

LISTERIA MONOCYTOGENES IN SILAGE : A MATHEMATICAL MODELLING APPROACH

Kelly L^{1,2}, Gettinby G², Gibson G³, Low JC⁴, Donachie W⁵

During the late 1980s an increasing incidence of ovine listeriosis was observed in Scotland. The disease, which is caused by the bacterium *Listeria monocytogenes*, was observed to be seasonal. Recently, listeriosis has been attributed to big-bale silage feeding. The pathways which lead to contamination of silage and the dynamics of *L. monocytogenes* in the farm environment are not fully understood. As a result, management strategies for feeding rely on pragmatic methods. A series of mathematical models was developed to introduce structure into the feed-stuff selection process. The models are at three distinct levels in relation to the microbe and in combination they can be used to provide a quantitative measure for the risk associated with feeding. This measure can be used to devise more effective disease control strategies.

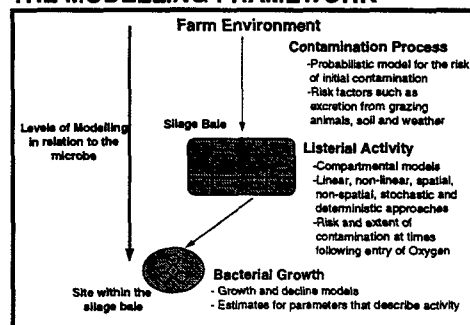
BACKGROUND

- Ovine listeriosis is an often fatal disease which is caused by the bacterium *Listeria monocytogenes*.
- It is recognised that the disease is associated with big-bale silage feeding (Low and Donachie, 1997).
- Big-bale silage is produced by anaerobic fermentation and problems occur if oxygen enters the bale.
- When oxygen enters, the fermentation process breaks down and conditions become favourable for the growth of *L. monocytogenes*.
- Any dormant organisms begin to grow, multiply and spread through the bale and when opened, the fodder may pose a risk to feeding animals.

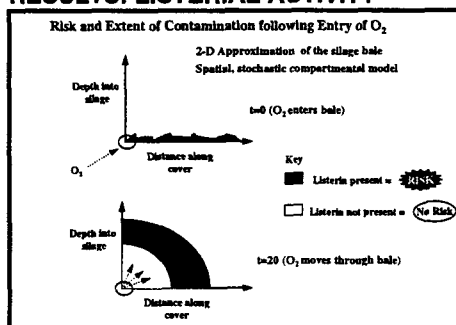
AIM

- To develop an initial framework for modelling the problem of *L. monocytogenes* in silage.

THE MODELLING FRAMEWORK



RESULTS: LISTERIAL ACTIVITY



CONCLUSIONS

- Development of the models has involved extensive collaboration between listeria experts from various disciplines; through these collaborations, an initial series of biological hypotheses has been generated.
- The models provide a stimulant for further research and data collection; as reliable data becomes available model testing is facilitated and an iterative process will be initiated.
- With reliable models for the individual aspects of the silage problem in place, integration to generate an overall quantitative risk model for silage feeding will be possible.
- An integrated model will introduce structure into the feeding process which will in turn aid in disease control.

BIBLIOGRAPHY

Low J.C. and Donachie W., 1997. A review of Listeriosis and *Listeria monocytogenes*. The Veterinary Journal (153), 9-29.

¹ Currently: Epidemiology Department, Central Veterinary Laboratory, Addlestone, Surrey KT15 3NB, U.K.
² Department of Statistics and Modelling Science, University of Strathclyde, Glasgow, U.K.
³ Biomathematics and Statistics Scotland, The Kings Buildings, University of Edinburgh, Edinburgh, U.K.
⁴ SACVS Edinburgh, Bush Estate, Penicuik, Midlothian EH26 0QE, U.K.
⁵ Moredun Research Institute, 408 Gilmerton Road, Edinburgh EH17 7JH, U.K.