

## Can plasma parameters reflect protein and lipid growth dynamics in fattening Charolais bulls? Towards individualized nutritional recommendations

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Despite individual variability in feed efficiency and growth potential, contemporary young bulls fattened in the same pen are typically fed identical diets. Recent research aims to refine feeding systems by considering individual nutritional needs to enhance efficiency and performance. The mechanistic INRA growth model predicts daily protein and fat deposition in cattle, which are key factors in determining energy and protein requirements. Initially designed for average animals of specific breeds and sexes, the model may also be calibrated for individual animals by adjusting coefficients for protein and lipid synthesis ( $\alpha$ ,  $\beta$ ), degradation ( $\gamma$ ,  $\delta$ ), or modulation of metabolizable energy use efficiency (cMEU). These individual coefficients have been found to be significantly correlated with *in vivo* recorded feed efficiency (Cantalapiedra-Hijar et al., 2023), making them crucial parameters for developing model-based precision feeding strategies. However, estimating these coefficients typically requires individual data on feed intake and body composition, which are difficult to measure in practice. Given that blood plasma metabolites reflect nutrient utilization capacity and body composition, this study aims to contribute to the long-term objective of using plasma metabolite profiles as a practical tool for estimating model coefficients, enabling implementation of model-based individualized feeding strategies. Thirty-six Charolais bulls were fattened on grass-silage-based diets, with or without rumen-protected methionine, over an average of  $228 \pm 9.6$  days. Individual daily metabolizable energy intake and fortnightly body weight were recorded. Body composition was estimated from subcutaneous adipocyte biopsies (begin and mid of the fattening period) and from 6th rib dissection at slaughter. Protein and lipid synthesis rates, degradation rates, or cMEU of the INRA growth model were separately adjusted using the optim function in R software to minimize model deviation from estimated kinetics in body composition. Blood plasma samples were obtained at the beginning of the fattening period and analysed for 13 classical biochemical parameters, natural abundance of  $^{15}\text{N}$  and  $^{13}\text{C}$  ( $\delta^{13}\text{C}$ ), and targeted metabolomic (around 300 metabolites quantification). No correlations greater than 0.5 or less than -0.5 were found between plasma parameters and protein synthesis or degradation rate coefficients (highest correlation,  $r = 0.49$  for a lysophosphatidylcholine). However, lipid synthesis and degradation rates were positively ( $r > 0.5$ ) and negatively ( $r < -0.5$ ) correlated ( $P < 0.05$ ) with plasma  $\delta^{13}\text{C}$ , total triglycerides, carnosine, oleic and linoleic fatty acids, and 26 triglyceride isomers, respectively. A partial least square regression model demonstrated that lipid synthesis and degradation rates could be predicted ( $Q^2 = 0.57$ ) using three plasma triglycerides isomers [TG(18:0\_32:1), TG(18:1\_32:0), TG(18:3\_36:1)]. In conclusion, our findings suggest that lipid deposition dynamics can be captured by a set of plasma metabolites measured at the beginning of the fattening period, advancing the potential for precision feeding strategies driven by metabolite profiles coupled with mechanistic modelling.

### Reference

Cantalapiedra-Hijar, G., Lerch, S. The INRA mechanistic beef growth model captures feed efficiency ranking in Charolais bulls. 74. Annual Meeting of the European Federation of Animal Science, INRAE, Aug 2023, Lyon, France.