PREDICTION OF INTRAMUSCULAR FAT CONTENT IN BEEF RIBEYE QUARTERED AT 5TH-6TH RIB USING A HAND-HELD CAMERA SOLUTION

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I. INTRODUCTION

An increased use of beef semen on the genetically lowest ranking females in the dairy herds have resulted in larger carcasses variation in offspring in Denmark [1]. Q-FOM™ Beef, a hand-held camera solution, is designed to efficiently predict marbling, eye muscle area, fat colour and meat colour of beef ribeye after quartering [2]. The camera has been calibrated and validated against visual grading performed by MSA accredited graders in Australia and is currently approved for predicting MSA and AUS-MEAT marbling, eye muscle area and fat colour of *M. longissimus thoracis* (LT) at the ribbing sites caudal to the 10th to 13th rib [2]. An implementation of Q-FOM™ at the European slaughter lines for predicting chemical IMF% would with time push the breeding programmes in a direction of genetically improved carcasses with higher meat quality. This study aims at characterising chemical IMF% and investigating the performance of Q-FOM™ IMF% prediction in LT between 5th and 6th rib from offspring of Holstein dairy cows sired by Angus (AA), Charolais (CH) and Danish Blue (BL).

II. MATERIALS AND METHODS

The study included 266 crossbred Holstein bulls and heifers slaughtered between 8 and 11 months of age with slaughter weights between 174 kg and 267 kg. An image of LT between 5th and 6th rib was taken with the hand-held Q-FOM™ Camera after 30 minutes of blooming. IMF% was determined by Weibull-Stoldt acid hydrolysis and Soxhlet extraction using HYDROTHERM and SOXTHERM® (C. Gerhardt GmbH & Co. KG, Germany). The 266 Q-FOM™ crossbred calves' images and images of additionally 106 highly marbled carcasses formed the basis of a prediction model for prediction of IMF% calibrated against chemical IMF% values of the same animals (IMF span: 0.9-22.9%).
Statistical analyses were conducted in R (version 4.2.2), generating lmer mixed models. For Q-FOM™ model performance, the root mean square error of calibration (RMSEC) and cross validation (RMSECV) and the coefficients of determination (R^2) were calculated. Additionally, R^2 and prediction error was calculated solely on the crossbred subpopulation of the model reference data to investigate model performance on crossbred calves' carcasses.

III. RESULTS AND DISCUSSION

The chemical IMF% and the Q-FOM™ predicted IMF% of LT in the animals are presented in Table 1.

Table 1: Chemical and predicted intramuscular fat (IMF%) of *M. longissimus thoracis* at 5th-6th thoracic vertebra in beef on dairy calves.

	AA		CH		BL		P-values		
	Bulls	Heifers	Bulls	Heifers	Bulls	Heifers	Breed	Gender	B × G
n	57	35	43	39	41	51	-	-	-
Chemical IMF, %	2.71^{b}	4.70^{d}	2.42^{ab}	3.84^{c}	1.77^{a}	2.95^{b}	***	***	ns
Predicted IMF, %	2.77^{ab}	4.53^{d}	2.58^{a}	3.80^{cd}	2.19^{a}	3.53^{bc}	***	**	ns

n—number of animals; AA—Holstein × Angus; CH—Holstein × Charolais; BL—Holstein × Danish Blue; B × G—Breed × Gender interaction; *P < 0.05, **P < 0.01, ***P < 0.001, ns—non-significant; ^{a,b,c,d,e} indicates significance.

There was no interaction between breed and gender, but both breed and gender had a significant effect on chemical IMF% with heifers having higher IMF% than bulls, CH higher than BL, and AA higher than CH and BL. This correlates well with the findings of Cafferky *et al.* [4].
The Q-FOM™ model performance R^2, RMSEC and RMSECV values for prediction of IMF% in LT are presented in Table 2. Stewart *et al.* performed a similar model calibration on chemical IMF% in 298 beef samples quartered at the $12^{th}/13^{th}$ rib with RMSEC = 1.84% and R^2 = 0.77 (IMF span 1.5-18.6% and mean 6.4 ± 3.85) and successfully validated the model on a unique dataset of 483 animals [5]. R^2 and prediction errors of the Q-FOM™ calibration model and cross validation model along with prediction errors approximately three times as low as standard deviations (SD) indicates acceptable performance of the overall model in this study with a prediction error of 1.58% IMF. It should be stressed, however, that a validation on a unique dataset must take place before further evaluation of overall model performance can take place. When the calf subpopulation with a smaller IMF% span (0.9-7.4%) was evaluated in isolation, the model only explains 27% of the variation. This indicates a poor prediction performance of the Q-FOM™ model in carcasses with low IMF%.

Table 2: Precision estimates for the calibration and cross validation of the Q-FOM™ model predicting chemical intramuscular fat (%) of *M. longissimus thoracis* at 5^{th}-6^{th} thoracic vertebra in beef on dairy calves.

		Prediction model		Chemical IMF%	
IMF%	*n*	R^2	Prediction error	Range	Mean ± SD
Calibration model	372	0.89	1.54[a]	0.9 - 22.9	5.5 ± 4.67
Cross validation model*	372	0.88	1.56[b]	0.9 - 22.9	5.5 ± 4.67
Veal subpopulation	266	0.27	1.47	0.9 - 7.4	3.0 ± 1.40

n—number of animals; R^2—coefficient of determination; IMF—intramuscular fat; SD—standard deviation; Prediction error—root mean square error of [a]calibration (RMSEC), [b]cross validation (RMSECV); *venetian blinds w/10 splits and 1 sample/split.

IV. CONCLUSION

This study showed that heifers had higher IMF% than bulls in measured chemically, CH had higher IMF% than BL, and AA had higher IMF% than CH and BL. Furthermore, it demonstrated the potential of a Q-FOM™ model to predict chemical IMF% in bovine LT between 5^{th} and 6^{th} thoracic vertebra. A unique sample set is required for validation of the model and potential implementation on the slaughter lines in Europe. Yet, the Q-FOM™ model was not able to predict IMF% with acceptable precision in carcasses with low IMF%, which limits the potential of implementation in countries with a large production of lean calf carcasses.

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