Evaluation Of Dual Energy X-Ray Absorptiometry For Phenotyping The Body Composition Of Meat Type Breeding Sheep

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Introduction

Sheep breeders need to improve the performance of their herds steadily for economic reasons -- especially in order to meet increasing consumer demands for lamb meat worldwide. A high percentage of lambs produced in Bavaria (Germany) does not meet fat and meat grades demanded by breeders and consumers. The use of improved performance testing and special breeding schemes in sheep, together with the use of new technologies such as dual energy X-ray absorptiometry (DXA), magnetic resonance imaging (MRI), or X-ray computer tomography (CT) scanning could help to decrease the generation interval and increase the accuracy of breeding value estimation. The time consuming tissue dissection during progeny testing is certainly not very efficient. A very few sheep breeding organizations use already X-ray computer tomography (CT) for performance testing (Junkuszew and Ringdorfer 2005, Macfarlane et al. 2009). Other promising methods are MRI (Streitz et al. 1995, Stanford et al. 1998) or DXA. The advantage of these methods is their non-invasive character already useable in living animals. X-ray computer tomography, however, requires massive protective measures, because the (long-time) exposure to X-rays may cause severe health problems especially to the personnel and also to the animals. The health risk for animals and for the personnel is much smaller when using magnetic resonance imaging or dual energy X-ray absorptiometry. There is no X-ray exposure with magnetic resonance imaging, while X-ray exposure is very low when using dual energy X-ray absorptiometry. Generally, the costs and efforts of data acquisition and analysis are lowest for dual energy X-ray absorptiometry compared with CT and MRI (Scholz and Baulain 2009). Only a very few groups used DXA for evaluating sheep body composition *in vivo* or *post mortem* (Clarke et al. 1999, Mercier et al. 2006, Dunshea et al. 2007, Pearce et al. 2008). The aim of this study is the evaluation of DXA scanning for the use in performance testing of male Merino (land type or “Wuerttemberger”) lambs.

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Material and methods

Totally 59 male lambs were studied by dual energy X-ray absorptiometry (DXA) at an average live body weight of 42.5 kg (±3.1 kg) and an average age of 110 days (±11.1 d). The male Merino lambs originating from seven different Bavarian breeders and from two Bavarian research herds were fattened at the central Bavarian performance test station. The performance test started at an age between 6 and 10 weeks of life and at a body weight between 20 and 24 kg. All lambs received a concentrate diet with 18 % crude protein and 10.5 MJ ME *ad libitum* and daily 300 g hay. At the end of the fattening period -- in addition to the "standard" ultrasound muscle and fat depth measurements -- a whole body scan was performed by DXA with a GE Lunar DPX IQ pencil beam scanner in order to measure the amount and percentage of fat tissue, lean tissue, and bone mineral *in vivo* (figure 1). Three days later, the lambs were slaughtered. The whole, empty carcass without head (19.4 ±2.0 kg) was X-rayed again with the GE Lunar DPX IQ scanner one day after slaughtering (figure 1). *In vivo*, the ′pediatric large′ whole body software mode with a pixel size of 3.6 mm x 7.2 mm was applied. The ′pediatric small′ whole body software mode (GE Lunar software version 4.7e) with a pixel size of 2.4 mm x 4.8 mm served for the scan of the carcasses. Finally, one half of the carcass was dissected into the main body tissues muscle (meat), fat, and bone as reference for the DXA data. The carcass half was split into the main body compartments: neck, shoulder, top of shoulder, back/top, breast/ribs/side, loin, hind leg + kidney fat.

Figure 1: DXA scanning of a lamb *in vivo* and of a lamb carcass

Statistics

Single and stepwise regression model procedures using SAS 9.2 were used to analyze the data. Coefficients of determination (R^2) and root mean squares errors (√MSE) are given in the tables as result. For stepwise regression, a significance level of $p<0.05$ for entry and stay of the variables within the equations was applied. The reference carcass data from DXA or dissection were used as dependent variable.

Results

There was a medium to high agreement between the *in vivo* and carcass DXA measurements for all traits (Table 1). The lower relationship between the DXA lean mass recordings is most likely affected by the varying filling state of the rumen *in vivo*. Unexpectedly, the highest coefficient of determination showed the DXA bone mineral (g) followed by DXA fat (g), and DXA fat or DXA lean (%).

Table 1: Relationship between *in vivo* and carcass DXA measurements

Trait	Adjusted R^2	√MSE	*F* value
DXA Fat mass (g)	.72	485	152.1
DXA Fat (%)	.69	2.10	131.7
DXA Lean mass (g)	.58	986	83.3
DXA Lean (%)	.69	2.05	129.5
DXA Bone mineral (g)	.86	39	365.7
DXA Bone mineral (%)	.51	.23	63.2

Carcass DXA traits as dependent variable; $P<.001$ in all rows, n=59

Table 2 shows the single relationship of the DXA data (*in vivo* or carcass) with the reference data from tissue dissection. Generally, carcass DXA data show a higher relationship with the dissection data than do the DXA data *in vivo*. The highest agreement was found between the DXA lean (g) and carcass meat yield (g) followed by fat (g). There was no significant relationship between DXA bone mineral (%) and carcass bone (%).

Table 2: Relationship of corresponding *in vivo* or carcass DXA measurements with dissection traits of one carcass half

Carcass Trait	DXA *in vivo*		DXA empty carcass	
	Adjusted R^2	√MSE	Adjusted R^2	√MSE
Fat (g)	.67	251	.82	185
Fat (%)	.59	2.13	.72	1.77
Meat (g)	.67	320	.84	223
Meat (%)	.49	1.96	.52	1.92
Bone (g)	.39	141	.42	138

Carcass dissection traits as dependent variable; $P<.001$ in all rows, n=59

In comparison with single regression, multiple stepwise regression analysis resulted only for carcass fat or carcass meat yield (g) traits in slightly higher coefficients of determination (and smaller √MSE), when all DXA traits (*in vivo* or *post mortem*) were considered as potential explanatory variables. Carcass meat yield (g) prediction can be improved from *carcass* DXA data by combining DXA lean (g) and DXA fat (g) with an R^2=0.88 and √MSE=193, or from DXA data *in vivo* by combining DXA lean (g) and DXA bone mineral (g) with an R^2=0.71 and √MSE=305. Similarly, carcass fat yield (g) shows a higher coefficient of determination (R^2=0.7; √MSE=241), when combing DXA lean (g) and DXA fat (g) from measurement *in vivo* or when combing DXA fat (g) and DXA bone mineral (g) from carcass measurement (R^2=0.83, √MSE=179). The contribution of the second explanatory variable in the above "multiple" regressions to the model R^2 is in all cases, however, very low (partial R^2<0.05).
Additionally, the "standard" traits ultrasound fat and muscle depth of the back region (last rib and middle of loin) are not very highly associated with the carcass dissection results in male Merino lambs at 42.5 kg live weight (R^2= not significant for ultrasound fat depth vs. carcass fat yield (g), R^2=0.13 or 0.25 for ultrasound muscle depth last rib or middle of loin vs. carcass meat yield (g)).

Conclusions

The low variation in the back fat (5.3 ±1.1 mm) of the Merino lambs leads to very low accuracies of ultrasound data for the prediction of carcass composition during performance testing. It is necessary to apply new technologies for phenotyping breeding sheep. Otherwise, it might be difficult to achieve further genetic progress. One alternative technique to those described by Stanford et al. (1998) could be DXA. There is medium to high agreement between DXA body composition data measured *in vivo* and *post mortem* (carcass). Additionally, DXA measurements *in vivo* or *post mortem* can predict the carcass composition of male Merino lambs with a relatively high accuracy and may be used for performance testing in meat type sheep.

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