

Comparison of ruminal degradability models using the number of runs of sign of residuals

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Introduction Various models are used to describe the degradation of feeds in the rumen. The use of a particular model in fitting a degradability data set and estimating the degradability parameters implies the model goodness-of-fit has been examined holistically, otherwise the validity of estimated parameters may be controvertible. There are different statistical tests for ranking and evaluating models and sometimes results from these different tests seem contradictory, so an overall assessment is needed in this situation. In this study, the goodness-of-fit of three models were evaluated using a single test, the number of runs of sign of residuals, when fitting whole soybean ruminal degradability data.

Materials and methods DM and CP degradability data of two Iranian soybean cultivars (Sahar and Williams) as raw, roasted and steep-roasted (6 feeds in total), which was recorded at fixed incubation periods (1, 2, 3, 4, 8, 16, 24, 36 and 48 h) for each feed and yielded a total of 6 disappearance curves, were used in this study. The evaluated models were: a segmented model with three spline-lines delimited by two nodes or break points, constraining splines 1 and 3 to be horizontal asymptotes, and follows zero-order degradation kinetics (model I); a simple negative exponential curve with first order kinetics and assuming a constant fractional rate of degradation (model II); and a rational function or inverse polynomial which assumes a variable fractional rate of degradation that declines with time (model III). The models were fitted to the DM and CP ruminal disappearance data by nonlinear regression using the PROC NLIN of the SAS (SAS, 1999) to estimate ruminal degradation parameters. The number of runs of sign of the residuals was calculated as Motulsky and Ransnas (1987). A run is a sequence of residuals with the same sign (positive or negative). For this test, the average residual of replicate observations was used for each incubation period.

Results All models could be fitted to the data using PROC NLIN of SAS, as convergence to a solution occurred in all cases and the degradability parameters could be estimated. The number of runs of sign of residuals was different (Table 1) for the three models. Model III gave a high percentage of curves with three or fewer runs (for both DM and CP components) indicating the residuals were not randomly distributed over the incubation times and this model was not as good as the other two for fitting these particular data.

Table 1 Percentage of curves (both DM and CP) for each number of runs of sign of the residuals observed when fitting each model

Number of runs of sign	Model I		Model II		Model III	
	DM	CP	DM	CP	DM	CP
≤ 3	0.0	0.0	0.0	0.0	66.7	66.7
4	0.0	0.0	0.0	0.0	16.7	33.3
5	16.7	16.7	16.7	33.3	16.6	0.0
6	66.7	16.7	16.7	16.7	0.0	0.0
≥ 7	16.6	66.6	66.6	50.0	0.0	0.0

Conclusion The results of this study showed that all three models could to describe the degradability data without systematically over- or underestimating any section of the DM and CP degradability curves and the number of runs of sign of residuals test could be a useful statistical test as other statistical criteria (R-square, Bayesian information criteria and lack-of-fit test, data are not shown) for assessing and ranking models.

References

- Motulsky, H.J., and L.A. Ransnas. 1987. Fitting curves to data using nonlinear regression: A practical and nonmathematical review. *FASEB J.* 1, 365–374.
- SAS, 1999. User's Guide: Statistics, 1999. Version 8.2. SAS Institute Inc., Cary, NC, USA.