other parts of Africa, where the disease is also endemic, were also examined by restriction enzyme analysis. The genomes of virus isolates from outbreaks in Tanzania and Cameroon were found to be different from each other and from the Malawi/Zambia group of viruses. It may therefore be possible in future to trace the origin of virus isolates by using restriction enzyme analysis.

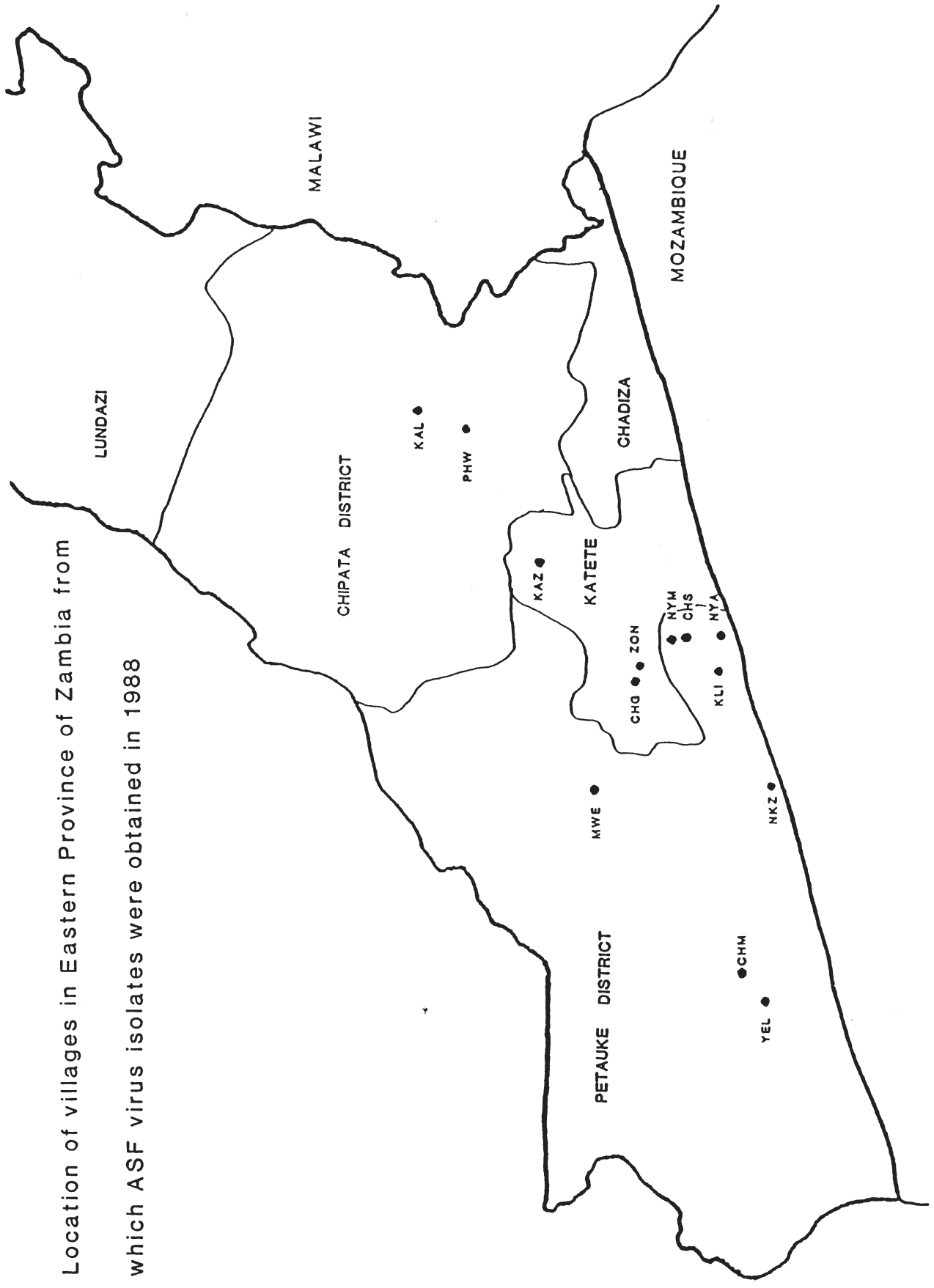
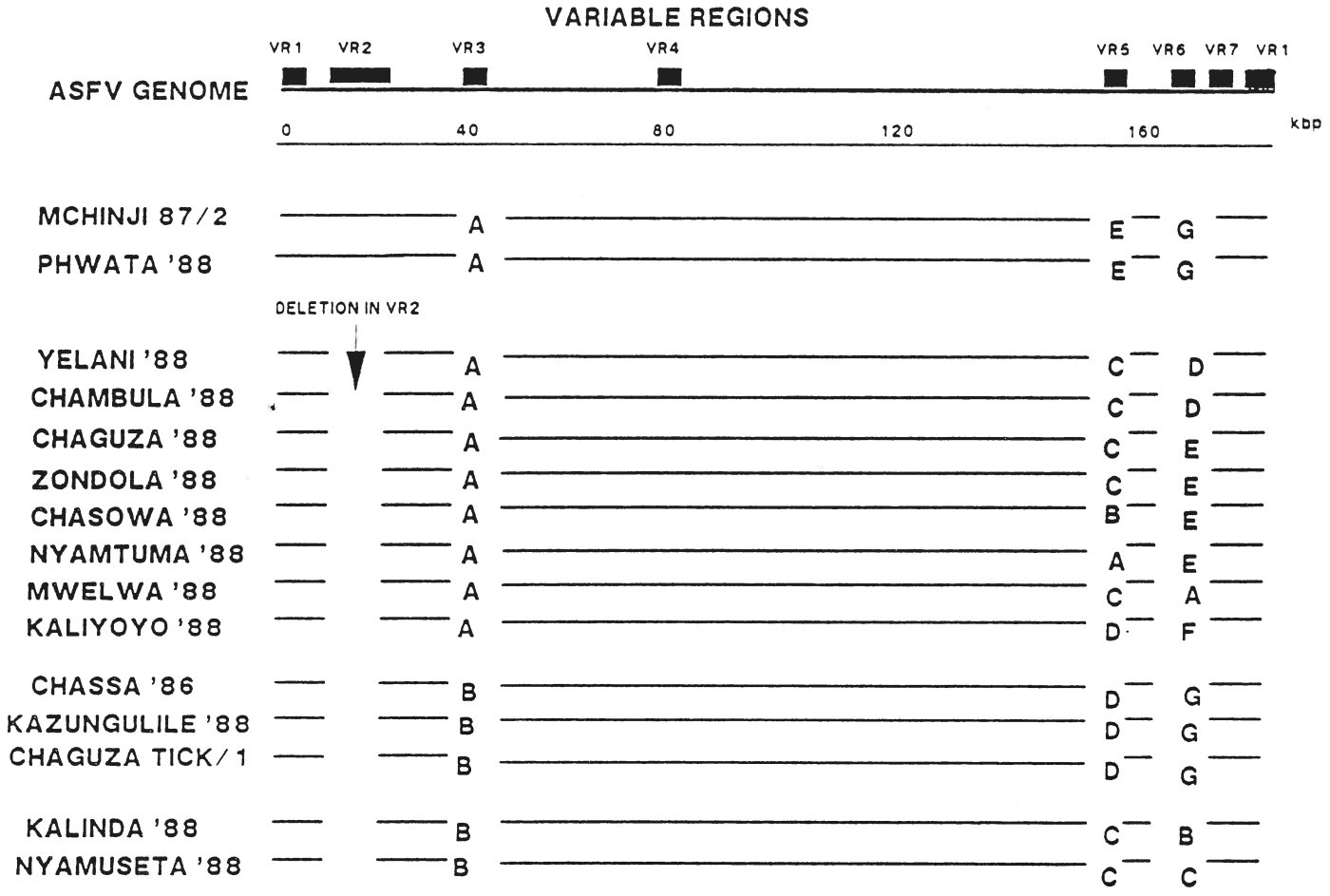


Fig.1 Location of villages in Eastern Province of Zambia from which ASF virus isolates were obtained in 1988

Fig. 2 **GENOME COMPARISONS OF ISOLATES FROM ZAMBIA (1986 and 1988) AND MALAWI (1987)**



THE LENGTH OF THE BamH1 FRAGMENTS THAT CONTAIN THE VARIABLE REGIONS VR3,VR5 AND VR6 HAVE BEEN COMPARED AND FRAGMENTS INDISTINGUISHABLE IN SIZE ASCRIBED A LETTER. THESE LETTERS REFER TO FRAGMENT LENGTH VALUES WITHIN AND NOT BETWEEN VARIABLE REGIONS. THE DELETION IN VR2 HAS BEEN MAPPED WITH Sau1 AND Nco1 ENZYMES.

EUROPE

ASF virus first occurred outside Africa when it was introduced into the Lisbon area of Portugal in 1957. This introduction was probably controlled successfully but was followed by the introduction of a different virus in 1960 which quickly spread throughout the Iberian Peninsula and led to the establishment of ASF as an endemic disease. Subsequently the disease spread in 1978 to Malta, from where it was eradicated by the destruction of the entire pig population (Wilkinson et al, 1980), and Sardinia, where it became endemic in the province of Nuoro. More recent outbreaks which occurred in Belgium in 1985 and Holland in 1986 were rapidly controlled and the virus eliminated. The outbreak in Belgium was attributed to the introduction of infected pig meat from Spain (Bironț et al, 1987) and this is the most common method by which ASF virus has been introduced into previously uninfected countries and is the most difficult means of introduction to control effectively.

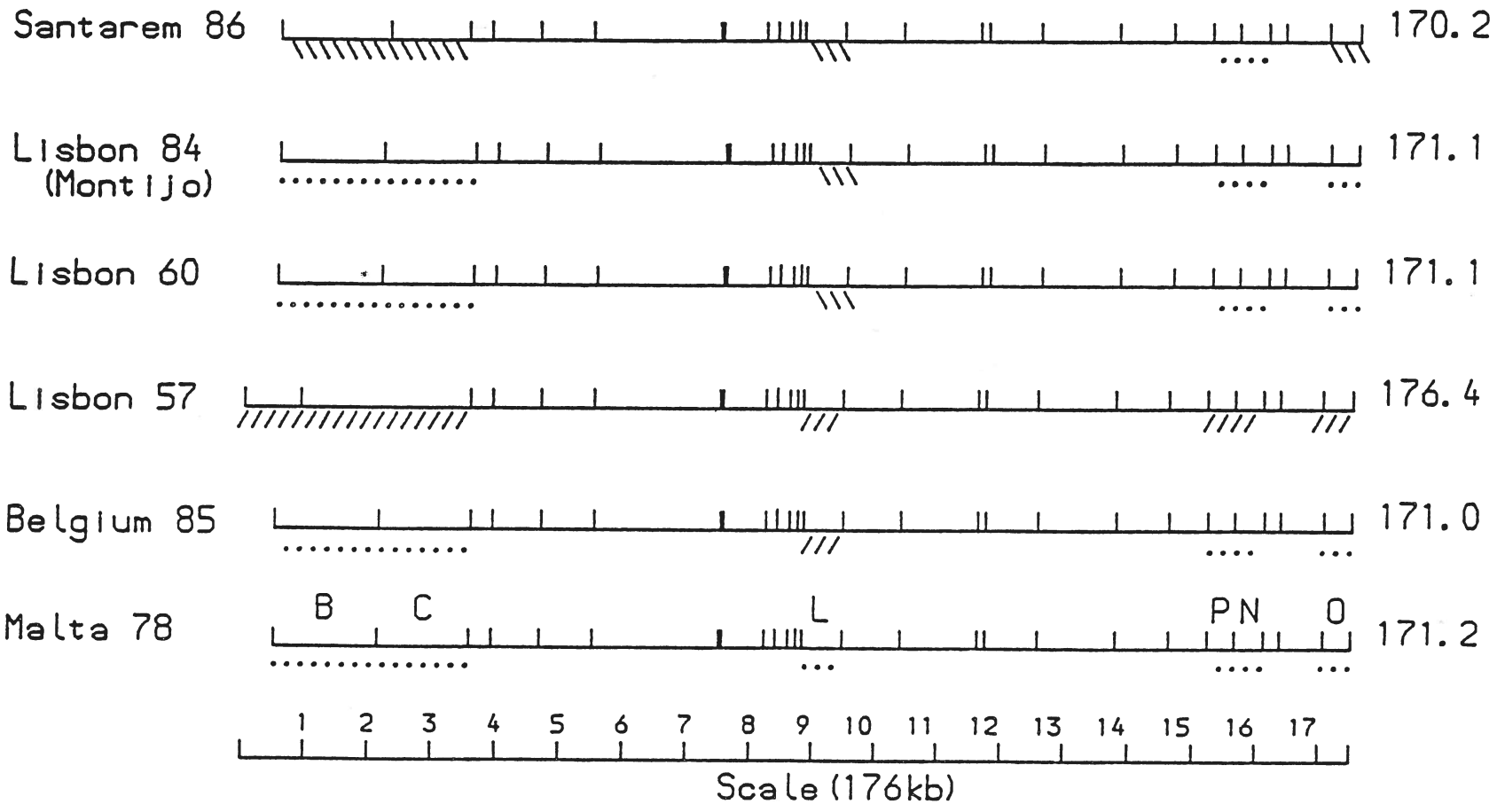
The relationship between virus isolates in Europe has been investigated by restriction enzyme analysis of genomes of virus isolates from Portugal (Lisbon 1957, Lisbon 1960, Lisbon 1984, Santarem 1986), Malta (1978) and Belgium (1985). These viruses were found to be closely related to each other (Figure 3), to isolates from Spain, Sardinia and Holland and also to the virus from Cameroon. It was also evident that the genomes of certain field isolates of virus are stable over long periods when circulating in domestic pigs.

The main methods of virus transmission within the endemic European countries are direct and indirect contact between infected pigs and pig meat products and susceptible animals because high levels of virus are present in the blood and tissues during the acute stages of the disease. Some of the virus isolates present in southern Europe are of low virulence and pigs which recover following infection with these mild strains may act as carriers of the virus for many weeks (McVicar, 1984; Wilkinson, 1984) although their role in the dissemination of virus in the field has never been clearly established.

In the south west region of Spain and parts of the southern half of Portugal the epidemiology of ASF is somewhat different (Sanchez Botija, 1982). These areas have pigs called 'Iberian' pigs which are kept under an extensive or semi-intensive system of management and are allowed free range in the evergreen oak forests of the region during part of the year. Their freedom of movement is not always limited and, as in Africa, this enables the disease to be spread by contact between different groups of pigs. In addition some parts of this region are infested by a soft tick, Ornithodoros erraticus, which lives in pig houses where it feeds on pigs and can act as a reservoir and vector of the virus. There are also wild boars (Sus scrofa) in the forests of this area and they have been found to be infected with ASF virus which produces an acute syndrome. The precise role of the soft ticks and wild boar in the epidemiology of ASF in Spain and Portugal is not at all clear but it is quite apparent that their presence in these areas will add to the difficulties in the ultimate eradication of ASF from southern Europe.

Following its introduction into Portugal and Spain in 1960 ASF was for many years widespread in both countries despite all attempts at control and eradication. Recently, however, an accelerated eradication programme was undertaken in Spain in which an extensive national serological survey was carried out to identify and slaughter herds in which infected pigs were present and to control the movement of both live pigs and meat products.

Fig.3 Comparison of the Bam HI restriction site maps of the genomes of European isolates of ASF virus



This programme also included the payment of compensation and financial incentives for improvement of pig herd health. As a consequence of this policy ASF was successfully eradicated from a large part of Spain and a request was made to the CEC that this part of Spain should be officially declared free from ASF. After discussion in Brussels this was agreed in the CEC Council Decision of 14 December 1988 which allows a derogation 'from prohibitions relating to African swine fever for certain areas in Spain' which lie north and east of a line running from the Portugese border to the north east of Salamanca southwards to Marbella on the Mediterranean coast. The area enclosed to the south and west of this line is still to be considered as an endemic area and is the part of the country in which Iberian pigs are kept and which also contains the soft tick O. erraticus.

The ultimate objective of all ASF control programmes in Europe must be the total elimination of the disease and the virus from the endemic regions of southern Europe and the recent eradication of ASF from a large part of the territory of Spain is an important contribution towards this goal. However the risk of ASF being introduced into other countries in Europe will remain so long as ASF persists in any part of southern Europe and every effort must be made to eliminate ASF from those regions in which it is still endemic.

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OPEN SESSION

THE EPIDEMIOLOGY OF SALMONELLA ENTERITIDIS INFECTION IN POULTRY FLOCKS IN NORTHERN IRELAND: ERADICATION AND PREVENTION

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Salmonella enteritidis has been recognised as a frequent pathogen of poultry in Great Britain since 1987 (O'Brien, 1988). The organism has been isolated from broiler, breeder and commercial egg laying flocks (Hopper and Mawer, 1988; Lister, 1988) and its presence in eggs has been associated with outbreaks of S. enteritidis food poisoning in man (Coyle, et al., 1988). S. enteritidis appears to replicate readily in poultry and rapidly becomes disseminated throughout an integrated organisation. "Vertical" transmission from infected parent flocks has been suggested, based on epidemiological observations (O'Brien, 1988) and the identification of S. enteritidis in ovarian tissue (Lister, 1988). Such a mechanism is highly effective in disseminating infection throughout the poultry industry, resulting in both contaminated poultrymeat and egg products. S. enteritidis was first isolated from poultry in Northern Ireland in 1986. This paper describes the successful control and eradication of S. enteritidis from an integrated broiler organisation and details the steps taken to minimise its reintroduction. The infection was restricted to one organisation and was not identified in other broiler and egg laying organisations by the existing comprehensive monitoring procedures employed.

CLINICAL DISEASE AND DIAGNOSIS

Five broiler flocks within a broiler organisation experienced an increased level of mortality during the first 48 hours of life. On average, such flocks frequently recorded a mortality of 2% during the first 48 hours and attained a cumulative mortality of 6% at five days of age. In addition, a morbidity rate of up to 20% was observed during the first five days of life. Affected birds were inappetant, very depressed, disinclined to move and frequently huddled together in groups. Individual, affected birds had a ruffled appearance and commonly exhibited vent staining. A consistent observation was the existence of many chicks standing on one leg and this was subsequently considered, by personnel of the broiler organisation involved, to be pathognomonic of S. enteritidis infection.

Culled live and freshly dead chicks from all five affected broiler flocks were submitted to the Veterinary Research Laboratories (VRL) for examination. Lesions of yolk sac infection were the most consistent

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pathological findings at post-mortem examination while some carcases exhibited fever and dehydration. On bacteriological examination S. enteritidis was isolated from most birds. The yolk sac, liver and intestinal contents were normally examined and all of these samples frequently proved positive for the organism. No other significant pathogenic micro-organisms were isolated. All isolates of S. enteritidis were identified by the Salmonella Reference Laboratory at Colindale as phage type 4.

Following the diagnosis of Salmonellosis, all personnel on affected broiler sites were alerted to the zoonotic implications of this disease and issued with detailed specific advice on precautions to be taken when handling infected chicks or their products. All other "at risk" personnel within the broiler organisation were similarly alerted and advised. Such actions were carried out under the terms and conditions of the Zoonosis Order (Northern Ireland) 1976. Concurrent with such actions, all morbid chicks in affected flocks were culled and buried. This resulted in the removal of approximately 10% to 16% of chicks from affected houses. Anti-bacterial therapy, consisting of the inclusion of 200 ppm of furazolidone in the drinking water, was immediately implemented in all flocks and maintained for seven days. Subsequent therapy consisted of 400 ppm of furazolidone in feed and this was maintained for a further seven days.

EPIDEMIOLOGICAL INVESTIGATIONS

The five affected broiler flocks were supplied with pelleted feedingstuffs manufactured at three separate feed mills indicating that a common contaminated feed source was unlikely. Furthermore, detailed investigations failed to identify any possible common vehicle for the lateral introduction of infection to the broiler sites. Notably, all affected flocks experienced mortality and morbidity within the first 24 hours of life, indicating early infection and suggesting transmission by a vertical route. Supporting this hypothesis was the finding that all flocks had been hatched over a common 2 day period. Individual broiler flocks were the progeny of between four and eight parent flocks. Detailed examination of the relevant hatchery records identified six parent flocks whose progeny was present in all five affected broiler sites. Following this finding all six suspect parent flocks were sampled for evidence of S. enteritidis infection. All these flocks were examined and found to be clinically normal and analysis of production data failed to identify any reduction in expected egg production, fertility or hatchability. Following sampling, all six suspect parent flocks were treated with 200 ppm furazolidone via the drinking water and subsequently via the feed.

At the hatchery, samples from all hatchers containing any of the six suspect parent flocks were taken for examination. In addition, ten culled chicks derived from each suspect parent flock were removed from the relevant hatcher tray. Pooled viscera and intestinal contents were cultured for Salmonellae. Samples were also obtained from each parent flock site. These consisted of pooled caecal droppings and ten birds. Pooled viscera and intestinal contents of these adult birds were examined for Salmonellae. Fifty blood samples were also collected from each parent flock and examined for antibodies to S. enteritidis using the tube agglutination test with specific "H" and "O" antigen. Environmental samples were obtained from each

house. These comprised a pooled dust and a pooled litter sample, each of which was obtained from four separate locations within each house.

Serum agglutination antibodies to both the "H" and "O" antigens were detected in two of the six suspect flocks. Subsequently, S. enteritidis was isolated from caecal droppings, culled chicks, fluffs, dust and litter originating from the same two parent flocks. Ongoing examination of imported day old parent chicks and chick box liners failed to indicate vertical transmission from the grandparent stock. However, it was established that both infected parent flocks were supplied with feedingstuffs from one feed mill and the introduction of infection by this route could not be discounted.

CONTROL

In addition to anti-bacterial therapy of all six suspect parent flocks the use of fresh eggs for human and animal consumption was prohibited in accordance with the Zoonosis Order (NI) 1976. All floor laid, soiled, cracked and thin shelled eggs were not used for hatching but were disposed of by burying. All eggs for hatching were immediately fumigated with formaldehyde on arrival at the hatchery and stored separately from all other hatching eggs. Any dirty, cracked or thin shelled eggs identified at this stage were again removed and destroyed. Vehicles and equipment used in the transport of eggs were thoroughly cleansed, disinfected and fumigated on each occasion after use. Eggs from suspect flocks were refumigated and placed in identified setters as a discrete group. Subsequently, each group was placed in specific hatchers containing only such eggs. On the day of hatching, hatchers containing chicks from all suspect flocks were vacated at the end of the day's production in order to minimise cross contamination with other chicks and to permit effective disinfection of the entire hatchery environments. After sexing, such chicks were placed on specific broiler sites where facilities and personnel were deemed best equipped to deal with possible infection during production. Vehicles and equipment used in the transport of such chicks were thoroughly cleansed, disinfected and fumigated on every occasion after use. Similar precautions and procedures were also applied to all hatchers and setters containing eggs from any of the six suspect parent flocks.

When infection was found to be restricted to two of the six parent flocks the above precautions and procedures were directed to the eggs and chicks of these two flocks only. In addition, preventative furazolidone treatment was administered to all progeny from these two flocks on arrival at each broiler site. Radical culling of all morbid chicks was also carried out. Twenty broilers from each broiler site in which S. enteritidis had been identified or suspected were submitted to the VRL one week before slaughter. Such birds were subjected to detailed pathological and bacteriological examinations and in all instances proved negative for Salmonellae.

ERADICATION

After consultation, the broiler organisation involved took a positive decision to eradicate the infection and agreed to immediately slaughter the

two infected parent flocks, following the necessary anti-bacterial withdrawal period. The parent flocks each contained approximately 4,000 birds. These birds were identified to the Veterinary Officer at the processing plant and subjected to detailed ante-mortem inspection with the rejection of any clinically affected birds. Following detailed post-mortem examinations the carcases were held in a cold store pending the results of laboratory examinations. Ten "New York dressed" carcases were examined and S. enteritidis was isolated from the intestines of two birds. Bacteriological examinations of lungs, livers, spleens, ovaries, oviducts and hearts failed to identify any indication of bacteraemia or ovarian/oviduct infection in these 10 birds. In addition, the ovaries and oviducts of 10 other carcases were examined and proved negative.

Litter from the two vacated parent houses was removed from the site and stacked for a minimum of six months before spreading on arable land. The houses and all equipment were thoroughly cleansed, disinfected and fumigated. Fumigation was repeated twenty-four hours later. The entire water system was drained and the tanks, lines and drinkers thoroughly cleansed and disinfected. Particular attention was paid to nest boxes and in one site, the wooden nest boxes were considered impossible to effectively decontaminate and were thus incinerated. Wild bird proofing and vermin control were assessed on each site and improved where necessary. On one site where a pet dog had access to the poultry house, stool samples from this animal were found negative for Salmonellae. Such access to poultry houses by pets was subsequently prohibited. All impervious areas surrounding the exterior of the houses were cleansed and disinfected. In other surrounding areas, where contamination was suspected, the top 15 cm of soil was removed and replaced by stone chips. Following all these procedures, swabs were taken from the concrete floors, walls, extractor fan outlets and all equipment within the house. Swabs were also taken from several locations on the exterior of the houses and the immediate surroundings. All swabs were found to be negative for Salmonellae and restocking was permitted. Similar decontamination and monitoring procedures were implemented on all broiler sites where S. enteritidis had been identified or suspected.

PREVENTATIVE MEASURES

Following the successful eradication of S. enteritidis infection a Working Group consisting of senior management from the broiler organisation and specialist veterinary staff from the VRL was formed. The remit of this Group was to implement procedures aimed at minimising the possibility of the reintroduction of Salmonellae and to devise a monitoring programme to identify Salmonella infection at an early stage. It was recognised that Salmonellae could be introduced by any of three principal routes; vertical transmission, feeding stuffs and other vehicles for lateral transmission such as personnel, other animal species and fomites.

Vertical transmission was minimised by ensuring that all levels of breeding flocks were regularly monitored for Salmonellae and deemed free from such infection. The status of grandparent flocks was assessed by examining samples of chick box liners from all batches of imported day old parent chicks. Furthermore, all mortalities occurring in the first seven days of life were submitted for bacteriological examination. All parent flocks (all under direct control of the broiler organisation concerned) were

regularly monitored throughout rearing and production by the examination of samples such as bloods, house dust, litter, caecal droppings, hatchery fluff and hatcher culls. In addition, the broiler progeny was monitored by the examination of culled chicks from flocks where any clinical disease was observed, at any stage of production and especially during the first seven days of life.

Whereas all broiler flocks in the organisation were fed on heat treated, pelleted feed, all parent flocks had been fed on non-heat treated mash. Since the epidemiological investigations indicated feed as a possible source of Salmonellae for the two infected parent flocks, measures to prevent such introductions were implemented. Such measures included subjecting all feedingstuffs to a minimum of 70°C for 12 minutes immediately prior to pelleting. Subsequent to pelleting (and crumbing where necessary) all finished feed was transported via dedicated lines, storage bins and vehicles to all poultry sites. Broilers thus continued to be fed on pelleted feed whilst all parent flocks now received a heat treated, crumbed product.

In an attempt to minimise all other routes of lateral transmission, detailed instructions were issued to all production personnel. Such instructions highlighted the role of vermin, birds, humans, other animals, vehicles and equipment in the introduction of Salmonellae into poultry sites.

DISCUSSION

This paper describes the successful control and eradication of S. enteritidis infection from an integrated broiler organisation. This was achieved by ongoing close co-operation between the organisation involved and the VRL. It was only possible through senior management of the organisation adopting a very positive and responsible attitude immediately following the diagnosis of infection and voluntarily implementing all measures recommended by the VRL. The early identification of infection was possible because of routine monitoring of all clinically affected broiler flocks for the presence of Salmonellae as an integral part of an established diagnostic service. Thus, the problem was identified and addressed before infection became widespread throughout the organisation. Complementing the early detection of infection in broiler flocks was the subsequent rapid removal of two valuable breeder flocks identified as the source of infection for the broilers.

It is highly probable that if such radical measures had not been taken and infection had become established throughout the organisation, subsequent eradication of S. enteritidis infection would have been economically impractical. In such circumstances S. enteritidis would become endemic and the only means of reducing the spread of infection available would be the continuous application of stringent control measures. Such a situation is obviously not desirable especially since "vertical" transmission occurs frequently when infection is present in parent flocks.

Vertical transmission normally implies transovarian transmission of an organism and such a mechanism may exist for S. enteritidis. Certainly, the organism is considered to be invasive and may localise in the ovary of poultry (Faddoul and Fellows, 1966; Snoeyenbos et al., 1969). However,

other possible methods of egg transmission of S. enteritidis exist and would also result in infection of the progeny. Thus, infection of the oviduct can result in the albumin becoming infected during egg formation. Furthermore, even after shell formation has been completed, Salmonellae from contaminated faeces can readily enter the egg and become resident on the egg membranes during the normal cooling process which occurs immediately after laying. Such an event preceeds the establishment of an effective proteinaceous cuticular barrier on the entire external surface of the egg. This is considered to be the primary method of preventing bacterial invasion of the egg (Board, 1968). A further method of egg transmission is via external contamination of the intact egg shell resulting in the establishment of infection in chicks during the hatching process. Obviously, if cracked eggs become contaminated, Salmonellae may become resident within the egg at any stage prior to hatching.

Irrespective of the relative frequency of each method of egg transmission of S. enteritidis infection it is clearly apparent from the epidemiological investigation that infected parents frequently result in infected progeny. The ability of S. enteritidis to frequently achieve "vertical" transmission is a major reason for its establishment as an important pathogen in both the broiler and egg laying sectors of the poultry industry.

Whilst such "vertical" transmission results in overt clinical signs in young chicks it is important to recognise that infection can be established in older birds without any apparent clinical signs or reduced production. This epidemiological observation is pertinent in that infection can become firmly established in both breeder flocks and commercial egg laying flocks at any stage of production and remain undetected unless effective monitoring procedures are carried out. This may be the reason why S. enteritidis infection has become established in some commercial egg laying flocks in Great Britain and the United States of America with obvious resulting zoonotic implications (Anon, 1989). Notably, S. enteritidis infection has only been identified in the broiler sector of the Northern Ireland poultry industry and the implementation of an effective eradication procedure for the egg laying sector has not been necessary. However, eradication of S. enteritidis infection from a large commercial egg laying site would present additional practical difficulties. Such sites are frequently not managed on an "all in - all out" basis and thus a total site depopulation and decontamination may be economically prohibited. In addition, the physical cleansing and disinfection of the vast surface area of a cage system presents considerable practical difficulties in effectively decontaminating such an environment.

The commonest vehicle for lateral transmission of Salmonellae into poultry flocks is via contaminated feedingstuffs (Stuart, 1984), and is probably the most important method by which S. enteritidis is initially introduced into a poultry organisation. Prior to the occurrence of S. enteritidis infection in Northern Ireland breeding flocks were fed on mash. Contamination of such diets with Salmonellae is entirely dependent on the status of the constituent raw materials and the ease with which contamination from other diets can occur during the milling process. It must be accepted that no raw material of either animal or vegetable origin can be guaranteed free of Salmonellae. Thus, the only practical means of effectively preventing the introduction of contaminated feedingstuffs to poultry is to produce a finished product in which all Salmonellae have been eliminated. Experimental work (Ellis; Personal Communication) has indicated that heat treatment of Salmonella contaminated feed at 70°C for 12 minutes

prevented infection in day old chicks. This time and temperature relationship was selected because of the known feasibility of attaining these conditions at a particular feed mill by the use of a conditioner/ripener immediately prior to pelleting Furthermore, having achieved such a product it is essential that recontamination does not occur at any stage before consumption of such feed by poultry. This necessitated the implementation of a totally dedicated system of lines, bins and vehicles for such decontaminated feed.

Codes of Practice for the Control of Salmonellae have been formulated in Great Britain, the Republic of Ireland and Northern Ireland. The common aims of these Codes are to prevent the introduction of Salmonellae to poultry, to detect infection and to effect control measures. A key element of the Northern Ireland Codes is the acceptance that, in spite of frequent monitoring, all raw feed ingredients are potentially contaminated and finished feedingstuffs must be treated by a method which renders them free from Salmonellae. Where feed mills do not have the facility to subject feed to 70°C for 12 minutes, using a conditioner/ripener process, then it is recommended that all finished feed should be subjected to a minimum of 80°C for one minute during the pelleting process. Furthermore, the prevention of recontamination can only be achieved by the use of a dedicated handling and transport system. A further key element is that the level of monitoring of poultry flocks must be adequate to identify infection at an early stage and thus facilitate effective control. Early detection is also a key element where the ultimate aim is the rapid eradication of specific Salmonellae, such as S. enteritidis, from the flock or organisation concerned.

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SOME EPIDEMIOLOGICAL OBSERVATIONS ON CANINE TESTICULAR TUMOURS

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Testicular tumours have been reported more frequently in the dog than in other domestic animals (Jubb et al.; 1985 Moulton, 1978) and man (Innes, 1942). They have accounted for over 10% of all reported tumours in male dogs, a morbidity second only to skin tumours (Hayes and Pendergrass, 1976).

Testicular tumours are classified into six categories (Nielsen and Lein, 1974):

1. germ cell tumours, including seminomas, embryonal carcinomas and teratomas;
2. sex cord-stromal tumours, including Leydig (interstitial) cell and Sertoli (sustentacular) cell tumours, and tumours of intermediate Leydig and Sertoli cell differentiation;
3. multiple primary tumours (combinations of 1 and 2, above, in the same testis);
4. mesotheliomas;
5. stromal and vascular tumours;
6. unclassified tumours.

Seminomas, Leydig cell tumours and Sertoli cell tumours are the three most common testicular tumours in dogs. There are also reports of fibroma, lipoma, haemangioma, sarcoma, carcinoma and granulosa-cell tumours of the canine testis (Jubb et al., 1985). Teratomas, seen frequently in the stallion, have not been reported in the dog (Cotchin, 1960; Dow, 1962). The three main tumour types occur in dogs with approximately equal frequency, with some reports conflicting on the relative frequencies (Dow, 1962; Hayes and Pendergrass, 1976; Innes, 1942; Lipowitz et al., 1973; Mulligan, 1949; Scully and Coffin, 1952). Leydig cell tumours are restricted almost entirely to the scrotal testis (Hayes and Pendergrass, 1976; Lipowitz et al., 1973), with 38% of seminoma and 52% of Sertoli cell cases having tumours recorded in an extrascrotal position (Lipowitz et al., 1973).

Most canine testicular tumours are benign; Jubb et al. (1985) suggest that metastases are more common from seminomas than the other tumour types. The major clinical problems thus are referable to the local and physiological effects of the tumours. Sertoli cell tumours may result in the production of

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increased amounts of oestrogens and are associated with a 'feminising syndrome', alopecia, pruritus, skin pigmentation, metaplasia of the prostate gland and myelotoxicosis. Leydig cell tumours may occur with lesions associated with high androgen levels - e.g., prostatic disease and perianal adenoma (Nielsen and Aftosimis, 1964) - but evidence for increased androgen production by these tumours is equivocal. After a period of slow growth seminomas enlarge suddenly with resultant haemorrhage and necrosis.

Testicular tumours tend to affect older dogs, commonly those over ten years of age (Lipowitz et al., 1973). There are very few reports of cases in animals under 3 years of age (e.g., Innes, 1942). Some authors have shown that the mean age at diagnosis is lowest for Sertoli cell tumours (Jones and Friedman, 1950; Cotchin, 1960; Lipowitz et al., 1973), whilst others have shown it to be lowest for seminomas (e.g. Dow, 1962). There also is evidence that the mean age at diagnosis varies between breeds (Lipowitz et al., 1973).

A relationship between cryptorchidism and testicular neoplasia is well-recognised. Although cryptorchidism has been shown to have a frequency less than 1% in the dog population (Bloom, 1954; Arthur et al., 1982), cryptorchid animals have an overall risk for any testicular tumour greater than that of normal males, estimates ranging from 8.6 (Reif et al., 1979) to 13.6 (Hayes and Pendergrass, 1976) times that of non-cryptorchid dogs.

The association between breed of dog and development of testicular tumours has been investigated by various authors in the United Kingdom (Cotchin, 1960; Weaver, 1983) and United States (Hayes and Pendergrass, 1976; Lipowitz et al., 1973), usually using data collected at veterinary clinics. The boxer is the only breed to have been shown to be at excessive risk of all three tumour types (Hayes and Pendergrass, 1976). The Weimaraner, Shetland sheepdog, cairn terrier, border collie and Pekingese have all been shown to be at excessive risk of Sertoli cell tumour development (Hayes and Pendergrass, 1976; Weaver, 1983). Seminomas are relatively common in the German shepherd dog (Hayes and Pendergrass, 1976; Robinson and Garner, 1973).

The current study was undertaken to ascertain whether or not the tumours' reported breed associations, age distribution and association with cryptorchidism, and relative frequencies of histological types of tumour are consistent in a population that is different than those investigated previously.

MATERIALS AND METHODS

Extraction and collation of data

The Small Animal Practice Teaching Unit (SAPTU) at the Royal (Dick) School of Veterinary Studies, University of Edinburgh maintains a computerised database of clinical case record summaries (Stone and Thrusfield, 1989; Thrusfield and Hinxman, 1981). Case notes are summarised, alphanumerically and numerically coded, and entered into the database after completion of one or more consultations for a particular patient problem. Information includes a patient's case record number, date of visit, breed and sex, and details of diagnoses and treatments. Results of auxiliary diagnostic tests, such as histopathological examination, are not recorded in detail in these summaries.

Listings of male animals, 3 years of age and over, that were entire at 3 years of age (to match partially by age), by breed and age (computed from the

date of birth) were produced for diagnoses of:

1. testicular tumours,
2. cryptorchidism (unilateral and bilateral, combined).

Counts by breed, age and diagnosis were entered into the 'Minitab' statistical package (Ryan, Joiner and Ryan, 1985) on a National Advanced Systems VL/80 mainframe computer to facilitate tabulation, totalling and comparison of figures.

Details of the histological types of tumour were obtained from the long-hand case notes after identification of cases in the database.

Frequencies of histological types of tumour were compared using a χ^2 statistic, and confidence intervals for the proportions of histological types of tumour were calculated using the Normal approximation to the binomial distribution (Bailey, 1981).

Measurement of association

The degree of association between breed of dog and testicular tumours, and between cryptorchidism and testicular tumours, was measured by the odds ratio (Thrusfield, 1986). Ninety-five percent confidence intervals for odds ratios were calculated using the method of Plackett (1981).

RESULTS

One hundred and twenty four cases of testicular tumours were identified in 5151 male animals, 3 years of age and older, that were entire when 3 years of age. No cases were recorded in animals under 3 years of age. Histopathological examination of the tumours was undertaken on 62 of the 124 cases. Sixty cases were of single primary tumours. Fifty-four cases had one tumour type in one testis. Six cases showed a different single tumour type in each testis. There were 2 cases of multiple primary tumours. The type of single primary tumour identified and the proportions of tumour type and their associated 95% confidence intervals are listed in Table 1.

The frequency distribution of the age at diagnosis of tumours and measures of position and dispersion are given in Table 2.

The frequencies by breed, and the associated odds ratios and 95% confidence intervals for dogs giving a statistically significant positive or negative association at the 5% level are presented in Table 3.

The odds ratio and 95% confidence interval for the association between cryptorchidism and testicular tumours is given in Table 4.

DISCUSSION

Tumour type

Table 1 suggests that seminoma is the most frequent tumour type. However, a χ^2 statistic, calculated on the assumption of equal frequency among the 3 single tumour types, has a value of 3.4 on 2 degrees of freedom which is not significant at the 10% level. There is thus insufficient evidence to suggest a

Table 1. Types of canine testicular tumour in 60 cases of single primary tumours diagnosed histopathologically (SAPTU database, January 1977 - October 1988).

Type	Number of types diagnosed*	Percentage of types diagnosed	95% confidence interval for percentage diagnosed
Sertoli cell	19	29	18, 40
Seminoma	29	44	32, 56
Leydig cell	18	27	16, 38
Totals	66	100	

* A different single tumour type was found in each testis in 6 cases.

difference in frequency among the 3 tumour types. This point is further illustrated by the overlapping 95% confidence intervals of the percentages of tumour types. However, less than 1 in 3 seminomas are detected on clinical examination (which was the method of identification of cases in this study) (Dow, 1962) and so the incidence of seminoma is likely to have been underestimated. The incidence of Leydig cell tumours, similarly, is likely to have been underestimated because they, too, may be clinically undetectable. The method of diagnosis used in a study (clinical examination vs. histological screening at routine post-mortem examination) may explain partly the disparity in relative frequency of tumour types among previous studies (Table 5).

Age at diagnosis

The descriptive statistics given in Table 2 are so similar as to render statistical tests for differences in measures of central tendancy among the tumour types redundant. The median age at diagnosis (Table 2: 11 years) is higher than that quoted by Reif and Brodey (1969) for Sertoli cell tumours and seminomas (from 8 to 10.5 years, depending on whether or not dogs are cryptorchid). Most other authors quote means rather than medians. Their results are compared with this series in Table 6, which reveals conflicting evidence, both for specific tumour types and for all tumours. The high median and mean ages in the present study may partly be explained by diagnoses being based only on clinical signs, resulting in tumours being detected relatively late in their development, compared to those detected by routine histopathological screening, as in Dow's (1962) study. However, other studies, also based on clinical diagnosis (Table 6), have produced values for the mean lower than the value in the current study. Comparisons of ages at diagnosis for all tumour types, combined, additionally are complicated by the different proportions of tumour types in the total sample, because of the variations in median and mean ages reported for the various types of tumour, although

Table 2. Frequency distribution of the age at diagnosis of 124 cases of canine testicular tumours (SAPTU database, January 1977 - October 1988).

Age at diagnosis (years)	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
Number of cases	0	0	1	0	1	2	3	7	6	16	21	20	22	11	9	3	1	1

Descriptive statistics

	Sample size*	Median age at diagnosis** (years)	Semi-interquartile range** (years)	Mean age at diagnosis (years)	Estimated standard error of the mean (years)
1. Sertoli cell	19	11.0	10.0 - 13.0	11.2	0.64
2. Seminoma	29	11.0	10.0 - 12.0	11.1	0.40
3. Leydig cell	18	12.0	10.5 - 13.0	11.7	0.54
4. All tumour types***	124	12.0	10.0 - 13.0	11.7	0.23

* Sample sizes for the 3 individual tumour types (1-3) based on the number of types diagnosed; sample sizes for all tumour types (4) based on the number of cases diagnosed.

** Exploratory data analysis (Tukey, 1977) revealed some evidence of skewness to the frequency distribution of the age at diagnosis of Sertoli cell tumours and all tumour types and so the median and semi-interquartile range have been included as measures of central tendency and dispersion, respectively.

*** Calculated for all cases of testicular tumours, including the 2 cases of multiple primary tumours and those on which no histopathological examination had been conducted.

Table 3. Odds ratios and 95% confidence intervals for dogs giving a statistically significant positive or negative association, at the 5% level, between breed and canine testicular tumours (SAPTU database, January 1977 - October 1988).

Breed	Cases	Controls	Odds ratio $\hat{\psi}$	95% confidence interval for ψ
Bearded collie	1	8	7.17	1.25, 41.07
Border collie cross	8	118	3.02	1.47, 6.21
Cairn terrier	8	147	2.41	1.18, 4.94
Chow chow	2	8	12.05	2.90, 49.93
Dalmatian	2	22	4.54	1.21, 16.98
Doberman pinscher	4	7	25.00	7.66, 81.57
Chihuahua	1	2	24.42	3.20, 186.30
Lhasa-apso	1	2	24.42	3.20, 186.30
Scottish terrier	1	2	24.42	3.20, 186.30
Springer spaniel cross	1	2	24.42	3.20, 186.30
Staffordshire bull terrier	1	1	40.70	4.20, 394.05
Labrador retriever	5	595	0.34	0.15, 0.81
Totals over all breeds in the study	124	5027		

Table 4. Frequency of testicular tumours in cryptorchid and non-cryptorchid dogs (SAPTU database, January 1977 - October, 1988).

	Testicular tumours present	Testicular tumours absent	Totals
Cryptorchid	10	74	84
Non-cryptorchid	114	4953	5067
Totals	124	5027	5151

$\hat{\psi} = 6.1$

95% CI for $\psi = 3.1, 11.9$

significant variations have not been demonstrated in this study. The present study's high median and mean ages at diagnosis could also be a function of current dog populations having a larger proportion of dogs surviving to old age than earlier populations on which previous studies were conducted. However, it is difficult to demonstrate changing trends in the age structure of companion animal populations using currently-available demographic data (Thrusfield, 1989).

Table 5. Comparison of the frequency of types of canine testicular tumour.

Percentage of testicular tumours (Number of testicular tumours)			Source
Sertoli cell	Seminoma	Leydig cell	
25 (15)	52 (32)	23 (14)	Innes (1942)
33 (13)	36 (14)	31 (12)	Mulligan (1949)
19 (33)	31 (55)	50 (88)	Scully and Coffin (1952)
26 (36)	33 (45)	41 (56)	Dow (1962)
26 (51)	28 (55)	46 (88)	Lipowitz et al. (1973)
38 (137)	35 (127)	27 (96)	Hayes and Pendergrass (1976)
29 (19)	44 (29)	27 (18)	Present series

Breed

Table 3 shows statistically significant positive associations between 11 breeds (including crosses) and testicular tumours. However, the point and interval estimates of the odds ratio are sensitive to small changes in the numbers in the contingency tables when some numbers are small. For example, considering border collie crosses, if the number of cases were reduced from 8 to 6, and the number of controls were increased from 118 to 120, then the point estimate and confidence interval become 2.23 and (0.99, 5.02) respectively, and the odds ratio is not statistically significant at the 5% level. Additionally, 5 breeds are represented by only one case and either one or two controls, resulting in imprecise estimates. When these are discounted, and moderate, rather than small, changes are made in numbers in the contingency tables, then

Table 6. Mean ages at diagnosis of canine testicular tumours.

Age (years)				Source
Sertoli cell	Seminoma	Leydig cell	All tumour types	
-	10+	12	-	[3]Schlotthauer et al. (1938)
8.7	9.9	9.6	9.5	[1]Innes (1942)*
7.6	11.1	12.1	-	[3]Jones and Friedman (1950)
10	11	10	-	[3]Scully and Coffin (1952)
9.3	-	-	-	[1]Brodey and Martin (1958)
8.5	10	11.5	-	[3]Cotchin (1960)
9.2	8.8	9.2	9.1	[2]Dow (1962)
9.4	9.8	-	-	[1]Reif and Brodey (1969)
9.2	10.0	-	10.2	[3]Lipowitz et al. (1973)
9.7	10.0	11.2	-	[3]Nielsen and Lein (1974)
9.5	-	-	-	[3]Weaver (1983)
11.2	11.1	11.7	11.7**	[1]Present series

1. Initial diagnosis made on clinical examination.
2. Diagnosis made on routine histopathological examination.
3. Methods 1 and 2, above, used in various proportions in the series of cases.

* The last age interval was defined as '13 and over'; '13' was used as the age of all dogs in this interval when calculating the mean, thus giving an estimated mean less than its true value.

** Calculated for all cases of testicular tumours, including those on which no histopathological examination had been conducted.

a significant positive association still holds for 3 breeds: the cairn terrier, Dalmatian and dobermann pinscher. The predisposition in cairn terriers is consistent with that identified by Weaver (1983), although his study only included Sertoli cell tumours; breed predisposition is known to vary between tumour type (Hayes and Pendergrass, 1976). Dalmatians and dobermann pinschers have not previously been reported to be at high risk in studies utilising reference population data. The boxer has been identified as being at individual risk of testicular tumours, in particular (e.g., Hayes and Pendergrass, 1976), and as having a diathesis to many tumours. generally (Howard and Nielson, 1965), but the present study does not substantiate the former.

One breed - the Labrador retriever - is identified in this study as having a significantly reduced risk of developing testicular tumours. This conflicts with some studies (e.g., Weaver, 1983) which suggest an increased risk.

The disparities in breed predisposition between studies may be explained by an environmental component to the cause of testicular tumours. Doll (1977) has contended that most cancers have environmental causes as either initiators or promoters, and there is evidence that human testicular tumours may, in part, be attributable to environmental carcinogens associated with rural or urban residence (Clemmesen, 1968; Graham and Gibson, 1972; Lipworth and Dayan, 1969; Sharma et al., 1972). However, the low risk of testicular tumours in mongrels, compared with purebred dogs, demonstrated in some studies (e.g., Hayes and Pendergrass, 1976), is evidence also of a genetic component to the cause of these tumours.

Cryptorchidism

The excess risk of testicular tumours in cryptorchid animals is illustrated in Table 4, with an odds ratio point estimate of 6.1 and associated 95% confidence interval of (3.1, 11.9). This result is in accord with the point estimates of Reif and Brodey (1969) (relative risk = 8.6 or 12.3, depending on the assumptions of the study), Pendergrass and Hayes (1975) (relative risk = 10.9) and Hayes and Pendergrass (1976) (odds ratio = 13.6), and is similar to relative risks demonstrated in man: 8.8 (Morrison, 1976) and 14 (Mostofi, 1973). The risk in cryptorchids, relative to non-cryptorchid animals, however, may be exaggerated because tumours in the former may be more easily detected on clinical examination than those in the latter. Nevertheless, it has been suggested that an excessive risk of cryptorchidism may predispose certain breeds to testicular tumours (Pendergrass and Hayes, 1975; Reif and Brodey, 1969). Additionally, there is individual breed variation in the risk of testicular tumours in cryptorchids (Hayes and Pendergrass, 1976) but there were insufficient cryptorchids in the present study to estimate breed-specific risks in cryptorchids. However, a breed predisposition to cryptorchidism cannot account, totally, for an excess risk of testicular tumours; in the current study, for example, no cases occurred in cryptorchids in the three breeds with high individual risks.

Conclusions

This study has substantiated previous workers' conclusions relating to the association between cryptorchidism and testicular tumours, and of the cairn terrier's predisposition to these lesions. Two additional breeds - the dobermann pinscher and Dalmatian - have been identified as having high individual risks. The average age at diagnosis appears to be higher than previously recorded.

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PRACTICAL EXPERIENCE OF USING SIMPLE MATHEMATICAL MODELS TO PREDICT THE EFFECT OF CHANGES IN DISEASE CONTROL SCHEMES

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When we have been asked to predict the effects of changes in disease control schemes, as in the examples we describe here, we have found ourselves without any ready-made computer simulation model to which we could turn for the answers. It may well be, in fact, that even if we had such models we would find them deficient in some small respect which was nevertheless crucial to the particular question we wished to ask. We have certainly found that there is rarely enough data available to model the disease and its control in great detail, and have been forced to rely on the simplest possible quantitative models, informed by whatever data exist .

CHANGING THE TUBERCULIN TESTING INTERVAL

Since 1950 cattle herds in the UK have been subject to regular tuberculin tests with a view to eradicating tuberculosis from the population. The frequency of these tests has been gradually reduced as the incidence of positive reactors has fallen, and most herds are now tested every three years. In some parts of South West England, however, it was realised in the 1960's that the incidence of positives was not falling, and herds in such areas have remained subject to annual testing. In 1971 it was discovered that wild badgers were infected, and it is now generally accepted that badgers are the source of most incidents of herd infection now occurring.

Annual testing is effective in limiting the severity of individual herd incidents, by revealing them before too many cattle are infected, and must also thereby limit the occurrence of herd to herd transmission. The question of whether a reduction of the testing interval to six months could have worthwhile benefits was therefore raised, and we were interested in predicting what the effects of such a change might be.

Table 1 shows the distribution of numbers of reactors in confirmed and unconfirmed incidents in these areas. Confirmed incidents occur when a positive reaction to the test is confirmed as due to tuberculosis by observation of a typical lesion on slaughter of the animal concerned or isolation of M. bovis. Unconfirmed incidents occur when a positive test result is not so confirmed.

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Table 1. Reactors in incidents in annually tested areas, 1979-1983

No. of reactors in incident	Confirmed incidents		Unconfirmed incidents	
	No. of incidents	No. of reactors	No. of incidents	No. of reactors
1	112	112	131	131
2	53	106	29	58
3-5	93	322	14	49
6-10	35	270	-	-
11-20	24	357	-	-
21-30	4	96	-	-
31-40	2	67	-	-
57	1	57	-	-
Total (5 years)	324	1387	174	238

We can make a fair attempt of prediction from this table alone. We would hope for a reduction in within – herd spread of TB, and thus of the average number of reactors per confirmed incident. We would hope for a decrease in the number of confirmed incidents per year as within-herd prevalence declines and herd to herd spread is reduced. We would, however, have to expect that those unconfirmed incidents that are due to transient infections with organisms other than M. bovis would occur at about the same frequency per test - or twice the frequency per year.

The last of these represented our greatest area of uncertainty, and we had to predict that anything from once to twice the number of unconfirmed incidents could occur. We could make some progress on the other two, however.

Number of reactors per incident

If we suppose that

(i) there is only one primary case per incident, and all other reactors in the herd are infected from it,

(ii) the primary case is equally likely to become infected at any time during the inter-test period, and from then on is uniformly infective to the other cows in the herd,

(iii) regular testing is the only means of detection,

then the number of secondaries will be directly proportional to the average time-to-next-test following a primary infection, and thus directly proportional to the testing interval. So the 1387/324 = 4.28 reactors per confirmed incident will be reduced to 1 + 3.28/2 = 2.64 per incident.

Now the assumptions are clearly not exactly true, but we can consider how a more accurate description might affect the prediction. Taking assumption

(i) first, there will be multiple primaries. To the extent that this occurs, the number of reactors is independent of the testing interval so we have underestimated the expected number of reactors. There must also be tertiary infection, particularly towards the end of a longer test interval, and these will nearly all be prevented, so we have tended to overestimate the number of reactors.

The first part of assumption (ii) is probably valid, and if we suppose that infectivity commences at the same time as test sensitivity then any incubation period is irrelevant. However it is very likely that infectivity increases thereafter as the disease progresses, and most of the consequence of this will be at the end of the longer period so again we have tended to over-estimate the number of reactors expected.

Other means of surveillance, ignored in assumption (iii), such as slaughter monitoring, become less effective as within-herd prevalence is reduced, so we have tended to under-estimate the expected number of reactors.

The balance between these separate effects is difficult to assess, but it seems likely that we have a slight over-estimate of the number of reactors. We have ignored those cases where one incident might turn into two, one in each six month period - in fact the intensive surveillance following discovery of a reactor in a herd would usually cause these to be considered part of the same incident.

Reduction in number of incidents

If prevalence is reduced, as it must be even ignoring a reduced incidence of secondaries, then the incidence of herd to herd transmission among herds subject to the same control will be reduced accordingly. The incidence of primary cases from other sources, particularly badgers and herds outside the areas, will be unchanged. Now we did have some information on the relative importance of herd to herd transmission from the origins of infection given in 544 incidents over all areas, while only 61 were attributed to purchased animals or spread from contiguous premises. In annually tested areas we would expect less, say no more than ten percent, to be due to local herd to herd spread.

Our simple assumptions do enable an expression to be derived for the number of infected animals to be expected in a population subject to testing at intervals T, given the primary incidence; it is

$$n = \frac{pT}{2} + \frac{psT^2}{6} \qquad (1)$$

where p is the rate of occurrence of primary cases, and s the rate at which each primary gives rise to secondary cases. We can estimate s from the secondary:primary ratio at annual tests, which should be one half of s. If we also assume that

$$p_2/p_1 = 0.9 + 0.1\, n_2/n_1 \qquad (2)$$

gives the change in p on reducing prevalence from n_1 to n_2, then we get p_2 to be 93 percent of p_1 on changing to six monthly testing. Of course this is an approximation subject to all the effects of mistaken assumptions described

above, but they are not very important beside the assumption, expressed in Eq. (2), that only ten percent of p_1 is susceptible to reduction.

A CLASSIFICATION OF EPIDEMIC MODELS

Our remaining examples are concerned more directly with the problem of herd infection rather than what goes on within herds, although the two can never be entirely separated.

There is a paper by Briscoe (1980) according to which there are only four types of (human) epidemic model, according to whether or not superinfection occurs and to whether or not the force of infection is determined by human environmental contamination. Now superinfection (of the individual) is characteristic of parasitic diseases; at the herd level it occurs in all diseases but we ignore it nevertheless, as a first approximation to predicting herd incidence. We are left with two types of model, type I where the weight of infection is determined by the number of infectious individuals, and type II where this is not the case. Briscoe's examples are typhoid (type I) and tetanus (type II).

The type I model

This is essentially the classical epidemic model where individuals exist in one of two possible states, susceptible and infective, and transition between these states occurs at the rates indicated in figure 1. Susceptible individuals become infected at a rate proportional to their number and to the number of infected individuals at the same time, since it is contact with an infected individual that causes the transition. Infected individuals become susceptible at a rate proportional only to their own number, that is each one behaves independently of the rest.

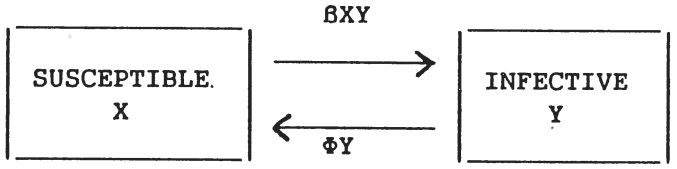

Fig. 1 Simplified model of disease type I

If we take X and Y to be proportions of the population, then X+Y=1 and we have a simple differential equation for Y;

$$\frac{dY}{dt} = (\beta-\Phi)Y - \beta Y^2 \qquad (3)$$

and provided $\Phi>\beta$ then Y is continuously driven downwards and eradication ensues. As Y ('prevalence') becomes small, the Y^2 term becomes negligible (it represents the 'wasted' infective to infective contacts) and the equation is that of simple exponential decay (Thrusfield and Gettinby, 1984); prevalence follows an exponential curve such that the natural logarithm of Y falls by an amount $\beta-\Phi$ per unit time.

The type II model

When infection does not derive from other infected individuals, but arises independently of prevalence, we have the transitions shown in figure 2.

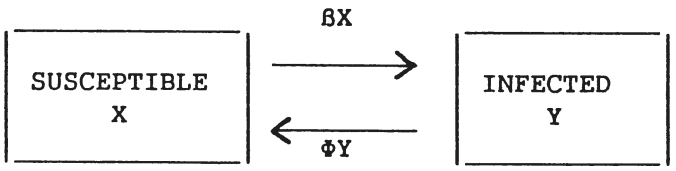

Fig. 1 Simplified model of disease type II

The differential equation for prevalence is now:

$$\frac{dY}{dt} = \beta-(\beta+\Phi)Y \qquad (4)$$

and the solution of this equation is:

$$Y_t = \frac{\beta}{\beta+\Phi} + \left(Y_o - \frac{\beta}{\beta+\Phi}\right) e^{-(\beta+\Phi)t} \qquad (5)$$

where Y_t is the prevalence at time t, and Y_o the prevalence at time zero. The solution represents a steady exponential decay of the difference between Y and $\beta/(\beta+\Phi)$, the steady level to which it is always attracted.

Comparison of the models

In these models β represents infection; infectivity in the case of type I and incidence in the case of type II. Recovery is represented by Φ, and in type I disease efforts are usually directed towards increasing Φ by detection and removal of infectives. In type II diseases, attention is directed towards decreasing β by reducing contact between animals and the source of infection.

BRUCELLOSIS TESTING

The brucellosis eradication programme in the UK proceeds by annual blood testing of all cattle, with the exception of cows producing milk for human consumption. The milk from dairy herds is subjected to a milk ring test (MRT), a cheap and effective method of screening dairy cows. The incidence of positives is now at a low level, and we were asked to consider what would be the effect of changing to blood testing beef herds every two years.

Brucellosis is a type I disease, and in the six years from 1981 to 1987 the annual number of reactors has fallen from 972 to 73. If we take these as proportional to prevalence, then the exponential decay is such that β-Φ is one sixth the logarithm of this ratio, or -0.43 yr^{-1}. The clear-up rate thus exceeds the contact rate by 0.43. If we were relying entirely on annual testing, then a change to two-yearly testing represents reducing Φ from two to one; it would appear that this would make β-Φ positive and reverse the progress towards eradication.

There are, however, two reasons for supposing that things might not be so bad. Brucellosis control depends on follow-up of recorded movements as well

as regular testing, and also the dairy sector (which would remain subject to MRT) provides a means of detecting contact infection in the beef herd.

Contact tracing is difficult to allow for in this simple model, but for contacts within the beef sector we can argue that it has little effect on the expected result of changing the testing frequency. Instead of individual herds, think of the units of the epidemic as 'nets' of herds joined by recorded movements or other traceable links. A net gives rise to another net when an unrecorded infectious movement takes place, and a net is removed in its entirety when one of its herds is detected at a regular test. If the average size of the nets has not changed over the years, then our estimate for $\beta-\Phi$ for this epidemic remains valid. The value of Φ should be greater than two for a 'net' of herds under annual testing, so halving it will tend, to this extent, to push the epidemic even more away from eradication.

It would appear then that an increase in the testing interval for beef herds would place more reliance on detection by contacts with dairy herds, where fortunately the MRT is available to rapidly reveal such contacts.

We would have more confidence in this analysis if results of control were available separately for beef and dairy herds and the extent of contact tracing within and between these sectors was recorded. The example does however show the danger of relaxing control without some assessment of the rate of decline of the epidemic under the existing regime.

TUBERCULOSIS IN CATTLE AND BADGERS

We return to the problem of tuberculosis in cattle in South West England, and specifically the link with infected badgers. The annual incidence of reactor herds was discussed in the Dunnett report (1986), where it was noted that the annual incidence from 1963 to 1984 is adequately described as constant until 1975/6, with a reduction at that time followed by a lower constant level. The report however has some difficulty relating this to the success of the badger gassing programme instigated in late 1975, since this "would have been expected to appear in the form of somewhat different statistical results" (page 66).

In fact, by seeing the gassing intervention as a reduction in β in a type II epidemic, the form of the results is entirely expected. Is this a reasonable model for the epidemic and for the intervention?

First of all it appears, both from data as discussed earlier and by analogy with other parts of the UK, that there is relatively little herd to herd spread, so that the epidemic in cattle herds is essentially of type II. The epidemic in badgers however is clearly self-contained, or type I, so we have to postulate that gassing was effective in limiting badger to cattle transmission but not so effective in limiting badger to badger spread as to result in a continuing decline in levels of badger infection.

This is plausible for two reasons. The first is that the badger epidemic is not close to eradication, so is not likely to respond much to moderate changes in the value of Φ. Secondly the areas chosen for gassing were selected on the basis of high incidence in cattle, so that any local variations in the relative infectivity of individual badgers for cattle and for other badgers would have contributed to this type of result.

So we conclude that badger gassing is a plausible cause of the reduction in incidence of cattle TB that occurred in 1975. This is not, of course, to criticise the decision to discontinue that policy which was based on other considerations.

CONCLUSIONS

The classification of epidemics into two types is based on gross simplification, but it is nevertheless a simplification that retains the most important characteristic of a disease that one might wish to control, whether or not it has a source outside the population to be controlled. If it does, incidence will be stable and control can only shift that stable level up or down. If it does not, then we have the conditions for eradication provided we apply sufficient control for long enough; controls may be relaxed, at the expense of a longer period to final eradication, but only after analysis of the progress of control to ensure that each infective individual is still removed before, on average, he infects one more.

Simplicity can be claimed as a virtue, leading to better understanding (Briscoe, 1980). We would echo that claim but feel that sometimes, due to lack of appropriate data, it is making a virtue of necessity.

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MILK COMPONENTS AS ROUTINE INDICATORS OF SUB-CLINICAL DISEASES AND USE IN EPIDEMIOLOGICAL RESEARCH

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Precise and frequent registration of the health status of individual cows, or groups of cows, is essential for an efficient application of modern preventive medicine in dairy herds. Health disturbances that lead to either clinically manifested diseases or severely impaired production, are easily observed and may also be easy to record. However, sub-clinical diseases or disturbances that lead to sub-optimal production, can seldom be observed. We therefore need other means to obtain information than the classical hands and eyes.

One example of such a diagnostic aid is the Compton Metabolic Profile Test (CMPT), which was presented almost 20 years ago and recently reviewed by Payne and Payne (1987). Since then it has been widely applied in the diagnosis of metabolic problems in dairy herds. However, the CMPT has also been criticized for being based more on possibilities of automated analysis than on biological relationships. Furthermore, the sampling of blood is cumbersome and limits its use for large-scale screening of the dairy cow population. Milk samples offer, at least from the sampling point of view, an alternative to blood samples that are suitable for mass analysis. Milk samples are already taken on a large scale in many countries, where they constitute the backbone of the milk recording scheme. It would thus be ideal if the same milk samples could be used to monitor the health status of the cows.

Milk has also been used for many years as a medium for diagnostic tests, notably the counting of somatic cells in milk as an aid in detecting mastitis. Methods to analyse milk samples for components other than the usual fat, protein, and lactose, and which may be related to the health status, are constantly being developed. Some of these methods can easily be automated and lend themselves readily to mass analysis. It is therefore conceivable that we will, in the near future, use a Milk Profile Test to help in diagnosing sub-clinical or sub-optimal conditions. In fact, there already exists knowledge of, and methods to analyse for, a number of milk components that can constitute some of the components in such a test. This paper discusses briefly some of these components and presents some results of epidemiological studies on such components pertaining to ketosis and virus infections.

POSSIBLE COMPONENTS IN A MILK PROFILE TEST

In looking for components to include in a milk profile test it is of interest not to disturb one basic property of the medium, i.e. that milk samples are

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cheap and easy to obtain, at least in most industrialized countries. Analyses should therefore be as simple and cheap as possible and it is preferable that the components can be extracted from milk samples already taken. For instance, bulk tank milk samples are frequently taken in order to monitor quality aspects (e.g. somatic cell counts, bacteria count, antibiotic residues), but other analyses could be made as well, to render the bulk samples useful for diagnosing health problems on the herd level. Furthermore, milk samples from individual cows are often taken in milk recording programs and analysed for fat and protein content. These analyses could also be supplemented by others, thus constituting a diagnostic aid on the individual or the herd level. It is especially suitable to use these samples in countries such as Sweden, where results from milk quality control laboratories, milk recording and artificial insemination activities, etc, form a single uniform database, as other sources of information may be needed in order to increase the interpretability of the milk profiles.

A milk profile test is not necessarily confined to monitoring health disturbances, but may also be used to detect deficiencies in feeding and problems with production. Such a broad use of the milk profile as a diagnostic aid, naturally affects its construction, i.e. what components should be included.

Milk yield

The daily milk yield of the individual cow is usually recorded every month in most milk recording programs. Variations in the milk yield may not be particularly useful in diagnosing a specific disease, but may nevertheless yield valuable information. The shape of the lactation curve may for instance be used to indicate energy-deficient diets or problems with ketosis. A sudden fall in the production of individual cows or groups of cows is usually caused by health or feeding problems that call for further investigation. It has been shown for instance that the milk yield may decrease already a couple of weeks before clinical signs are observed, in certain metabolic disorders (Lucey et al., 1986; Rowlands & Lucey, 1986). A more frequent registration of the milk yield, as can be done in individual herds, is naturally even more informative.

Milk fat

A constant monitoring of the milk fat concentration may quickly detect problems with the so-called 'low milk fat syndrome', i.e. a sudden reduction in milk fat concentration usually caused by too little roughage in the ration. Early detection is beneficial, as it minimizes the losses for the farmer. Changes in the milk fat content also occur in conjunction with several diseases, but these changes are usually not large enough to be of use in diagnosing the disease.

Somatic cells

The somatic cell count has been used for many years as an indicator of mastitis and is therefore a self-evident component in a milk profile test. The use of bulk tank or quarter milk samples has a longer tradition, but the use of composite milk samples from individual cows has attracted increasing interest, as the milk already sampled in the milk recording scheme can be used for such analyses. In Sweden, as in many other countries, farmers are now given monthly somatic cell counts for individual cows on a routine basis. The use of somatic cells as an indicator of mastitis has proved reliable and is a well established procedure that does not need to be elaborated on here. However, it deserves mention that mastitis is indeed a dynamic process and that the somatic cell

count is affected by other physiological factors besides mastitis. Consequently, the cell counts that are reported to the farmers in Sweden are currently adjusted for breed, parity, milk yield, and stage of lactation. It should also be kept in mind that the interpretations will be more reliable if a sequence of cell counts is used rather than a single count.

Acetone

The concentration of acetone in milk can be used as an indicator of hyperketonaemia (Andersson, 1988) and semiquantitative methods to test for ketone bodies in milk have been used for several years in preventive veterinary medicine. Recently, a reliable procedure has been developed to quantitatively assess the acetone concentration in milk (Marstorp et al., 1983). This procedure, based on flow injection analysis (FIA) technique, is cheap and easy to perform, insensitive to diurnal variation and sample treatment, and the ordinary milk samples taken in the milk recording scheme can be used. Thus, this method constitutes a means for routine screening of the cow population for hyperketonaemic individuals or for herds with problems with sub-clinical or clinical ketosis. This can identify herds that need advice on feeding in order to reduce the prevalence of hyperketonaemia. Such a reduction may also cut costs for the farmer since impaired production and fertility can be an effect of hyperketonaemia (Andersson et al., 1988) However, a sampling interval of one month, as in the Swedish milk recording scheme, may be too long for using the milk acetone determinations to help in deciding on treatment for individual cows. Furthermore, factors other than feeding must be considered when interpreting prevalence of sub-clinical ketosis based on milk acetone measurements, since it has been shown that the acetone concentration is affected by systematic factors such as breed, lactation number, season (e.g. Andersson & Emanuelson, 1985).

Urea

The concentration of urea in blood is related to the intake of crude proteins, or rather to the relation between the intake of protein and energy (Payne & Payne, 1987). However, it has been shown by Oltner and Wiktorsson (1983) that there is a strong correlation between levels of urea in serum and milk, and also that there is a strong correlation between milk urea concentration and the ratio between protein and energy in the ration. Thus, a high level of urea indicates feeding of excess amounts of crude protein, usually together with too little easily digestible energy feed. Low levels often indicate extensive feeding with low protein diets. Milk urea analyses could consequently be used to screen for herd owners needing feeding advice. However, this is not only of interest from a purely nutritional aspect, since there may be a negative association between urea concentrations and fertility (Ropstad & Refsdal, 1987). Again, correction of the milk urea concentration may be necessary, as it has been shown to be influenced by factors such as season, live weight, age, etc. (e.g. Oltner at al., 1985; Payne & Payne, 1987).

Progesterone

Rapid and accurate laboratory tests for progesterone in milk are available and good cow-side tests are also emerging, thus promoting a more systematic use of progesterone testing in fertility management. Although it is often beneficial to get immediate answers when dealing with heat detection, for example, the time consuming but more accurate laboratory tests can still be useful e.g. for early, negative pregnancy checks, to detect sub-fertile cows for further investigation, to monitor the effects of cyst treatments, etc.

Virus antibodies

Antibodies against a number of viruses can be detected in milk by using the enzyme-linked immunosorbent assay (ELISA) technique. The use of milk instead of serum is especially valuable, since it is possible to use milk already sampled for other purposes in the analyses, and the milk samples can be frozen without prior centrifugation. Bulk tank milk samples can also serve as a meaningful, combined sample from all milking cows in the herd. Such samples could thus be used to screen for positive herds, in which all cows could be sampled subsequently. Examples of viruses that can be detected by analysing milk samples for antibodies are infectious bovine rhinotracheitis (IBR) virus (Bommeli & Kihm, 1982), bovine leukaemia virus (BLV) (Florent, 1988) bovine virus diarrhoea virus (BVDV) (Niskanen et al., 1988), and bovine corona virus (BCV) (Larsson et al., 1989).

Other components

The components mentioned above would probably form the backbone of a milk profile test, although other components may also find their place there. The number of possible components will probably continue to increase as new techniques to analyse milk samples are developed. Some speculations on other potential components can be offered:

Lactose and citric acid: Lactose and citric acid are two components that are easy to obtain, since most modern apparatuses that are used to analyse for milk fat and protein are capable of measuring them simultaneously. Both components have been proposed as alternatives to or to complement somatic cells as indicators of mastitis (e.g Renner, 1980; Oshima & Fuse, 1981), but more research into their suitability is called for. There are also a number of other alternatives to somatic cell counting, e.g. conductivity, bovine serum albumin, *N*-acetyl-ß-D-glucosaminidase (e.g. Miller, 1984; Emanuelson et al., 1987), but they all need special measuring equipment.

Trace elements: Payne and Payne (1987) state that "all essential trace elements merit inclusion in the profile test", and that copper and selenium come first in priority. The analysis of such elements in milk should not give rise to any insuperable problems and may be of value in a milk profile test, once the biological interpretation of the values found in milk has been substantiated.

EPIDEMIOLOGICAL STUDIES

The great advantage of a milk profile test is that the milk is easy to obtain and the test is reasonably cheap, and can therefore be used as a routine indicator of sub-clinical diseases. Such a use also yields large materials for use in epidemiological studies. This is especially valuable for studies on production diseases, which are multifactorial and therefore require very large materials in order to be able to draw firm conclusions. Large materials are also necessary when studying the genetic background of diseases and pertinent parts of the milk profile outlined above have been used to study the heritability of ketosis and mastitis (e.g. Emanuelson & Andersson, 1986; Emanuelson, 1987, 1988a). Examples of the use of tests performed on milk in epidemiological studies are presented in the following.

Virus antibodies in milk

Bovine virus diarrhoea virus: Infections with BVDV in cattle have been reported from a number of countries and the virus has a worldwide spread (Stöber, 1984). BVDV, which infects susceptible, pregnant cattle, can cross the placenta and invade the fetus. The outcome of infection can vary from fetal death to the birth of healthy or apparently healthy, but persistently infected, calves. Fetal death or abortion in cows during the first trimester of pregnancy usually passes unobserved and is perceived as infertility (Carlsson et al., 1988). In Great Britain, BVDV is considered to be the most serious viral pathogen causing reproductive failure. The financial losses attributable to BVDV infections are difficult to estimate, however, due to current lack of suitable data on the incidence and outcome of this infection in dairy cows (Richards, 1987). Epidemiological studies are therefore needed, and such studies would also be of importance when formulating control strategies for BVDV. The indirect ELISA for detection of antibodies to BVDV in individual milk samples, as described by Niskanen et al. (1988), will certainly be helpful in obtaining datasets suitable for epidemiological studies.

In an ongoing epidemiological study of BVDV, milk samples from more than 3000 cows in 150 dairy herds in different parts in Sweden have now been analysed using this ELISA technique. Data from this study have shown that bulk milk samples (BMS) can give representative information on herd immunity to BVDV (Niskanen, unpublished results). Thus, herds that have low absorbance values (0.00-0.03) in undiluted BMS can be regarded as uninfected as regards BVDV. Usually all cows in these herds are completely seronegative to BVDV, though a very small proportion may have low antibody titres to BVDV. In contrast, some 90-100% of cows in herds with high absorbance values (0.80-1.20) in the BMS, have antibody titres to BVDV.

Consequently it is feasible to get a good picture of the BVDV status in a large number of herds with this indirect ELISA method, as it is easy and inexpensive to perform. Recently, BMS from 244 dairy herds in two counties in central Sweden were analysed, using this technique; 86 (35.2%) of these herds had low absorbance values (0.00-0.03) and were classified as uninfected with BVDV. The majority of the other 158 herds, classified as infected, had high absorbance values in the BMS, indicating a large proportion of seropositive animals in these herds. The owners of the 244 dairy herds in this study were asked in a questionnaire if they had purchased any cattle (calves, heifers or cows) during the preceding 5 years. 111 (70.3%) of the owners of the 158 infected herds stated that they had purchased animals during this period, compared with 43 (50.0%) of the owners of the 86 uninfected herds.

Preliminary analyses of data from 42 dairy herds in the county of Skaraborg (southwest Sweden), indicate that uninfected herds appear to have a better general fertility than infected herds. The mean 56-day non-return rate for first calvers in the 14 dairy herds classified as non-infected was 70%, compared with a mean of 59.5% ($p<0.01$) in the 28 herds classified as infected. However, this apparent correlation between fertility and BVDV infection is rather uncertain, as the BVDV status of these herds was determined on the basis of only one BMS from each herd and the fertility data were calculated on records from the year before the testing of the BMS. In the above-mentioned epidemiological study of BVDV, milk samples will be taken twice, with a one-year interval, from all cows in altogether 200 dairy herds, approximately. Fertility can then be compared between herds with active BVDV infections among the cows during that period, and herds with seropositive cows but no seroconversions, or BVDV-free herds. When completed, this study will hopefully give a better understanding of the effects

of BVDV on fertility and health in dairy herds.

Bovine corona virus: The causative agent of winter dysentery or epizootic enteritis among cows is often described in the literature as unknown. We now have serological evidence that outbreaks of epizootic diarrhoea in Sweden are caused by BCV (Alenius et al., 1989), thereby confirming the results of other authors indicating that BCV was the etiological agent of winter dysentery (Takahashi et al., 1980; Espinasse et al., 1982). BMS from 299 herds in two counties in Sweden were recently examined for antibodies to BCV, using an indirect ELISA. Antibodies to BCV were detected in 298 of the samples. Absorbance values, in the ELISA for BCV antibodies, were significantly ($p<0.001$) higher in milk samples from 87 herds where outbreaks of contagious diarrhoea had occurred during the last 2 years, than in the other herds. This association indicates that examinations of BMS can be used to measure the status of immunity to BCV in a herd and to predict the risk of appearance of winter dysentery. Screening of BMS could then be used in order to study how BCV may affect production and also its influence on other disorders, e.g. sub-clinical mastitis, acetonaemia, etc.

A study of hyperketonaemia

Ketosis has been the subject of numerous epidemiological studies and, consequently, much is already known about its etiology. However, in the view of the complexity of ketosis, a large database is required in order to thoroughly analyse certain relationships, e.g. with fertility and production. Milk tests for acetone content may be the best way to get the datasets needed, since large databases with clinical recordings are available in only a few countries, e.g. Norway, Finland and Sweden (Solbu, 1983; Gröhn et al., 1986; Emanuelson, 1988b). Using milk acetone to indicate hyperketonaemia also gives another advantage, as it has been shown that the clinical recordings may underestimate the true prevalence considerably (e.g. Andersson & Emanuelson, 1985).

A large field study, where milk acetone determinations were used as indicators of hyperketonaemia, has recently been concluded in Sweden. About 470 herds were randomly selected to participate and recordings were made over 3 years. Milk samples for acetone determinations were taken at the regular monthly production tests within 60 days after calving, from all cows in all the herds. The cows were categorised according to their highest milk acetone value into classes 1-4, representing milk acetone concentrations of $\leq$0.4, 0.41-1.00, 1.01-2.00 and >2.00 mmol/l, respectively. Milk acetone concentrations exceeding 0.4 mmol/l were considered as denoting hyperketonaemia, according to Andersson (1988). Data on milk yield and fertility were collected from the milk recording scheme and the official artificial insemination (AI) records. The data for calvings that took place during the first 1½ years of the study have already been analysed (Andersson et al., 1988). This material comprised information on 15,438 cows, of which 5,633 were first calvers. The cows were of mainly the two dominant dairy breeds in Sweden, Swedish Red and White (SRB) and Swedish Friesian (SLB).

In order to study the effect of hyperketonaemia on milk production a least-squares analysis of variance was carried out. The model included the combined effect of herd-year-season (HYS) of calving, the effect of cow within HYS, and the effect of stage of lactation, and the analyses were performed within breed (SRB or SLB), parity (first calver or older cow), and milk acetone class (1-4). The resulting lactation curves (Figs. 1-4) show that there was a fall in milk yield during peak lactation for cows with hyperketonaemia (acetone classes 2-4). This milk loss increased with increasing acetone concentration, the worst

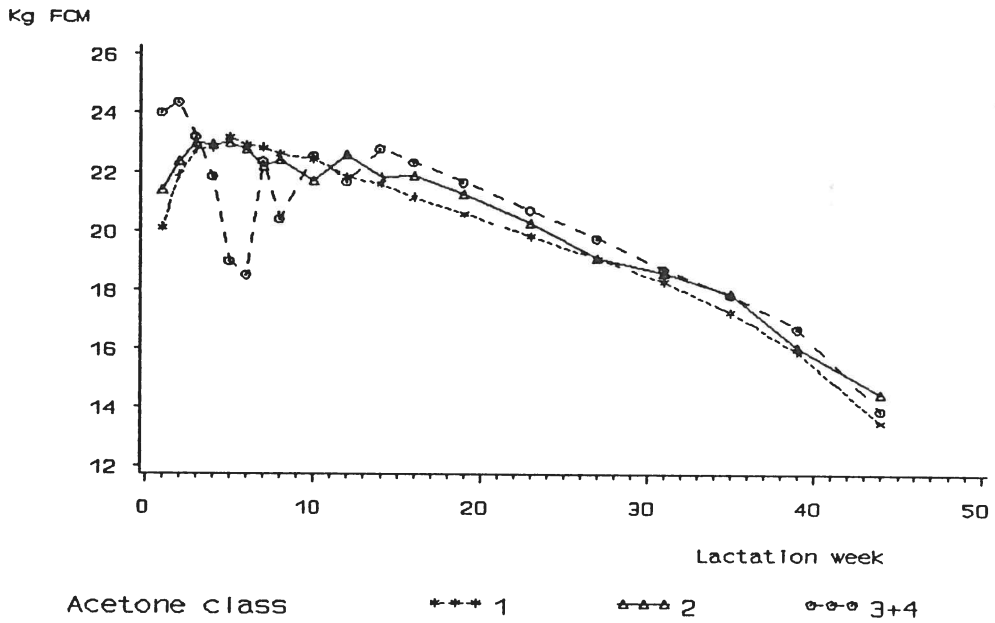

Fig. 1 Daily milk yield (kg FCM) in acetone classes 1-4 for Swedish Red and White cattle in lactation number 1, presented per lactation week (LS means).

affected category being multiparous SRB cows in acetone class 4. The production loss during peak lactation in acetone classes 2 and 3, seems to be compensated later in the lactation. This was verified in other analyses, on 305-day lactation yields, where cows in acetone classes 2 and 3 gave at least the same yield as cows in acetone class one. The lactation curves indicate that the milk yield early in lactation increased with increasing acetone class. Other analyses also showed that there were indeed significant differences in kg FCM at the first test after calving, between cows in different acetone classes. Undoubtedly it would be interesting to study possible differences between groups of cows that have equally high initial milk yields, but where one group develops hyperketonaemia and the other does not. Such a comparison might be feasible using the complete material from this study.

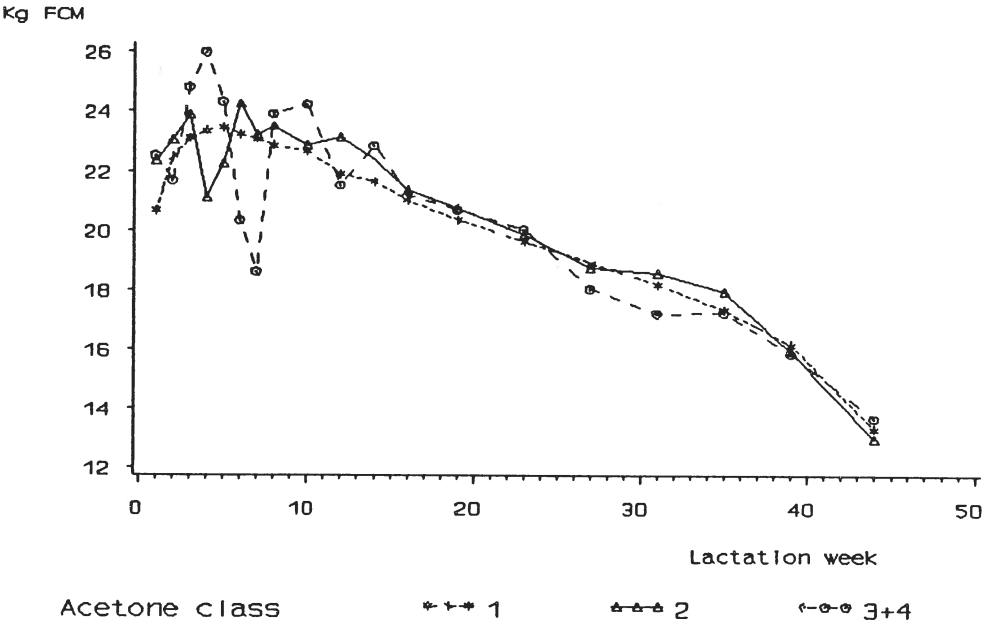

Fig. 2 Daily milk yield (kg FCM) for acetone classes 1-4 for Swedish Friesian cattle in lactation number 1, presented per lactation week (LS means).

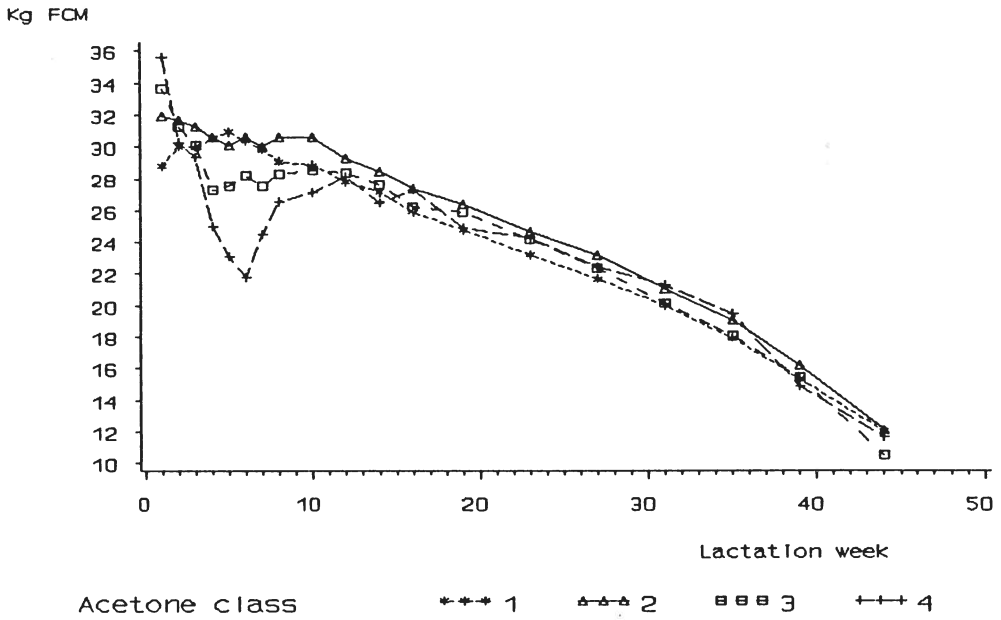

Fig. 3 Daily milk yield (kg FCM) in acetone classes 1-4 for Swedish Red and White cattle in lactation number >1, presented per lactation (LS means).

Only preliminary analyses of the relationship between hyperketonaemia and fertility have been conducted so far. Table 1 shows some fertility measures and there is a marked tendency towards an impaired fertility with increasing acetone concentrations. The differences proved significant ($p<0.05$) when tested with ordinary *t*-tests (the chi-square test for ovarian cysts).

CONCLUDING REMARKS

It is beyond doubt that a milk profile test is useful for general management, and also for health management, of dairy herds. The milk profile can be made more or less sophisticated, depending on the purpose of its use and on the cost of obtaining the different components. Such a profile will probably be valuable

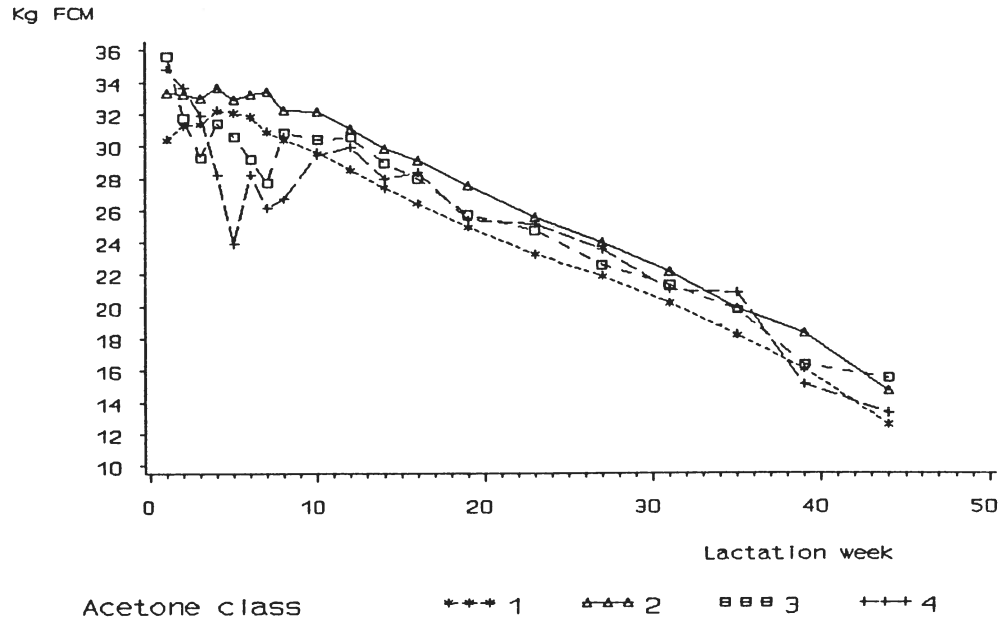

Fig. 4 Daily milk yield (kg FCM) in acetone classes 1-4 for Swedish Friesian cattle in lactation number>1, presented per lactation week (LS means).

Table 1 Overall means of intervals from calving to first service and to last service, number of AI, and frequency of ovarian cysts for cows in different acetone classes

	Acetone class			
	1	2	3	4
Calving - first AI (days)	81.2	85.1	85.6	89.6
Calving - last AI (days)	103.5	110.4	112.3	116.5
Number of AI	1.77	1.80	1.84	1.96
Ovarian cysts (%)	0.98	1.75	2.93	4.11

for both farmers and veterinary practitioners, as well as for others involved in managemental advisory work, provided they are given ample information on how to interpret the profile. Further research is advocated in order to substantiate the interpretations of the already existing components and to explore other possible components.

Currently, no unified milk profile test has yet been introduced in Sweden, although some components of such a test are already in routine use. Thus, milk yield, milk fat and protein content, and somatic cell counts are components in a milk profile test that are already being measured every month in herds in the official milk recording scheme. Educational efforts are currently in train in order to make farmers and veterinarians aware of the value of these measurements for determining the causes of sub-clinical diseases or sub-optimal production. Analyses of milk acetone and urea content performed at central laboratories can currently be provided for special investigations. However, it is possible that these analyses will be made on routine basis in a few years, but, in that case, they will be offered as an option for the farmers. Progesterone analysis is not used to any great extent in Sweden at present, but it is likely to increase in the future. A project has recently been initiated in order to evaluate both a cow-side and a laboratory test for progesterone and to learn how they are best used in practice.

Tests for antibodies to viruses in bulk milk samples have given promising results, showing that they can be used in control programs. Thus, a program, whose goal is to reduce the incidence of BLV in Swedish dairy herds is currently being outlined, where this technique will be utilized. Bulk milk samples will be screened for antibody-positive herds in the first step, and milk samples from individual cows in these herds will be tested in the second step. Continuous monitoring of bulk milk samples can then be used to verify the results of the measures taken in positive herds.

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CATTLE EPIDEMIOLOGY AND PREVENTIVE MEDICINE

ANALYSIS OF RISK FACTORS FOR INFECTION OF CATTLE HERDS WITH LEPTOSPIRA INTERROGANS SEROVAR HARDJO

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Leptospira interrogans serovar hardjo (L. hardjo) is recognised as an important cause of reproductive failure and agalactia in cattle and a cause of human illness in persons exposed to cattle (Pritchard, 1986). Numerous surveys in the U.K. have shown that about one third of aborting cattle have antibodies to L. hardjo but the prevalence of herd infection has received less attention. Clearly such information is of considerable value in planning control measures for L. hardjo. In South West Wales a study by Morgan et al.(1981), using 10 sera from each of 90 herds, 59% of herds had at least one animal with antibody to L. wolffii (a leptospire which is closely related antigenically to L. hardjo). It is known that cattle are the major maintenance host for L. hardjo although some studies have suggested sheep may also act as maintenance hosts. L. hardjo has been found in a wide range of species sharing their habitat such as horses, pigs, deer and man (Pritchard, 1986). Although wildlife in the U.K. are infected with an antigenically related serovar (L. saxkoebing) there is no evidence that wildlife act as a reservoir of L. hardjo infection (Little et al.,1986). Leptospires are known to be excreted in the urine and in secretions of the reproductive tract. Experimental infection has been transmitted by the venereal route as well as by the conjunctiva, mucous membranes and abraded skin. The contamination of surface waters with leptospires has been shown to be an important mode of spread of leptospires (Faine, 1982). Transmission of leptospires in the U.K. tends to be seasonal with peaks coinciding with warm wet weather in summer and autumn. The entry and spread of L. hardjo into a fully susceptible herd is often accompanied by a propagating epidemic of milk drop and abortion in the cows, and by human disease. The source of L. hardjo in such cases can often be traced to the purchase of infected heifers, cows or bulls but occasionally follows flooding of the farm with run off waters from neighbouring infected farms. Rarely the source in closed herds appears to be the introduction of infected sheep (Pritchard,1988,unpublished data).

A systematic random sample of 183 herds was taken from all the herds in the county of Herefordshire by selecting blood samples from routine screening tests (Pritchard et al.,1987). From this sample of farms, 22 accepted invitations to further blood sampling and to complete a questionnaire. As this response was insufficient, a further sample was sought and 56 more farms volunteered. This paper reports the results of this "questionnaire survey" on 78 farms with respect to antibodies to L. hardjo and their relationship to a variety of demographic, husbandry and management factors. Details of results of tests for antibody to other leptospiral serovars and disease histories will be published separately.

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ERRATUM

Page 131, Table 1, column 2, row 12 in the body of the table : for 'farms by cattle' read 'farms with cattle'.

Page 132, line 19: for 'Bull' read 'Purchase', and, after line 21, insert: 'Bull – value = 1 if bull present on farm or natural service used'.

Page 134, Table 3, column headings: for 'With hardjo antibody' read 'Without hardjo antibody'; for 'Without hardjo antibody' read 'With hardjo antibody'

MATERIAL AND METHODS

The questionnaire consisted of a computer input form in which each answer was coded as detailed in Table 1. Additional case history of interest was also noted to assist in coding forms. The questionnaire was completed during a farm visit. To standardise results the four interviewers were each briefed on the detail required to code each answer so that an agreed standard was maintained. This frequently involved asking the same question in several different ways to ensure that interviewees, (usually the owner, herd managers and cattle men) fully grasped the issue at stake.

Table 1

Summary of data collected by Questionnaire.

Factor	Measure
Farm reference	County Parish Holding Number
Farm type	Dairy, Beef or, mixed - coded 0,1,2.
Dairy cattle herd	Number of bulls, cows, heifers and calves
Beef cattle herd	Number of bulls, cows, heifers and calves
Sheep flock	Number of ewes, rams
Goat flock	Number of goats
Horses	Number of horses
Dogs	Number of dogs
Grassland	Number of hectares
Arable	Number of hectares
Drainage - rivers	Access to rivers or streams by cattle
Drainage - waters	Access to run-off from other farms by cattle
Rodent control	never = 0 when problem = 1 regular >monthly = 2 regular <monthly = 3
Housing cows	none=0, cubicles=2, cowshed=3, yard=4
Milking parlour	Bucket=1, Tandem=2, Abreast=3, Chute=4
Time in parlour	hours a.m and p.m
Purchase or leasing	during last 5 years - none=0, any=1
Mating cows	own bull=1, hired bull=2, AI=3, DIY AI=4
Mating heifers	own bull=1, hired bull=2, AI=3, DIY AI=4
Sheep/cattle cograze?	no=0, yes=1
Heifers/cows cograze?	no=0, yes=1
Heifers/sheep cograze?	no=0, yes=1
Heifers/calves cograze?	no=0, yes=1
Age heifers calves	2, 3 or 4 years
Calf feeding	suckled = 1, cross-suckled = 2, milk substitute = 3
Calf/cows housed	together = 1, separate = 2
Calf/cows grazed	together = 1, separate = 2
Heifers reared	same farm = 1, different farm = 2
Calves reared	same farm = 1, different farm = 2
Abortions	number of abortions recalled by farmer in last 5 years
Milk drop	whether herd milk drop seen in herd in last 5 years
Agalactia	Number of cases of agalactia recorded in last 5 years

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Adult (over one year old) heifers, bulls and cows were selected for blood sampling at this visit to obtain a stratified sample for the adult herd (Anon, 1988. At the blood sampling visit further questions were asked in order to corroborate the data. Live antigen microscopic agglutination test (MAT) were conducted as described by Pritchard (1986) with the addition of serovar hardjo strain b215. This strain has been shown by restriction endonuclease analysis (Pritchard D.G. and Woolley J.C., unpublished data 1986) to be similar to genotype hardjo-bovis described by Marshall et al.(1985).Cattle with sera giving 50% or more agglutination at a serum dilution of 1/100 were regarded as positive. A herd was regarded as positive if one or more sera from the herd were positive to L. hardjo. Sera from negative herds was also tested by a blocking ELISA assay using peroxidase labelled mouse monoclonal antibody (K1-10) (Stevens et al.,1985) specific for the Sejroe serogroup.

Analysis of results were conducted using standard statistical techniques using Minitab program (Ryan et al.,1976). From the questionnaire data the following "summary" variables were produced:

Herd size - total number of cattle on farm.
Stocking rate - total livestock units/grassland hectares (Nix,1988).
Bull - value = 1 if any cattle purchased in previous 5 years; if not = 0.
River - value = 1 if river present on farm; if not = 0.
Sheep - value = 1 if sheep present on farm except on winter keep; if not = 0.

A step-wise linear regression was performed using the presence of L. hardjo antibody in the cattle herd (coded as: present = 1; absent = 0). The independent variables consisted of the "summary" variables and all variables in Table 1 and variables used to produce "summary" variables. At a 95% probability this identified herd size, the use of a bull, purchase of animals, a river and the presence of sheep as significant variables. The GLIM computer program (Baker & Nelder,1978) was used to estimate the odds ratios of these variables using a logistic transformation and multiple regression analysis.

RESULTS AND DISCUSSION

Antibody to L. hardjo was found in 66 (84.6%) of 78 herds completing the questionnaire. Overall 3408 cattle were tested and 825 (24.2%) had antibody to L. hardjo. Both herd prevalence and cattle prevalence in the questionnaire sample were significantly higher than those found in the systematically selected random selected of this population. (The random sample had a herd prevalence of 115/183 (63%) (Chi square = 12.2 $P<0.005$) and a cattle prevalence of 579/2691 (21.5%) (Chi square = 6.15 $P = 0.008$)). It is clear that the questionnaire sample is biased towards herds with L. hardjo antibodies. The questionnaire sample was also significantly biased towards dairy herds as it had 56 dairy herds (71% of all herds in the sample) compared to the random sample which contained 83 dairy herds (45%) of all herds (Chi square = 13.36 $P<0.005$). The systematic randomly selected sample was not significantly different to the actual distribution of dairy and beef herds in Herefordshire.

While the questionnaire sample is not representative of farms in Herefordshire the use of this study base for examining the relationships between L. hardjo infection and possible risk factors is valid. The study base for investigating causal relationships is a matter of choice as it is not inherent to a particular problem and is likely to be independent of spatiotemporal effects (Miettinen,1985).

Although there was a tendency for farms with L. hardjo to be larger, and have larger herds of cattle and flocks of sheep, these effects did not reach the 5% significance level (Table 2).

Table 2

Summary of farm size and animal numbers in herds with and without antibodies to serovar hardjo.

factor	With hardjo antibody mean	Without hardjo antibody mean	F value
Dairy Cattle	124.4	82.1	2.20
Beef Cattle	13.8	9.3	0.21
Sheep	148.2	35.6	2.61
Goats	-	-	-
Horse	0.8	1.8	1.80
Dog	2.1	2.0	0.03
Grass (hectares)	78.1	53.5	1.44
Arable(hectares)	43.6	30.2	0.41
Herd size (cattle)	138.2	91.4	3.56
Stocking density units/hectare	0.72	0.69	0.03

Table 3 lists the distribution of factors in herds with and without L. hardjo and gives the chi square statistic for unadjusted data. Both exposure to rivers and access to run-off waters are more common in L. hardjo infected herds but only the river factor variable reached significance. This factor was also selected by stepwise regression.

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Table 3

Distribution of factors in herds with antibody and in herds without antibody to L. hardjo

Factor	With hardjo antibody %with factor	Without hardjo antibody %with factor	Chi square +
River	41.6	77.2	6.35
Drain	25.0	39.3	0.90
Rodent control			
never (4 farms)	75	25	
when a problem (28 farms)	71	28	
regular >monthly (34 farms)	97	3	
regular <monthly (12 farms)	83	17	8.08*
Out wintered	16.2	4.5	2.48
Kennel/Cubicle	66.6	66.6	0
Cow shed	8.3	7.5	0.008
Covered yard	41.6	51.5	0.29
Bull purchase	25.0	56.0	3.92
Cow purchase	55.3	71.2	0.79
Heifer purchase	25.0	62.1	5.60
Calf purchase	41.6	48.4	0.18
Cow mating : own bull	0	41.0	15.17
" " : hire bull	16.6	21.2	0.129
" " : A.I.	91.6	80.3	0.89
" " : DIY A.I.	0.0	6.0	0.76
Co-grazing with sheep	33.3	37.8	0.09
Calf rearing	33.3	34.8	0.01
Calf/yearling grazing	27.2	33.8	0.184
Calf/cow grazing	36.3	20.0	1.45
Calf/yearling housed	18.1	30.7	0.72
Calf/cow housed	18.1	26.1	0.31
Heifer/cow grazing	75.0	59.0	1.08
Heifer/sheep grazing	9.0	37.0	3.49
Heifer mating : own bull	0	53	11.54
" " : hire bull	16.6	13.6	0.71
" " : A.I.	83.3	53.0	3.82
" " : DIY A.I.	0	6.0	0.7
Heifer keep	16.6	34.8	1.54
Calf feeding			
Dam	58.3	60.6	0.02
Cross suckling	8.3	19.7	0.89
Artificial milk	33.3	46.9	0.76
Cows milk	66.6	46.9	1.56
Summary variables			
Bull	33.3	78.9	10.36
Sheep	25.0	68.18	7.99
Purchase	66.7	92.4	6.60

+ Chi square with 1 degree of freedom except where marked *.
* 3 degrees of freedom

No evidence was found of associations between housing, co-grazing of cows/heifers/calves or calf and heifer rearing variables and L. hardjo infection. Only one farm did not house cattle, 58 farms used one housing method, 18 used two methods, and one farm used three methods. It has been suggested that spread of L. hardjo may be increased by housing cattle but this could not be adequately examined in this study, since only 5 farms outwintered cattle. Interestingly 3/56 infected farms outwintered compared to 2/10 non-infected farms.

Purchase of bulls and of heifers were both significantly associated with L. hardjo infection. Purchase of cows and calves were not associated. Only qualitative measures of purchase over the last 5 years could be readily and reliably obtained. An analysis of quantitative measurement of class and number of animals purchased and their source (farm or market of dealer) may prove informative. The purchasing policy of most farmers was to buy heifers, and bulls and unweaned calves. Very few cows were purchased. As purchases of different classes of cattle were correlated a single measure of purchase was produced which was identified as a significant variable in the stepwise regression.

Obtaining a reliable co-grazing history of cattle and sheep proved very difficult and this variable had to be coded as a missing value on several farms. There did however appear an association between co-grazing of heifers and sheep and L. hardjo infection. A more valid variable was the presence or absence of sheep on the farm on the day of the questionnaire visit, which was more strongly associated with L. hardjo infection.

Natural service using the owners bull on both cows and heifers was significantly associated with L. hardjo, whereas artificial insemination was more common in herds without L. hardjo antibody. As a correlation existed between the use of bulls for natural service in heifers and cows, a combined variable was produced for use in regression analysis.

The frequency of rodent control was apparently associated with L. hardjo infection but this variable was not selected in the regression analysis. It appears that this is due to a confounding effect with herd size; larger herds tend to use more frequent rodent control. L. hardjo has not been recorded as being isolated from rats or mice in the U.K. (Pritchard, 1986; Little et al. 1986) although these species are recognised as carriers of other serovars.

The 5 variables selected by step-wise linear regression were subjected to a logistic regression analysis to produce the odds ratios shown in Table 4. The (approximate) 95 per cent confidence limits of the odds ratios were estimated using the errors from the regression equation. The lower limits were above 1.0 for the presence of a river and the presence of sheep but were less than 1.0 (i.e. non-significant) for 'bull' and 'purchases'. Given the small sample size of 78 farms it was not surprising that these estimates had such wide confidence limits.

Table 4

Estimates of risk factors for antibody to hardjo among cattle herds from logistic regression analysis.

Factor	Odds Ratio	95% Confidence Limits Lower	Upper
Herd Size	1.02	1.00	1.03
River	7.94	1.28	49
Sheep	6.65	1.09	40
Bull	3.90	0.75	20
Purchase	1.97	0.19	19

It appears from these analyses that herd size, the presence of a river and of sheep, the use of a bull and purchases of cattle may be useful predictors of the risk a herd becoming infected with L. hardjo. Prospective studies have shown that a proportion of cattle maintain a serological response to L. hardjo for several years (and some for their life) following infection. Thus the presence of antibody in a herd at a particular time is in part a measure of the cumulative incidence over the previous years. The presence of L. hardjo antibodies in a herd is a measure of four events (i) the introduction of L. hardjo in to the herd, (ii) its spread through the herd and vertical spread from cows and bulls to foetuses, calves, heifers and young cows, (iii)the persistence of antibody in individual animals, and (iv) the survival rate in the herd. Vaccination can also induce a transient agglutinating antibody response but none of the herds in the trial used leptospiral vaccines prior to sampling. In general most herds with antibody to L. hardjo will have been L. hardjo-infected (if not infectious) cattle, unless vaccination or antibiotic therapy has been used. Occasionally, antibody is only present in a cohort of purchased cattle or a cohort which has undergone exposure to L. hardjo outside the farm (e.g. heifers at keep) or aged cattle which, although in contact with the herd for several years, have not transmitted infection to susceptible cattle. Sporadic antibody titres to L. hardjo may also be due to paradoxical reactions to infections with other leptospires. Unless any of these situations apply, herds with L. hardjo antibody should undergo a control programme involving vaccine and strategic use of antibiotics. This is necessary not only to prevent human infections but also to reduce losses due to reproductive failure and milk loss (see Pritchard,1986; Pritchard et al.,1987).

In herds which do not have antibody to L. hardjo it is necessary to assess the likely risk of introduction of L. hardjo into the herd. The logistic model described in Figure 1 was used to predict whether a herd would become infected, using all the variables in the equation. If the predicted prevalence is plotted against herd size then a sigmoid curve is produced. Adding risk factors to the equation results in increasing prevalence. For example, in a herd of 100 cows without any risk factors the predicted prevalence (probability that the herd contains animals with antibody) is about 19%. If a 'purchase' risk is added, this increases to about 24%. If a 'river' risk

is added, it rises to about 56%. The potential for developing such a predictive model and examining its validity was explored by comparing the predicted prevalence (from the model) with the actual prevalence using data from the 78 farms. The results are tabulated by the number of the four risk factors which applied on each particular farm in Table 5. There appears to be good agreement between actual and predicted prevalence, suggesting that the model may prove useful.

Clearly this model could be refined by further quantifying the risk factors and by testing a larger number of herds. The model has proven useful in explaining the complexities of assessing the risk for L. hardjo infection and may help in choosing between a vaccination and a monitoring policy for L. hardjo free herds.

Table 5

Comparison of risk factors, actual prevalence and predicted prevalence of antibody to hardjo using a logistic model.

Risk Factors	hardjo Antibody		Actual Prevalence	Predicted Prevalence
	No	Yes		
0	3	0	0%	19%
1	2	2	50%	43%
2	4	13	75%	72%
3	2	23	92%	91%
4	1	28	97%	98%

The survey led to an increase in awareness of L. hardjo in the area and the most interesting finding was that most farmers interviewed did not appreciate the significance of clinical signs of L. hardjo infection in their herds and did not realise the potential benefits of control for both cattle and human health. Clearly more publicity and extension work is required by both the veterinary and medical professions. The introduction of the Cattle Health Scheme L. hardjo Program (Anon, 1988) provides a framework for practitioners with L. hardjo infection of their herds.

SUMMARY

A questionnaire survey was conducted on 78 cattle farms in Herefordshire, England to collect details of farms, animals, methods of housing, husbandry and drainage. The leptospiral status of each herd was established by either testing all the cattle in the herd or a sample designed to detect 3% and antibody prevalence of 5% (5% confidence level) using 18 different leptospiral serovars. Twenty two of these farms were responders in a random sample of cattle herds in Herefordshire and 56 were volunteers. 85% of these 78 farms had evidence of Leptospira interrogans serovar hardjo infection.

Associations between factors and presence of L. hardjo in herds were examined using tabulation and logistic regression analysis. Stocking density, rodent control, methods of housing, grazing, calf or heifer rearing, and the presence of dogs and horses were not associated with L. hardjo antibody. The odds ratios of risk factors >1 estimated by logistic regression were as follows: River 7.92, Sheep 6.65, Bull 3.90, Purchase of cattle 1.97 and Herd size 1.02. The relationship between these factors and the ability of this model to predict herd infection is discussed.

Most farmers interviewed did not appreciate the significance of clinical signs of L. hardjo infection in their herds and did not realise the potential benefits of control for both cattle and human health.

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ECONOMIC LOSSES DUE TO CLINICAL AND SUB-CLINICAL PARATUBERCULOSIS IN DAIRY CATTLE

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The economic losses due to paratuberculosis (Johne's disease) vary with the area and farm (Riemann & Abbas, 1983). In herds affected with Johne's disease the losses may be so large that profitable farming cannot be continued (Merkal, 1983). This is one of the reasons why a voluntary eradication scheme was organized in the Netherlands.

There is little published information concerning the extent of the economic consequences due to Johne's disease, and as the scale of economic loss increases, more stringent measures are required and farmers are stimulated to take the appropriate preventive steps.

The present investigation attempted to quantitate the economic losses which were due to clinical and sub-clinical Johne's disease on farms participating in the organized eradication scheme. The losses were found to be due to one or more of the following factors (Renkema & Dijkhuizen, 1979):

* the losses prior to culling, due to the loss of milk production and the cost of examination and treatment;
* the losses on culling, due to the reduced slaughter value of the animals and inefficient use of capital and equipment;
* the losses due to premature culling, i.e. the unrealized future income.

The information available makes it possible to quantify the production losses and the losses in future income.

MATERIAL AND METHODS

Losses prior to culling

Production loss: The percentage production loss prior to culling was determined from data on Friesian-Holstein dairy cows examined between January, 1979 and February, 1984. Johne's disease was verified after slaughter by histological examination of the intestines and adnexa. Two categories of animals were used.

Group 1 consisted of 61 animals from 11 farms which were taking part in an organized Johne's disease eradication scheme. These animals were culled because they showed clinical symptoms of Johne's disease.

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Group 2 consisted of 52 animals from 7 farms. In the eradication scheme, these animals were requisitioned by the Animal Health Department because of the results of the annual allergic and serological examination for Johne's disease (Benedictus, 1985) and they were removed from the farm with minimal if any evidence of clinical disease.

In order to make it possible to calculate the decrease in production, the milk production of the animals was initially adjusted to a mature equivalent (Dijkhuizen, 1983; Dijkhuizen et al., 1985) by correcting it for age (up to eight years), for month of calving (up to February), lactation period (up to 305 days) and year of production (up to the period from July 1, 1982 to June 30, 1983). The starting point in estimating the annual effect was data supplied by the Milk Controlling Service of Friesian dairy cattle in the Netherlands and the Province of Friesland from July 1, 1972 to June 30, 1983. Individual productions were first converted using an estimated genetic progress of one per cent per annum. Subsequently, the corrected production data of the various annual periods were expressed in percentages of the data of the period from July 1, 1982 to June 30, 1983 (Dijkhuizen, 1980). These percentages are the correcting factors and are listed in Table 1. The corrected individual productions were divided by the respective correction factors for the period in question.

Table 1. Annual correction factors for production

Dried-off animals from July 1 to June 30	kg of milk	% fat	% protein
1972-73	0.920	0.980	1.005
1973-74	0.920	0.980	1.005
1974-75	0.920	0.970	1.020
1975-76	0.940	0.980	1.010
1976-77	0.960	0.985	1.005
1977-78	0.970	0.990	1.005
1978-79	1.000	0.990	1.015
1979-80	0.985	0.990	1.005
1980-81	0.975	0.985	1.000
1981-82	0.980	0.995	1.005
1982-83	1.000	1.000	1.000

The extent and duration of the loss in production was established in terms of kg of milk and analysed in three ways:

(1) The percentage decrease of the corrected production in the lactation of culling was determined with respect to the previous lactation in the animals which were culled in the second lactation or later. The percentage production decrease in these animals was equal to 100-{LL/(LL-1) x 100}, in which LL is the production in the lactation of culling, and (LL-1) is the production in the previous lactation.

(2) The percentage decreases in the final and the previous lactation with regard to the prior lactation was calculated in animals culled in the third lactation or later.

(3) To determine the number of lactations which had been affected, the possible production losses in all the lactations of a culled animal were calculated with regard to the production of the animal as a heifer.

Costs of examination and treatment: These costs were estimated on the basis of the experience of the first author in his own practice, because recorded information was not available.

Loss at culling

Reduced slaughter value: The day value of an animal is the sum of the normal slaughter value and the 'norm loss' on culling (i.e. the expected future income if continuation of normal production had been possible). The official day value and official slaughter value of each animal were recorded by a qualified valuer. These values were available in only 18 animals from one farm in group one. It was therefore possible to calculate the relationship between the day value and the slaughter value at the time of culling. From the data shown later in Table 6 it is possible to compute the normal day and slaughter values of animals comparable in age and stage of lactation. A change in this relationship gives an impression of the reduction in slaughter value attributable to clinical Johne's disease.

Table 2. Assumptions used in the replacement model

* Every lactation is divided into periods of 20 days, except the first period which is 25 days	
* The price of milk, having an average solid content:	£0.2127/kg
* The average price per calf:	£114
* The average slaughter value of healthy animals:	£514
* The average value of a heifer:	£686
* The cost of concentrate per energy equivalent:	£0.17
* The additional cost per cow at the time of culling: (consisting of reduced slaughter value (£41), production loss (£41), idle production factors (£21) and others (£24)).	£127
* The average production in kg of milk in 305 days, with a content of 4.04 per cent fat and 3.43 per cent protein:	5330 kg
* Age at first calving:	24 months
* Calving interval:	365 days
* Annual genetic improvement in milk production:	1 per cent
* Average duration of herds:	3.9 years
* Preference for immediate over future income. All future costs and revenues are readjusted to the time of calculation by using an adjustment factor of 4 per cent per year. This is done by multiplying by 1/1.04i, in which i is the time in years between the time of calculation and the time at which the costs and revenues concerned are sustained or realised.	

Idle production factors: When an animal is culled, there is often a period during which a replacement animal is not available. There are still costs due to the continuing expenditure on wages, buildings and machinery (Renkema & Dijkhuizen, 1979).

Loss due to premature culling

In animals in good health and with normal production potential, the average income increases with age (Dijkhuizen et al., 1985). The loss resulting from forced premature culling can be calculated by computing the difference between the income per animal over its remaining expected life span (with normal probabilities of disposal as a result of other common forms of disease) and the expected average income over the same period produced by a replacement heifer with a normal production potential and normal likelihood of being culled. Dijkhuizen (1983) developed a replacement model in which 'norm losses' (= unrealized future income) can be calculated for culling at various stages of lactation. The most important assumptions for the computer model are summarised in Table 2.

The 'norm losses' are mainly dependent on:

- the age of the culled animal;
- the relative production potential as compared with others in the herd;
- the stage of lactation at the time of culling (Dijkhuizen et al., 1985).

To determine these values for the animals with Johne's disease, the data on animals of groups 1 and 2 were used. The relative productive capacity of the culled animals was determined using the heifer production of the culled animals.

RESULTS

The percentage production losses are shown in Table 3. Table 4 shows the production potential of the culled animals compared with the herd average. Animals culled in the third lactation or later showed a relative production potential as heifers of more than 100. For the animals in group 1 this is highly significant ($P<0.005$). In group 2, there was no significant relationship because of the small number of animals ($P = 0.07$).

The average length of the lactation in which culling took place was 208 days for the animals in group 1 and 215 days for the animals in group 2, although there was a considerable spread of 107 and 104 days respectively. The computer model divides a lactation into periods of 20 to 25 days (see Table 2). The calculations are therefore based on an average length of the last lactation of 85, 205 and 305 days.

The age distribution of the culled animals is shown in Table 5. The average slaughter value of the animals with clinical Johne's disease was £305, the average day value of these animals being £721. The price at slaughter is normally 65 per cent of the day value. In cases of clinical Johne's disease, however, the figure is 42.3 per cent ($P<0.005$). The reduction in the slaughter value of clinically affected animals is therefore estimated at approximately 20 (65 minus 42.3) per cent of the day value. This agrees with about 30 (100/65 x 20) per cent of the normal slaughter value.

Table 3. Percentage decrease in production per kg of milk in the various lactations in animals of group 1 (clinical Johne's disease) and group 2 (sub-clinical Johne's disease).

Animal	Group 1 n	Group 1 mean	Group 1 s.e.	Group 2 n	Group 2 mean	Group 2 s.e.
Culled in second lactation or later: LL-(LL-1)[a]	47	13.8***	2.2	48	10.3***	3.4
Culled in third lactation or later: LL-(LL-1)	38	15.5***	2.4	37	9.6***	4.2
(LL-1)-(LL-2)	38	5.9**	2.3	37	6.4*	2.5
LL-HL	38	19.6***	2.5	37	16.8***	3.0
(LL-1)-HL	38	4.1	2.5	37	5.9	2.6
(LL-2)-HL	27	-3.5[b]	2.6	21	-2.0[b]	3.3
(LL-3)-HL	14	-5.8[b]	3.5	13	-8.6[b]	4.7
(LL-4)-HL	6	3.7	2.0	8	-6.8[b]	5.5
Average decrease:						
LL-(LL-2)		19.5%			16%	
(LL-1)-(LL-2)		5%			6%	

[a] LL Lactation of culling
LL-1 Lactation prior to culling
LL-2 Lactation prior to last two lactations
LL-3 Lactation prior to last three lactations
LL-4 Lactation prior to last four lactations
HL Production as heifer

*** P<0.005
** P<0.01
* P<0.05

[b] Non significant increase in production in animals culled in the fourth lactation or later

Table 4. Productive capacity of culled animals (at mature equivalent)

Animals	Relative production potential as heifer: Group 1 n	Group 1 Percentage	Group 2 n	Group 2 Percentage
All animals	48	104	28	104
Culled in first lactation	13	95	4	88
Culled in third lactation or later	27	108***	13	109

*** P<0.005

Table 5. Age distribution of the culled animals

Age (years)	Group 1	Group 2
2-3	14.8%	3.8%
3-4	11.5%	17.3%
4-5	22.9%	28.9%
5-6	22.9%	19.2%
6-7	16.4%	15.4%
7-8	6.6%	5.8%
8-9	4.9%	9.6%
>9	0%	0%
Number of animals	61	52
Mean age (years)	5.54	5.81

Table 6 shows the 'norm losses', i.e., unrealized future income due to premature culling at various stages of lactation for different corrected production levels (in percentages of the herd average).

Table 6. 'Norm losses' (in £) due to premature culling within 85, 205 and 305 days after calving (lost future income)

Lactation	Days after calving								
	85			205			305		
	108[a]	109	Normal slaughter value	108	109	Normal slaughter value	108	109	Normal slaughter value
1	303	320	469	360	377	503	301	323	546[c]
2	398	419	489	353	373	517	365	385	551
3	391	413	517	327	348	537	330	351	560
4	345	367	526	270	291	546	273	294	566
5	306	326	506	232	252	520	237	255	537
6	260	279	489	182	199	503	190	208	517
7	195	212	480	118	133	494	125	139	509
8	134	149	471	61	73	486	67	79	500
9	78	87	469	17	23	483	22	30	497
10	40	49	460	-[b]	-	474	3	5	486

a Corrected production level (% of herd average).
b Where no amount is listed, culling caused no loss (because retention of the animal would have resulted in less income than replacement).
c The day value, not shown in the table, can be calculated as lost future income + normal slaughter value.

Culled animals with clinical Johne's disease

The average culled animal with clinical Johne's disease is five and a half years of age and approximately 200 days after calving. On the basis of production as a heifer, the production potential is about 108 per cent of the herd average.

On the basis of age distribution of the culled animals (see Table 5) and the average normal production per lactation (see Table 7), the average anticipated production in the year of culling is 5943 kg, and in the previous lactation 5732 kg, provided Johne's disease is not present.

Table 7. Milk production per stage of lactation (%) and per lactation (kg) (Dijkhuizen,1980)

Lactation	Production per stage of lactation (%)			Production per lactation	
	1-85 days	86-205 days	206-305 days	kg	%
1	35.3	40.8	23.9	4225	69.5
2	38.0	40.6	21.4	5063	83.3
3	38.6	40.9	20.5	5610	92.3
4	38.8	40.8	20.3	5818	95.7
5	38.7	41.1	20.2	5923	97.4
6	38.8	41.1	20.1	6026	99.1
7	38.8	41.1	20.1	6079	100.0

Loss prior to culling

Production loss: There is a 19.5 per cent reduction in lactation during the year of culling. The quantity of milk produced at 200 days averages about 80 per cent of the expected annual total milk production (see Table 7). The loss therefore is 19.5 per cent of 4753 kg of milk at £0.21 = £196. The production loss in the previous lactation is 5 per cent of 5732 kg at £0.21 = £61.

In calculating the production losses and loss of slaughter value of animals culled for disease, a corrective factor is applied because of reduced feed intake (Dijkhuizen, 1980). In this feed correction, it is assumed that no concentrate was required for the milk not produced. A reduction of 0.5 kg of concentrate/kg milk, at a price of £0.17 per energy equivalent, is used. The maximal saving in the use of concentrate per animal culled from group one is: 606 kg x 0.940 energy equivalent at £0.17 = £96. Because appetite is affected, animals showing reduced production ingest less concentrate. In Johne's disease however, the appetite continues to be healthy, even in the clinical stages (Reinders, 1963). The loss of weight, which contributes to the reduced slaughter value, is caused by malabsorption and protein-losing enteropathy (Buergelt, 1976). Ingested foodstuffs are lost and not used for production. The extent of this loss is not known. The reduced feed costs are thus partially offset. The applied concentrate correction is therefore arbitrarily set at 50 per cent of the maximum concentrate correction. Thus the applied correction for concentrate correction is £48.

The net loss due to production losses for the average culled animal with clinical Johne's disease is, therefore, £209.

Cost of examination and treatment: In the majority of cases clinical examination of an affected animal is done by a veterinary practitioner. A few animals were treated for diarrhoea prior to culling. This cost amounts to approximately £11.40 per animal.

Loss at culling

Reduced slaughter value: The reduced slaughter value amounts to 30 per cent of £526 (Table 5 and Table 6) {(0.15 x 503) + (0.11 x 517) + (0.23 x 537) + (0.23 x 546) + (0.16 x 520) + (0.07 x 503) + (0.05 x 494)} = £158 for the average culled animal.

As the animals in group one have a lower slaughter weight as the result of loss of weight, an additional correction has to be applied. Lower costs of feed have to be reckoned for animals showing lower body weights. Energy becomes available from the loss of weight, and Dijkhuizen (1980) has assumed 3.4 energy equivalent per kg of loss in weight. This energy is translated into kg of concentrate, at a price of £0.17 per energy equivalent. Thus, if an animal has lost 100 kg, the lowered slaughter price of the animal is offset by a maximum of 100 x 3.4 x 0.17 = £58. The concentrate corrective factor applied is 50 per cent. The reduction in slaughter values is thus reduced by £29 to result in a net reduced slaughter loss of £129.

Idle production factors: The exact amount is not known but was estimated by Dijkhuizen (1980) at £19, assuming that the reduced use of facilities continues for two weeks. At current costs, this amount is approximately £21.

Loss due to premature culling

The average 'norm loss' is computed from Table 6 by considering the 'norm losses' at 205 days after calving, a relative production level of 108 per cent, and the age distribution of the culled animals (Table 5) in group 1. The average 'norm loss' then amounts £279.

The total farm cost amounts to £650 (209 + 11.40 + 129 + 21 + 279) for each clinically affected animal culled.

Culled animals with sub-clinical Johne's disease

The average culled animal with sub-clinical Johne's disease is 5.8 years of age and approximately 200 days after calving. On the basis of production as a heifer, the productive capacity is 109 per cent of the herd average (Table 4). The average production is found by considering the normal average production in the Netherlands and the age distribution of culled animals (Tables 5 and 7). The applied expected production in the lactation of culling is 6,119 kg of milk, and 5,901 kg of milk in the previous lactation.

The farm loss then consists of loss prior to culling, at culling and from premature culling.

Production loss: The decrease in production in the last lactation is 16 per cent. About 80 per cent of the total annual production is realized in a lactation of approximately 200 days. The loss therefore is 16 per cent of 4,895 kg of milk at £0.21 = £165. In the prior lactation a decrease of 6 per cent occurs, which corresponds with a loss of 6 per cent of 5,901 kg of milk at £0.21 = £75. The applied correction for reduced feed intake is £45. The net loss due to production loss, therefore, is £195.

Costs of examination or treatment are not applicable.

The slaughter value is normal. A loss of £21 is caused by idle production factors.

The average 'norm loss' is computed by considering the 'norm loss' values at a relative production level of 109 per cent 205 days after calving (Table 6) and the age distribution of the culled animals (Table 5). The average 'norm loss' therefore is £295.

The total farm loss thus amounts to £510 (195 + 21 + 295) per average culled animal not showing any clinical symptoms of Johne's disease, and which is requisitioned by the Animal Health Department.

DISCUSSION

Larsen (1973) stated that cows shed Mycobacterium paratuberculosis and show few if any symptoms of Johne's disease from six months to two years prior to the clinical stage. This is why reduced production in the lactation of culling and in the previous lactation was investigated. As seen in Table 3, there is no reduction in production in the lactations previous to the last two lactations. The period during which there is reduced production thus coincides with the period of shedding of M. paratuberculosis.

The loss of production in group 2 was high compared with that of animals with clinical Johne's disease in group 1. Only post-mortem histological examination was done in the culled animals and bacteriological cultures of M. paratuberculosis were not made. Animals showing minimal lesions, therefore, were unlikely to have been detected. It is possible that the average age of the culled animals was higher than that in the work reported by Buergelt and Duncan (1978).

All animals of group 2 were found to be positive for Johne's disease on morbid-anatomical examination of the intestines and adnexa. These animals accordingly showed obvious lesions.

Doyle (1956) reported that highly productive animals infected with M. paratuberculosis are more likely to develop clinical symptoms. Table 4 shows that the relative productive capacity of animals with Johne's disease is approximately eight to nine per cent larger than that of the herd average (when mature). Accordingly, there is a relationship between the productive capacity and the likelihood of culling for Johne's disease. When examining an animal suspected of infection with Johne's disease, the veterinary practitioner should take this into account and compare the productive capacity of the animal as a heifer and as a patient.

Animals not showing any clinical symptoms of Johne's disease on a farm which is not part of an organized eradication scheme do not have to be culled. In these animals, the loss sustained by the farm consists only of the decrease in the production of milk, fat and protein.

Using the findings of this study and previous publications (Benedictus, 1985; Dijkhuizen, 1980) the economic loss may be calculated for individual animals with Johne's disease, the productive capacity, age and time of culling after calving each playing a role.

CONCLUSION

A considerable decrease in production occurs in the culling lactation and the lactation prior to culling in animals with clinical or sub-clinical Johne's disease. The animals culled because of a suspicion of Johne's disease, and those with clinically apparent disease, had a productive potential above the herd average in this study.

The quantified farm loss for the average animal clinically affected with Johne's disease is £650. On a farm which takes part in an eradication scheme, the loss per average cow culled for sub-clinical disease is £510.

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EPIDEMIOLOGICAL FACTORS ASSOCIATED WITH A HIGH INCIDENCE OF SOLE ULCER AND WHITE LINE DISEASE IN DAIRY CATTLE

G.P. DAVID*

Lameness in British dairy cattle is a major cause of financial loss to farmers and pain and discomfort for their livestock. Although a number of surveys have been carried out to determine the incidence of disease (Russell et al., 1982; Whitaker, 1981; Eddy and Scott, 1980; Prentice and Neal, 1972) the exact magnitude of the problem is not known. It is however generally accepted that it ranks only after mastitis and reproduction failure as a cause of economic loss to the dairy industry and annual losses of between 36 and 40 million pounds have been quoted. In many herds it is the most important disease process and a major contributor to poor reproductive performance as demonstrated by Lucey et al.(1986).

The emergence of lameness as a major disease problem in dairy cattle has followed the increased intensification of the industry. Rowlands et al. (1983) showed lameness to be more common in large herds and a particular problem of the winter housing period.

It is now clear that in order to fully understand the disease process and develop an effective preventative strategy, it must be approached as a disease affecting the herd rather than the individual. This type of approach is standard practice for diseases such as mastitis. The investigation and control of mastitis outbreaks rely on the identification of the aetiological agent which not only indicates the most effective treatment but also the areas of management and husbandry requiring most attention. Lameness can and should be approached in a similar manner with the difference that it is the demonstration of a specific causative lesion rather than a bacterial pathogen that suggests the areas of husbandry and management for investigation and consequently the correct control strategy.

Russell et al. (1982) confirmed that the majority of lameness lesions occur in the feet (81.3 per cent), in particular the hind feet with the outer claw of the hind foot being particularly at risk. Although these authors listed a total of 15 lesions, this paper restricts itself to the most important of these, sole ulcer and white line abscess/separation and their sequelae, which are responsible for the majority of lameness problems in intensively housed dairy cattle. If these lesions were to be adequately controlled, lameness in dairy cows would not be the problem it is presently perceived to be.

The incidence of both lesions varies widely between farms and may reach epidemic proportions in some herds (David, 1986). Both diseases have a complex multifactorial epidemiology. A high incidence of sole ulcer has been related to feeding, housing system, management and behaviour. A simplified causative web for sole ulcer is shown in Fig 1. A similar one could be constructed for white line disease. Naturally, all factors do not carry equal weight and, although for many of the factors these weights have not been quantified, and indeed are the subject of some debate, an attempt is made here

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to ascribe some relative importance to particular predisposing factors, this being an essential prerequisite to the practical prevention of disease at the farm level.

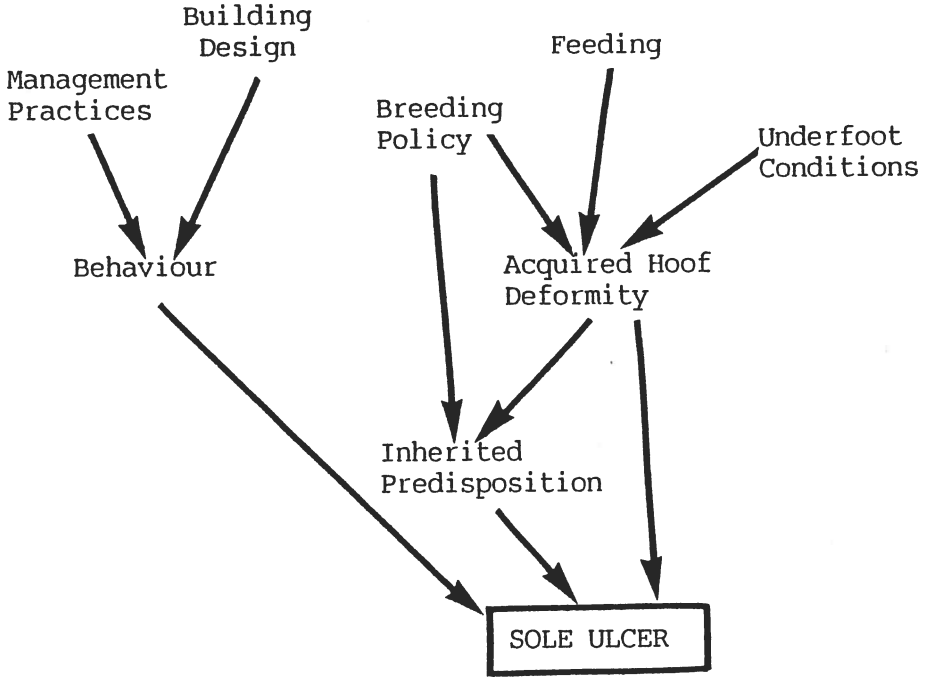

Fig. 1. A simplified causative web for sole ulcer.

SOLE ULCER (Pododermatitis circumscripta)

Classically this appears as a circumscribed lesion in the region of the sole/heel junction that is nearer the axial than the abaxial margin. The underlying sensitive tissues are exposed and there may be a protrusion of granulation tissue through the horn defect. It is nearly always situated in the outside claw of the hind foot. Long-standing lesions may have an atypical superficial appearance due to a development of an overlying flap of horn obscuring the true area of ulceration. The lesion may be complicated by the separation of the sole/heel junction with under-running. The lesion commonly occurs bilaterally, and lameness tends to be progressive with septic pedal arthritis as a common sequel.

Predisposing Factors

Sole ulcer is a common cause of lameness and is associated with environments with hard floors particularly cubicle systems with concrete floors (Rowlands et al., 1983). In many herds it can account for more than 80% of the cases of lameness. The author has investigated what appear to be outbreaks of the disease following major building alterations (David, 1986). Bee (1986) also described similar findings. Rowlands et al. (1983) indicated that the lesion was more common during the housing period and was virtually absent in animals kept mainly at pasture. It was also found to be less common in straw yards than in cubicle systems.

The basic lesion is caused by pressure necrosis of the corium in the typical site. The very specific site of the lesion indicates that anatomical and mechanical factors play an important part in its pathogenesis. Zantinga (1973) suggested that compression of the solar corium at the posterior axial border of the pedal bone is involved. Excessive compression of solar corium was also suggested by Rusterholtz (1920) with his original theory. Nillsson (1966) indicated that vascular changes caused by laminitis could also be important, and this theory was supported by MacLean (1971). The compression of the solar corium, caused by the basic anatomical flaw outlined by Zantinga, may be exacerbated by such factors as hoof overgrowth, poor hoof and leg conformation and erosive heel lesions as suggested by Bomer (1958), Toussaint Raven (1969) and others. Smedegaard (1964) successfully reproduced the lesion using a special type of shoe. Because of the mechanical factors involved in the pathogenesis, it would also seem logical to assume that the likelihood of developing the lesion is directly related to the amount of time cows spend standing, especially where under-foot conditions are unyielding as in the case of concrete.

Table 1 here shows a summary of information gained from 10 herds investigated by the author between 1982 and 1988. These herds were selected because they had a high incidence of sole ulcer and because the unacceptably high incidence of lameness on these farms was caused almost exclusively by this lesion. The findings are similar to those of Rowlands et al. (1983) with respect to the association of disease with season, building type and herd size. Table 2 shows that all 10 herds were housed in cubicles. Of particular interest in these herds was the appearance of a possible precipitating factor in 8 out of 10 herds. This took the form of recent major modifications of the cubicles. In all cases the cubicle bases were changed from earth to concrete. It was also common for inadequate bedding to be supplied (David, 1986). Cubicle divisions in these herds were commonly too narrow for the predominant Friesian Cross Holstein type cows and positioning devices (such as head rails) were incorrectly sited. Both factors can markedly affect the ease of rising and lying down and consequently the cubicle acceptability (Cermak, 1983). It has been established that cows spend much less time lying down (resting time) on concrete cubicles without significant bedding (7 hours) than on Enkamat (14 hours). Not suprisingly resting time is markedly improved by the provision of a deep straw bed (14.1 hours) (Cermak, 1983). The resting time will be markedly affected in any situation where the design of the cubicle does not satisfy the space requirements of the animal.

Table 1. Summary of information collected from ten herds with a high incidence of sole ulcer (1982-1988).

Average herd size	Average yield (litres)	Average lameness incidence %	Peak seasonal occurrence	Hoof trimming	Foot bath	Recent major changes to cubicle house
123 (44-250)*	6037 (5000-6500)	44 (10-89)	Winter 9/10 Winter/ Spring 1/10	5/10	4/10	8/10

* Ranges in parentheses

Toussaint Raven (1969) and others have suggested that hoof overgrowth predisposes to sole ulcer formation. Because of the large forces exerted during movement, weight distribution over the bearing surface of the hoof must be correct. Any abnormality causing unequal weight-bearing, either between claws or on an individual area of a particular claw, predisposes to sole ulcer formation. Toussaint Raven (1969) described how the outer claw of the hind foot tends to become overgrown and to bear more weight than the inner claw. This partially explains the predilection of the lesion for that particular claw. In his original theory, Rusterholtz suggested that excessive length of wall horn resulted in increased load bearing of the sole/heel junction leading to exostoses and pressure necrosis of the corium. Restoration of correct load bearing of the bovine hoof must, therefore, be a potentially valuable preventative technique.

Table 2. Summary of housing details for the 10 herds.

Housing type	Cubicle type	Length	Width	Base	Bedding
Cubicles 10/10	Newton Rigg 8/10	7'0"	3'9"	Concrete 9/10	Straw 5/10
	Timber 1/10				
	Dutch Comfort 1/10	6'8"-7'6"	3'8"-4'	Bitmac + concrete	Shavings/ sawdust 5/10

Arkins and Hannan (1982) showed a beneficial effect of routine chiropody on the incidence of sole ulcer, although it had no effect on the overall incidence of lameness. The efficacy of chiropody in reducing the incidence of sole ulcer in a herd depends largely on the adoption of a rational hoof trimming policy and the vigour and enthusiasm of its execution. Hoof trimming alone is unlikely to be sufficient to offset other major casual factors. Table 1 shows that 5 out of the 10 herds which suffered a high incidence of sole ulcer had practised some form of chiropody. An attempt to select cows most at risk may make chiropody more effective. This can be achieved by the use of on-farm lameness records and by detecting abnormalities in gait.

Load bearing of the bovine digit is also determined by inherited factors associated with hoof and leg conformation. Long narrow claws with insufficient depth of heel and insufficient angle of pastern and hock may confer increased susceptibility to sole ulcer and other lesions. Russell (1986) has described an inherited predisposition to sole ulcer which may be related in part to these physical characteristics.

Toussaint Raven (1969) has also suggested the heel erosion (erosio ungulae) may contribute to sole ulcer formation by reducing the weight-bearing capacity of the heel bulb. Arkins and Hannan (1982) demonstrated the efficacy of formalin footbathing in alleviating this condition. Footbathing alone, however, has little or no effect on the incidence of sole ulcer.

Wet hoof horn has only one third of the hardness of dry horn. The fact that most British dairy cattle spend long winter periods paddling in slurry has been blamed for the high incidence of lameness in the national herd. Certainly, wet conditions soften hoof horn, and it is likely that these

conditions increase the incidence of sole ulcer and white line disease. It is, however, difficult to envisage an intensive (or extensive for that matter) system in British conditions being sufficiently dry underfoot to prevent hydration of hoof keratin. There are suggestions that formalin hardens hoof horn, but there is little scientific evidence to support this.

A great deal of interest has been shown in recent years in the link between diet and aseptic laminitis. Nillsson (1966) suggested that laminitis predisposed cows to sole ulcer and that this was due to vascular injury. MacLean (1971) described sole ulcer as a sequel to acute laminitis caused by overfeeding of concentrates. Livesey and Fleming (1984) describe the occurrence of laminitis and subsequent ulceration in heifers fed a diet with a 40/60 forage/compound DM ratio. The current hypothesis is that certain types of feed lead to abnormal fermentation in the rumen which results in the release of vasoactive factors causing vascular changes characteristic of laminitis. Damage to the vascular supply to the corium predisposes cows to sole ulcer and white line disease in particular. MacLean (1971) demonstrated that the hoof horn of cows which had been affected by acute laminitis caused by nutritional factors contained significantly less cystine and methionine than normal horn. It is also suggested that horn of this type is softer, more yellow and has a waxy consistency, lacking the resilience and hardness of healthy horn. Numerous components of the diet have been suggested as the precipitating factor, including fibre content, concentrate/forage DM ratio, rate of increase in concentrate feeding, easily fermentable starchy foods, silage pH and the protein content of concentrate rations.

Attempts to reproduce aseptic laminitis experimentally have been disappointing (Mortensen et al, 1986). Surveys have been conducted using solar haemorrhage as an external marker for the presence of aseptic laminitis. Bergsten et al. (1986) failed to show any association between the severity and incidence of such hoof lesions and the amount of concentrate rations fed, nor did Peterse et al. (1984) show any association between these lesions and the rate of increase in concentrate feeding after calving. Smit et al. (1986) failed to show any relationship between the haemorrhagic hoof lesions and the level of concentrate feeding or incidence of sole ulcer. Peterse et al. (1984) suggested that a forage/concentrate dry ratio of 50/50 was the trigger factor. However, this is contrary to the studies of Livesey and Fleming (1984) which suggest that diets with a ratio of 50/50 cause little disease compared with those with a ratio of 60/40 and above. Bazeley and Pinsent (1984) described a relationship between high silage ammonia nitrogen levels (> 15%), protein intake and laminitis with subsequent sole ulcer in heifers.

The results of the author's investigations (Table 3) show a forage/ concentrate DM ratio falling somewhere between the figures suggested by Livesey and Fleming (1984) and Peterse (1986) as a trigger factor. Low silage pH would not appear to be a factor, and this is consistent with the findings of Anderson (1981). Silage ammonium nitrogen level was not excessive (< 15%) although figures were only available for 5 out of 10 herds examined. Concentrate usage was not excessive by British standards and was usually fed in more than two feeds per day, the maximum feed in all but one case being 4 kg or less. These herds were certainly not employing extreme feeding practices, and were not different from other herds in the region with lower incidences of sole ulcer.

It is clear that there may be a relationship between dietary intake and incidence of sole ulcer (and other lesions such as white line disease) through the effects of aseptic laminitis. What is not clear is the mechanism through which this occurs. The paucity of empirical scientific experimental evidence does not help.

Table 3. Summary of feeding details for the ten herds.

Forage concentrate DM ratio	Silage analysis pH	DM	NH_3 %	Concentrate feeding Feeds /day	Maximum feed (kg)	CP	kg/l
46:54 (32:67-50:50)* (16-21)(0.2-0.45)	4.3 (3.7-5.3)	25.75 (18.5-30.4)	10.58+ (8.8-13)	3	2.6 (5.4-0.5)	17.8	0.37+

* ranges in parentheses
\+ figures from 5 herds only

It is worth mentioning that aseptic laminitis may also be caused by trauma referred to as overloading laminitis by Nillsson (1966) and described by Dewes (1979). The published literature suggests that diets containing forage/concentrate DM ratios of 50/50 or greater, concentrate rations with crude protein levels less than 18% and silage ammonia levels less than 15% would not predispose to a high incidence of sole ulcer. There are, however, herds which feed rations conforming to, or even exceeding, these recommendations which suffer unacceptable levels of sole ulcer (and white line disease) (Bee, 1986). In the author's view it is unlikely that, in the majority of cases where there is a high incidence of sole ulcer, significant improvements can be achieved by dietry manipulation alone.

Sole ulcer can be a particular problem in heifers following calving, often associated with attacks of acute laminitis (Bazeley and Pinsent, 1984; Livesey and Fleming, 1984). In 6 out of 10 herds described in Tables 1-3, first lactation animals were the worst affected group, and in 2 cases were the main reason for seeking assistance. Outbreaks of laminitis and subsequent sole ulcer formation in heifers are usually associated with this sudden introduction to the adult herd, to concrete surfaces, and to production rations following calving. Often there is also a failure to train heifers to use cubicles prior to calving, and so they are being introduced into a totally alien environment. The combined stress of calving, nutritional changes, introduction to an established dominance hierarchy and failure to adapt to an unfamiliar housing system are probably responsible for the high level of disease in heifers. In the author's experience attention to each of these stress factors can significantly affect the level of disease.

WHITE LINE DISEASE (White zone disease)

This is manifested as a separation of the white line which extends to the germinal layers at the junction of the laminar and solar corium. The lesion is usually found in the outer claw of the hind foot on the abaxial border close to the junction with the heel. Gravel or small flints may be impacted in the lesion. Infection gains entry via this lesion and most often tracks upwards to erupt at the coronary band. Less often it affects the solar corium resulting in separation at the skin/horn junction of the heel. Septic navicular bursitis and pedal arthritis may be a sequel.

Predisposing Factors

Greenhough et al. (1962) ascribed the typical site of the lesion to the fact that this region of the abaxial wall is under the most stress, especially at the first impact when walking, because spreading of the hoof is greatest at this site. Edwards (1980) considered that this factor was exacerbated by any rotation of the hoof on contact with the ground and suggested that malformation due to overgrowth, chronic laminitis and heel erosion were important predisposing factors. Rowlands et al. (1985) observed that the lesion was more common in larger heavier cows and this may be explained by the increased twisting forces experienced by such animals. Although a number of factors are involved with the development of this lesion, the occurrence of a high incidence within a herd would seem to depend upon three main factors: firstly, the ability of the hoof to withstand the torsional forces involved in locomotion; secondly, the amount of physical activity involving twisting and torsional forces experienced by the animals in the herd; thirdly, the condition of the underfoot surface.

White line disease is a common cause of lameness. Russell et al. (1982) indicated that it was responsible for 20% of cases of lameness in their survey. Bee (1986) described high incidence herds where white line disease accounted for 60-70% of the total lameness. He attributed the high incidence of disease to poor underfoot conditions, particularly in areas where silage was fed. Silage effluent has an erosive effect on concrete, resulting in the development of a very rough surface where the aggregate stands proud. It may even be released onto the surface, and become impacted into the white line by rotational movements during locomotion. Herds investigated by the author have shown similar factors to be present. Murphy (1986) described how the abrasion of the hoof wall by slatted floors was a contributory factor to the development of the lesion. Kirchner and Boxberger (1987) indicated that excessively wide slots in slatted floors caused contusion of the sole and exungulation. They recommended slot widths of no more than 25-30 mm. Poorly designed and constructed slatted floors can lead to considerable problems with lameness, particularly white line disease.

It is clear that animal behaviour may well have an influence on the incidence of white line lesions within a herd. Murphy (1979) showed a significant association between the incidence of lameness (principally caused by white line lesions) and available trough space in Irish beef cattle housed on slats. Reduction of trough space per animal resulted in a significant increase in the incidence of lameness. This was attributed to the extra activity brought about by increased competition. Such agonastic activity is associated with considerable twisting forces, particularly on the hind feet. There are a number of places where a high level of activity may occur with intensively housed dairy cattle. A primary one is the feeding area where, as described above, there may be poor conditions underfoot. Poorly designed loose-housing layouts may also impede the flow of animals, resulting in an increase in unwanted agonistic activity. Any factors which increase the amount of unwanted activity within the herd, particularly those associated with poor building design and management, may increase the incidence of white line disease.

Dewes (1978) related lameness to bulling activity. The lesions he described were principally associated with the thinning of the sole but white line separation and abscessation were also involved. This may be relevant in herds with very compact calving interval, leading to concentrated periods of bulling behaviour.

Russell et al. (1982) and Eddy and Scott (1980) found that white line disease and sole ulcer were commonly associated with hoof overgrowth. This probably relates to the abnormal weight-bearing characteristics of the overgrown hoof, which exacerbates the physical factors described above.

Maclean (1971) described white line lesions as a sequel to acute nutritional laminitis, and Edwards (1980) stresses its importance as a cause of hoof deformity. It is possible that chronic laminitis reduces horn quality and increases the susceptibility of the hoof to the physical factors already described. It is interesting to note, however, that the concentrate intake of the herds described by Bee (1986), and also of the most severely affected herd investigated by the author, was low.

There is some suggestion that susceptibility to white line lesions may be heritable (Russell, 1986). Hoof and leg conformation are bound to affect weight may be bearing characteristics and consequently the potential to develop the lesion.

CONCLUSIONS

The effective control of sole ulcer and white line disease would dramatically reduce the incidence of lameness in the national herd, with consequent improvements in animal welfare and reduced financial losses to the industry.

The genetically determined susceptibility of the cows in the national herd to these lesions can only be altered significantly by a long-term breeding policy. Such a policy would require a large data base as described by Russell (1986). Were such information to be available, then the development of resistant strains of cattle could be achieved by the use of modern embryo transfer techniques.

In the short-term, a great deal can be achieved to limit the predisposing factors already discussed. Control strategies, however, need to involve several aspects of husbandry management.

It is obvious that there is no panacea. In the author's experience much can be achieved by attention to underfoot conditions, cow behaviour and comfort, cow management and correct hoof trimming policies. Diets for dairy cows need to be assessed with regard to the degree of risk of causing nutritional laminitis. In cases with an identifiable trigger factor, such as poor slat design or installation of inadequate cubicles, attention to that trigger factor alone can bring dramatic results. Most farms, indeed all those involved in planning new dairy production systems, should consider all the epidemiological factors discussed above.

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