Material and methods: At the upper level, a bioeconomic model aims at maximizing the average daily return with respect to feeding and shipping strategy. It simulates the growth of each pig with an individual-based model (Cadéro et al., 2018) on a daily basis throughout the fattening period, and calculates the economic results and environmental impacts according to a cradle-to-farm gate life cycle assessment. Decisions are live weight at the diet change, percentage of the average lysine requirement met by the feed delivered at the start of each phase (α), maximum amount of feed supplied per pig per day, target weight for slaughter, and the maximum fattening duration. At the lower level, a linear feed formulation seeks to minimize feed cost. The carbon taxes are specified in both objective functions.

With this model, we investigated the effects of carbon tax levels (from 0 € to 100 €/ton CO_2-eq) in four economic average contexts: low pork (1.20 €/kg carcass) and feed prices– (Lfeed_Lpork) from May 2018 to July 2018, low pork (1.17 €/kg carcass) and high feed prices from November 2018 to January 2019 (Hfeed_Lpork), high pork (1.66 €/kg carcass) and low feed prices from August to October 2019 (Lfeed_Hpork), and high feed (November 2018 to January 2019) and pork (August to October 2019, 1.66 €/kg carcass) prices (Hfeed_Hpork). In each scenario, we run the model in three ways: optimizing both feeding and shipping strategies, and feed formulas (OBF), optimizing only feed formulas with optimal feeding and shipping strategies obtained without tax (OF), using the optimal feeding and shipping strategies as well as feed formulas obtained without tax (Ptax).

Results and discussion: Optimizing the management of the pig-fattening unit always reduced the carbon footprint of the production, by 1–43 % depending on the economic context and the tax level. OF reduced the carbon footprint vs. Ptax, and OBF obtained further reduction. At the same time, OBF limited the reduction of the annual income by up to 30 % in all contexts, except Lfeed_Lpork where carbon footprint was already relatively low without carbon tax. All decisions variables were affected by the economic context and the tax level. In OBF with high feed prices, while carbon tax increases from 0 to 30 €/t CO_2-eq, the optimized lysine content dropped from 9.6 g/kg feed to 8.5 g/kg in average in the growing feed, and from 8.2 g/kg to 7.3 g/kg feed in average in the finishing feed. This adaptation of the lysine level allowed the substitution of soybean meal by protein crops to reduce carbon footprint. At the same time, feed conversion ratio (FCR) increases in average from 2.6 to 2.7 kg feed/kg gain. Then after, lysine content and FCR remained almost stable with higher levels of tax.

Conclusion and implications: The bi-level optimization model for pig-fattening units captures various effects, including the economic contexts and the various levers of optimization associated to feeding and shipping strategies. The results highlighted that both optimization of feeding/shipping strategies at the upper level and feed formulation at the lower level can contribute to the mitigation of climate change impact and to prevent the loss of income when applying a carbon tax. Therefore, policy makers could benefit from this bi-level optimization model to define the environmental mitigation target for the pig sector.

References:

Cadéro, A., Aubry, A., Brossard, L., Dourmad, J.Y., Salaün, Y., Garcia-Launay, F., 2018. Modelling interactions between farmer practices and fattening pig performances with an individual-based model. Animal 12, 1277–1286. https://doi.org/10.1017/S1751731117002920.

47. Relationship between coefficients from the INRA mechanistic beef growth model and muscle metabolites in Charolais bulls

H. Nguyen-Ba [a], S. Lerch [b], G. Cantalapiedra-Hijar [a]

[a] Université Clermont Auvergne, INRAE, VetAgro Sup, UMR 1213 Herbivores, 63122 Saint-Genès-Champanelle, France
[b] Ruminant Nutrition and Emissions, Agroscope, 1725 Posieux, Switzerland

Corresponding author: H Nguyen-Ba. E-mail: hieu.nguyen-ba@inrae.fr

Introduction: The development of precision feeding strategies for growing beef cattle is critical to address the sustainability challenges facing the beef sector by formulating diets that closely align with the nutritional requirements of each individual within a herd. The INRA model (Hoch and Agabriel, 2004) predicts the daily processes of body protein and lipid synthesis and degradation of growing beef cattle, crucial factors for estimating nutrient requirements and formulating diets. A previous attempt of model calibration for individual Charolais bulls showed significant correlations between its metabolic coefficients and *in vivo* feed efficiency metrics (Cantalapiedra-Hijar and Lerch, 2023). The model could therefore support precision feeding tool by predicting individual's potential. However, estimating model's coefficients requires daily feed intake and kinetics of body weight and composition, which are difficult to record in practice. As the first approach, this study aimed to test the potential of using various metabolites analyzed on muscle tissue, as proxies for predicting the model's coefficients related to protein and lipid synthesis and degradation.

Material and methods: Cantalapiedra-Hijar and Lerch (2023) previously calibrated the INRA beef growth model at the individual level for 32 Charolais growing bulls by separately adjusting coefficients for rates of body protein and lipid synthesis (α and β), or degradation (γ and δ) based on daily metabolizable energy intake and three estimations of body compositions (d0, d84 and d200). The present study is based on the same experimental setup. A total of 285 muscle metabolites directly quantified by mass spectrometry with the MxP Quant 500 Assay from Biocrates, were obtained after slaughter and used to explore relationships with adjusted metabolic coefficients of INRA model using Pearson correlation (r) and partial least squares (PLS) regression.

Results and discussion: For protein synthesis and degradation, only Lysophosphatidylcholine 18:1 showed a correlation greater than 0.5 with α ($r = 0.51$, $P < 0.05$), while both 3-Methylhistidine and Lysophosphatidylcholine 18:1 showed correlations less than -0.5 with γ ($r = -0.54$ and -0.50, respectively, $P < 0.05$). Conversely, lipid synthesis and degradation were positively ($r > 0.5$) and negatively ($r < -0.5$) correlated ($P < 0.05$) with 18 metabolites including 3-Methylhistidine, Diacylglyceride 17:0_18:1, three Lysophosphatidylcholines, ten Phosphatidylcholines and three Triacylglycerides. The PLS regression model indicated that the body lipid growth dynamics could be moderately predicted ($Q^2 \geq 0.47$) using only a subset of Phosphatidylcholines isomers, such as 32:3, 34:3 and 42:1 for synthesis and 32:3, 42:1, 42:2 and 44:3 for degradation (Table 1).

Table 1 Partial least square (PLS) regression for predicting INRA model's coefficients from muscle biomarkers.

INRA growth model's coefficients	Number of metabolites initially used ($r < -0.4$ or $r > 0.4$)[a]	Final PLS regression model			
		Number of retained metabolites	Q^2	R^2Y	RRMSEE (%)[b]
α	32	4	0.19	0.27	7.33
β	42	3	0.49	0.52	10.98
γ	10	2	0.25	0.34	25.25
δ	42	4	0.47	0.51	30.14

a Markers are correlated with the model's coefficients ($P < 0.05$).

b RRMSEE: Relative Root Mean Square Error of Estimation.

Conclusion and implications: In this study, modelling the dynamics of body lipid deposition in individual Charolais growing bulls could be achieved by only a small subset of muscle metabolites. This highlights the potential for developing precision feeding strategies based on the use of metabolite biomarkers for adjusting mechanistic model coefficients at the level of individual cattle. In the next step, plasma metabolites measured at various growth time-points could be evaluated to enhance the early identification of individual cattle's requirements.

References:

Cantalapiedra-Hijar, G., Lerch, S., 2023. The INRA mechanistic beef growth model captures feed efficiency ranking in Charolais bulls. In: Proceedings of the 74. Annual meeting of the EAAP, Aug 2024, Lyon, France, p. 332.

Hoch, T., Agabriel, J., 2004. A mechanistic dynamic model to estimate beef cattle growth and body composition: 1. Model description. Agricultural Systems 81, 1–15. https://doi.org/10.1016/j.agsy.2003.08.005.

48. Predicting dry matter intake in dairy goats using artificial neural networks

C. Fernández [a], C. Vicente [a], I. Hernando [b], M. Martínez-Álvaro [a]

[a] Instituto de Ciencia y Tecnología Animal. Universitat Politècnica de Valencia, Spain
[b] Facultad de Magisterio y Ciencias de la Educación. Universidad Católica de Valencia, Spain

Corresponding author: Carlos Fernández. E-mail: cjfernandez@dca.upv.es

Introduction: The Valencian Murciano-Granadina Goat Breeders Association (AMURVAL) was created with the aim of improving breed performance. Official dairy milk control is the basic tool for starting the genetic improvement program, as it provides production data such as milk production, chemical composition and somatic cell count. No information is available about intake. Any tool for predicting dry matter intake (DMI) would be highly beneficial for AMURVAL. Multiple linear regression (MLR) and artificial neural networks (ANN) were used to predict DMI as linear and non-linear model, respectively. There is not much information on ANN application in animal nutrition (Meng et al., 2019; Cavallini et al., 2023). Because ANN can capture nonlinear relations between traits and are flexible in terms of model assumption and structure, we hypothesized that ANN could be used to simulate the complex physiological process of DMI. The objective of this study was to predict DMI based on milk performance data using MLR and different ANN structures.

Material and methods: Models were calibrated and validated using DMI and milk performance data from 421 dairy goats from the Universitat Politècnica de Valencia, Spain. Milk performance traits recorded were milk yield, fat, protein, lactose, total solids, dry extract, cheese extract and fat to protein ratio. The whole data set was randomly split into calibration (70 %) and validation (30 %) data set. In the MLR model, study was included as a random effect, and milk performance traits as covariates. In ANN, we tested one layer (ANN1), two layers (ANN2) and three hidden layers (ANN3) with different activation functions. The accuracy of the model predictions was evaluated through comparison of predicted and observed values in the train and test data sets using RMSE and, goodness of fit was measured by R^2. As a practical application, the best model obtained was used to predict DMI from AMURVAL database ($n = 22{,}063$). Data analyses were conducting using R (2016) libraries lme4 (1.1–37), nnet (7.3–20), neuralnet (1.44.2) and keras (2.15.0).

Results and discussion: Both ANN and MLR models showed similar accuracies. During calibration, RMSE (kg/d) was 0.15, 0.13, 0.17 and 0.12 for MLR, ANN1, ANN2 and ANN3, respectively. The marginal R^2 was 0.59, 0.68, 0.73 and 0.75 for MLR, ANN1, ANN2 and ANN3, respectively. In the test set, the RMSE was 0.14 except for ANN2 which was 0.31 and, R^2 was 0.61 in all models. All models shown better accuracy for training than test dataset. During validation, ANN3 (Table 1) exhibits the best model performance in predicting DMI (average values of 1.90 and 1.88 kg DM/d for observed and predicted, respectively). Increase in milk yield led to an increase of DMI, as expected. However, ANN3 underpredict DMI at values around 1.30 kg/d, and overpredict DMI as the predicted DMI increase above 2.15 kg/d.