

The results help explain differences in the efficiency of microbial protein synthesis.

1. France J, Thornley JHM (1984) *Mathematical Models in Agriculture* Butterworths, London
2. France J, Theodorou MK, Davies D (1990) *J Theoret Biol* 147, 413-422
3. Dijkstra J (1994) *Br J Nutr* 72, 679-699
4. Dijkstra J, France J, Tamminga S (1997) *J Agric Sci, Camb* (submitted)

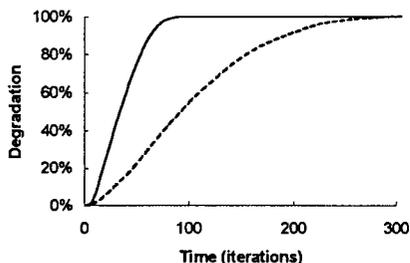
Computer simulation of cell wall degradation using cellular automata

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The kinetics of cell wall degradation by rumen micro-organisms *in vivo* are complex, and difficult to model mathematically in a biologically meaningful way. Measurement of cell wall degradation in sacco provides an overall degradation curve showing the rate at which cell wall material is lost. Similarly, measurement of gas production by rumen micro-organisms in

incubated with plant material *in vitro* provides information about the rate of cell wall degradation indirectly. The shape of these degradation curves is determined by many factors including forage quality, and has been the subject of several exponential models of cell wall degradation. The degradation curve itself represents an overall measure of the underlying kinetics, and provides useful information about the degradation process as a whole. However, many different factors combine to determine the overall shape of the degradation curve and it is almost impossible to assess their relative contribution by fitting curves to simple exponential models.

An alternative approach is to simulate the degradation process using a computer model. In this case, the continuous functions used to represent the overall degradation process in the exponential model are replaced by discrete numerical functions for which no analytical solution exists. The advantage of this approach is that the process can be modelled in a biologically meaningful way. Cellular automata are useful to describe processes that have a spatial component. An automaton is simply a computational 'cell' or unit which is arranged in an array of similar units. The automata process data in discrete steps or iterations, and share data with neighbouring automata. Typically an automaton can exist in a number of different states and obeys rules controlling the transition from one state to another. In the case of our cell wall degradation model, each automaton represents a small cube of cell wall material (or the solution in which a larger cube of plant material is incubated) and the automata rules have been defined to simulate the diffusion of cell wall degrading enzymes and the loss of cell wall material. The 'cut surface'



The 'cut surface' curve (solid line) represents degradation where all the cell wall is accessible to enzymes and the 'within tissue' curve (dashed line) represents degradation where access is restricted by other tissue.

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PROTEIN METABOLISM

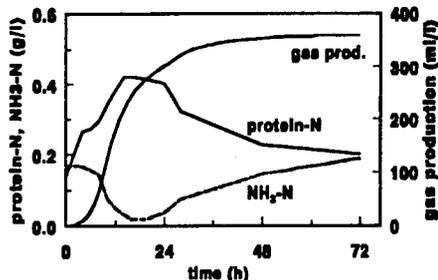
Turnover of microbial protein during in vitro rumen fermentations.

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Recently developed techniques using continuous measurement of gas production in vitro are being used to study the fermentation kinetics of ruminant feeds [1]. Cumulative gas production curves can be described by a three-phasic model. The first two phases represent fermentation of soluble and insoluble carbohydrates respectively. The third phase, starting after c. 16h, had an unknown source. The present study indicates that the final phase is caused by degradation of microbial mass.

Strained rumen fluid was diluted with 2 volumes of buffer and incubated with glucose, starch or cellulose at 39°C for 72h. Maximal microbial protein concentrations were reached after 8 (glucose) to 16h (cellulose). After 48 and 72h incubation protein levels had decreased to, respectively, 25-50% and 10-25% of the maximal levels. No effect of the type of substrate on the maximal protein level was observed. Ammonia concentrations mirrored that of protein, demonstrating the dual role of ammonia as

a precursor of protein synthesis and end-product of protein degradation. The observed protein degradation was at least partially dependent on the presence of protozoa. Rumen fluid from which protozoa were removed by centrifugation (10min 200g) showed a 2-3 fold reduced rate of protein degradation.



Cumulative gas production and protein-N and ammonia-N concentrations during incubation of crystalline cellulose in buffered rumen fluid.

1. Cone JW, van Gelder AH, Driehuis F (1997) *Anim. Feed Sci Technol* 66, 31-45

A role for plant enzymes in the early stages of herbage protein digestion in ruminants. W-Y Zhu, MK Theodorou, DR Davies, RJ Merry, H Thomas (*Institute of Grassland and Environmental Research, Plas Gogerddan, Aberystwyth, Ceredigion, SY23 3EB, UK*)

Proteolytic enzymes in plants are intimately involved in controlled cell-death (apoptosis) during plant senescence. They also cause much of the digestion of plant proteins in the silo after cutting grass for silage. Although in ensiled herbage it is accepted that plant enzymes initiate the conversion of herbage proteins to low molecular weight peptides [1], microor-