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AVALIAÇÃO E CALIBRAÇÃO DE UM OSTEODENSITÔMETRO PARA ESTIMAÇÃO DA COMPOSIÇÃO QUÍMICA CORPORAL E COMPOSIÇÃO DE TECIDOS DISSECADOS DE SUÍNOS

TESE DE DOUTORADO

Marcos Kipper da Silva

Santa Maria, RS, Brasil
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Marcos Kipper da Silva

Tese apresentada ao Curso de Doutorado do Programa de Pós-Graduação em Zootecnia, Área de Concentração em Produção Animal, da Universidade Federal de Santa Maria (UFSM, RS), como requisito parcial para obtenção do grau de
Doutor em Zootecnia.

Orientador: Dr. João Radünz Neto
Coorientador: Dr. Candido Pomar

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como requisito parcial para obtenção do grau de
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A você, Ines, minha linda esposa, que sempre esteve ao meu lado tanto nas horas boas como nas ruins. Você que sempre me apoiou e teve paciência comigo.

Eu te dedico este trabalho.

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Se você quer saber como foi seu passado,
olhe para quem você é hoje.
Se quer saber como vai ser seu futuro,
olhe para o que está fazendo hoje.

(Provérbio chinês)

RESUMO
Tese de Doutorado
Programa de Pós-Graduação em Zootecnia
Universidade Federal de Santa Maria

AVALIAÇÃO E CALIBRAÇÃO DE UM OSTEODENSITÔMETRO PARA ESTIMAÇÃO DA COMPOSIÇÃO QUÍMICA CORPORAL E COMPOSIÇÃO DE TECIDOS DISSECADOS DE SUÍNOS
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Uma série de estudos foram desenvolvidos para avaliar e calibrar um equipamento de densitometria óssea (*Dual-energy X-ray Absorptiomentry* – DXA) como método indireto para avaliação corporal, de carcaça e de cortes cárneos suínos. Assim, a tecnologia foi testada quanta à sua precisão em condições de repetibilidade e reprodutibilidade; além dos efeitos de borda da amostra, temperatura e espessura da amostra; e do efeito da modificação da composição da amostra pela adição de tecidos. Os pacotes de softwares também foram avaliados quanto às suas configurações. Por fim, um protocolo foi desenvolvido para calibrar o método para estimação da composição química corporal e de meia carcaça suína, além da composição de tecidos dissecados de meia carcaça e cortes primários. A repetibilidade e reprodutibilidade do equipamento foram em geral satisfatórias. Porém, algumas regiões de interesse devem ser evitadas, como a do tronco. A redução do perímetro da borda não modificou os resultados fornecidos pelo equipamento. A temperatura apresentou um leve efeito sobre os resultados, no entanto é necessária uma grande variação de temperatura para gerar uma pequena variação nos resultados DXA. A variação da espessura de uma amostra com composição constante foi um dos fatores que mais influenciaram as medidas tomadas com o equipamento. Visto isso, a padronização de técnicas considerando esse fator é fundamental para viabilizar a utilização desta tecnologia. Os softwares avaliados foram o *Total body* e *Small animal* cada um com suas três configurações totalizando seis estudos. Os dois softwares puderam ser empregados para estimação da composição de tecidos dissecados. No entanto, quanto mais extensiva foi a dissecção menor foi a precisão do método. Assim, a estimação da quantidade de um determinado tecido em uma meia carcaça foi mais precisa do que a estimação da composição de mesmo tecido nos cortes primários. Através da calibração do método, foi possível obter modelos de tradução com boa acurácia e precisão para estimar a composição química e de tecidos dissecados. Além disso, medidas tomadas em uma condição puderam ser utilizadas para estimar a composição em outra. Assim, a digitalização da meia carcaça pode ser utilizada para estimar a quantidade de músculo da paleta, por exemplo. No entanto, quanto mais específica foi a medida maior foi a precisão da estimativa. Resultados precisos foram alcançados depois de pequenos ajustes metodológicos, uma vez que, os fatores de influência sobre os resultados foram quantificados e eram de fácil correção através de padronização dos métodos. A ferramenta DXA mostrou-se um importante instrumento para avaliação animal. Portanto, a DXA deve ser considerada em futuras pesquisas.

Palavras-chave: Análises químicas. Dissecção. DXA. Método indireto. Zootecnia de precisão.

ABSTRACT
Doctoral Thesis
Programa de Pós-Graduação em Zootecnia
Universidade Federal de Santa Maria

EVALUATION AND CALIBRATION OF AN OSTEODENSITOMETER TO ESTIMATE BODY CHEMICAL COMPOSITION AND DISSECTED COMPOSITION IN PORK
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Site and Date of Defense: Santa Maria, February 20th, 2015.

A series of studies have been developed to evaluate and calibrate a bone densitometry device (Dual-energy X-ray Absorptiometry – DXA) as an indirect method for body, carcass, and pork evaluation. Thus, the technology was tested for its precision in repeatability and reproducibility conditions. The effect of the sample edge, temperature, and thickness of the sample, and the effect of modifying the composition of the sample by the addition of tissue were also tested. In addition, software packages were evaluated. Finally, a protocol was developed to calibrate the method estimating the chemical composition of entire body and half carcass; and the dissected tissue composition of half carcass and primary cuts. The repeatability and reproducibility of the equipment were in general satisfactory; however, some regions of interest should be avoided, such as the trunk. The reduction of the edge perimeter did not change the results provided by the device. The temperature had a slight effect on the results; however, a wide variation in temperature is necessary to generate a small change in DXA results. The thickness variation of a sample with constant composition was one of the factors that most influenced the DXA measurements. For this reason, the techniques for standardization considering this factor are crucial to enable this device utilization. The evaluated software were Total body and Small Animal, each one with its three configurations totaling six studies. Both software could be used to estimate the composition of dissected tissues; however, the more extensive was the dissection the lower was the accuracy of the method. Thus, estimating an amount of a particular tissue in a half carcass was more accurate than estimating the same tissues in the primal cuts. The calibration procedure allowed obtaining translation models with good accuracy and precision to estimate the chemical composition and dissected tissues. In addition, measurements took in a condition could be used to estimate the composition in another one. However, when the measurement was more specific then greater was the precision of estimation. Accurate results were achieved after small methodological adjustments. This happened because the factors affecting DXA measurements were quantified and easily corrected with method standardization. The DXA is an important tool for animal evaluation. Thus, DXA should be considered in future studies.

Key words: Chemical analyses. Dissection. DXA. Indirect method. Precision farming.

SUMÁRIO

INTRODUÇÃO

A preocupação com a produção de alimentos e seus efeitos na economia são questões que vêm sendo discutidas há décadas no país (BARROS e GRAHAM, 1978). Estas discussões, aliadas à influência da indústria, promoveram desde a década de 1970 uma profunda modificação nos sistemas de produção, com consequente aumento na oferta de alimentos (FAOSTAT, 2014). No entanto, a população mundial continuou crescendo e há estimativas de que se aproxime dos 9,6 bilhões de pessoas em 2050. Esse aumento populacional terá como consequência um crescimento estimado de 100% no consumo de alimento (TILMAN et al., 2002).

A suinocultura se destaca entre os maiores sistemas de produção de alimentos como importante fonte de proteína para alimentação humana. A cadeia respondeu em 2012 pelo fornecimento diário médio de 110 kcal de energia e 3,9 g de proteína para cada habitante do planeta e é atualmente responsável pela produção anual de mais de 105,5 milhões de toneladas de carne (ABPA, 2014; FAOSTAT, 2014). Porém, os sistemas atuais de produção não são suficientes para suprir a futura demanda. Assim, novas tecnologias incorporadas aos grandes sistemas de geração de alimentos serão fundamentais para suprir o crescente consumo. Estima-se que 70% do excedente de produção deverá ser provido por tecnologias inovadoras (SIMMONS, 2011). No entanto, elas não virão para substituir as antigas tecnologias, e sim para corrigir falhas e restaurar o potencial produtivo ou o rendimento do sistema (GODFRAY et al., 2010).

Novos métodos e conceitos para aumentar a produção de um sistema devem ser testados antes de sua aplicação prática. A avaliação animal é uma importante etapa para o melhoramento genético, bem como para a avaliação de técnicas de manejo e nutrição. Usualmente, a avaliação de carcaça utiliza a análise química ou a dissecação com posterior pesagem dos tecidos como técnicas "padrão ouro" (POMAR et al., 2009). A grande desvantagem destas abordagens é a necessidade do abate, impedindo a avaliação dos animais durante seu crescimento. Uma das técnicas alternativas é o abate comparativo, no qual animais com elevada semelhança e criados sob mesmas condições são utilizados dentro de um mesmo grupo. Nesta condição, alguns indivíduos são abatidos e considerados como representativos dos animais que permaneceram vivos. Porém, a variabilidade individual não pode ser considerada neste método e é consequentemente inserida como uma fonte de variação nos estudos.

Este problema pode ser contornado com a utilização de metodologias indiretas de avaliação. Em geral, estas técnicas utilizam medidas que apresentam alta correlação biológica com as variáveis de interesse para a avaliação animal. Além de reduzir o erro devido à variabilidade individual, as técnicas indiretas reduzem os custos no processo de avaliação, pois um número menor de animais permite as mesmas conclusões nos estudos e também por poupar do abate indivíduos com alto valor genético ou econômico.

Um método rápido, acurado, pouco invasivo e que necessite de poucos dados é considerado adequado para prover informações sobre o animal (MITCHELL et al., 2003). Exemplos de técnicas indiretas são: análise da impedância bioelétrica (*Bioelectrical impedance analyses - BIA*), eletrocondutividade corporal (*Total body electrical conductivity - TOBEC*), ultrassonografia, absorciometria por dupla emissão de raios-X (*Dual-energy X-ray absorptiometry* - DXA), ressonância magnética (RM) e tomografia computadorizada (TC). Todas essas tecnologias necessitam ser previamente calibradas por análise química ou dissecação. Somente TOBEC e ultrassom foram testadas em linhas automatizadas de abate para avaliação de carcaças em tempo real (BERG et al., 1994; LIU e STOUFFER, 1995). O TOBEC é de difícil manuseio por ser um equipamento em formato de tubo onde o animal precisa ser inserido, além de ser pouco preciso. Já a ultrassonografia possui a desvantagem de não permitir uma análise completa do corpo. Os métodos TC, RM e DXA são os que apresentam maior precisão, porém, os dois primeiros são dispositivos extremamente caros em relação ao último. Assim, a tecnologia DXA surge como um método alternativo, preciso, de fácil utilização e com custo acessível. Porém, os escâneres DXA foram desenvolvidos para a avaliação corporal de humanos e, portanto, fornecem resultados calibrados para tal, sendo necessária a transformação dos resultados para representar as condições do animal em estudo.

Alguns equipamentos DXA já foram calibrados e validados para estudos com animais (LÖSEL et al., 2007; MARCOUX et al., 2005; MITCHELL et al., 1998c), mas a tecnologia tem evoluído muito nos últimos anos. Neste contexto, novos equipamentos DXA estão disponíveis no mercado. No entanto, não se sabe qual o impacto que as melhorias nos sistemas podem causar na sua aplicação para avaliação animal. Os trabalhos apresentados nesta tese foram desenvolvidos com o objetivo de avaliar a precisão desta tecnologia em diversas condições, para propor modelos de estimação da composição química e dissecada de suínos, bem como para entender as consequências de sua utilização. O problema de pesquisa e as questões a serem respondidas são apresentados nesta tese em um estudo bibliográfico, um estudo preliminar, cinco artigos científicos, uma discussão geral e as conclusões e perspectivas mais importantes.

1 REVISÃO BIBLIOGRÁFICA

1.1 Histórico e evolução da tecnologia

O emprego de fótons para estimar a composição corporal iniciou com a utilização de absorciometria por emissão de fóton único (*Single photon absorptiometry - SPA*). Esta técnica foi estabelecida nos anos 1960 e apresentava várias dificuldades, sendo substituída pela dupla emissão de fótons nos anos 1980 (DEVITA e STALL, 1999). O objetivo inicial da SPA era avaliar a massa óssea do antebraço como medida representativa de todo o corpo (CAMERON e SORENSEN, 1963). Assim, esse método era falho na sua aplicação uma vez que a avaliação de um osso não pode ser atribuída aos demais. Outra grande dificuldade era a sua sensibilidade à variação da espessura do braço. Para contornar isso, medidas eram tomadas no antebraço não dominante mergulhado em água, como forma de padronização da espessura da amostra digitalizada (TOTHILL, 1995).

Apesar dos bons resultados obtidos pela SPA, ela não permitia a avaliação do esqueleto axial. Assim, esse método não apresentava grande aplicabilidade, uma vez que fraturas na coluna vertebral apresentam consequências muito mais graves em relação às demais regiões (TOTHILL, 1995). Além disso, a composição da massa óssea do antebraço era influenciada pela massa não óssea, cuja composição não era conhecida, o que impedia a correção da interferência. Visto estas dificuldades, o desenvolvimento de um novo método era necessário.

A absorciometria por dupla emissão de fóton (*Dual photon absorptiometry - DPA*) permitiu a obtenção de boas medições de coluna vertebral e de fêmur devido ao seu excelente contraste na imagem (PEPPLER e MAZESS, 1981). No entanto, esses equipamentos utilizavam 153 Gd para geração de fótons. Por se tratar de um radionuclídeo caro e que precisava ser anualmente substituído, o equipamento exigia instalações e cuidados especiais (PIETROBELLI et al., 1996). Além disso, o procedimento de digitalização era demorado, podendo levar em torno de uma hora para ser realizado completamente (TOTHILL, 1995). As medidas tomadas eram de boa qualidade e pouco afetadas pela espessura da amostra. No entanto a exposição à radiação era consideravelmente alta (GOODSITT, 1992).

Como alternativa para a utilização de radionuclídeo na geração de fótons, foi proposta a sua substituição por um tubo de raios-X (TOTHILL, 1989). Isso permitiu a produção de alto

fluxo de fótons em um feixe de pequeno diâmetro, mais preciso, que gerava menor exposição à radiação e aumentava a velocidade do processo (DEVITA e STALL, 1999; LASKEY, 1996). Com isso nascia a tecnologia DXA. Este escâner foi apresentado em 1987 e foi incorporado nas práticas de rotina em clínicas humanas (BLAKE e FOGELMAN, 2010). Além disso, procedimentos de calibração do dispositivo foram implantados para garantir ainda mais precisão. Isso é feito com a utilização de fantasmas (*phantoms*), que são peças artificiais que simulam tecidos ósseos e não ósseos e que possuem composição conhecida (DEVITA e STALL, 1999).

Os fótons produzidos pelo tubo de raios-X são divididos em dois níveis energéticos para obtenção do contraste da imagem. Esta divisão é obtida basicamente por duas técnicas: a primeira utiliza variação na voltagem da corrente elétrica e a segunda utiliza corrente elétrica constante e um filtro para que os raios-X sejam divididos em dois (GOODSITT, 1992). Dentre as vantagens da DXA podem ser citados ainda: ser rápida, não invasiva, não gerar desconforto, permitir avaliação regional, aplicável em diferentes idades e sofrer pouco ou nenhum erro dependente do operador (BLAKE e FOGELMAN, 1997; DEVITA e STALL, 1999; NORD, 1998). Dentre as desvantagens, podem ser citadas: variação dos resultados dependendo do fabricante do dispositivo; exposição à radiação; criação de uma imagem/projeção bidimensional que limita a avaliação óssea; estimação (e não medição) do tecido não ósseo em regiões ósseas; algoritmos desenvolvidos para avaliar humanos (uma desvantagem na avaliação de animais ou outros objetos de estudo); e sensibilidade à espessura da amostra (BLAKE e FOGELMAN, 1997; DEVITA e STALL, 1999; NORD, 1998).

1.2 Descrição da tecnologia DXA

Escâneres DXA desenvolvidos para medicina humana ou osteodensitômetro são constituídos por uma mesa, que representa o equipamento de raios-X propriamente dito, e por um computador com o pacote de softwares responsável pela análise dos dados (Figura 1.1) (BLAKE e FOGELMAN, 1997). O escâner captura uma imagem bidimensional projetada, semelhante às obtidas em radiografias para constatação de fraturas e outros diagnósticos por imagem (Figura 1.2). Esta “fotografia” é formada por centenas de pixels, que são as menores unidades de uma imagem bidimensional (TOTHILL, 1995). O tamanho do pixel dependerá da configuração do software que é feita antes da digitalização. Estas unidades podem ser de dois

tipos distintos. Assim, a unidade é chamada de pixel de tecido macio (em uma região corporal onde não existe osso) ou pixel ósseo (em região onde existe osso). Esta tecnologia se diferencia de outras pela emissão de raios-X em duas intensidades (ou níveis energéticos), característica essa que dá nome a técnica. No entanto, a informação mais importante coletada pelo DXA é o coeficiente de atenuação dos raios-X, que juntamente com valores de referência, servem para a medição e estimação corporal do indivíduo ou amostra sobre a mesa. Para isso, o software utiliza um modelo com três compartimentos, sendo: conteúdo mineral ósseo, gordura e magro (material que não é osso nem gordura).

Figura 1.1 – Equipamento Lunar Prodigy Advance

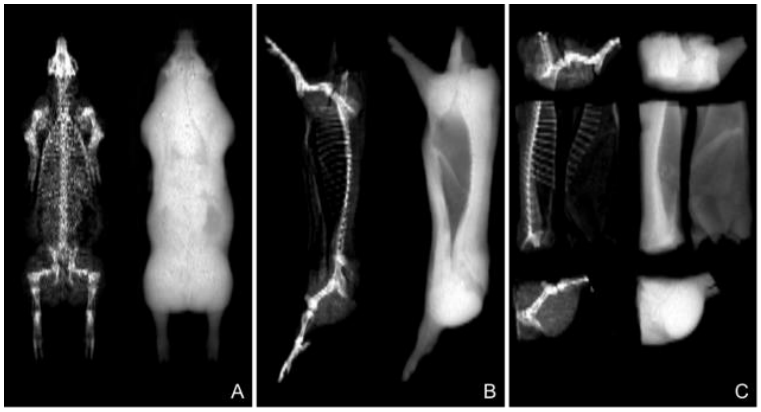

Figura 1.2 – Exemplos de imagens obtidas pela DXA; A: imagem de um suíno vivo com aproximadamente 90 kg; B: imagem de uma meia carcaça suína; C: imagem de cortes cárneos

O conceito chave da tecnologia DXA é a atenuação dos raios-X em diferentes níveis energéticos (PIETROBELLI et al., 1996). Um tubo ou lâmpada de raios-X é o responsável pela geração de fótons com energia constante (KIM, 2010). A energia do fóton emitido e recebido é conhecida, o que permite estimar a composição da amostra. A perda de intensidade se dá quando um fóton encontra algum material em sua trajetória e interage com a órbita de elétrons dos átomos do referido material. Na tecnologia DXA, esta interação pode ser classificada em dois eventos. No primeiro, o fóton atinge um elétron que está mais afastado do núcleo atômico e que, por isso, está mais fracamente ligado a ele. Esta colisão fará com que o elétron mude para uma camada eletrônica ainda mais afastada do núcleo, além de defletir a trajetória original e reduzir parte da energia do fóton. Este fenômeno é conhecido como efeito Compton (*Compton scattering*) e sua principal consequência é a retirada do fóton de sua trajetória, fazendo com que ele não atinja o receptor (PIETROBELLI et al., 1996). No segundo evento, o fóton atinge um elétron mais próximo do núcleo e, por isso, mais fortemente ligado a ele. Nesse tipo de colisão, o fóton transfere toda sua energia para o elétron e, por consequência, deixa de existir (KIM, 2010). Esse fenômeno é chamado de colisão fotoelétrica (*photoelectric collision*) e sua consequência é a aniquilação do fóton que deixa de atingir o receptor (PIETROBELLI et al., 1996). O resultado em ambos os eventos é a redução ou atenuação exponencial da energia fotoelétrica incidente durante sua passagem através do material (JEBB, 1997).

Enquanto uma fonte monoenergética de raios-X é capaz de mensurar a massa de uma amostra homogênea, uma fonte de dupla energia é necessária para estudar uma amostra com dois componentes. O corpo ou carcaça de um suíno, por exemplo, pode ser dividido em seis elementos básicos, a saber: água, carboidratos, cinzas ósseas, cinzas não ósseas, lipídios e proteínas (Figura 1.3). O software do DXA redistribui estes seis elementos em dois modelos com dois componentes cada. Um primeiro modelo foi desenvolvido para pixel onde não existe tecido ósseo. Nele o lipídio é separado dos outros quatro elementos, o primeiro compartimento é chamado de massa gorda (*fat mass*) e o restante de massa magra (*lean mass*). No segundo modelo, as cinzas ósseas são separadas dos outros cinco elementos. Assim, o primeiro compartimento é chamado de conteúdo mineral ósseo (*bone mineral content* - BMC) e o restante de tecido macio (*soft tissue mass*). O software então combina a informação dos dois modelos de dois compartimentos para criar um modelo de três compartimentos (LASKEY, 1996). Esta integração é necessária, pois em pixel ósseo o software calcula a massa de tecido macio mas não é capaz de diferenciá-la em massa gorda ou magra. Para isso, a tecnologia DXA usa como referência o pixel de tecido macio mais próximo do pixel ósseo e supõe que a composição da massa macia do segundo seja igual ao do primeiro (MITCHELL e SCHOLZ,

2009; PIETROBELLI et al., 1996). Esta suposição pode trazer uma série de imprecisões para o modelo, uma vez que em grandes áreas ocupadas por ossos (por exemplo, na escápula) o pixel de tecido macio de referência está muito afastado de um pixel localizado no centro desta grande área.

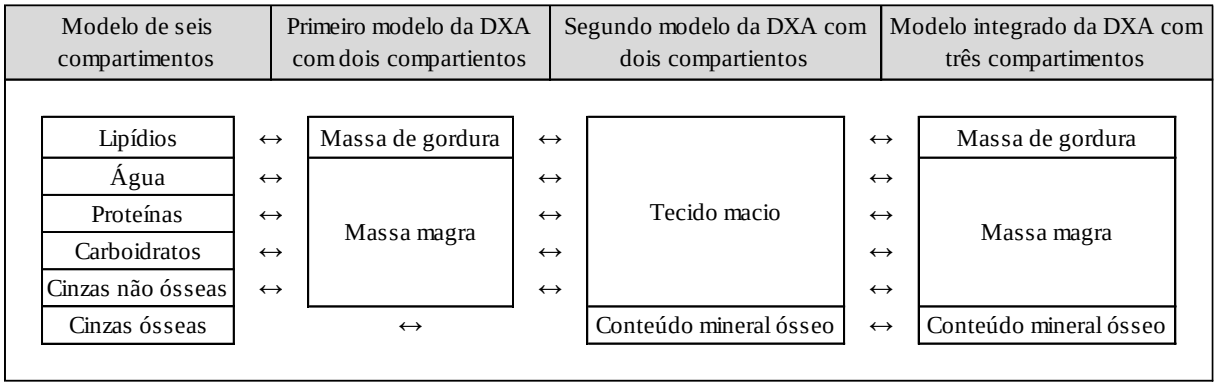

Figura 1.3 – Representação de um modelo com seis compartimentos para composição corporal de suínos, os dois modelos de dois compartimentos e o modelo integrado com três compartimentos da tecnologia DXA

1.3 Descrição dos modelos matemáticos utilizados pela DXA

A capacidade de estimar a massa contida em um pixel foi o fator que permitiu a utilização da DXA na estimação da composição corporal de indivíduos. Neste procedimento, são conhecidos: a energia do fóton emitido (I_0) e recebido (I), além do valor do coeficiente de atenuação de massa (μ_m). A partir deles, é possível determinar a massa por unidade de área (M) em uma amostra com composição homogênea (Equação 1) (LASKEY, 1996). Quanto maior o número atômico do material em estudo, maior será o valor de μ_m. Por outro lado, quanto maior a energia do raio-X, menor será o μ_m. Com o intuito de padronizar posteriores explicações, alta e baixa energia serão consideradas nesta revisão como 70 e 40 keV, respectivamente. O coeficiente de atenuação de massa é estimado através de ensaios científicos e é constante em um determinado nível energético para um dado material que pode ser homogêneo ou heterogêneo em sua composição de elementos atômicos (KIM, 2010). A Tabela 1.1 apresenta alguns exemplos de coeficientes em materiais homogêneos e heterogêneos. A apesar da água

ser considerada heterogênea aqui, ela pode ser considerada homogênea se não apresentar impurezas. Vale ressaltar que a emissão de fótons é necessária em somente um nível energético para determinação da massa de uma amostra de composição homogênea.

$$In(I/I_0) = \mu_m * M \quad (1)$$

Tabela 1.1 – Exemplos de coeficientes de atenuação de massa (μ_m) e coeficientes de atenuação (*R-value*) a dois níveis energéticos em materiais homogêneos e heterogêneos

Tipo de material	**Material**	μ_m		***R-value***
		40 keV	**70 keV**	
Materiais homogêneos	Hidrogênio	0,3458	0,3175	1,0891
	Carbono	0,2047	0,1678	1,2199
	Nitrogênio	0,2246	0,1722	1,3043
	Oxigênio	0,2533	0,1788	1,4167
Materiais heterogêneos	Ácido oleico	0,2273	0,1872	1,2143
	Ácido linoleico	0,2268	0,1857	1,2208
	Proteínas	0,2363	0,1831	1,2906
	Água	0,2636	0,1942	1,3572

Fonte: Adaptado de Pietrobelli et al (1996).

A utilização de raios-X em dois níveis permite também obter mais uma variável de interesse: o coeficiente de atenuação, *Ratio value* ou simplesmente *R-value* (Equação 2). Este valor é gerado pela divisão de dois μ_m de um mesmo material tomados em energias diferentes (BRUNTON et al., 1993; MITCHELL et al., 1998b). Sua função é servir como referência para a determinação da composição da amostra. Assim, para a avaliação corporal existem três valores de *R-value* de referência que são obtidos por ensaios científicos e representam os três compartimentos do modelo DXA (Figura 1.3). Eles são gordura (*fat* - F), material magro (*lean* - L) e osso (*bone* - B); e possuem os valores de 1,211 (Equação 3); 1,412 (Equação 4); e 3,125 (Equação 5), respectivamente. O termo magro se refere ao compartimento que engloba os elementos que não são osso ou gordura. Outro elemento importante é a massa de tecido macio (*soft tissue* - ST) que representa a soma de gordura e magro. Uma pressuposição importante neste caso é de que existe uma relação linear entre o *R-value* de 100% gordura até 100% magro.

$$R = In(I_0^{40}/I_{ST}^{40})/In(I_0^{70}/I_{ST}^{70}) = \mu_m^{40}/\mu_m^{70} \quad (2)$$

$$R_F = 0{,}23/0{,}19 = 1{,}211 \quad (3)$$

$$R_L = 0{,}27/0{,}19 = 1{,}421 \quad (4)$$

$$R_B = 1{,}00/0{,}32 = 3{,}125 \quad (5)$$

Segundo a metodologia utilizada pela DXA, o animal ou carcaça em estudo é composto pela mistura dos três componentes supracitados. Assim, a análise de uma amostra começa pela avaliação do pixel de tecido macio. Primeiramente é calculado o *R-value* deste pixel através da combinação da informação da energia emitida e recebida nos dois níveis (Equação 6). A pressuposição de que existe uma relação linear entre material magro e gordura permite que o cálculo do segundo valor. Isso vale tanto para o pixel de tecido macio, quanto para a porção macia de um pixel ósseo. O cálculo é expresso em percentual, representando a relação dos *R-values* de referência e o *R-value* obtido para o tecido macio (Equações 7 e 8). Após, os valores estimados para percentual de gordura e de material magro são relacionados com os valores de μ_m de referência (μ_m da gordura ou magro) para obtenção do μ_m do tecido macio específico do pixel em estudo (Equações 9 e 10).

$$R_{ST} = In(I_0^{40}/I_{ST}^{40})/In(I_0^{70}/I_{ST}^{70}) \quad (6)$$

$$Magro\ \% = [(R_{ST} - R_F)/(R_L - R_F)] * 100 \quad (7)$$

$$Gordura\ \% = 100 - Magro\ \% \quad (8)$$

$$\mu_{m\,ST}^{40} = \lceil (magro\ \% * \mu_{m\,L}^{40})/100 \rceil + [(gordura\ \% * \mu_{m\,F}^{40})/100] \quad (9)$$

$$\mu_{m\,ST}^{70} = \lceil (magro\ \% * \mu_{m\,L}^{70})/100 \rceil + [(gordura\ \% * \mu_{m\,F}^{70})/100] \quad (10)$$

A estimação das massas pode ser iniciada a partir destas informações. Primeiramente, a massa total do pixel de tecido macio é obtida utilizando os valores de referência e os calculados (Equação 11) (LASKEY, 1996). Esse último valor é relacionado com a informação obtida pelas Equações 7 e 8, sendo possível decompor a massa de tecido macio em massa gorda e massa magra.

$$M_{ST} = \frac{In(I_B^{40}/I_0^{40}) - [R_B * In(I_B^{70}/I_0^{70})]}{(R_B * \mu_{m\,ST}^{70}) - \mu_{m\,ST}^{40}} \quad (11)$$

Para a estimação da composição de um pixel ósseo, um pixel de tecido macio mais próximo a ele é tomado como referência (ROUBENOFF et al., 1993). Esse procedimento é

realizado pois não é possível calcular o *R-value* e o μ_m de tecido macio em um pixel ósseo. A massa óssea de um pixel ósseo é calculada (Equação 12) através das informações de referência juntamente com o *R-value* da massa de tecido macio do pixel que está sendo utilizado como referência. Já a estimação da massa de tecido macio de um pixel ósseo é realizada da mesma forma que a de um pixel de tecido macio (Equação 11). Por último, os valores obtidos pelas equações 7 e 8 do pixel de tecido macio de referência são assumidos como iguais para o pixel ósseo em questão. A densidade mineral óssea é então obtida bela divisão do BMC pela área total de pixels ósseos.

$$M_B = \frac{[R_{ST} * In(I_B^{70}/I_0^{70})] - In(I_B^{40}/I_0^{40})}{\mu_{m\,B}^{40} - (\mu_{m\,B}^{70}) * R_{ST}} \quad (12)$$

1.3.1 Inovações introduzidas à tecnologia DXA

Novas tecnologias de informática têm sido consideradas recentemente para correção de alguns fatores, o que aumentou a precisão dos softwares desenvolvidos para os equipamentos DXA. Dentre estas modificações, podem ser citadas a utilização de algoritmos e pressuposições. Novos algoritmos que melhoraram a classificação de pixel em macio (*R-value* < 1,421) ou ósseo (*R-value* > 3,125) foram desenvolvidos principalmente para distribuir pixels que ficam entre estas duas classes (*R-value* entre 1,421 e 3,125). Outros algoritmos foram utilizados para delimitar áreas de pixels macios em função da sua distância à regiões ósseas, auxiliando na correção do valor percentual de gordura na região estudada (NORD e PAYNE, 1995).

A inclusão de algumas pressuposições também modificou a forma como a estimação é realizada. Uma das premissas mais conhecidas é o uso de um valor fixo de percentual de gordura para ossos, o que depende da marca comercial do equipamento. Como descrito anteriormente, a relação teórica entre o *R-value* e o percentual de gordura é linear, sendo obtido 100% de massa gorda quando o *R-value* é igual a 1,211 e 0% de massa gorda quando igual a 1,421. Considerando que o osso apresenta 4% de gordura e tendo como referência o GE Lunar Prodigy Advance (equipamento utilizado nesta tese), o menor percentual de gordura obtido pela DXA em qualquer tipo de tecido estudado não será inferior a esse valor. Este efeito já foi verificado em uma série de estudos, onde a relação perde sua linearidade quando o *R-value* é maior que

1,38 ou, em outras palavras, quando o percentual de gordura for menor que 4 a 5% (MITCHELL et al., 1998b; SWENNEN et al., 2004). Relação semelhante também foi observada para tecido adiposo dissecado (MERCIER et al., 2006). Neste contexto, apesar do conhecimento disponível sobre os fundamentos da DXA, é importante considerar que os novos softwares possuem seus aperfeiçoamentos. Estas modificações devem ser percebidas e entendidas, uma vez que a maioria delas são segredos industriais e não são disponibilizadas em manuais. Assim, alguns testes devem ser realizados antes da utilização de equipamentos DXA para garantir a veracidade dos resultados fornecidos por esta tecnologia.

Os equipamentos DXA modernos receberam, além das modificações nos softwares, também inovações estruturais. A utilização de feixes de raios-X em leque pode ser citada como um dos maiores avanços na utilização da DXA (BARTHE et al., 1997). Equipamentos de primeira geração utilizavam feixes estreitos de raios-X (SVENDSEN et al., 1993). Com isso era dispendido mais tempo para a digitalização, além de representar maior tempo de exposição à radiação. Os feixes em leque permitem que uma maior faixa da amostra seja digitalizada ao mesmo tempo, tornando o processo mais rápido (FELSENBERG et al., 1995). No entanto, algumas questões relacionadas com esta nova tecnologia ainda não foram respondidas, tais como: o grau de modificação na precisão das medidas e qual seu impacto sobre a estimação da composição química e dissecada de suínos.

1.4 Comparação de metodologias para avaliação corporal em suínos

Os principais métodos disponíveis atualmente para a avaliação corporal de suínos são as análises químicas e a dissecção de tecidos. Dentre estes, a análise química é considerada como método padrão para avaliação da composição corporal.

As diferenças mais importantes entre os princípios metodológicos devem ser conhecidas quando um procedimento é utilizado para calibrar outro. Assim, grande parte da falta de concordância ou de ajuste em modelos para transformação de dados pode estar relacionada com o que cada resultado realmente significa. A seguir serão discutidas as principais diferenças entre medidas obtidas por análise química ou por dissecção com medidas obtidas pela DXA, focando na estimação dos dois primeiros em função do último método.

1.4.1 Análise química e DXA

Como revisado anteriormente, os modelos matemáticos da DXA redistribuem os seis componentes corporais em três compartimentos: BMC, massa gorda e massa magra. No entanto, os métodos tradicionais de análise química também não são utilizados para medir esses seis componentes, uma vez que os níveis corporais de carboidratos são normalmente baixos (sendo ainda menores na carcaça) e que os minerais ósseos e não ósseos não são distinguidos (NIELSEN, 1973). A relação entre os seis componentes básicos, a análise química e os resultados DXA é detalhada na Tabela 1.2. A primeira coluna mostra a composição corporal dividida em seis compartimentos, já a segunda e a terceira colunas mostram como os seis compartimentos são redistribuídos segundos a metodologia DXA e química. Essa analogia ajuda a explicar parte da dificuldade no uso da DXA como ferramenta para predizer algum constituinte químico, em especial proteínas (MITCHELL et al., 1998b). A dificuldade na estimação das proteínas pode se originar de duas condições: (1) a forma como a análise química classifica as proteínas - relação da primeira com a segunda coluna; e (2) a forma como o DXA classifica as proteínas - relação da primeira com a terceira coluna.

Tabela 1.2 – Relação entre componentes corporais determinados pela DXA e análise química

Componentes corporais principais	**Análise química**	**DXA**
Lipídios	Extrato etéreo	Massa gorda
Água	Água	Massa magra
Proteínas	Nitrogênio	Massa magra
Carboidratos	Nitrogênio	Massa magra
Minerais não ósseos	Cinzas	Massa magra
Minerais ósseos	Cinzas	Conteúdo mineral ósseo

Fonte: Adaptado de Pietrobelli et al. (1996) e St-Onge et al. (2004).

A primeira condição que afeta a precisão da DXA na estimação das proteínas vem da forma como as análises químicas as determinam. O método químico determina o conteúdo proteico através da mensuração do nível de nitrogênio total da amostra. No entanto, nem todo o nitrogênio é proteico, sendo que alguma porção dele pode ser proveniente de carboidratos,

ácidos nucleicos ou frações inorgânicas (EMMANS e KYRIAZAKIS, 1997). Como forma de contornar essa falta de especificidade do nitrogênio total, foi proposto um fator de correção para proteína animal de 6,25. Isso significa dizer que para cada 100 g de proteína animal existem 16 g de nitrogênio proteico (NIELSEN, 1973). Apesar do viés gerado pela primeira condição ser considerado menor do que na segunda condição, não foram encontrados estudos em que estes efeitos tenham sido mensurados para determinar seu real impacto sobre as medidas DXA.

Para entendimento da segunda condição, leva-se em conta que a variável DXA que está relacionado com as proteínas é a massa magra. No entanto, dentro deste último compartimento também estão incluídos os carboidratos, os minerais não ósseos e a água (PIETROBELLI et al., 1996). Destes três componentes, os dois primeiros representam apenas um pequeno percentual da massa total. No entanto, a água é um fator com grande representação (EMMANS e KYRIAZAKIS, 1997). A grande importância da água neste cenário é que ela não apresenta uma constância em volume relativo, sendo que seu valor reduz ao longo do período de crescimento e maturidade do animal (WANG et al., 1999). Uma vez que a maioria dos estudos de composição corporal *in vivo* são realizados para avaliar animais que ainda não são adultos, o percentual de água (que está contido dentro de massa magra do DXA) pode ser uma fonte importante de viés na estimação da proteína.

Apesar de parte das cinzas químicas estarem contidas dentro da massa magra do DXA, a comparação da BMC e das cinzas é simples, pois a proporção de minerais não ósseos é relativamente constante em tecido não ósseo. A composição da matéria seca do tecido magro dissecado pode variar dependendo do tipo de animal, mas geralmente fica em torno de 78% proteína, 20% cinzas e o restante sendo carboidrato (NIELSEN, 1973). Por isso, se for considerado que as cinzas são razoavelmente constantes dentro de um genótipo e que a proporção de minerais não ósseos também é constante, então uma simples relação percentual poderia ajudar na obtenção de seus valores. Um fator de transformação de 0,15 foi proposto para a obtenção do conteúdo mineral não ósseo em função das cinzas (JEBB et al., 1995). No entanto, em condições de desbalanço mineral da dieta, essa relação pode não ser constante, pois o nível de minerais ósseos pode variar (RYAN et al., 2011). Nesta condição de desbalanço, a obtenção do valor de minerais não ósseos fica comprometida. Por isso, a calibração de modelos de ajuste para transformar medidas DXA em cinzas é importante para condições não convencionais de mineralização óssea.

As pressuposições utilizadas pela DXA em relação aos ossos também devem ser salientadas, uma vez que a tecnologia não foi desenvolvida para avaliar a composição interna do osso. Assim, o teor de gordura da medula óssea é considerado constante entre 4 a 5%, com

exceção do crânio onde a composição de 17% é considerada devido ao alto teor de lipídios no sistema nervoso central (HOLOGIC, 1996). No entanto, esses valores são dependentes da marca comercial do equipamento. Esta pressuposição pode ser considerada como um importante viés na comparação dos métodos, uma vez que a análise química considera o conteúdo real de lipídios, enquanto que o método DXA meramente extrapola o conteúdo para as condições humanas.

Por fim, os *softwares* DXA foram desenvolvidos para avaliação de seres humanos, com exceção de alguns módulos para estudos em pequenos animais. Assim, sempre que algum ajuste para melhor estimar a composição corporal de pessoas for incluído nestes softwares (geralmente informações consideradas segredos industriais), uma nova fonte de viés pode estar sendo incluída para a avaliação animal.

1.4.2 Dissecção e DXA

A relação entre o método DXA e a dissecção é um pouco mais abstrata, pois os tecidos obtidos por dissecção são na verdade "misturas" de vários componentes químicos. Sendo assim, a DXA também identificará seus diferentes componentes dentro de cada tecido dissecado (Tabela 1.3). Os tecidos adiposo e muscular apresentam seus respectivos teores de massa magra e gorda enquanto que o tecido ósseo além de apresentar esses dois componentes ainda apresenta o BMC (PIETROBELLI et al., 1996). O que torna possível relacionar a dissecção com os valores da DXA é que o tecido adiposo apresenta forte correlação com a massa gorda, o tecido muscular é correlacionado com a massa magra, e o tecido ósseo é altamente relacionado com BMC e massa magra (MARCOUX et al., 2005). Isso ocorre pois tecido adiposo é rico em lipídios que, por sua vez são, os materiais de referência da massa gorda da DXA, já o tecido muscular apresenta correlação com massa magra, uma vez que porções de carne bovina foram utilizadas como referência para massa magra medida pela DXA (PIETROBELLI et al., 1996). O tecido ósseo, por sua vez, apresenta relação com BMC devido a calibração da DXA com peças artificiais que simulam ossos e com massa magra devido à forte relação positiva existente entre músculo e osso (PIETROBELLI et al., 1996; SCHOENAU, 2005). Assim, deve ser levado em conta que a forma como um tecido hipotético é classificado por um método de dissecção qualquer afeta consideravelmente o modelo para estimação de seus valores em função de medidas DXA.

Tabela 1.3 – Relação entre medidas obtidas por dissecção e DXA

Dissecção	**DXA**
Tecido adiposo	Massa gorda
	Massa magra
Tecido muscular	Massa gorda
	Massa magra
Tecido ósseo	Massa gorda
	Massa magra
	Conteúdo mineral ósseo

Em algumas condições, devido às questões comerciais ou práticas, os tecidos são considerados como sendo relacionados pela dissecção. No entanto, quimicamente ou do ponto de vista da DXA, eles podem ser completamente diferentes. Exemplo disso são as cartilagens e a pele que são considerados na dissecção (pelo método utilizado nesta tese) como osso e tecido adiposo (MARCOUX, 2001). A cartilagem é um dos exemplos mais contrastantes entre os princípios metodológicos, onde a DXA nem sequer mede traços de BMC. O viés inserido nos modelos é maior quanto maior a proporção de cartilagem na amostra analisada, principalmente nas costelas (MARCOUX et al., 2003; MERCIER et al., 2006). Outro ponto a ser salientado é que as patas inteiras podem ser classificadas como osso na dissecção, no entanto a pele e tendões estarão incluídos nesse compartimento, gerando outro viés. A pele é considerada tecido adiposo no método de dissecção, porém, esta porção corporal apresenta uma proporção muito menor de lipídios em comparação com o restante das porções contidas neste compartimento. Esta diferença química também é percebida pela DXA, onde o tecido adiposo (sem pele) apresenta em torno de 58% de massa gorda, enquanto que a pele apresenta somente 28% (dados não publicados). Neste caso, a importância se detém mais na diferença entre indivíduos pois, quanto maior for a diferença no percentual de pele entre os animais, maior será o viés inserido no modelo. No entanto, quanto menor o peso da amostra estudada, menos importante será esta imprecisão. Algo muito parecido também é observado na classificação da papada. Esta parte é considerada como tecido adiposo na dissecção, no entanto, uma pequena porção de tecido muscular está presente nesta área.

1.5 Utilização da DXA para estimação da composição corporal

Como qualquer método, a tecnologia DXA apresenta vantagens e desvantagens. Alguns pontos importantes serão expostos em relação a sua utilização para estudos de avaliação corporal.

1.5.1 Vantagens

Métodos não destrutivos, como a DXA, permitem a construção de modelos mais precisos. Estas tecnologias permitem, por exemplo, o desenvolvimento de modelos de crescimento para animais utilizando dados obtidos no mesmo indivíduo ao longo do seu desenvolvimento. Assim, a utilização da DXA em detrimento de métodos, como o abate comparativo, pode reduzir o erro devido a variabilidade individual (SUSTER et al., 2006). Além disso, equipamentos DXA apresentam boa reprodutibilidade e um reduzido efeito do operador (RAFFAN et al., 2006; SUSTER et al., 2006). Outro ponto importante remete ao tamanho dos animais, uma vez que o efeito do operador é bastante frequente na avaliação de suínos jovens, principalmente na técnica de dissecção (MITCHELL et al., 1998a).

A metodologia DXA apresenta outras vantagens que não estão relacionadas diretamente com os modelos. Pelo fato de não serem necessários abates, o gerenciamento de questões logísticas se torna mais fácil devido ao menor número de animais necessários na experimentação. Além disso, a tecnologia permite testar um maior número de tratamentos em um experimento com o mesmo número de animais. O método é extremamente rápido, sendo que os resultados estão disponíveis imediatamente após a obtenção e interpretação da imagem. Assim, se em um experimento hipotético alguma decisão deve ser tomada no decorrer do ensaio em função de um período anterior, não será necessário esperar pelos resultados (muitas vezes demorados) de análises químicas laboratoriais ou pelo término da dissecção das carcaças. Por fim, contrastando com os dois métodos destrutivos de referência, o uso da DXA na seleção de animais para programas de melhoramento poderia poupar do abate comparativo aqueles indivíduos que apresentam características vantajosas ou com alto valor genético e econômico.

1.5.2 Desvantagens

Uma das maiores dificuldades encontradas na utilização desta tecnologia é a sua impotência quanto ao nível de umidade da amostra, ou seja, quanto ao nível de água nos tecidos livres de gordura (TLG) (EMMANS e KYRIAZAKIS, 1997; ST-ONGE et al., 2004). O conteúdo de água varia nos animais, sendo um maior percentual registrado em indivíduos jovens (EMMANS e KYRIAZAKIS, 1995). O conteúdo aumenta com o crescimento dos animais e, após atingirem a maturidade, a relação água:TLG permanece constante em torno de 0,732 nos mamíferos (WANG et al., 1999). Porém, a suinocultura moderna abate seus animais antes da maturidade, ou seja, os indivíduos de interesse em pesquisas são justamente aqueles que apresentam grandes variações no conteúdo de água corporal. Fazendo um paralelo com humanos, a relação água:TLG é de aproximadamente 0,81 em crianças recém nascidas, sendo que este valor reduz para 0,75 aos dez anos de idade e para em torno de 0,73 na maturidade (FOMON et al., 1982). Por isso, apesar dos dados fornecidos pelo DXA serem relacionados com os valores dos métodos químicos, eles não representam a realidade, sendo necessária a utilização de regressões de ajuste com base em análises químicas. Estes ajustes se justificam também pela concepção original do equipamento para análises em humanos. Como descrito anteriormente nesta revisão, os aparelhos DXA e seus softwares têm seu foco na medicina humana e, por isso, utilizam padronizações que nem sempre são plenamente adequadas para os testes com animais.

1.6 Justificativa

A importância desta tese se deve a ideia inovadora do projeto. As questões a serem respondidas serão apresentadas em uma sequência lógica, considerando:

1.6.1 Efeitos da amostra

Existem poucos estudos sobre a potencialidade da DXA para avaliação de peças de carne (KRÖGER et al., 2006). A aplicação desta tecnologia pode ser realizada em diferentes etapas dentro de uma unidade de processamento de carne ou em pesquisas científicas, incluindo momentos onde peças podem estar resfriadas ou congeladas. Um estudo já demostrou um leve efeito da temperatura da amostra sobre medidas ósseas da DXA (WAHNERT et al., 2009). No entanto, nenhuma informação está disponível para outras medidas.

Alguns estudos também sugerem a existência de um efeito de borda (BARTHE et al., 1997; LANG, 2010). No entanto, pouco é conhecido a respeito de sua intensidade e importância, em especial na análise de produtos cárneos. Portanto, o efeito de borda deve ser verificado. Além disso, desde a concepção da DXA, a espessura da amostra é conhecida como um dos fatores mais limitantes para utilização da tecnologia (GOODSITT, 1992). Assim, esse efeito também deve ser verificado.

Os questionamentos relativos a estes efeitos serão apresentados ao longo da tese. O efeito de borda será abordado no Capítulo 2, enquanto que a temperatura e a espessura serão abordadas no Capítulo 3.

1.6.2 Efeito da precisão do equipamento

A precisão deste tipo de equipamento é fortemente questionada devida a sua utilização em medicina humana (LOHMAN et al., 2009). Portanto, estes equipamentos foram desenvolvidos para avaliação corporal de pessoas e respeitam suas características intrínsecas. Assim, sua precisão deve ser novamente verificada antes da aplicação em animais, não apenas na questão de variabilidade entre resultados mas também em como esta tecnologia identifica modificações artificiais (desossa e congelamento, por exemplo) que muitas vezes ocorrem na manipulação de cortes cárneos.

Estes questionamentos serão apresentados na forma de artigos científicos. A questão da precisão de medidas está contida nos Capítulos 4 e 5, já o tema dos cortes cárneo é apresentado no Capítulo 6.

1.6.3 Calibração e avaliação das fontes de erro para os modelos

Estudos anteriores mostraram a capacidade do equipamento DXA na predição da composição química e de tecidos dissecados (LÖSEL et al., 2007; MITCHELL et al., 1998c). No entanto, existe pouca ou nenhuma informação a respeito de como a evolução/atualização do equipamento (tal como apresentado na seção 1.3.1.), alterou a precisão ou a capacidade dele em predizer corretamente a composição química. Da mesma forma, existem poucos estudos que avaliaram a relação entre medidas obtidas por DXA e por dissecção em suínos (LÖSEL et al., 2007; MARCOUX et al., 2003, 2005). Por isso, muitas dúvidas ainda existiam, como por exemplo, qual a melhor condição para obter bons dados para predição da composição dissecada, ou em outras palavras, se seria recomendado digitalizar animais vivos, meias carcaças ou corte primários para gerar modelos mais precisos. Estas questões serão abordadas na forma de um artigo e apresentadas no Capítulo 7.

2 EFEITO DE BORDA DA AMOSTRA NAS MEDIDAS DXA

2.1 Introdução

Alguns estudos anteriores sugerem a existência de um efeito de borda sobre as medidas DXA (BARTHE et al., 1997; LANG, 2010). No entanto, pouco é conhecido a respeito de sua intensidade e importância, em especial na análise de produtos cárneos. Portanto, o objetivo deste teste foi estudar o efeito de borda e sua possível interação com outras variáveis e com configurações do modo de leitura da DXA.

2.2 Material e métodos

Doze ventres suínos desossados (panceta + costela) com peso médio de 3,753 kg foram adquiridos em um estabelecimento local e distribuídos em quatro grupos. Cada unidade de um grupo foi padronizada para que apresentasse exatamente a mesma largura e comprimento, e consequentemente, o mesmo perímetro de borda. Os perímetros iniciais de cada grupo foram 130, 139, 135 e 136 cm para os grupos 1 a 4, respectivamente. A digitalização das amostras foi realizada com o software *total body* uma vez em cada uma das duas configurações selecionadas (*thin* e *standard*) em três etapas (Figura 2.1). Na primeira etapa, os ventres foram digitalizados inteiros, uma unidade de cada grupo foi adicionada por vez seguida de uma digitalização, totalizando seis imagens. Na segunda etapa, as unidades foram cortadas ao meio no sentido da borda de menor comprimento. Assim, os perímetros aumentaram para 180, 184, 184 e 223 cm para os grupos 1 a 4, respectivamente. Na terceira etapa todas as partes dos ventres foram cortadas novamente ao meio no mesmo sentido, onde os perímetros aumentaram para 260, 277, 270 e 272 cm para os grupos 1 a 4, respectivamente. As digitalizações da segunda e terceira etapas foram realizadas como procedido na primeira, com a diferença de que as partes dos ventres eram posicionadas lado a lado sem se tocar. As unidades de cada grupo foram sempre acrescentadas na mesma ordem.

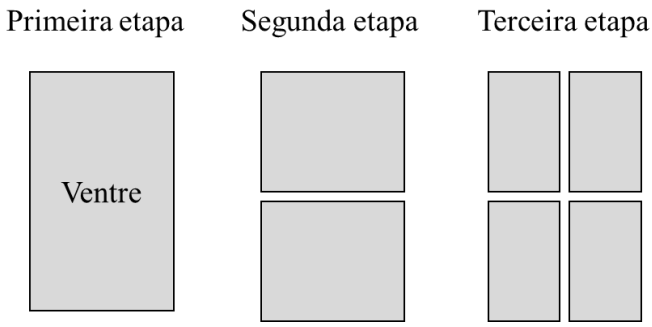

Figura 2.1 – Representação do corte e posicionamento de um grupo de ventres sobre a DXA nas três etapas sequenciais para estudar o efeito de borda

A análise das imagens foi realizada através do software EnCORE v.13.40.038 utilizando duas metodologias distintas. Primeiramente, os quatro grupos foram delimitados dentro das 18 imagens obtidas compreendendo as 72 amostras. No primeiro procedimento de análise, as 72 amostras foram avaliadas através de uma região personalizada que abrangia todas as partes de um mesmo grupo ao mesmo tempo. No segundo procedimento, os grupos foram analisados com múltiplas regiões personalizadas, ou seja, uma para cada parte cortada do grupo sendo os resultados posteriormente somados para representar o todo.

Os dados foram analisados estatisticamente utilizando análise de covariância pelo PROC GLM. As medidas DXA de percentual de gordura e massas de tecido macio, gorda e magra foram as variáveis dependentes. A configuração do modo de leitura e o procedimento de análise da imagem foram inseridas no modelo como variável qualitativa e o perímetro e o peso da amostra como covariáveis. Quando uma covariável era significativa ($P < 0,05$), uma regressão era gerada pelo PROC REG com objetivo de estudar sua dinâmica. Todas as análises foram realizadas utilizando o software SAS v.9.3 (SAS Inst. Inc., Cary, NC).

2.3 Resultados e discussão

Nas condições estudadas, as medidas DXA foram afetadas ($P < 0,05$) pelo peso da amostra. As configurações do software (*thin* ou *standard*), o procedimento para análise da imagem (grupo ou individual por parte), o perímetro e todas as interações não foram

significativas ($P > 0,05$). Também, não houve correlação entre o perímetro e o peso ($P > 0,05$). O delineamento não permitiu isolar os efeitos de aumento de peso e espessura, uma vez que para aumentar a espessura mantendo o mesmo perímetro era necessário acrescentar mais uma camada. Assim, o efeito da espessura foi desconsiderado na análise estatística sendo necessário desenvolver um delineamento exclusivo para seu estudo.

O único valor de referência para a composição dos ventres era o peso, que podia ser extrapolado para a massa de tecido macio, uma vez que os ventres eram desossados. Assim, uma superestimação foi observada para essa relação, onde a DXA identificava 1,198 g para cada grama da amostra (massa de tecido macio = - 2034 + 1,198 × peso; DPR: 573; R^2: 0,977). Vale ressaltar que a comparação do peso estimado e real não serve de referência para determinar a veracidade dos resultados DXA. Porém, a correta determinação do peso é um requerimento mínimo para sua aplicação (MITCHELL e SCHOLZ, 2009).

O efeito de borda vem sendo estudado desde a concepção da DXA. No entanto, seu foco é direcionado para o estudo de bordas ósseas para segmentação da imagem em pixels ósseo e de tecido macio (LANG, 2010). Em estudos com peças fantasmas, os autores posicionaram as regiões de interesse a três mm da borda lateral do fantasma para evitar qualquer efeito sobre as medidas (BARTHE et al., 1997). Além disso, em softwares para avaliação corporal de pessoas, os algoritmos são calibrados para tentar encontrar ossos em regiões onde elas ocorrem naturalmente (LANG, 2010). No presente estudo não foi possível identificar nenhum efeito de borda, provavelmente porque esse efeito apresenta pouca importância prática na avaliação de amostras pesadas. Os procedimentos de análise das imagens não diferiram ($P > 0,05$) entre si, o que concorda parcialmente com os resultados que serão apresentados no Capítulo 5.

Neste estudo foi possível observar, portanto, que o efeito de borda da amostra não afeta o valor das medidas DXA. A pequena variação nos resultados se deve a inclusão de nova camada com composição um pouco diferente das camadas anteriores.

3 ÉVALUATION DE LA TECHNOLOGIE DXA POUR ÉTUDIER LA COMPOSITION DES CARCASSES DE PORC ET DE SES COUPES PRINCIPALES

Este capítulo apresenta um artigo aprovado (revisão por pares) para publicação nos anais do evento *Journées de la Recherche Porcine*. A formatação original foi modificada para permitir sua inclusão neste documento, mas segue as principais normas do evento.

Évaluation de la technologie DXA pour étudier la composition des carcasses de porc et de ses coupes principales

Cette étude vise à déterminer la précision de l'absorptiométrie biphotonique à rayons X (DXA, pour dual energy X-ray absorptiometry) et l'effet de facteurs qui pourraient interférer dans l'estimation de la composition des carcasses de porc et des coupes de viande. La répétabilité et la reproductibilité de cette technologie ont été estimées par les coefficients de variation (CV, %) obtenus dans des conditions spécifiques de mesure. Nous avons également étudié l'effet des régions (rectangulaire, tête, tronc, bras et jambes), de la température de l'échantillon et de l'épaisseur de la coupe sur les mesures DXA. L'erreur de répétabilité était de moins de 1% dans toutes les conditions de mesures, sauf pour la masse de graisse où elle atteignait 4,1% dans la région du tronc. Dans les conditions de reproductibilité, les CV étaient inférieurs à 3% lorsque les estimations étaient faites dans la région de la tête, des bras ou des jambes, mais certaines mesures pouvaient avoir des CV supérieurs à 5% lorsqu'elles étaient réalisées dans la région du tronc. L'effet de la température de l'échantillon était de moins de 0,1%. L'augmentation de l'épaisseur de l'échantillon n'a pas eu d'influence sur la mesure de la masse grasse, mais elle a réduit la masse maigre (43%). La technologie DXA utilisée dans cette étude s'est avérée une technologie précise pour évaluer la composition des coupes et des carcasses de porc.

Evaluation of DXA technology to study the composition of pig carcasses and primal cuts

The objective of this study is to assess the precision of dual energy X-ray absorptiometry (DXA) and the effect of factors that could be interfering in the estimation of pig carcass and meat cuts composition. The repeatability and reproducibility were estimated by the adjusted coefficients of variation (CV, %) in repeatability and reproducibility conditions, which served to estimate the reliability of this technology. The effect of the measurement regions (custom, head, trunk, arm, and leg), the temperature, and the thickness of the piece was also studied. The repeatability was less than 1% for all measurement conditions studied, except for fat

mass, which was 4.1% when estimated in the trunk region. In reproducibility conditions, CV were less than 3% when estimated in the head, arms and, legs regions, but some measurements had CV higher than 5% when measured in the trunk region. The effect of temperature of the sample was negligible because it was less than 0.1%. Increasing the thickness of the sample did not affect the measurement of fat mass, but it reduced the lean mass (43%). The DXA technology used in this study accurately estimates pork cuts and carcass composition.

INTRODUCTION

L'absorption biphotonique à rayons X (DXA pour dual energy X-ray absorptiometry) est une méthode d'imagerie médicale utilisée pour déterminer la composition corporelle des humains, notamment la densité minérale osseuse. Ces appareils DXA émettent des rayons X à deux intensités, pour être captés après être passés à travers l'échantillon analysé. Les rayons X perdent toutefois de l'intensité en traversant l'échantillon, ce qui permet d'estimer sa composition (Pietrobelli et al., 1996). Ces appareils ont un grand potentiel scientifique, par exemple pour l'évaluation de la composition corporelle des animaux pendant leur croissance (Mitchell et al., 1996) ou la composition des carcasses (Marcoux et al., 2005). Toutefois, peu d'études ont porté sur l'évaluation des coupes principales. Le manque de données précises dans ce domaine peut être partiellement comblé par les connaissances générées à l'aide d'objets artificiels. Cependant, de nombreuses caractéristiques intrinsèques de la viande sont difficiles à simuler. Notre étude visait donc à vérifier l'exactitude d'un appareil DXA lors de la détermination de la composition des carcasses ainsi que l'effet de la température et de l'épaisseur de l'échantillon sur l'estimation de la composition de ses coupes primaires.

1. MATÉRIEL ET MÉTHODES

La répétabilité et la reproductibilité des mesures DXA faites sur des carcasses et les effets de la température et de l'épaisseur des échantillons sur l'estimation de la composition des coupes ont été évalués à partir de trois études indépendantes.

1.1. Répétabilité et reproductibilité des mesures DXA

La répétabilité et la reproductibilité des mesures DXA ont été étudiées sur 9 demi carcasses de porc comprises dans un intervalle de poids de 38,5 à 53,1 kg et une épaisseur de gras dorsal allant de 14 à 22 mm. Les demi-carcasses ont été obtenues auprès d'une entreprise commerciale après préparation selon les normes canadiennes. Les carcasses ont été radiographiées (GE Lunar Prodigy Advance, Madison, WI, É. U.; logiciel version 13.40.038) en mode corps entier et configuration standard.

La répétabilité mesure l'erreur inhérente à la lecture DXA et a été déterminée en radiographiant dix fois consécutives chacune des carcasses sans les manipuler. La reproductibilité mesure la variation inhérente à la position de la carcasse sur la table de l'appareil et sa mesure inclut la variation due à la répétabilité. La reproductibilité a été déterminée dans cette étude en radiographiant chaque carcasse dans dix positions différentes obtenues en tournant les carcasses (peau vers le haut ou vers le bas), et en changeant la direction du balayage (de la tête vers les pieds arrière ou des pieds arrière vers la tête), la disposition de la carcasse sur la table (droite ou en diagonale) et la présentation de la poitrine (étendue ou repliée). Les conditions de répétabilité et de reproductibilité ont été adaptées à partir de celles proposées dans de normes internationales (ISO, 1993).

Toutes les images obtenues dans les conditions de répétabilité et de reproductibilité ont été analysées en introduisant les images manuellement dans une région d'intérêt (ROI pour *region of interest*) rectangulaire ou en utilisant les 4 ROI proposées par le fabricant de cet appareil pour le corps humain. Ces dernières ROI ont été obtenus en plaçant successivement la carcasse dans la région de la tête, du tronc, des bras et des jambes. Les

coefficients de variation (CV) ont été calculés pour chaque carcasse individuellement, puis de manière combinée, en respectant une distribution de la variance normale (Glüer et al., 1995). Les mesures obtenues avec DXA sont la densité minérale osseuse (DMO, g cm^{-2}), le contenu minéral osseux (CMO, g), la masse totale (kg) et la masse de tissus mous (kg), ces derniers étant constitués de gras et de maigre. Les moyennes ont été comparées entre les ROI en conditions de répétabilité et reproductibilité et pour chaque ROI entre ces deux conditions à l'aide du test de Tukey ($P < 0,05$).

1.2. Effet de la température de l'échantillon

Pour l'évaluation de l'effet de la température de l'échantillon, une truie de réforme a été abattue au Centre de Recherche d'Agriculture et Agroalimentaire Canada à Sherbrooke dans le respect des règles de bien être animal (CCAC, 2009). Après l'abattage, 5 échantillons ont été prélevés dont 2 sur la longe, pesant 2,1 et 2,7 kg et trois autres sur la poitrine, dont un pesant 3,7 kg sans os et deux autres pesant 2,6 et 3,9 kg et comprenant des côtes. La température interne des échantillons mesurée au thermomètre (Copper-Atkins DFP450W, Middlefield, CT, É.-U.) était de 39,4, 40,2, 39,7, 26,2, 34,4 et 40,2 ^{o}C, respectivement dans les échantillons de longe, poitrine désossée et poitrine avec os. Immédiatement après la mesure de la température, les échantillons ont été emballés dans des sacs sous vide pour éviter toute perte d'eau.

L'analyse DXA a été faite en trois étapes, avec huit répétitions pour chaque échantillon de viande, pour un total de 120 radiographies. Les morceaux de viande n'ont pas été déplacés entre les répétitions et ont toujours été radiographiés dans la même position. L'appareil DXA a été réglé en mode Corps entier et configuration standard. Les images ont été analysées à l'aide de la ROI rectangulaire prévue pour l'expérience. Les échantillons ont été radiographiés 1) immédiatement après avoir été emballés sous vide (première étape), 2) après 24 heures de réfrigération à 4 °C, et 3) après 24 heures à -18 °C. Les conditions auxquelles les échantillons ont été soumis reflètent celles régnant dans les salles de refroidissement (4°C) et de congélation (-18°C) en conditions commerciales.

Les analyses statistiques ont été faites avec la procédure MIXED de SAS (SAS Inst. Inc., Cary, NC, É.-U.), en considérant les différentes mesures DXA comme les variables dépendantes, ainsi que la température de l'échantillon (effet fixe) et l'échantillon de viande (effet aléatoire) comme variables indépendantes.

1.3. Effet de l'épaisseur de l'échantillon

Huit poitrines commerciales désossées ayant un poids moyen de 3,6 kg ont été obtenues dans une boucherie locale et groupées en paires de 6,5, 6,6, 8,1 et 8,1 kg. Les poitrines de chaque paire avaient été découpées pour qu'elles aient les mêmes longueur et largeur. Les radiographies ont été effectuées en trois étapes (figure 1). Pour chaque étape, nous avons utilisé trois modes de balayage pour un total de 36 radiographies. Le balayage en mode Corps entier a été utilisé avec les options mince (pour les échantillons de moins de 16 cm d'épaisseur), normale (pour les échantillons de 16 à 25 cm), et épaisse (pour les échantillons de 25 cm et plus). Les poitrines ont d'abord été placées sur la table de balayage de manière à former quatre piles (une par groupe). Dans la deuxième étape, les poitrines ont été coupées en deux sur le sens de la largeur. Les moitiés ont ensuite été superposées à l'intérieur de chaque groupe. Finalement, tous les morceaux ont été coupés encore une fois sur le sens de la longueur et superposés de nouveau, toujours à l'intérieur de chaque groupe. Cette stratégie a permis d'augmenter l'épaisseur de l'échantillon tout en maintenant constants le poids et la composition de l'échantillon. L'épaisseur moyenne des piles de poitrines était de 6,6, 11,8 et 23,4 cm pour chacune des étapes.

Les données ainsi obtenues ont été analysées par covariance avec la procédure GLM de SAS. Le mode de lecture, l'épaisseur de l'échantillon et l'interaction ont été considérés comme des variables indépendantes, tandis que les différentes mesures de tissus mous DXA ont été considérées comme les variables dépendantes. La procédure REG de SAS a permis de générer les régressions linéaires, quadratiques et cubiques pour toutes les mesures DXA sur lesquelles l'épaisseur a eu un effet ($P < 0,05$). Pour choisir le meilleur modèle, nous avons tenu compte de l'écart type résiduel et du coefficient de détermination de ces régressions.

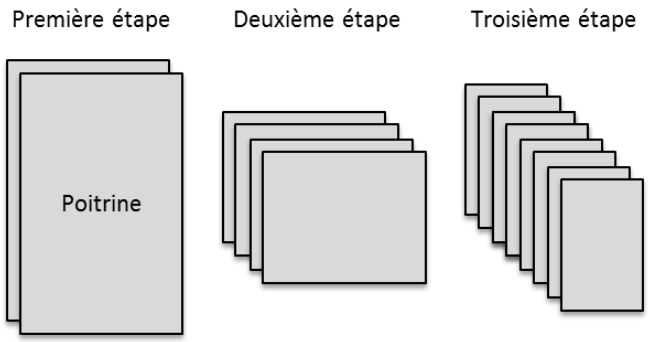

Figure 1 – Coupe et disposition des morceaux de poitrine dans les trois étapes de l'étude visant à évaluer l'effet de l'épaisseur de l'échantillon sur les mesures DXA.

2. RÉSULTATS ET DISCUSSION

2.1. Répétabilité et reproductibilité des mesures DXA

Les CV obtenus en conditions de reproductibilité étaient toujours plus élevés que ceux obtenus dans des conditions de répétabilité (tableau 1), ce qui signifie que la technologie DXA utilisée était correctement calibrée. Une méthode avec une reproductibilité inadéquate peut être ajustée et améliorée alors qu'une méthode avec répétabilité inadéquate est peu fiable et les concepts de base de la méthode elle-même doivent être revus (Burdick et al., 2005).

En général, les mesures obtenues dans les deux conditions de mesure étaient différentes ($P < 0,05$; données non présentées), mais avec trois exceptions qui sont le poids total de l'échantillon et le poids des tissus mous dans la ROI de la tête et le CMO dans la région du tronc. D'un autre côté nous avons observé une différence de 22% dans la masse grasse et 5% dans la masse maigre dans cette même région du tronc. Le reste des estimations DXA avaient une différence moyenne de 0,1%. Par conséquent, à quelques exceptions près, les mesures obtenues dans les conditions de répétabilité et de reproductibilité, tout en étant différentes, sont peu variables.

En comparant les valeurs moyennes entre ROI, le poids total et des tissus mous n'étaient pas différents, pendant que le CMO et la masse grasse étaient les plus différents. Les différences de DMO entre régions étaient de 0,5 et 0,8% en conditions de répétabilité et reproductibilité, respectivement et de 4,7 et 5,6% pour la répétabilité et la reproductibilité de la masse maigre.

Les ROI de la tête, des bras et des jambes ont présenté les plus basses erreurs de mesure dans des conditions de répétabilité et reproductibilité. Ainsi, en moyenne, ces erreurs étaient respectivement de 0,31, 0,36 et 0,36% pour la répétabilité et de 0,79, 0,84 et 0,82% pour la reproductibilité.

La répétabilité des mesures DXA de cette étude était, en général, inférieure à 1%, et la reproductibilité était inférieure à 3%. C'est la masse totale et des tissus mous qui ont été les plus répétables (moyenne de 0,3 et 0,4%, respectivement) et reproductibles (moyenne de 0,4 et 0,6%, respectivement) dans toutes les régions d'intérêt. À l'inverse, la masse grasse est la mesure DXA qui a été la moins répétable et reproductible (moyenne de 20 et 22%, respectivement) dans la ROI rectangulaire et de la tête conduisant au fait qu'elles se sont démarquées des autres ROI.

La ROI rectangulaire utilisée dans cette étude n'a pas permis d'estimer de manière précise le CMO, mais a permis d'obtenir des valeurs acceptables pour la DMO. La région du tronc n'a pas permis d'obtenir d'estimation précise de la masse grasse ce qui peut être expliqué par le fait que cette région d'analyse est configurée par le fabricant pour analyser une région avec peu de tissus mous chez l'homme.

2.2. Effet de la température de l'échantillon

Les écarts types des mesures de composition déterminée par DXA sont élevés, ce qui reflète une variation importante de la composition des échantillons (données non présentées). Le poids des échantillons obtenus par DXA a été sous estimé de 3,6% par rapport au poids déterminé par pesée (3003 vs 2895 g). À l'exception des mesures de CMO, les relations entre la température et les mesures DXA étaient généralement négatives (tableau 2). La température n'a pas eu d'effet sur la mesure de la masse maigre DXA ($P > 0,05$), mais

elle a eu un effet limité sur les autres mesures DXA. Le pourcentage de variation de la mesure DXA par degré de variation de température (pente de la régression/moyenne de la mesure, %) était de -0,07% pour la DMO, 0,02% pour le CMO et la masse de tissus mous et 0,05% pour la masse de gras. Autrement dit, pour une augmentation de température de 10°C, on observe une réduction de 0,007 g cm^{-2} de la DMO, 0,225 g de CMO, 1,98 g de gras et une réduction de 4,24 g de tissus mous. Le coefficient de variation de l'erreur résiduelle des mesures DXA prises aux différentes températures (ETR/moyenne, %) variait entre 0,6% pour le poids des tissus mous à 4,7% pour la masse grasse. Une partie de cette variation est due à la reproductibilité des mesures, car les échantillons ont été déplacés pour le refroidissement et la congélation, et replacés sur la table DXA pour chaque radiographie. Ces résultats sont similaires à ceux de DMO et CMO mesurés avec un Lunar Prodigy Advance par Wahnert et al. (2009) sur des fémurs congelés et dégelés (températures variant de -27 à 20 °C) montrant que les mesures différaient selon la région de l'os analysé, avec des variations de 1,2 et 1,4% pour la DMO le CMO, respectivement.

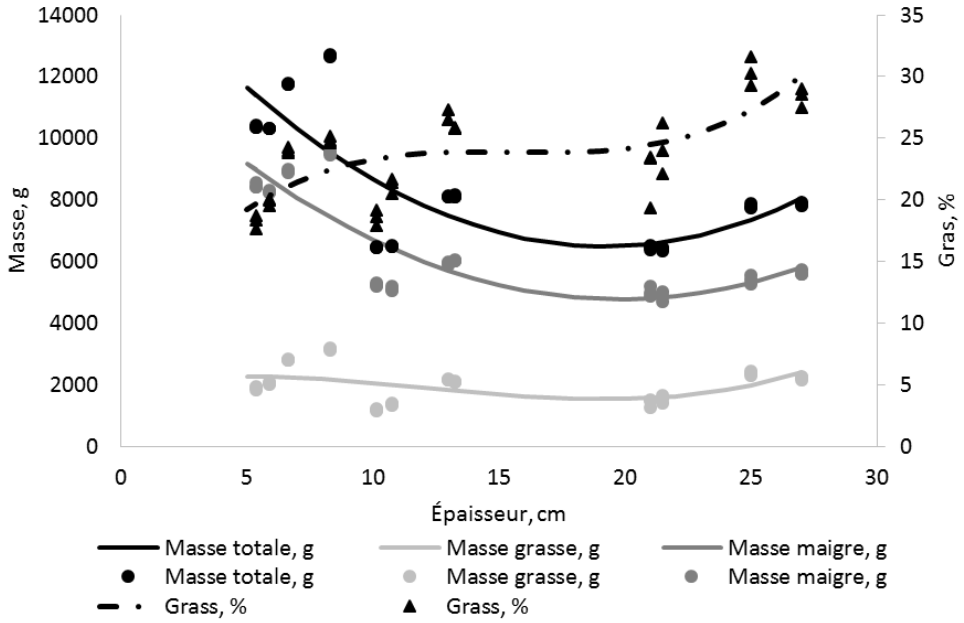

Figure 2 - Variation des mesures de DXA en fonction de l'épaisseur d'échantillons de poids constant. Les lignes continues et pointillées représentent les régressions. Les cercles et les triangles représentent les mesures.

2.3. Effet de l'épaisseur de l'échantillon

Il a été reconnu qu'un des facteurs de variation limitant l'utilisation du DXA est l'épaisseur de l'échantillon (Goodsitt, 1992). Dans cette troisième étude, le mode de lecture et ses interactions avec l'épaisseur de l'échantillon n'ont pas eu d'effet sur les mesures DXA ($P > 0,05$). L'épaisseur de l'échantillon a cependant affecté ($P < 0,05$) la mesure des tissus mous et du maigre, mais pas ($P > 0,05$) celle du gras (figure 2). La fonction quadratique est celle qui représente le mieux la relation entre l'épaisseur de l'échantillon et la masse de tissus mous et maigres. L'estimation de la masse maigre a varié de 43% entre l'épaisseur la plus faible et la plus grande. D'après ces résultats, la gamme d'épaisseur de tissu maigre pour laquelle on obtient les résultats les plus stables se situe entre 17 et 23 cm approximativement.

La configuration et le mode de lecture n'ont pas eu d'effet sur les mesures DXA dans les conditions expérimentales de cette étude. Le mode de balayage a été établi selon l'épaisseur de l'échantillon en raison du phénomène physique du durcissement du faisceau (*beam hardening*) caractérisé par une atténuation disproportionnée et plus prononcée des rayons X de faible énergie. Cet effet réduit les valeurs R (ratio des coefficients d'atténuation des rayons X) et par conséquent, augmente l'estimation de la teneur en gras. De plus, le durcissement du faisceau est plus important dans les substances ayant une valeur R plus élevée (Goodsitt, 1992). Ainsi, plus le pourcentage de masse maigre est élevé, plus il sera sous estimé à cause de cet effet. Nous n'avons toutefois pas observé cet effet ($P > 0,05$) entre les différents modes de lecture. Comme les configurations ont été créées pour tenir compte de cet effet, on peut en déduire que cette configuration ne fonctionne pas correctement. Étant donné que nous avons évalué des poitrines désossées dans cette étude, on peut supposer que l'effet de l'épaisseur (et le durcissement du faisceau) est plus prononcé lorsque les os sont présents dans les échantillons. Cependant, il faut pousser les recherches davantage dans ce domaine pour mieux évaluer cet effet.

Les mesures de DXA ont révélé plusieurs profils d'évolution par rapport à l'épaisseur de l'échantillon. Les tissus mous et la masse maigre présentent un profil d'évolution quadratique, tandis que celui de la masse grasse n'a presque pas varié. Ces résultats s'accordent avec ceux de publications antérieures sur l'effet de l'épaisseur des échantillons ayant différents pourcentages de gras (Jebb et al., 1995). Ces derniers auteurs ont montré

qu'à faible épaisseur, il y a surestimation des faibles pourcentages de gras (> 15%) et sous estimation des forts pourcentages de gras (< 25%). En revanche, les fortes épaisseurs donnent toujours lieu à une surestimation du gras, et ce biais est encore plus important lorsque le pourcentage de gras est faible. Dans une autre étude, les chercheurs ont utilisé une combinaison d'assiettes en plastique pour simuler différentes épaisseurs toujours avec le même pourcentage de gras, et ils ont trouvé que le biais positif augmentait avec l'épaisseur de l'échantillon (Gotfredsen et al., 1997). Il faut noter cependant que ces deux dernières études ont été faites avec des appareils DXA différents (Hologic et Norland) de celui de la présente étude et puisque chaque fabricant utilise des algorithmes qui leur sont propres, les résultats obtenus avec un appareil ne peuvent pas être extrapolés directement aux autres. Aucune étude n'a été trouvée à ce sujet dans la littérature, ce qui fait ressortir son importance pour l'évaluation future des coupes de viande.

CONCLUSION

La technologie DXA utilisée dans cette étude permet d'obtenir des résultats précis sur l'évaluation des carcasses et des coupes principales. La répétabilité a été considérée comme excellente avec toutes les régions d'intérêt, sauf pour le gras dans la région d'intérêt du tronc. La reproductibilité a été considérée comme bonne pour toutes les régions d'intérêt, sauf pour le gras dans la région du tronc et pour le CMO dans la région rectangulaire utilisée pour les objectifs de la présente expérience.

L'effet de la température de l'échantillon sur les mesures DXA est faible. Il est possible cependant de corriger les résultats DXA lorsque les mesures ont été prises sur des échantillons de viande dont la température n'a pas été normalisée, ou dans les cas où l'on compare des résultats obtenus chez des animaux vivants avec ceux obtenus sur carcasses froides.

Dans les conditions expérimentales utilisées, l'épaisseur de l'échantillon a un effet marqué sur certaines mesures DXA. Ainsi, la masse de graisse est peu affectée par l'épaisseur alors que celle des tissus mous et du maigre varient avec l'épaisseur de l'échantillon selon un modèle quadratique. La meilleure plage d'épaisseur d'échantillons de viande pour leur analyse avec un appareil GE Prodigy est de 17 à 23 cm.

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Tableau 1 – Moyennes et coefficients de variation ajustés des mesures de DXA obtenues avec des demi-carcasses de porc placées dans différentes régions d'intérêt dans des conditions de répétabilité et de reproductibilité[1]

Mesure/région d´intérêt	Rectangulaire		Tête		Tronc		Bras		Jambes		ETM
	Moyenne	CV[2]	Moyenne	CV	Moyenne	CV	Moyenne	CV	Moyenne	CV	
Test de répétabilité											
DMO[3], g cm^{-2}	0,91^{ab}	0,61	0,92^{a}	0,52	0,91^{a}	0,57	0,90^{b}	0,53	0,91^{a}	0,56	0,004
CMO[4], g	949^{b}	0,68	883^{c}	0,56	983^{ab}	0,68	1008^{a}	0,56	995^{a}	0,55	10,3
Masse totale, kg	46,98	0,07	47,23	0,04	46,92	0,10	46,87	0,04	46,86	0,04	0,536
Tissus mous, kg	46,03	0,07	46,35	0,05	45,93	0,11	45,87	0,05	45,87	0,04	0,528
Masse grasse, kg	9,65^{a}	0,77	5,27^{c}	0,59	8,09^{b}	4,10	8,54^{b}	0,80	8,51^{b}	0,78	0,236
Masse maigre, kg	36,38^{b}	0,24	41,08^{a}	0,09	37,84^{b}	0,96	37,32^{b}	0,17	37,36^{b}	0,17	0,439
Test de reproductibilité											
DMO, g cm^{-2}	0,90^{ab}	0,64	0,91^{a}	0,64	0,90^{a}	0,67	0,89^{b}	0,67	0,90^{a}	0,62	0,004
CMO, g	967^{a}	3,59	877^{b}	0,59	986^{a}	2,20	1004^{a}	0,52	990^{a}	0,60	10,6
Masse totale, kg	46,91	0,24	47,21	0,32	46,65	0,78	46,82	0,32	46,82	0,22	0,539
Tissus mous, kg	45,94	0,29	46,34	0,24	45,67	0,81	45,83	0,22	45,83	0,22	0,531
Masse grasse, kg	9,79^{a}	2,23	5,21^{c}	2,63	9,84^{a}	20,69	8,68^{b}	2,75	8,64^{b}	2,78	0,247
Masse maigre, kg	36,15^{b}	0,77	41,12^{a}	0,29	35,83^{b}	6,17	37,14^{b}	0,54	37,19^{b}	0,49	0,451

[1]Les moyennes affectées de lettres différentes sur une même ligne sont significativement différentes (P < 0,05). [2]Coefficient de variation ajusté pour tenir compte de la distribution normale de la variance entre les carcasses. [3]Densité minérale osseux. [4]Contenu minéral osseux.

Tableau 2 – Moyennes des mesures de DXA des échantillons de porc et régressions obtenues sur les relations entre les mesures de DXA et la température des échantillons

Mesure	Analyse descriptive			Analyse de régression				
	n	Moyenne	Écart type	Écart type résiduel	Point d'interception		Température, °C	
					Coefficient	*p*	Coefficient	*p*
DMO[1], g cm^{-2}	96	1,06	0,36	0,03	1,07	0,014	-0,0007	< 0,001
CMO[2], g	96	125	70	2	125	0,045	0,0225	0,042
Masse totale, g	120	2895	635	18	2898	< 0,001	-0,4067	< 0,001
Tissus mous, g	120	2795	687	17	2798	0,001	-0,4240	< 0,001
Masse grasse, g	120	382	254	18	384	0,039	-0,1979	0,005
Masse maigre, g	120	2424	590	84	2427	0,001	-0,3871	0,240

[1]*Densité minérale osseuse.* [2]*Contenu minéral osseux.*

4 REPEATABILITY AND REPRODUCIBILITY OF MEASUREMENTS OBTAINED BY DUAL-ENERGY X-RAY ABSORPTIOMETRY ON PORK HALF CARCASS

Este capítulo é apresentado de acordo com as normas para publicação no periódico *Journal of Animal Science*.

Repeatability and reproducibility of measurements obtained by dual-energy X-ray absorptiometry on pork half carcass

ABSTRACT: The aim of this study was to evaluate the precision of a DXA device in terms of repeatability and reproducibility of measurements took on pig half carcasses. Nine pigs left half carcasses with large variability in weight and body fat were acquired in a local company. Image analyses were generated through an adaptation of the standard grid for human body, using the region of interest (**ROI**) of Head, Trunk, Arm, and Leg, as well as a Custom ROI. Each ROI was manually expanded to encompass the entire half carcass using the DXA software. In repeatability condition, the half carcasses were scanned by DXA 10 times in the same position, without being moved during the procedure. In reproducibility condition, the carcasses were scanned once in 10 different positions. Reasonable results were found for the repeatability of all bone related variables in all studied ROI, given that all CV values were lower than 1.06%. Head, Arm and Leg ROI showed good reproducibility results for bone mineral density, bone mineral content, bone area; and soft tissues, fat, and lean masses. In contrast, Trunk ROI showed poor reproducibility for fat and lean masses. Custom ROI showed deficiency on reproducibility for bone mineral content and bone area. Trunk showed poor reproducibility in all variables except for total weight, soft tissue, and bone mineral density. The results demonstrated that different grid adaptations can be explored to obtain more precise results, because the algorithms used to calculate the composition of different regions have peculiarities and adjustments, and consequently can produce different repeatability and reproducibility. As conclusion, Custom ROI show deficiency in reproducibility from BMD and bone area; the Head, Arm and Leg ROI present good reproducibility in all studied variables.

Key words: composition, DXA, precision, repeatability, reproducibility, ROI

INTRODUCTION

Dual-energy X-ray absorptiometry (**DXA**) devices emit X-ray beams at 2 different energies, which are captured after passing through the sample (Pietrobelli et al., 1996). The attenuation of the X-ray beams differs between body tissues and the ratio between the lower and higher energy X-ray beam attenuations are used to calculate a coefficient of attenuation (**R-value**) (Genton et al., 2002) which is used afterwards to estimate the sample composition (Tothill, 1995).

The DXA devices are used to assess body composition in humans (Makovey et al., 2007), pet animals (Jeusette et al., 2010), farm animals (Hunter et al., 2011), and carcasses (Ribeiro et al., 2011). These devices have great potential in animal studies because they allow evaluating the body composition of live animals throughout its growing period, as well as estimating its carcass composition (Pomar et al., 2009). However, DXA devices are being improved on issues such as image quality, radiation exposure, and algorithms for human composition assessment. The question emerging from this process is how these improvements may change the precision of these devices and its implications on scientific research based on the DXA measurements of pig and pork. Furthermore, the repeatability and reproducibility of these devices should be evaluated especially when they are used for non-conventional measurements as those took in animal studies. The objective of this study was therefore to evaluate the repeatability and reproducibility measurements took on pork half carcasses in different regions of interest (**ROI**).

MATERIAL AND METHODS

Carcasses

Nine pork left half carcasses selected from the slaughter line to present moderate variability in weight and backfat thickness measured by a Destron grading probe (model PG100, Anitech Identification System Inc., Markham, Canada; Table 1) were acquired in a local meat packing plant in Québec, Canada. The selected half carcasses followed the standard commercial procedures for refrigeration and preparation, including the removal of the head, kidney, and leaf fat (CPI, 1995). Half carcasses were transported under refrigeration (4 °C) to the Agriculture and Agri-Food Canada Research Centre at Sherbrooke (Quebec, Canada) and stored in plastic bags under the same temperature. Carcasses were not frozen to prevent water losses during thawing.

Dual-energy X-ray absorptiometry device

Half carcass composition was estimated by DXA using the GE Lunar Prodigy Advance (GE Healthcare, Madison, WI, USA) device equipped with the GE Lunar Encore (v. 13.40.038) package provided by the same company. This device generates two-dimensional projected images with pixels classified as bone or soft tissue (pixel segmentation) based on each pixel R-value. Because 2 X-ray beams are used in this and similar devices, only 2 pixel components can be quantified. Thus, in pixels with bone, the amount of bone and soft tissue is measured while in pixels without bone (i.e., soft tissue pixels) the amount of fat and lean tissue is estimated. Finally, the composition of the soft tissue within bone pixels is extrapolated from the composition of soft tissue pixels around it (Pietrobelli et al., 1996). For the overall scanned body, this device provides results of bone area (**BA**, cm^2), bone mineral content (**BMC**, g), and masses of soft tissue, fat, and lean (kg). Bone mineral density (**BMD**, g cm^{-2}) is the BMC/BA ratio calculated in bone pixels. The calibration procedure following the manufacturer's recommendations was performed daily before scanning.

Repeatability and reproducibility tests

Two sequential and complementary tests were performed to estimate the device measurement repeatability and reproducibility. In both tests, the half carcasses were individually weighted and then positioned laterally on the device table before scanned in total body software with standard configuration. However, the scan table was narrower than the carcass and, for this reason, the front foot was disarticulated at the carpometacarpal joint and positioned perpendicularly to the ventral face of the fore arm. For the repeatability test, the 9 half carcasses were scanned 10 times each (10 replicates) in the same position ensuring that carcasses were not moved during this procedure. These measuring conditions are identified in this document as the repeatability conditions (**REPEAC**). The methodology provide a unique source of variation, and was used in this study to estimate the repeatability variance or, in other words, the error inherent to the DXA device. The half carcasses were stored again under refrigeration after this scanning procedure.

For the reproducibility test, the 9 half carcasses were scanned once (1 replicate) in 10 different positions (Table 2). This design was developed to include the same reproducibility error in all carcasses. This design is not symmetrical because the position was not the object of the study. These measuring conditions are identified in this document as the reproducibility conditions (**REPROC**). These REPROC provided 2 additive sources of variation: the first was the inherent variation of the DXA device under REPEAC conditions, and the second being the variation inherent to the carcass positioning on the scan table (i.e., reproducibility), this later variation meanly induced by the inherent error of the software pixel segmentation.

The half carcass images obtained from these 2 tests were analyzed by GE Lunar Encore package using 5 different ROI. First, the entire half carcass was included within a rectangular Custom ROI of this software while 4 other analyses were performed by including the entire

carcass in the Head, Trunk, Arm, and Leg ROI of the human body predefined regions. It should be noted that the absence of the head in the carcass and its lateral positioning on the scan table did not allow to correctly matching the carcass morphology with the proposed human ROI and, therefore, this later ROI analysis was not performed.

Statistical analyses

The guidelines of the International Organization for Standardization (ISO, 1993) were used to estimate the repeatability and adapted for the reproducibility of DXA measurements. The dispersion of the data collected under REPEAC and REPROC conditions was calculated for each DXA measurement in each ROI. Repeatability was associated with the variance between measurements of the same carcass on REPEAC conditions. An average value of variance was obtained combining all the carcasses and then the standard deviation was calculated as the square root of the variance (Glüer et al. 1995). On the other hand, reproducibility was calculated for each carcass by the difference between the variances obtained under REPROC and REPEAC conditions. Means comparisons of DXA measurements in the different ROI or conditions were performed, when necessary, using Tukey test at 95% of significance or ANOVA with the GLM procedure of SAS (SAS Inst. Inc., Cary, NC).

RESULTS

Means and CV were obtained for each ROI (Table 3). A similar pattern of means comparison was observed among ROI when analysing BMD in REPEAC and REPROC conditions. In both tests the Arm ROI showed the lowest ($P < 0.05$) value of BMD, while the Head ROI showed the lowest ($P < 0.05$) values of BMC and BA.

The BMD is the BMC/BA ratio that is presented in Figure 1. The reference line represent BMD equal to 1. The distribution followed reference line in parallel until around 1100

cm^2 and then it started to diverge from the reference. This pattern was also observed when studying each ROI individually.

A similar pattern of means comparison was also observed among ROI when analysing fat and lean masses in REPEAC and REPROC conditions, except for fat mass of Trunk ROI. For fat, the greatest value was observed using Custom followed by Arm or Leg and the lowest values were observed for Head ROI. The Head ROI showed the greatest ($P < 0.05$) value for lean mass compared to all other ROI. Fat and lean measured using Trunk ROI presented unexpected behavior. When the condition changed from REPEAC to REPROC there was an increase of 22% in fat and a reduction of 5% in lean. Total weight and soft tissue did not differ among ROI in both conditions.

The analyses also allowed to compare REPEAC and REPROC conditions. Regardless of the ROI, the REPEAC condition presented the greatest ($P < 0.05$) values of BMD. However, the REPROC condition presented the greatest ($P < 0.05$) values of BA, except for Head ROI that showed similar result in both tests. In fact, Head was the ROI with best agreement between conditions, with 3 out of 7 measurements being similar in REPEAC and REPROC.

All the dispersion values (CV) obtained in REPEAC were smaller than the respective measurements obtained in the REPROC. In general, the repeatability was adequate for all ROI, except for the fat measured by Trunk ROI. In all studied ROI, the CV of BMD, total weight, and soft tissue were lower than 1% in both measuring conditions. The reproducibility for BMC and BA in Custom ROI were considered inappropriate because they are greater than 2.5%. In addition, fat mass CV were greater than 2.5% in all ROI, except for Custom. Lean measured by Trunk (REPROC) was neither acceptable.

DISCUSSION

In this study, the repeatability is the precision (in terms of imprecision or error) of DXA measurements obtained under REPEAC. In this condition, results from independent tests are obtained using the same method, in identical test items, in the same laboratory, by the same operator, using the same equipment, within short intervals of time. Similarly, reproducibility is defined as the precision obtained under REPROC. In this condition and according to ISO (1993), the results are obtained with the same method, on identical test items, in different laboratories, with different operators, using different equipment. These REPROC condition have however be adapted to animal studies in which live animals are scanned throughout their growing period to evaluate the impact of experimental treatments in body composition. Therefore, REPROC condition is defined in this study as that in which just the carcass positioning on DXA table was changed.

The DXA showed good repeatability result in all studied ROI, supporting that this technology is adequate for assessing carcasses composition (Nielsen et al., 2004; Pomar et al., 2009; Ribeiro et al., 2011). Deep modifications on the technique are necessary to reduce even more the repeatability error, while the reproducibility imprecision can be reduced by minor methodological adjustments (Burdick et al., 2005). It is important to note that repeatability should be lower than reproducibility (since less variability is included in the REPEAC condition). This statement was observed in the present study, indicating that the tests succeed in obtaining the information desired. Knowing the magnitude in which repeatability and reproducibility contribute to the global error is important to improve the precision of a method.

The software utilized in this study to evaluate pork half carcasses was originally developed to study human body using adjustments (algorithms) that account for specific anatomical characteristics to increase the trueness and the precision of the results obtained when a person is scanned (Nord and Payne, 1995). Normally the software split the human body image

in up to 5 regions (ROI: head, trunk, spine, arms, and legs) and adequacies were developed for each ROI, depending on the manufacturer. Those adjustments may reduce the precision of any DXA measurement obtained in non-human subject and, consequently, calibration is necessary before its application (Hunter et al., 2011, Ribeiro et al., 2011). Calibration is also necessary to deal with the non-linear pattern found in BMD (Figure 1), which could be related with the DXA software or with some animal issue. Future studies using phantom pieces with known BMC and BA could better explain the relation between these variables.

The adaptation on grid of ROI proposed for human body by changing the position of the lines that split the image as an approach to improve live animal evaluation is a concept that has been explored in recent years (Suster et al., 2006; Hunter et al., 2011). Previous publications comparing measurements obtained using the standard grid and 3 modified grids during the pig growth showed that some adaptations may reduce the CV of results obtained in the same live animal, specially for fat evaluation (Suster et al., 2003, 2006). These findings demonstrated that the software can be explored to reach more precise DXA results, which was also evidenced in the present study by comparing the values obtained in different ROI.

The variation observed between values obtained by the same ROI in REPEAC or REPROC conditions is mainly due to the inclusion of the variability related to the carcass positioning in the second test. Little is known about how the algorithms used in each ROI may influence the DXA measurements, but it is possible that some of them could better adapt itself to a great number of carcass positioning, producing constant results in REPEAC and REPROC conditions. In the current study, just the Head and the Trunk showed at least one similar responses in both tests. However, the experimental design did not allow exploring further this issue.

Custom region of interest

Custom ROI showed near or less than 1% of repeatability for all DXA measurements. However, this region showed reproducibility greater than 3.5% for BMC and BA. Perhaps this lack of reproducibility may be related to the fact that Custom is not adjusted to any specific part of the human body. This finding is important since some studies had been developed using small Custom ROI to evaluate specific body areas (Burkhart et al., 2009; Shepherd et al., 2010).

Nielsen et al. (2004) have developed a protocol to evaluate bone mineralization in pigs as function of DXA measurements took using Custom ROI in the front feet. The results observed in this previous study indicated that the feet repositioning on DXA table slightly influenced the CV of BMD measurement. The size of the Custom ROI influenced the precision of the results, with small ROI producing greater variability.

Head, Arm, and Leg regions of interest

In a previous study performed with live pigs, the precision of fat and BMC results were improved when the Head ROI was positioned over the skull in comparison to the use of Arm ROI encompassing the whole animal (Suster et al., 2006). However, just few studies had been developed to evaluate the effect of different grid adaptations to analyze animal images, which emphasises the pioneering of the current study in this field.

Head, Arm, and Leg ROI showed similar dispersion for all DXA responses. Reproducibility values of these 3 ROI indicated a great potential of using DXA for carcass evaluation. However, it is important to be aware that some softwares may have especial corrections in the Head ROI to deal with fat content of the brain (Hologic, 1996). Therefore, Arm and Leg ROI may be more appropriated to assess pork half carcass with good repeatability and reproducibility.

Trunk region of interest

The Trunk ROI showed the worst precision for fat result under REPROC condition. However, previous study found similar CV values for DXA measurements using Trunk ROI or the standard grid proposed for human body (Suster et al., 2006).

The soft tissue composition in a pixel with bone is predicted based on the soft tissue pixel near its edge (Mazess et al., 1990; Jebb, 1997). However, the human thorax is a complex region with great amount of overlapped bones and presence of air, which increases the difficulties in predicting its soft tissue composition. In the current study, the Trunk ROI presented good reproducibility for soft tissue measurement (0.81%), but it showed great variability in the identification of fat and lean. This problem was observed even using half carcasses laterally positioned on the DXA table, which decreases the overlapping of bones on rib cage compared to a live animal image.

Another important point about the Trunk ROI is the presence of a sub-region called Android. In humans, this sub-region is positioned outside the rib cage, specifically in the abdominal/lumbar region. When the Trunk ROI was used to analyze the carcasses, the Android region moved automatically to the lower portion of the image. During data collection, it was observed that the composition of fat inside Android affect the composition of Trunk measurements. Part of the repeatability and reproducibility of fat and lean values in Trunk ROI may be attributed to the Android effect, especially in REPROC condition since the region located into Android changed with the scanning direction (positioned over the ham in head-to-hind foot direction or over the jowl in hind foot-to-head direction). Therefore, the results were adjusted for a greater fat concentration in some scans and, to a lower fat concentration in others. In the same way, lean measurements were also affected by the Android region. An alternative would be to expand the Trunk region in order to locate the Android outside the carcass, however this was not possible due to the large dimension of the sample.

In conclusion, DXA provide precise result to evaluate pork half carcass composition. The Custom, Head, Arm, and Leg ROI present adequate repeatability. However, the Custom ROI shows inappropriate reproducibility for BMC and BA measurements.

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Table 1. Characteristic of the 9 pork left half carcasses.

Carcass	Sex	Hot carcass weight[1], kg	Backfat thickness, mm	Half carcass weight[2], kg
1	Male	86.1	14.0	38.5
2	Male	99.6	16.5	44.7
3	Male	102.6	21.5	48.4
4	Female	102.8	18.5	46.2
5	Male	107.3	17.5	47.5
6	Female	108.6	15.5	39.0
7	Male	115.4	14.0	51.0
8	Male	115.8	20.0	51.4
9	Female	118.7	20.0	53.1
CV, %		9.5	15.5	11.1

[1] With head and without visceras;
[2] Without head, kidney and leaf fat.

Table 2. Description of the 10 positions used to scan 9 pork half carcasses in the reproducibility test.

Position	Skin	Centralization[1]	Belly	Scan direction
1	Up	Centralized	Extended	Head-to-hind foot
2	Up	Centralized	Folded	Head-to-hind foot
3	Up	Diagonal	Extended	Head-to-hind foot
4	Up	Centralized	Extended	Hind foot-to-head
5	Up	Centralized	Folded	Hind foot-to-head
6	Down	Centralized	Extended	Head-to-hind foot
7	Down	Centralized	Folded	Head-to-hind foot
8	Down	Diagonal	Extended	Head-to-hind foot
9	Down	Centralized	Extended	Hind foot-to-head
10	Down	Centralized	Folded	Hind foot-to-head

[1] The carcass in relation to DXA table.

Table 3. Dual-energy X-ray absorptiometry (DXA) measurement means and CV obtained under repeatability and reproducibility conditions in 9 cold half carcasses analyzed in different software regions of interest[1]

Item[2]	Region of interest (ROI)										SEM – Comparison between ROI
	Custom		Head		Trunk		Arm		Leg		
	Mean	CV	Mean	CV	Mean	CV	Mean	CV	Mean	CV	
Under repeatability condition (REPEAC)											
BMD[3], g cm^{-2}	0.91^{ab}	0.61	0.92^{a}	0.52	0.91^{a}	0.57	0.90^{b}	0.53	0.91^{a}	0.56	0.004
BMC[4], g	949^{b}	0.68	883^{c}	0.56	983^{ab}	0.68	1008^{a}	0.56	995^{a}	0.55	10.3
Bone area, cm^2	1045^{c}	1.06	963^{d}	0.72	1074^{bc}	0.91	1120^{a}	0.78	1087^{b}	0.81	8.2
Total weight, kg	46.98	0.07	47.24	0.04	46.92	0.10	46.87	0.04	46.87	0.04	0.536
Soft tissue, kg	46.03	0.07	46.35	0.05	45.93	0.11	45.87	0.05	45.87	0.04	0.528
Fat tissue, kg	9.65^{a}	0.77	5.27^{c}	0.59	8.09^{b}	4.10	8.54^{b}	0.80	8.51^{b}	0.78	0.236
Lean tissue, kg	36.39^{b}	0.24	41.08^{a}	0.09	37.84^{b}	0.96	37.32^{b}	0.17	37.37^{b}	0.17	0.439
Under reproducibility condition (REPROC)											
BMD, g cm^{-2}	0.90^{ab}	0.64	0.91^{a}	0.64	0.91^{a}	0.67	0.89^{b}	0.67	0.90^{a}	0.62	0.004
BMC, g	967^{a}	3.59	877^{b}	0.59	986^{a}	2.20	1004^{a}	0.52	990^{a}	0.60	10.6
Bone area, cm^2	1073^{b}	3.75	964^{c}	0.85	1087^{b}	2.37	1125^{a}	0.79	1093^{ab}	0.85	8.8
Total weight, kg	46.91	0.24	47.21	0.32	46.65	0.78	46.82	0.32	46.82	0.22	0.539
Soft tissue, kg	45.94	0.29	46.34	0.24	45.67	0.81	45.83	0.22	45.83	0.22	0.531
Fat tissue, kg	9.79^{a}	2.23	5.21^{c}	2.63	9.84^{a}	20.69	8.68^{b}	2.75	8.64^{b}	2.78	0.247
Lean tissue, kg	36.15^{b}	0.77	41.12^{a}	0.29	35.83^{b}	6.17	37.14^{b}	0.54	37.19^{b}	0.49	0.451
SEM – Comparison between conditions											
BMD, g cm^{-2}	0.001***		0.001***		0.001***		0.001***		0.001***		
BMC, g	2.7***		0.7***		1.7		0.8***		0.8***		
Bone area, cm^2	3.2***		1.0		2.2***		1.2**		1.2**		
Total weight, kg	0.010***		0.009		0.025***		0.008***		0.008***		
Soft tissue, kg	0.011***		0.009		0.026***		0.008***		0.008***		
Fat tissue, kg	0.018***		0.012***		0.138***		0.018***		0.018***		
Lean tissue, kg	0.023***		0.011*		0.161***		0.018***		0.018***		

[1] Mean values are arithmetic means. Within a row, means followed by same or no letter did not differ ($P > 0.05$) according to Tukey's test. Within a column, comparison of means were performed using ANOVA considered * $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$ of significance.
[2] Repeatability conditions are those in which carcasses are scanned (10 times) in the same position; carcasses were placed in different positions when scanned (10 times) under reproducibility conditions.
[3] Bone mineral density.
[4] Bone mineral content.

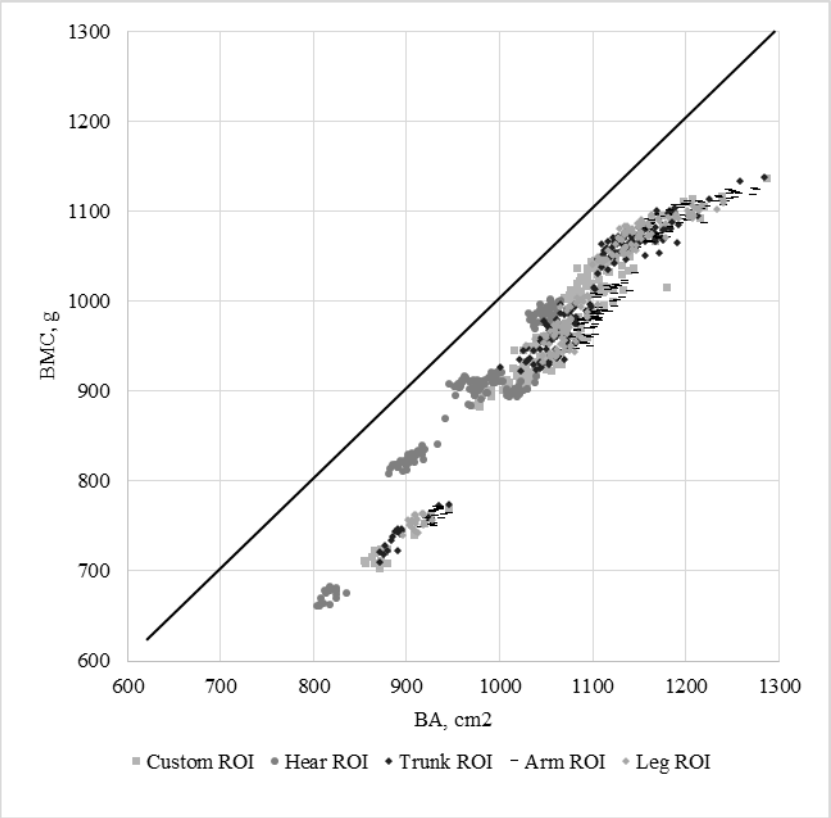

Figure 1 – Relationship between bone mineral content (BMC, g) and bone area (BA, cm^2) of pork half carcass measured in repeatability and reproducibility conditions. Black solid line represent BMC/BA ratio equal to 1.

5 ACCURACY, TRUENESS, AND PRECISION OF MEASUREMENTS OBTAINED BY DUAL-ENERGY X-RAY ABSORPTIOMETRY ESTIMATING PORK HALF CARCASS AND PRIMAL CUT DISSECTED COMPOSITIONS

Este capítulo é apresentado de acordo com as normas para publicação no periódico *Journal of Animal Science*.

Accuracy, trueness, and precision of measurements obtained by dual-energy X-ray absorptiometry estimating pork half carcass and primal cut dissected compositions

ABSTRACT: The goal of this study was to evaluate the accuracy, trueness, and precision of DXA measurements taken on pork half carcasses and primal cuts using different region of interest (ROI) and softwares estimating its dissected composition. Nine left half carcass were acquired in a local meat packing plant. They were scanned using different ROI and configurations of softwares. The ROI used were: Custom, Head, Trunk, Arm, and Leg; while the softwares were: total body (with thick, standard, and thin configurations) and small animal (with heavy, medium, and light configurations). After scanning, primal cuts were dissected in adipose tissue (including skin), muscles, and bones (including cartilage). Firstly, it was verified if the dissection values matched with DXA measurements. Therefore, adipose tissue was considered as corresponding of fat mass measured by DXA; muscle as matching of lean mass; and bone weight obtained by dissections as corresponding of BMC measured by DXA. The correspondence between the two methods was verified as: (1) overall accuracy, considering the mean square of the prediction error; (2) trueness, as error in central tendency plus error due to regression; (3) and precision, as error due to disturbances (ED). Finally, regression analyses were performed considering dissection as dependent variable and DXA measurement as the independent one. In this study, Custom ROI presented the best overall accuracy and Head ROI the worst. Scale weight, soft tissue, and bone weight were estimated with more accuracy and trueness by Arm and Leg ROI, while the more precise was Head ROI. The total cut, soft tissue, and lean mass weights measured by DXA were similar ($P < 0.001$) between softwares for all primal cuts. Fat mass measured by different softwares were similar in loin and ham, but differed

($P < 0.001$) in shoulder and belly. Results from all ROI using half carcass and from all softwares using primal cuts can be employed to generate regressions predicting dissected composition. Precision expressed in ED was in general low allowing the application of regressions to adjust the DXA measurements.

Key words: belly, composition, DXA, ham, loin, shoulder

INTRODUCTION

The interest of using dual-energy X-ray absorptiometry (**DXA**) technology to evaluate live pigs and carcasses as a method to obtain their chemical and dissected composition had increasing in the last few years (Marcoux et al., 2005, Andretta et al. 2014). The DXA is an important method because it allows taking measurements without killing the animal. Therefore, studies with growing animals can be performed with less repetitions and reduced cost. In addition, studies on carcass yield can be performed without dissection, and being consequently faster and cheaper (Marcoux et al., 2003).

Despide its importance in animal projects, DXA was not originally developed for those objectives. The softwares currently used to evaluate live pigs and half carcasses were developed to evaluate human beings. For this purpose, especial algorithms were developed and used taking into account the human body characteristics (Nord and Payne, 1995). Those adjustments work very well in human medicine, but they can insert some sort of error when other subjects are being studied. For this reason, calibration procedures should be performed to generate translation models and to obtain better DXA measurements (Suster et al., 2004).

In addition, modern softwares allow exploring new possibilities for the evaluation of DXA images, like increased flexibility on the manipulation of regions of interest (**ROI**), or new configurations to better adjust the scanning methodology considering different characteristics of the sample. For this reason, the objective of the current study was to evaluate the accuracy,

trueness, and precision of DXA measurements taken on pork half carcasses and primal cuts using different ROI and softwares estimating its dissected composition.

MATERIAL AND METHODS

Data collection

Carcasses. Nine pork left half carcasses selected from the slaughter line to present moderate variability in terms of weight were acquired in a local meat packing plant in Québec, Canada. The selected carcasses followed the standard commercial procedures for refrigeration and preparation, including the removal of the head, kidney, and leaf fat (CPI, 1995). The half carcasses were transported under refrigeration (4 °C) to the Agriculture and Agri-Food Canada Research Centre at Sherbrooke (Quebec, Canada) and stored in plastic bags under the same temperature. Carcasses were not frozen to prevent water losses during thawing.

Dual-energy X-ray absorptiometry device. Carcass composition was estimated by DXA using the GE Lunar Prodigy Advance (GE Healthcare, Madison, WI, USA) device equipped with the GE Lunar Encore (v. 13.40.038) platform provided by the same company. This device generates two-dimensional projected images with pixels classified as bone or soft tissues (pixel segmentation) based on each pixel ratio value (**R-value**). For the overall scanned body, this device provides results of bone area (**BA**, cm^2), bone mineral content (**BMC**, g), soft tissue and fat masses (kg). Bone mineral density (**BMD**, g cm^{-2}) is the BMC/BA ratio calculated in bone pixels, while the lean mass (kg) is calculated by the difference between soft tissue and fat masses in all pixels. The calibration procedure following the manufacturer's recommendations was performed daily before scanning.

Region of interest test. The first series of scans was performed to evaluate the impact of using different ROI when estimating the dissected composition of pork primal cuts. To this

end, the carcasses were placed on the DXA table, with skin side up, and scanned with total body software using the standard configuration.

The half carcass images obtained were analyzed by the GE Lunar Encore package using 5 different ROI. First, the entire half carcass was included within a rectangular Custom ROI of this software, while the other 4 analyses were performed by including the entire carcass in the Head, Trunk, Arm, and Leg ROI of the human body predefined regions.

Software and configuration test. A second series of scans was performed to evaluate the impact of using different softwares and configurations when estimating the dissected composition of pork primal cuts. To this end, the carcasses were prepared in a uniform manner and into primal cuts (shoulder, loin, belly, and ham) using standard Canadian cutting procedures as previously described by Marcoux et al. (2005). During these tests, the primal cuts of each carcass were placed on the DXA table, with skin side up, and scanned using 2 softwares (total body and small animal), using 3 different configurations in each software, for a total of 6 scans per carcass. Total body software was configured to the sample thicknesses thick (> 25 cm), standard (16 to 25 cm), and thin (< 16 cm). The small animal software was configured to the sample weights heavy (> 20 kg), medium (2 to 20 kg), and light (< 2 kg). Each primal cut was analyzed with a rectangular Custom ROI.

Dissection. After the scans, primal cut bones (including cartilage), adipose tissue (including skin), and muscle were dissected following Canadian reference methods (CPI, 1995, Marcoux et al., 2003). The feet and jowl were not dissected but they were considered respectively as bone and adipose tissue. Half carcass dissection composition was obtained by adding the dissected cut tissues (fat, bone, and muscle).

Statistical analyses

Half carcass and primal cut DXA measurements obtained with different ROI or with combinations of softwares and their configurations were compared using Tukey test with the GLM procedure of SAS (SAS Inst. Inc., Cary, NC) at 95% of significance. The relationships between half carcass, cuts, and dissected tissue weights (i.e., dependent variables) and the corresponding DXA measurements (i.e., independent variables) within each ROI were obtained by linear regression using the REG procedure of SAS.

Evaluating the accuracy of an instrument implies the evaluation of the closeness between its measurements and the accepted reference values in terms of trueness and precision. The trueness of a measurement indicates the degree of agreement between the expected and reference value, while the precision indicates the degree of internal agreement between independent measurements made under specific conditions (Theil, 1966). A device is considered accurate when it is true, i.e., when its measurements adjust to the true values, and considered precise when there is no spread around the true value (ISO, 1993). The accuracy of DXA total sample weight and dissected tissue weight measurements was evaluated following the procedure of Theil (1966) adapted by Pomar and Marcoux (2005). Briefly, the mean square of the prediction error (**MSPE**) was calculated as the sum of the square difference between dissected (i.e., observed) and DXA (i.e., predicted) values divided by the number of experimental observations. The MSPE was then decomposed into error in central tendency (**ECT**), error due to regression (**ER**), and error due to disturbances (**ED**). Error in central tendency is the difference between the average observed weight of dissected tissue and the corresponding average DXA measurement. Error due to regression represents the value it would have been obtained if dissection and regression were in complete agreement, in other words ER is the deviation of the least square regression coefficient from one. Error due to disturbances is the variation in dissection weight that is not accounted for a least squares regression to predict

dissection using DXA measurements. In this paper, trueness was estimated by adding the values of ECT and ER, precision was associated with the ED error, and the overall accuracy with the MSPE prediction error.

The coefficient of determination (**R^2**), the residual standard deviation (**RSD**), and the coefficient of variation of the error (**CV**) were obtained by the linear regressions between the weight of total sample, bone, soft tissues (dissected no-bone tissue), dissected adipose tissue, and dissected muscle weights (i.e., dependent variables) and the respective sample weight, BMC, soft tissues, fat, and lean DXA measurements (i.e., independent variables). Dissection predicted variables were assumed true while its precision was evaluated by the RSD.

RESULTS

Measurement errors of DXA readings by region of interest

The agreement between carcass dissection and DXA measurement was evaluated in terms of MPSE, ECT, ER, and ED that gives an evaluation of overall accuracy, trueness, and precision (Table 1). In this study, Custom ROI presented the best overall accuracy (average MSPE across weight of dissected tissues = 37.5) and Head ROI the worst accuracy (average MSPE = 74.4). Arm and Leg ROI were the more accurate and true ROI estimating total weight, soft tissue, and bone weight, while the more precise was Head ROI. However, there were few differences between the trueness and the precision of these models. In the estimation of adipose and muscle tissues, the more accurate, true, and precise was the Custom ROI. Head ROI showed the worst trueness in all DXA tissue measurements, but this same ROI showed the best precision, or near the best, in all measurements other than muscle. Trunk ROI showed the worst precision in the estimation of adipose tissue, that was 7 times worse than in Custom or Arm ROI. In addition, Head was the less accurate, true, and precise ROI for muscle dissected tissues.

The ability of DXA measurements to predict dissected tissue weights in the studied ROI was evaluated in terms of regression analyses (Table 1). The CV were lower than 5% for all the studied relationships. In terms of R^2 and RSD, Custom was the best ROI followed by Arm, Leg, Head, and Trunk ROI. The obtained R^2 were greater than 0.73 for all the studied relationships. The lowest R^2 were obtained for the relationship between bones and BMC. Head ROI presented a 16 % inferior R^2 than Custom in the estimation of muscle and 15% superior than Trunk in the estimation of bone. Custom ROI had a 7% greater R^2 than Trunk in the estimation of adipose tissue. Similar R^2 were observed among ROI in the estimation of scale and soft tissue weighs using DXA.

Measurement errors of DXA readings by different softwares and configurations

Software comparisons were performed for shoulder, loin, belly, and ham DXA measurements (Tables 2, 3, 4, and 5). Total cut, soft tissue, and lean mass weights were similar among softwares and configurations for all primal cuts. Loin and ham presented similar DXA fat weight between softwares and configurations. However, the shoulder and belly presented significant differences ($P < 0.001$) for DXA fat weight. For the shoulder, the greatest value of fat mass was obtained with the small animal software using light configuration, that was 26% greater than the value obtained with thin configuration of total body. Meanwhile, for the belly, the greatest value of fat mass was also found with the small animal software in light configuration that was 37% greater than the value for standard configuration of total body. In all cuts, BMC measured by small animal was greater than the measured by the total body mode. For the small animal, the greatest value of BMC was obtained with the thin configuration, followed by the medium and heavy ones. Within the total body software, the greatest BMC was obtained using the thin configuration, followed by the standard and thick ones.

Shoulder. In average, the small animal software was more accurate in the estimation of shoulder dissected tissues than the total body (Table 2). Scale and soft tissue weights in the shoulder were more accurate (i.e., MSPE) when estimated by the total body than by the small animal software (respectively, 0.17 vs 0.27, and 2.06 vs 2.13). In addition, scale and soft tissue weights were also truer (i.e., ECT + ER) in the total body than using the small animal software for this cut (respectively, 0.15 vs 0.25, and 2.05 vs 2.12). The small animal software estimated respectively bone, adipose and muscle tissues 1.2, 8.9, and 1.8 times more accurately and 1.2, 11.2, and 1.8 times truer than the total body software. However, precision (i.e., ED) tended to show inverse pattern than trueness, with the exception of soft tissues. For the scale and soft tissue weights, the R^2 of the corresponding regressions were almost similar across softwares and configurations. For should bone, total body in standard configuration presented a 26% greater R^2 than with the small animal software in heavy configuration. The thin configuration of total body presented a 7% greater R^2 than the light small animal configuration when estimating adipose tissue weight in this cut.

Loin. Similar to the shoulder, the loin composition was in general more accurately predicted using small animal software (Table 3). Total body was 1.7 and 1.1 times more accurate and truer in the estimation of scale weight and soft tissue weight, respectively. Small animal was 1.2, 3.5, and 1.4 times more accurate and truer in the estimation of bone, adipose tissue and muscle. Precision showed opposite pattern to trueness for total, bone, and muscle weights. The R^2 was almost similar between softwares and configurations in the estimation of total and soft tissue weight. Total body standard presented a 15% superior R^2 than small animal light in the prediction of bone, and 4% inferior than small animal medium in the prediction of adipose tissue. Estimating muscle total body and thick configuration presented a 5% superior R^2 than small animal and light configuration.

Belly. The small animal was the best software to estimate belly composition, however bone was well predicted using total body it this same cut (Table 4). Small animal was more accurate, true, and precise in the estimation of total, adipose tissue, and muscle weight. In addition, this last software was more accurate and true to estimate bone, while total body was more accurate and true in the estimation of soft tissues. The total body and small animal formed 2 distinct groups, with the second software showing slight better results in the analyses of total, soft tissues, and muscle weights. Total body with thick configuration was 5% superior to total body with thin configuration in the estimation of bone.

Ham. Scale weight and adipose tissue were 1.5 and 2.7 times more accurate and truer estimated using total body software (Table 5). Small animal software was 1.4 and 2.9 times more accurate and 1.4 and 3.5 truer in the estimation of bone and muscle, respectively. Scale weight presented the same mean precision in both softwares. Total body was 2.7, 1.3, 3.3, and 3.5 times more precise than small animal in bone, soft tissues, adipose tissue, and muscle evaluation. The R^2 were almost similar between softwares and configurations in ham estimation of total and soft tissue weight. Thick configuration of total body presented a 26% greater R^2 than small animal heavy in the estimation of bone, 5% superior than light configurations of small animal in the estimation of adipose tissue, and 3% superior than thin configurations of total body in the estimation of muscle.

DISCUSSION

Although MSPE was considered as overall accuracy in this study, the measurement can be decomposed as ECT, ER, and ED. Trueness was considered as ECT plus ER, indicating the agreement between observed and estimated values and being both systematic errors that can be corrected by regression. Error of central tendency is the square difference between observed and predicted values, while ER is related with the regression slope (Pomar and Marcoux, 2005).

Precision is the variation in the observed value that is not accounted by the predicted value; while means a random error that is not liable for correction (Benchaar et al., 1998). Therefore, with few exceptions, most of the disagreement between dissection and DXA measurements came from ECT plus ER. This observation indicates that DXA did not provide true values and mathematical models are necessary to correct these results.

In an overall analysis, the total weight was the most accurate variable estimated by DXA, since it showed low MSPE values. An exception was found in the evaluation of half carcass weight, with this problem probably being related to the methodology used to estimate the total scale weight (considering the sum of bones, adipose tissue, and muscle weight), and to scan the primal cuts (6 combination of softwares and configurations were used and some water could be lost by evaporation during the process). The same procedure to obtain the scale weight was adopted in all primal cuts, however a similar problem was not observed for these variables.

The accuracy increased when dissection was applied to obtain the weight of tissues and it was due to the increment of ECT in most of the variables. The different approach used in DXA and dissection procedures could be the main reason for the increasing MSPE in dissected tissue evaluation. The GE Lunar Encore software of the GE Lunar Prodigy Advance DXA device used in this study is calibrated to differentiate body tissues like bone, fat, and lean using physical concepts (Pietrobelli et al, 1996) and, therefore, it is not calibrated to estimate dissected tissue weights. However, the dissection method used in this study, which is in accordance with industry standards, split the carcasses into 3 tissues using anatomic concepts.

Bones and BMC showed the weakest relationship in this study, presenting the smallest R^2 and the greatest difference among ROI or softwares and configurations, especially in the belly. On the other hand, the relationship between scale and DXA weights was the strongest in all primal cuts, showing the greatest R^2. Adipose tissue and fat mass also showed a weak

relationship, since CV was great for all primal cuts. The relationship between muscle and lean mass in belly presented also a great CV in comparison to the other primal cuts. Although these variances were observed, the methodologies could be satisfactorily calibrated by regression equations (with at least 0.59 of R^2).

Measurement errors of DXA readings by region of interest

Few studies had evaluated the effect of using different ROI over DXA measurements (Suster et al., 2006; Hunter et al., 2011). The previous studies indicated that adaptations on the standard grid for human body can be used to obtain more precise data on the evaluation of carcass composition. The present study supported the previous publications demonstrating that the choice of the ROI influence the data variability.

Measurement errors of DXA readings by different softwares and configurations

The DXA devices were used in some studies to predict the dissected tissue composition of pork primal cuts. Two publications used a DXA device equipped with narrow beam and scanned the samples previously divided into primal cuts (Marcoux et al., 2003, 2005). Another studies used DXA devices equipped with pencil and fan beam to scan entire half carcass, and used the software to split the carcass image into primal cuts (Mitchell et al., 1998; Suster et al., 2004). These studies used only one software in each project and, for this reason, it is not possible to determine if there is a better software or configuration to obtain good predicting results. In addition, these studies used older versions of the softwares with less configurations for obtained image and few options for analyses compared to newer versions.

Current results showed that the softwares may provide measurements with little variability, which can be used to create models predicting the dissected tissue composition of primal cuts. In conclusion, DXA represents a good tool to provide precise result in the

evaluation of carcass and primal cut compositions. Results obtained in all ROI using half carcass and in all softwares using primal cuts can be employed to satisfactorily (i.e., low ED) predict dissected composition.

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Table 1. Trueness (ECT + ER), precision (ED), and accuracy (MPSE) of dual X-ray absorptiometry (DXA) tissue measurements taken in half pork carcasses analyzed in different software regions of interest (ROI) relative to dissected tissues[1]

Weight	Mean, kg[2]	Accuracy analysis				Regression analysis		
		MSPE	MSPE			R^2	RSD	CV
			ECT	ER	ED			
Half cold carcass weight								
Scale	43.36							
DXA by ROI								
Custom	46.98	13.82	13.12	0.43	0.28	0.99	0.52	1.20
Head	47.24	15.76	15.01	0.51	0.24	0.99	0.48	1.10
Trunk	46.92	13.37	12.64	0.41	0.32	0.99	0.56	1.29
Arm	46.87	13.02	12.34	0.40	0.28	0.99	0.53	1.23
Leg	46.87	12.96	12.28	0.40	0.28	0.99	0.53	1.23
P	0.988							
SEM	0.54							
Dissected bone and DXA BMC[3]								
Dissected	3.75							
DXA by ROI								
Custom	0.95[b]	7.93	7.87	0.04	0.02	0.81	0.14	3.80
Head	0.88[c]	8.30	8.24	0.05	0.01	0.88	0.11	2.95
Trunk	0.98[ab]	7.74	7.68	0.03	0.03	0.74	0.17	4.46
Arm	1.01[a]	7.60	7.54	0.03	0.02	0.77	0.16	4.16
Leg	0.99[a]	7.67	7.61	0.03	0.02	0.78	0.15	4.08
P	<0.001							
SEM	0.01							
Dissected and DXA soft tissues								
Dissected	39.61							
DXA by ROI								
Custom	46.03	42.27	41.29	0.69	0.28	0.98	0.54	1.37
Head	46.35	46.51	45.48	0.82	0.21	0.99	0.47	1.18
Trunk	45.93	40.99	40.01	0.67	0.32	0.98	0.58	1.47
Arm	45.87	40.14	39.16	0.66	0.32	0.98	0.57	1.44
Leg	45.87	40.19	39.21	0.66	0.32	0.98	0.57	1.44
P	0.964							
SEM	0.53							
Dissected adipose tissue and DXA fat mass								
Dissected	13.56							
DXA by ROI								
Custom	9.65[a]	15.37	15.29	0.02	0.06	0.99	0.24	1.75
Head	5.27[c]	70.91	68.66	2.18	0.07	0.99	0.27	2.02
Trunk	8.09[b]	30.33	29.92	<0.01	0.41	0.93	0.64	4.72
Arm	8.54[b]	25.24	25.18	<0.01	0.06	0.99	0.26	1.90
Leg	8.51[b]	25.61	25.53	<0.01	0.07	0.99	0.26	1.92
P	<0.001							
SEM	0.24							

Dissected muscle and DXA lean mass

Dissected	26.05							
DXA by ROI								
Custom	36.39[b]	108.13	106.83	1.12	0.18	0.98	0.43	1.64
Head	41.08[a]	230.35	225.90	2.82	1.63	0.82	1.28	4.93
Trunk	37.84[b]	141.18	139.12	1.35	0.71	0.92	0.85	3.26
Arm	37.32[b]	128.59	127.13	1.23	0.24	0.97	0.49	1.88
Leg	37.37[b]	129.52	128.05	1.23	0.24	0.97	0.49	1.89
P	<0.001							
SEM	0.44							

[1] Mean square prediction error (MSPE), error of central tendency (ECT), error due to regression (ER), and error due to disturbances (ED) are calculated from the differences between DXA and the equivalent dissected tissues. Coefficient of determination (R^2), residual standard deviation (RSD) and CV are calculated from the regression of DXA on dissected measurements.

[2] In the Mean column and within each tissue, means followed by same or no letter dido not differ ($P > 0.05$) according to Tukey's test.

[3] Bone mineral content (BMC).

Table 2. Trueness (ECT + ER), precision (ED), and accuracy (MPSE) of dual X-ray absorptiometry (DXA) tissue measurements taken in half pork shoulders analyzed in different softwares and using Custom region of interest analysis[1]

Weight	Mean, kg[2]	Accuracy analysis				Regression analysis		
		MSPE	MSPE			R^2	RSD	CV
			ECT	ER	ED			
Shoulder weight								
Scale	11.56							
DXA by software								
TB[3] Thick	11.89	0.16	0.11	0.03	0.02	0.99	0.14	1.21
TB Standard	11.89	0.16	0.11	0.03	0.02	0.99	0.14	1.21
TB Thin	11.94	0.19	0.14	0.03	0.01	0.99	0.13	1.14
SM[4] Heavy	11.93	0.18	0.14	0.03	0.01	0.99	0.13	1.15
SM Medium	12.05	0.28	0.24	0.02	0.01	0.99	0.13	1.10
SM Light	12.11	0.34	0.30	0.03	0.01	0.99	0.14	1.17
P	0.999							
SEM	0.46							
Dissected bone and DXA BMC[5]								
Dissected	1.37							
DXA by software								
TB Thick	0.31[c]	1.14	1.13	0.01	<0.01	0.91	0.05	3.29
TB Standard	0.31[c]	1.13	1.12	0.01	<0.01	0.92	0.04	3.03
TB Thin	0.33[bc]	1.11	1.09	0.01	<0.01	0.89	0.05	3.67
SM Heavy	0.39[ab]	0.98	0.97	<0.01	0.01	0.66	0.09	6.42
SM Medium	0.40[a]	0.95	0.94	0.01	0.01	0.71	0.08	5.98
SM Light	0.44[a]	0.88	0.87	0.01	<0.01	0.76	0.07	5.38
P	<0.001							
SEM	0.01							
Dissected and DXA soft tissues								
Dissected	10.19							
DXA by software								
TB Thick	11.59	2.06	1.97	0.07	0.02	0.99	0.15	1.43
TB Standard	11.58	2.01	1.93	0.07	0.01	0.99	0.13	1.30
TB Thin	11.61	2.11	2.02	0.07	0.01	0.99	0.13	1.23
SM Heavy	11.55	1.93	1.85	0.06	0.02	0.99	0.14	1.33
SM Medium	11.65	2.19	2.13	0.05	0.01	0.99	0.13	1.30
SM Light	11.67	2.27	2.19	0.06	0.02	0.99	0.14	1.33
P	1.000							
SEM	0.45							
Dissected adipose tissue and DXA fat mass								
Dissected	3.11							
DXA by software								
TB Thick	2.25[ab]	0.74	0.73	<0.01	0.01	0.96	0.11	3.50
TB Standard	2.26[ab]	0.74	0.73	<0.01	0.01	0.94	0.13	4.17
TB Thin	2.16[b]	0.91	0.91	<0.01	0.01	0.97	0.09	3.03
SM Heavy	2.81[ab]	0.12	0.09	0.01	0.02	0.91	0.16	5.00
SM Medium	2.87[ab]	0.08	0.06	0.01	0.01	0.95	0.12	3.88

SM Light	2.91[a]	0.07	0.04	<0.01	0.03	0.89	0.17	5.45
P	0.003							
SEM	0.18							
	Dissected muscle and DXA lean mass							
Dissected	7.08							
DXA by software								
TB Thick	9.33	5.15	5.05	0.08	0.02	0.97	0.16	2.21
TB Standard	9.32	5.12	5.02	0.07	0.03	0.96	0.19	2.63
TB Thin	9.45	5.75	5.63	0.10	0.02	0.97	0.15	2.17
SM Heavy	8.74	2.93	2.76	0.13	0.04	0.95	0.21	2.91
SM Medium	8.78	2.99	2.87	0.10	0.03	0.97	0.18	2.50
SM Light	8.76	2.99	2.82	0.15	0.03	0.97	0.17	2.44
P	0.609							
SEM	0.40							

[1] Mean square prediction error (MSPE), error of central tendency (ECT), error due to regression (ER), and error due to disturbances (ED) are calculated from the differences between DXA and the equivalent dissected tissues. Coefficient of determination (R^2), residual standard deviation (RSD) and CV are calculated from the regression of DXA on dissected measurements.

[2] In the Mean column and within each tissue, means followed by same or no letter did not differ ($P > 0.05$) according to Tukey's test.

[3] Total body (TB) software configured to thick (> 25 cm), standard (16 to 25 cm), and thin (< 16 cm) options.

[4] Small animal (SM) software configured to heavy (> 20 kg), medium (2 to 20 kg), and light (< 2 kg) options.

[5] Bone mineral content (BMC).

Table 3. Trueness (ECT + ER), precision (ED), and accuracy (MPSE) of dual X-ray absorptiometry (DXA) tissue measurements taken in half pork loins analyzed in different softwares and using Custom region of interest analysis[1]

Weight	Mean, kg[2]	Accuracy analysis				Regression analysis		
		MSPE	MSPE			R^2	RSD	CV
			ECT	ER	ED			
Loin weight								
Scale	12.15							
DXA by software								
TB[3] Thick	12.66	0.30	0.26	0.01	0.03	0.99	0.17	1.44
TB Standard	12.64	0.28	0.25	0.01	0.03	0.99	0.18	1.46
TB Thin	12.66	0.31	0.27	0.01	0.03	0.98	0.19	1.54
SM[4] Heavy	12.71	0.35	0.31	0.01	0.02	0.99	0.16	1.32
SM Medium	12.85	0.52	0.49	0.01	0.02	0.99	0.15	1.27
SM Light	12.91	0.61	0.58	0.01	0.02	0.99	0.17	1.38
P	0.997							
SEM	0.49							
Dissected bone and DXA BMC[5]								
Dissected	1.10							
DXA by software								
TB Thick	0.23[d]	0.77	0.76	<0.01	<0.01	0.79	0.05	4.13
TB Standard	0.23[d]	0.76	0.76	<0.01	<0.01	0.83	0.04	3.70
TB Thin	0.24[cd]	0.73	0.73	<0.01	<0.01	0.83	0.04	3.80
SM Heavy	0.28[bc]	0.67	0.66	<0.01	<0.01	0.70	0.05	4.94
SM Medium	0.30[ab]	0.64	0.64	<0.01	<0.01	0.80	0.04	4.04
SM Light	0.33[a]	0.58	0.57	<0.01	<0.01	0.69	0.06	5.09
P	<0.001							
SEM	0.01							
Dissected and DXA soft tissues								
Dissected	11.05							
DXA by software								
TB Thick	12.43	1.97	1.92	0.02	0.03	0.98	0.18	1.67
TB Standard	12.41	1.91	1.87	0.02	0.03	0.98	0.18	1.66
TB Thin	12.42	1.93	1.87	0.02	0.04	0.98	0.20	1.84
SM Heavy	12.46	1.93	1.89	0.01	0.03	0.98	0.19	1.73
SM Medium	12.56	2.29	2.25	0.02	0.03	0.98	0.19	1.68
SM Light	12.61	2.36	2.31	0.02	0.04	0.98	0.19	1.76
P	1.000							
SEM	0.49							
Dissected adipose tissue and DXA fat mass								
Dissected	4.02							
DXA by software								
TB Thick	3.02	1.04	1.00	<0.01	0.03	0.96	0.18	4.53
TB Standard	2.99	1.09	1.05	0.01	0.03	0.96	0.19	4.81
TB Thin	3.00	1.05	1.03	<0.01	0.01	0.99	0.11	2.68
SM Heavy	3.31	0.34	0.32	0.01	0.01	0.99	0.11	2.83
SM Medium	3.33	0.37	0.36	0.01	0.01	0.99	0.09	2.21

SM Light	3.37	0.20	0.17	0.01	0.03	0.97	0.16	4.05
P	0.832							
SEM	0.29							
Dissected muscle and DXA lean mass								
Dissected	7.03							
DXA by software								
TB Thick	9.42	5.77	5.70	0.04	0.02	0.97	0.17	2.38
TB Standard	9.42	5.80	5.73	0.04	0.03	0.97	0.18	2.57
TB Thin	9.41	5.75	5.68	0.03	0.03	0.96	0.19	2.76
SM Heavy	9.15	3.85	3.76	0.05	0.05	0.95	0.21	2.95
SM Medium	9.23	4.48	4.39	0.05	0.04	0.96	0.19	2.75
SM Light	9.24	3.86	3.72	0.09	0.05	0.93	0.25	3.58
P	0.990							
SEM	0.37							

[1] Mean square prediction error (MSPE), error of central tendency (ECT), error due to regression (ER), and error due to disturbances (ED) are calculated from the differences between DXA and the equivalent dissected tissues. Coefficient of determination (R^2), residual standard deviation (RSD) and CV are calculated from the regression of DXA on dissected measurements.

[2] In the Mean column and within each tissue, means followed by same or no letter did not differ ($P > 0.05$) according to Tukey's test.

[3] Total body (TB) software configured to thick (> 25 cm), standard (16 to 25 cm), and thin (< 16 cm) options.

[4] Small animal (SM) software configured to heavy (> 20 kg), medium (2 to 20 kg), and light (< 2 kg) options.

[5] Bone mineral content (BMC).

Table 4. Trueness (ECT + ER), precision (ED), and accuracy (MPSE) of dual X-ray absorptiometry (DXA) tissue measurements taken in half pork bellies analyzed in different softwares and using Custom region of interest analysis[1]

Weight	Mean, kg[2]	Accuracy analysis				Regression analysis		
		MSPE	MSPE			R^2	RSD	CV
			ECT	ER	ED			
Belly weight								
Scale	7.94							
DXA by software								
TB[3] Thick	7.60	0.24	0.12	0.09	0.04	0.97	0.21	2.58
TB Standard	7.60	0.24	0.11	0.09	0.04	0.97	0.21	2.61
TB Thin	7.60	0.25	0.12	0.09	0.04	0.97	0.21	2.62
SM[4] Heavy	8.12	0.05	0.03	<0.01	0.01	0.99	0.10	1.24
SM Medium	8.25	0.11	0.10	<0.01	0.01	0.99	0.10	1.31
SM Light	8.36	0.19	0.18	0.01	0.01	0.99	0.11	1.37
P	0.582							
SEM	0.43							
Dissected bone and DXA BMC[5]								
Dissected	0.42							
DXA by software								
TB Thick	0.03[c]	0.15	0.15	<0.01	<0.01	0.76	0.03	7.82
TB Standard	0.03[c]	0.15	0.15	<0.01	<0.01	0.74	0.03	8.17
TB Thin	0.04[bc]	0.14	0.14	<0.01	<0.01	0.71	0.04	8.66
SM Heavy	0.06[ab]	0.13	0.13	<0.01	<0.01	0.72	0.04	8.53
SM Medium	0.06[a]	0.13	0.13	<0.01	<0.01	0.71	0.04	8.63
SM Light	0.06[a]	0.13	0.13	<0.01	<0.01	0.74	0.03	8.15
P	<0.001							
SEM	<0.01							
Dissected and DXA soft tissues								
Dissected	7.52							
DXA by software								
TB Thick	7.57	0.14	0.00	0.11	0.03	0.97	0.20	2.60
TB Standard	7.57	0.14	0.00	0.10	0.03	0.97	0.20	2.61
TB Thin	7.55	0.14	0.00	0.10	0.03	0.97	0.20	2.62
SM Heavy	8.10	0.32	0.30	0.01	0.01	0.99	0.12	1.59
SM Medium	8.19	0.47	0.44	0.01	0.01	0.99	0.12	1.62
SM Light	8.32	0.63	0.60	0.01	0.02	0.99	0.13	1.70
P	0.615							
SEM	0.42							
Dissected adipose tissue and DXA fat mass								
Dissected	3.49							
DXA by software								
TB Thick	1.59[b]	3.67	3.64	0.01	0.02	0.97	0.14	4.15
TB Standard	1.57[b]	3.73	3.69	0.02	0.02	0.97	0.14	4.08
TB Thin	1.65[ab]	3.43	3.39	0.01	0.02	0.97	0.15	4.40
SM Heavy	2.14[ab]	1.93	1.88	0.04	0.01	0.98	0.13	3.66
SM Medium	2.21[ab]	1.68	1.63	0.03	0.01	0.97	0.14	3.93

SM Light	2.49[a]	1.04	1.00	0.03	0.01	0.98	0.12	3.38
P	0.011							
SEM	0.21							
Dissected muscle and DXA lean mass								
Dissected	4.03							
DXA by software								
TB Thick	5.98	4.00	3.82	0.12	0.06	0.84	0.26	6.51
TB Standard	5.99	4.06	3.88	0.12	0.06	0.83	0.27	6.74
TB Thin	5.90	3.70	3.52	0.12	0.06	0.85	0.26	6.36
SM Heavy	5.96	3.77	3.68	0.07	0.02	0.94	0.16	3.97
SM Medium	5.98	3.87	3.78	0.07	0.02	0.95	0.15	3.84
SM Light	5.83	3.24	3.15	0.07	0.02	0.95	0.15	3.83
P	0.998							
SEM	0.30							

[1] Mean square prediction error (MSPE), error of central tendency (ECT), error due to regression (ER), and error due to disturbances (ED) are calculated from the differences between DXA and the equivalent dissected tissues. Coefficient of determination (R^2), residual standard deviation (RSD) and CV are calculated from the regression of DXA on dissected measurements.

[2] In the Mean column and within each tissue, means followed by same or no letter did not differ ($P > 0.05$) according to Tukey's test.

[3] Total body (TB) software configured to thick (> 25 cm), standard (16 to 25 cm), and thin (< 16 cm) options.

[4] Small animal (SM) software configured to heavy (> 20 kg), medium (2 to 20 kg), and light (< 2 kg) options.

[5] Bone mineral content (BMC).

Table 5. Trueness (ECT + ER), precision (ED), and accuracy (MPSE) of dual X-ray absorptiometry (DXA) tissue measurements taken in half pork hams analyzed in different softwares and using Custom region of interest analysis[1]

Weight	Mean, kg[2]	Accuracy analysis				Regression analysis		
		MSPE	MSPE			R^2	RSD	CV
			ECT	ER	ED			
Ham weight								
Scale	11.71							
DXA by software								
TB[3] Thick	12.05	0.15	0.11	0.01	0.02	0.99	0.15	1.26
TB Standard	12.04	0.13	0.10	0.01	0.02	0.99	0.14	1.23
TB Thin	12.06	0.15	0.12	0.01	0.02	0.99	0.15	1.24
SM[4] Heavy	12.04	0.14	0.11	0.01	0.02	0.99	0.14	1.17
SM Medium	12.17	0.24	0.20	0.02	0.02	0.99	0.15	1.29
SM Light	12.18	0.25	0.22	0.01	0.02	0.99	0.15	1.24
P	1.000							
SEM	0.48							
Dissected bone and DXA BMC[5]								
Dissected	0.86							
DXA by software								
TB Thick	0.223[c]	0.41	0.41	<0.01	<0.01	0.85	0.03	3.98
TB Standard	0.230[bc]	0.40	0.40	<0.01	<0.01	0.67	0.05	5.79
TB Thin	0.249[abc]	0.38	0.37	<0.01	<0.01	0.74	0.04	5.11
SM Heavy	0.266[abc]	0.30	0.30	<0.01	0.01	0.59	0.06	6.48
SM Medium	0.269[ab]	0.32	0.31	<0.01	<0.01	0.74	0.04	5.19
SM Light	0.290[a]	0.24	0.24	<0.01	<0.01	0.79	0.04	4.59
P	<0.001							
SEM	0.01							
Dissected and DXA soft tissues								
Dissected	10.85							
DXA by software								
TB Thick	11.83	0.99	0.94	0.03	0.02	0.99	0.14	1.33
TB Standard	11.81	0.95	0.91	0.03	0.02	0.99	0.15	1.34
TB Thin	11.81	0.96	0.92	0.02	0.02	0.99	0.15	1.34
SM Heavy	11.76	0.82	0.76	0.03	0.02	0.98	0.15	1.40
SM Medium	11.88	1.08	1.02	0.03	0.02	0.98	0.15	1.42
SM Light	11.88	0.97	0.92	0.03	0.02	0.98	0.16	1.47
P	1.000							
SEM	0.43							
Dissected adipose tissue and DXA fat mass								
Dissected	2.94							
DXA by software								
TB Thick	2.51	0.19	0.18	<0.01	<0.01	0.99	0.06	1.96
TB Standard	2.54	0.18	0.16	0.01	0.01	0.95	0.11	3.74
TB Thin	2.64	0.12	0.09	0.02	0.01	0.96	0.11	3.62
SM Heavy	2.60	0.38	0.12	0.23	0.03	0.96	0.10	3.42
SM Medium	2.76	0.20	0.06	0.12	0.02	0.96	0.10	3.31

SM Light	2.66	0.72	0.57	0.12	0.02	0.93	0.13	4.46
P	0.946							
SEM	0.18							
Dissected muscle and DXA lean mass								
Dissected	7.92							
DXA by software								
TB Thick	9.31	2.01	1.95	0.04	0.02	0.97	0.15	1.93
TB Standard	9.27	1.91	1.82	0.06	0.03	0.96	0.19	2.42
TB Thin	9.18	1.69	1.59	0.05	0.05	0.94	0.23	2.90
SM Heavy	9.16	0.72	0.28	0.30	0.13	0.96	0.19	2.46
SM Medium	9.12	0.87	0.58	0.19	0.10	0.96	0.20	2.51
SM Light	9.22	0.34	0.04	0.19	0.11	0.95	0.21	2.62
P	0.999							
SEM	0.37							

[1] Mean square prediction error (MSPE), error of central tendency (ECT), error due to regression (ER), and error due to disturbances (ED) are calculated from the differences between DXA and the equivalent dissected tissues. Coefficient of determination (R^2), residual standard deviation (RSD) and CV are calculated from the regression of DXA on dissected measurements.

[2] In the Mean column and within each tissue, means followed by same or no letter did not differ ($P > 0.05$) according to Tukey's test.

[3] Total body (TB) software configured to thick (> 25 cm), standard (16 to 25 cm), and thin (< 16 cm) options.

[4] Small animal (SM) software configured to heavy (> 20 kg), medium (2 to 20 kg), and light (< 2 kg) options.

[5] Bone mineral content (BMC).

6 THE EFFECT OF ADIPOSE TISSUE, BONE, AND WATER DISTRIBUTION SURROUND PORK LOIN ON DUAL-ENERGY X-RAY ABSORPTIOMETRY COMPOSITIONAL EVALUATION

Este capítulo é apresentado de acordo com as normas para publicação no periódico *Meat Science*.

The effect of adipose tissue, bone, and water distribution surround pork loin on dual-energy X-ray absorptiometry compositional evaluation

Abstract

The goal of this study was to evaluate the addition of materials (adipose tissue, bone, and water) in different spatial distributions on pork loins and to identify their consequent effects on DXA measurements. Four commercial pork loins, three square pieces of adipose tissue, three water bags, and six scapulae bones were used in this experiment. Three independent tests were performed to evaluate the effect of each material. In each test, four procedures of addition were performed, being: Over, Staked, Individual, and Collective. Individual and Collective procedures did not allow to correct identify all mass disposed on the DXA table. Over and Staked procedures showed consistent results for the total weight of the added materials. When adipose tissue was added on the loins, the best agreement was found for fat mass, while for water addition the best result was found for lean mass estimation. All procedures present distinct behaviors in terms of DXA and reference method agreement.

Keywords: DXA, meat, pig, primal cut, soft tissue, total mass.

1 Introduction

Dual-energy X-ray absorptiometry (DXA) devices were first developed in order to evaluate bone mineralization (Roubenoff, Kehayias, Dawson-Hughes, & Heymsfield, 1993). Over time, this technology was being improved allowing its use for assessing body composition in terms of fat and lean masses. Nowadays, it is a useful tool in monitoring healthy people or the effect of some diseases over body composition (Koo & Hammami, 2011; Pichard, Kyle, & Slosman, 1999).

This technology also has been used in research to evaluate farm animal, both live and carcass for several years (Marcoux, Faucitano, & Pomar, 2005; Pearce, et al., 2009). However, just few studies have evaluated primal cuts using DXA. The lack of specific information in this area can be partially filled with knowledge generated through tests using phantoms. However many intrinsic conditions of meat are not easily simulated by them. So, using meat cuts is indicated to obtain better understanding the implications of using DXA in their assessment. Furthermore, manipulating the meat during its preparation for the market can produce a number

of artificial factors compared to the carcass (such as bone or adipose tissue removal) that may affect DXA measurements.

In addition, a brief literature review shows that different types of devices have their own peculiarities. Data earlier published demonstrate that the addition of no-bone-tissues over a phantom may reduce (Barthe, Braillon, Ducassou, & Basse-Cathalinat, 1997), increase (Mazess, Collick, Trempe, Barden, & Hanson, 1989) or shown no effect on bone mineral density (BMD) measure by DXA (Gotfredsen, Bæksgaard, & Hilsted, 1997). Each DXA device has characteristics that are intrinsic in terms of technology and algorithms, which may lead to different results. These intrinsic factors must be checked before the assessment of meat using a DXA device because this knowledge is useful to archive good result in real time. Thus, the goal of this study was to evaluate the addition of materials (adipose tissue, bone, and water) in different spatial distributions surround pork loins and to identify their consequent effects on DXA measurements.

2 Material and methods

2.1 Material

Four commercial pork loins were used in this experiment. The loins were skinless and with bone (commercial presentation). Three square pieces of adipose tissue (dorsal fat) and six scapulae bones from a local company were also used in the study. The material was transported under refrigeration (4 °C) to the Agriculture and Agri-Food Canada Research Centre at Sherbrooke (Québec, Canada). Loins were stored (4 °C) in the original package, while the adipose tissue and the bones were stored in vacuum plastic bags until the day of scan. Bags of drinking water were used in order to simulate meat (no-fat and no-bone tissue).

2.2 DXA device

The device used in this study was a Lunar Prodigy Advance equipped with the package of softwares Lunar Encore v. 13.40.038. Calibration procedure using manufacturer's recommendations was performed before the scanning. Two scans were performed in each sample. The software used was total body configured with standard and thin options. Standard configuration is recommended for samples with average thickness between 16 and 25 cm, and thin is recommended for samples with less than 16 cm. All images were analyzed using a rectangular custom region of interest (ROI).

2.3 Scanning procedures

The weights of adipose tissues, water bags, and scapulae bones were measured by scale and those materials were added always in the same order (Table 1). The loins were positioned on DXA table, and were not moved until the end of the tests to avoid any additional effect in the measurements.

Three independent tests were performed to evaluate the effect of each added material (adipose tissue, water, and bone) on DXA measurements. In each test, four procedures of addition were performed (Fig. 1). In Over procedure, the material was spread over the loin one by one without superposition. In Stacked procedure, the material was also added over the loin, but each piece of material was added in the same place with superposition. In Over and Stacked procedures, a scan was performed with the loin alone plus a scan for each addiction. In Individual procedure, just a scan was performed including all added material placed on the DXA table side by side with the loin without superposition and neither touching each other. In this situation, each material was analyzed using an individual ROI, and their values were added to the loin value. This procedure was performed always in the same sequence of pieces. And finally, in Collective procedure, it was used the same image obtained to Individual procedure but a different method was used to analyze it. In this last procedure, the ROI was increased to fit the added material, beginning with the loin and changing the shape of the region to include each piece of material one by one.

The variables included in the study were the scale weight of the added material (g), and DXA measurements for BMD (g cm^{-2}), bone mineral content (BMC, g), bone area (cm^2), and fat and lean masses (g). To assess how DXA identify only the added material, the DXA measurements took in the loin alone were subtracted from the respective measurements with added material. This methodology allowed focusing the study on the variations generated by the addition of material.

2.4 Calculations and statistical analyses

Analyses of covariance (ANCOVA by GLM) were performed to study the effect of different procedures of material addiction and the effect of software configurations. In this analyses DXA measurements were considered as dependent variable; the weight of the added material was considered as covariate; software configuration (standard or thin), procedure of addiction (Over, Stacked, Individual, and Collective), and all interactions were considered in

the model. After this first step, linear regressions were generated when the weight of the added material was significant ($P < 0.05$). Specific equations were generated for each software configuration when these factors showed significant ($P < 0.05$) effect in the model. All analyzes were performed using the SAS statistical package.

Total mass measured by DXA was calculated to evaluate the capability of it to identify all mass disposed on the table. This was performed by summing the slopes from BMC, and fat and lean masses. Soft tissue mass (i.e., no-bone-mass) was also considered as the sum of fat and lean masses. The regression slopes for fat and lean masses were summed to assess the effect of adding material and its consequence on soft tissue mass. This procedure allowed understanding if adipose tissue and water bags were completely identified by DXA.

3 Results

3.1 Addiction of adipose tissue

In the studied condition, the choice between standard or thin configuration did not affect ($P > 0.05$) any of the studied variables (Table 2). The interaction between the amount of added adipose tissue and the procedure was significant ($P < 0.05$) for BMC, bone area, fat mass, and lean mass, indicating that each procedure affects DXA measurements in a different way. The BMD was not affected ($P > 0.05$) by any independent variable.

The effect of the addiction of adipose tissue on total mass was accessed through the sum of regression slopes of fat and lean masses, and BMC (Fig. 2). For each gram of addition of adipose tissue, DXA could estimate a total mass of 1.0005, 1.0132, 0.8707, and 0.8715 for Over, Stacked, Individual, and Collective procedures, respectively. These results showed that this device was not able to correctly identify all adipose tissue disposed on the table in Individual and Collective procedures.

The addition of adipose tissue also changed the measurement of soft tissue. The slopes for soft tissue mass were 1.0134, 1.0291, 0.8707, and 0.8715, respectively for Over, Stacked, Individual, and Collective. These slopes represent the amount (in grams) of soft tissue mass that was identified for each addition of one gram of adipose tissue in the sample. Over and Stacked procedures overestimated in 0.0134 and 0.0291 g the real added mass; while Individual and Collective procedures underestimated in 0.1293 and 0.1285 g the added soft tissue mass.

The relationship between addition of adipose tissue and fat mass measured by DXA was positive. However, if dissection is considered as the reference method, then DXA was not able

to correctly discriminate the added tissue. The slopes of the regressions for Over, Stacked, and Individual showed that DXA underestimated the added fat mass. In this scenario, for each one gram of adipose tissue added, it is estimated just 0.6979, 0.5908, and 0.6982 g of fat mass in Over, Stacked, and Individual procedures, respectively. On the other hand, Collective procedure overestimates the addition, identifying 1.4242 g of fat mass for each gram of added adipose tissue.

When Over or Stacked procedures were performed, the addiction of adipose tissue occurred over bone pixels, generating a reduction in the amount of BMC measured by DXA. On the other hand, when Individual or Collective procedures were performed, the addiction occurred beside the loin (i.e., outside bone pixels) and BMC remained constant. This relation was more pronounced in the Stacked procedure. Similar pattern observed in BMC was also observed for bone area, in which the superposition of bone pixels with adipose tissue reduced the bone area. Regressions generated for BMC and bone area presented high RSD and low R^2.

3.2 Addiction of water

The software configuration did not affect ($P > 0.05$) any of the studied variables (Table 3). The interaction between the amount of added water and the procedure of addiction was significant ($P < 0.05$) for BMD, BMC, and fat and lean masses. Bone area was not affected ($P > 0.05$) by any independent variable.

The values of total masses obtained by the sum of regression slopes were 1.0094, 0.3693, and 0.3694 for Over, Individual, and Collective procedures, respectively (Fig. 3). These results indicated that, DXA was not able to correctly identify all disposed water on the table in Individual and Collective procedures.

The effect of addiction of water over soft tissue measured by DXA was also verified. For one gram of addiction of water there was an overestimation of 0.0071 g of soft tissue mass in the Over procedure. On the other hand, Individual and Collective showed a great underestimation, where for each one gram of added water only 0.3693 g was identified by DXA as soft tissue mass.

The relationship between addition of water and lean mass was positive. However, if dissection is considered as the reference method, than water should provide 100% lean. In this context, all three procedures underestimated the added mass. For each gram of added water,

DXA estimated 0.9146, 0.3402, and 0.3810 g of lean mass in Over, Individual, and Collective procedures, respectively.

A relationship between the BMC and the addiction of water was observed just in Over procedures. On the other hand, the BMD was sensitive to water addition only in Over and Collective procedures. For each gram of added water, it was expected an increase of $6x10^{-6}$ in BMD for Over procedure. In Collective procedure, this effect was even lower. A similar result was found in the relation between amount of added water and BMC. Regardless the amount of added water, the BMC was not affected in Individual and neither in Collective procedures. Water addition affected BMC in the Over procedure in a very small proportion, with an increase of 0.0023 g for each gram of added water. However, RSD of the regression generated for BMD and BMC were very high and R^2 was not satisfactory. For this reason, although the effect of addition was significant ($P < 0.05$), it was considered null for BMD and BMC in the studied conditions.

3.3 Addiction of bone

The interaction between addition of bone and the software configuration was significant ($P = 0.051$) to BMC (Table 4). The interactions between the addition of bone and the procedure were significant ($P < 0.05$) for all variables, indicating that DXA measurements are affected in a different way in each condition.

The estimated total masses (BMC plus fat and lean masses) were 1.0682, 1.0021, 0.2457, and 0.6550 for each added gram in Over, Stacked, Individual, and Collective procedures, respectively (Fig. 4). As for adipose tissue and water additions, these results showed that DXA was not able to correct identify all disposed bone on the table in Individual and Collective procedures.

The BMD was affected differently when bones are added over loins or beside them. Over and Stacked procedures presented a positive relationship between BMD and addiction of bone. However, Individual and Collective showed a negative relationship for the same combination of variables. The BMC increased in a similar pattern in all procedures being a little more pronounced in Over. The addition of bone also increased bone area, and it was more pronounced in Individual and Collective procedures. The regression for BMC in thin configuration had a slope 5.9% greater than the slope for standard configuration.

The addition of bones affected fat and lean masses. However the RSD and the R^2 from fat mass regressions did not allowed drawing accurate conclusions. The Over and Stacked procedures showed R^2 considerably greater in the relation between addition of bone and lean mass. However, the RSD were higher too, indicating poor precision. The Collective was the procedure with a more precise pattern and Individual did not showed good R^2 values.

4 Discussion

Regressions were generated to study the relationship between adding materials on the loins and its consequent effect on DXA measurements. Linear regressions were generated since linearity is an inherent aspect to this type of test and reflects the device accuracy (Tothill & Hannan, 2006). The DXA provided measurements which allowed obtaining regressions with good fit, underscoring the high accuracy of this technology (Lohman, Tallroth, Kettunen, & Marttinen, 2009; Margulies, et al., 2005).

The Over and Stacked procedures provided superposition of tissues, and this situation could generate two different issues. The first one is known as beam hardening and it happens when the increasing sample thickness generates a higher attenuation of the low energy X-ray compared with the high energy X-ray, changing the coefficient of attenuation (R-value) and consequently incrementing the sample leanness (Goodsitt, 1992; Pietrobelli, Formica, Wang, & Heymsfield, 1996). The second issue is the superposition of tissues near to bone edge that can influence the DXA measurements. The mass estimation of a pixel (bone or not) is calculated based on the X-ray attenuation (Kelly, Berger, & Richardson, 1998). However, the quantification of fat and lean masses in bone pixels is estimated assuming that the composition of soft tissue mass of bone pixels is similar to the composition of pixels immediately near to the bone (Laskey, 1996). Therefore, if fat or lean masses are added only on bone pixels, DXA is able to estimate the added mass but is not able to discriminate the amount of added fat and lean masses. If the added tissue is not completely overlapped on the bone pixels, thus DXA is capable to differentiate just part of the added material.

The Individual and Collective procedures did not provided superposition of tissues, since the added materials (adipose tissue, water, and bone) were positioned beside the loin. This condition may promote an interference related to the low thickness of the sample, because when the materials are very thin, the X-ray can pass very easily through the sample, not being possible to completely identify the scanned mass (Goodsitt, 1992). In this situation, DXA underestimates

the added mass. Assuming that DXA is able to identify all material disposed on its table is required to evaluate the experimental design (Goodsitt, 1992). The Individual and Collective procedures did not reached this proposition, as showed in the results with adipose tissue, water, and bone additions. Even pieces of bone were not correctly identified by DXA when disposed directly on the table, probably due to the low BMD and it influence on the software sensitiveness in identifying the bone edges (Barthe, et al., 1997). In addition, this situation is influenced by the characteristics of the software that are developed to study human body. Thus, these two procedures were not liable to be used in the conditions proposed for the project, and they will be not further discussed in this paper.

4.1 Addiction of adipose tissue and water

Using dissection as the reference method, the added adipose tissue should be 100% identified as DXA fat mass. However, it was observed that just 70 and 58% of adipose tissue were identified as fat mass in the Over and Stacked procedures respectively. In other words, these two procedures underestimated the addiction of fat mass. Nevertheless, when considering the added adipose tissue as DXA soft tissue mass, it was observed an overestimation of 1.3 and 1.6% for each gram of added adipose tissue in Over and Stacked procedures. However, DXA underestimated BMC in 1.3% and 1.6% for each gram of adipose tissue in the same procedures. These results suggest that DXA estimate the total added mass with a good accuracy because the overestimation on soft tissue is compensated by the underestimation in bone measurements. Nonetheless, the underestimation in fat mass was not compensated.

A similar parallel was drew between added water and dissected muscle. The Over procedure estimated the added material as being 91% lean mass. This procedure also estimated the added soft tissue mass very accurately (100%). Although water is not meat, similar results are expect for both materials since previous tests showed that DXA recognized around 92 to 96% of lean mass in meat while around 90 to 94% of lean is recognized in water (unpublished data). Comparing the tests with adipose tissue and water allowed to observe that DXA was more precise predicting the real added water weight than estimating the weight of added adipose tissue.

Previous studies reported controversial results when assessing the influence of soft tissues over bone related DXA measurements. A negative effect of the addition of soft tissue (by increasing the thickness) over BMD was observed in a Hologic device (Barthe, et al., 1997).

In other studies, an increase in all bone measurements was observed when adipose tissue was added over phantoms of bone tissue or people (Mazess, et al., 1989; Tothill & Hannan, 2006). Another experiment demonstrated that the addition of blocks of meat and/or lard over phantoms or people caused significant difference between real and DXA measurements only for soft tissue (Gotfredsen, et al., 1997). Finally, the addition of lard or muscle homogeneously over phantoms did not cause any change in BMD, while this measurement was influenced when muscle were added intercalated side-by-side with lard (Hansen, et al., 1990). This leads to the conclusion that each device has characteristics that are intrinsic to the technology and to the algorithms in use. These intrinsic factors must be verified before using DXA devices for meat assessment.

4.2 Addiction of bone

Similar results were observed in both procedures (Over and Stacked) when assessing the effect of bone addition over BMC. The small difference observed between the slopes of the regressions is probably due to the effect of beam hardening, since Stacked procedure promoted a greater superposition of bones. This condition is not naturally found in animal body, but assessing it is important for better understanding the DXA technology.

Bone mineral density is derived from the ratio between BMC and bone area and, for this reason, BMD provided by DXA is an area-related or two-dimensional result (Heaney, 2005). Thus, when there is superposition of bones, it must be considered that an amount of BMC is added in a constant bone area that consequently increased the BMD. This can be easily observed when comparing the different procedures of bone addition, since the Over procedure is dealing with a greater increase in bone area comparing to the Staked procedure.

5 Conclusion

All procedures present distinct behaviors in terms of agreement between DXA and reference methods. In the proposed conditions, total body software configured with standard or thin options do not influence the results. A great addiction of water over the loin is required to promote a small change in BMC and BMD. Further studies are necessary to encompass all observed patterns and to better understand DXA technology.

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Table 1 – Increasing scale weight of materials used in each addition step

Addition	Material (g)		
	Adipose tissue (Dorsal fat)	Bag of water	Bone (Scapulae)
First	888	1183	474
Second	1415	2316	1037
Trird	1919	2909	1568

Table 2 – Probability from covariance analyses to evaluate the addition of adipose tissue to pork loins

Independent variables	Probability				
	BMD (g cm^{-2})	BMC (g)	Bone area, (cm^2)	Fat mass (g)	Lean mass (g)
Proc[a]	0.914	0.959	0.980	0.405	0.343
Con[b]	0.937	0.799	0.868	0.806	0.843
Proc × Con	0.993	0.986	0.974	1.000	0.998
AT[c]	0.813	<0.001	<0.001	<0.001	<0.001
AT × Proc	0.897	<0.001	<0.001	<0.001	<0.001
AT × Con	0.137	0.296	0.546	0.427	0.267
AT × Proc × Con	0.471	0.550	0.563	0.564	0.583

[a] Procedures: Over, Stacked, Individual, and Collective.
[b] Configurations: DXA total body software configured to standard or thin.
[c] Addition of adipose tissue, in grams.

Table 3 – Probability from covariance analyses to evaluate the addition of water to pork loins

Independent variables	Probability				
	BMD (g cm^{-2})	BMC (g)	Bone area, (cm^2)	Fat mass (g)	Lean mass (g)
Proc[a]	0.997	0.763	0.609	0.866	0.757
Con[b]	0.930	0.745	0.723	0.840	0.909
Proc × Con	0.995	0.899	0.872	0.961	0.996
W[c]	0.007	0.045	0.513	<0.001	<0.001
W × Proc	<0.001	0.019	0.689	<0.001	<0.001
W × Con	0.897	0.797	0.666	0.166	0.449
W × Proc × Con	0.967	0.936	0.795	0.784	0.850

[a] Procedures: Over, Individual and Collective.

[b] Configurations: DXA total body software configured to standard or thin.

[c] Addition of water in grams.

Table 4 – Probability from covariance analyses to evaluate the addition of bone to pork loins

Independent variables	Probability				
	BMD (g cm^{-2})	BMC (g)	Bone area, (cm^2)	Fat mass (g)	Lean mass (g)
Proc[a]	0.008	0.898	0.098	0.763	0.590
Con[b]	0.553	0.778	0.542	0.712	0.822
Proc × Con	0.994	0.989	0.967	0.989	0.956
B[c]	<0.001	<0.001	<0.001	0.063	<0.001
B × Proc	<0.001	<0.001	<0.001	0.007	<0.001
B × Con	0.808	0.051	0.586	0.858	0.961
B × Proc × Con	0.947	0.990	0.928	0.998	0.904

[a] Procedures: Over, Stacked, Individual, and Collective.

[b] Configurations: DXA total body software configured to standard or thin.

[c] Addition of bone, in grams.

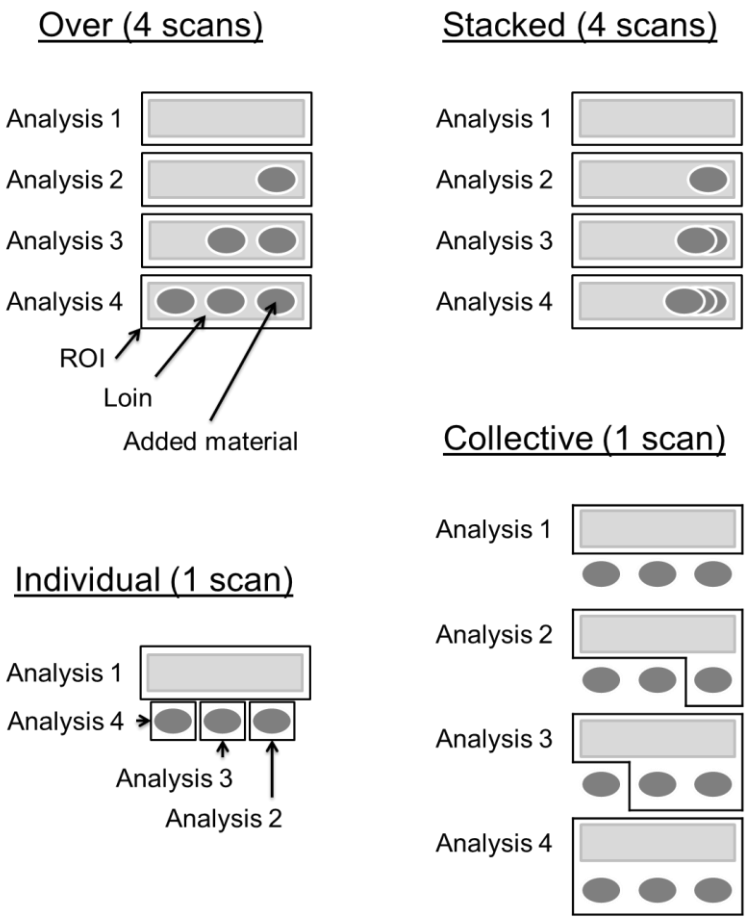
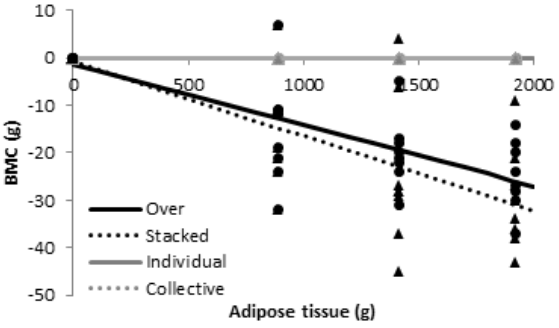
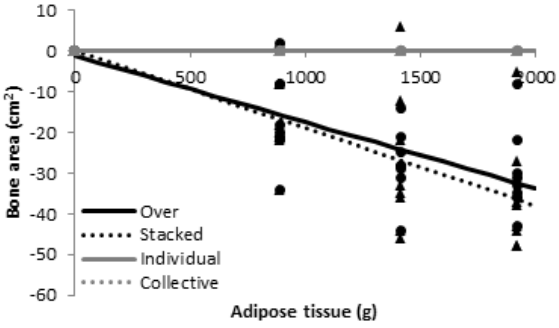


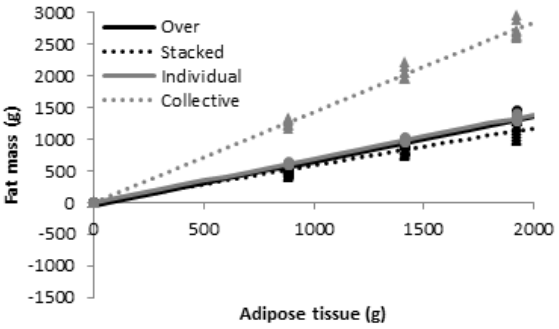
Fig. 1 – Layout of the procedures used to study the effect of adding materials to pork loin. ROI represents custom regions of interest used in software EnCORE. Each ellipse represents a piece of adipose tissue, a bag of water, or two pig scapulae.

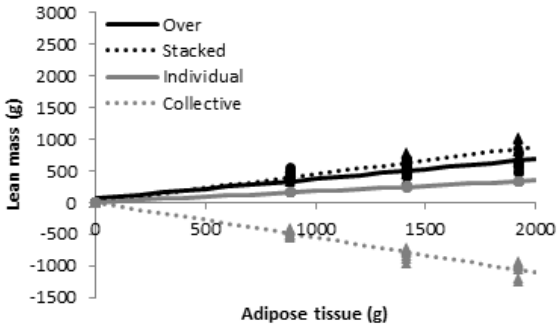




Procedure	RSD	R^2	Intercept	Slope
Over	8	0.598	-1.42	-0.0128
Stacked	11	0.530	-0.70	-0.0158
Individual	-	-	-	-
Collective	-	-	-	-

Procedure	RSD	R^2	Intercept	Slope
Over	9	0.649	-1.14	-0.0163
Stacked	12	0.569	0.16	-0.0191
Individual	-	-	-	-
Collective	-	-	-	-

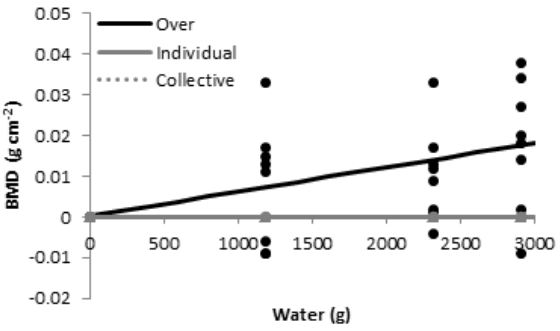


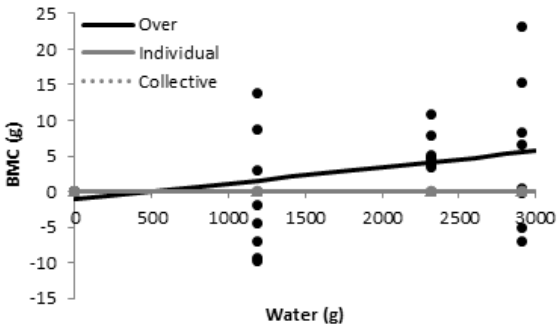


Procedure	RSD	R^2	Intercept	Slope
Over	81	0.975	-46.41	0.6979
Stacked	81	0.965	-2.01	0.5908
Individual	26	0.997	-3.78	0.6982
Collective	85	0.993	2.68	1.4242

Procedure	RSD	R^2	Intercept	Slope
Over	102	0.832	59.34	0.3154
Stacked	104	0.902	10.49	0.4382
Individual	9	0.995	6.30	0.1725
Collective	71	0.969	-0.11	-0.5527

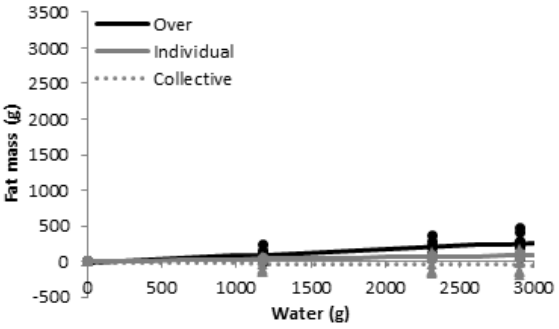
Fig. 2 – Effect of adipose tissue addition to pork loins and its effect on DXA measurements; Lines represent regression and forms represent observed values (● Over procedure, ▲ Stacked, ● Individual, and ▲ Collective); RSD: residual standard deviation; R^2: coefficient of determination.

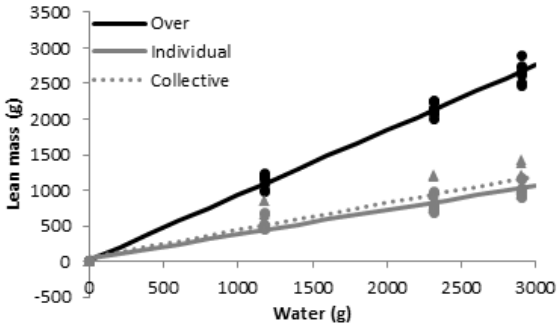




Procedure	RSD	R^2	Intercept	Slope
Over	0.012	0.220	0.00023	0.000006
Individual	-	-	-	-
Collective	<.0001	0.044	0.00004	<.000001

Procedure	RSD	R^2	Intercept	Slope
Over	7	0.128	-1.1	0.0023
Individual	-	-	-	-
Collective	-	-	-	-

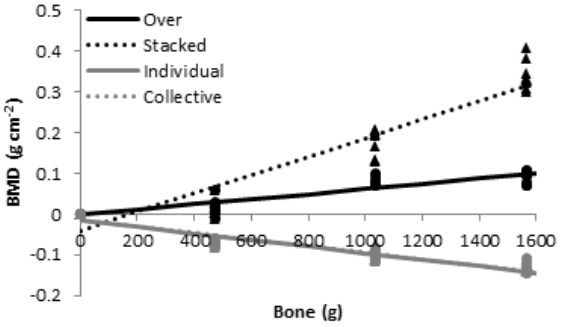




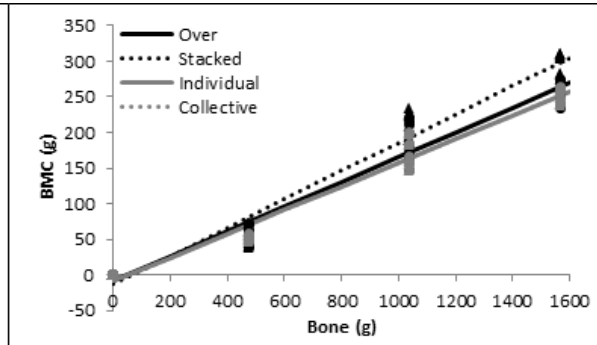
Procedure	RSD	R^2	Intercept	Slope
Over	86	0.595	-13.4	0.0925
Individual	9	0.926	1.2	0.0291
Collective	95	0.019	-14.4	-0.0117

Procedure	RSD	R^2	Intercept	Slope
Over	91	0.992	18.7	0.9146
Individual	94	0.944	43.7	0.3402
Collective	165	0.873	59.4	0.3810

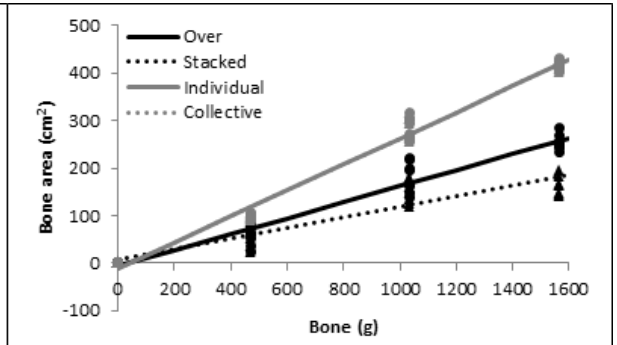
Fig. 3 – Effect of water addition to pork loins and its effect on DXA measurements; Lines represent regression and forms represent observed values (● Over procedure, ● Individual, and ▲ Collective); RSD: residual standard deviation; R^2: coefficient of determination.



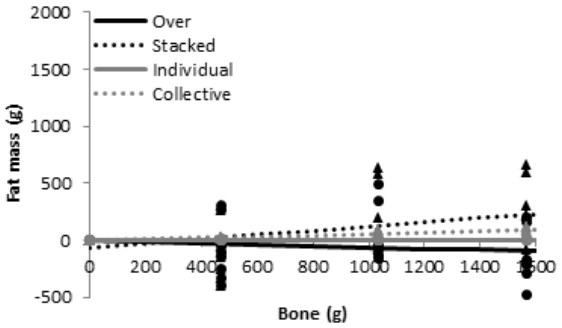
Procedure	RSD	R^2	Intercept	Slope
Over	0.017	0.830	-0.0015	0.0001
Stacked	0.044	0.906	-0.0399	0.0002
Individual	0.016	0.906	-0.0147	-0.0001
Collective	0.016	0.905	-0.0148	-0.0001



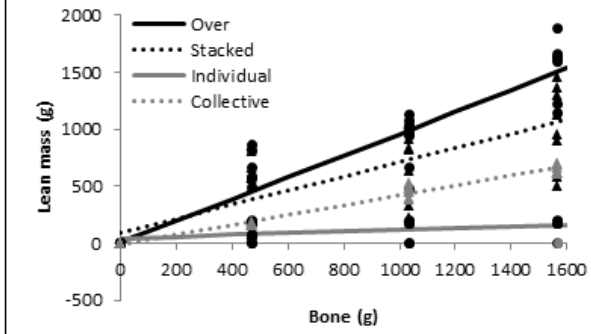
Procedure	RSD	R^2	Intercept	Slope
Over	21	0.961	-7.77	0.1731
Stacked	21	0.970	-13.23	0.1988
Individual	16	0.976	-9.12	0.1667
Collective	16	0.976	-9.04	0.1666



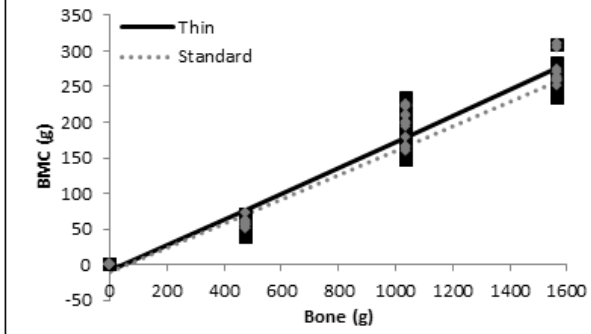
Procedure	RSD	R^2	Intercept	Slope
Over	22	0.954	-5.87	0.1680
Stacked	25	0.876	8.51	0.1105
Individual	18	0.988	-11.10	0.2741
Collective	18	0.988	-11.07	0.2738



Procedure	RSD	R^2	Intercept	Slope
Over	211	0.027	-2.53	-0.0582
Stacked	239	0.175	-61.26	0.1836
Individual	3	0.241	1.82	0.0031
Collective	20	0.757	-2.31	0.0592



Procedure	RSD	R^2	Intercept	Slope
Over	220	0.871	8.68	0.9534
Stacked	279	0.638	91.14	0.6197
Individual	80	0.243	44.25	0.0759
Collective	35	0.982	-8.77	0.4292



Configuration	RSD	R^2	Intercept	Slope
Thin	20	0.967	-9.03	0.1817
Standard	22	0.957	-10.54	0.1709

Fig. 4 – Effect of bone addition to pork loins and its effect on DXA measurements; Lines represent regression and forms represent observed values values (● Over procedure, ▲ Stacked, ● Individual, and ▲ Collective; ■ thin configuration of total body software, and ♦ standard configuration); RSD: residual standard deviation; R^2: coefficient of determination.

7 CALIBRATION OF DUAL-ENERGY X-RAY ABSORPTIOMETRY ESTIMATING PIG BODY COMPOSITION

Este capítulo é apresentado de acordo com as normas para publicação no periódico *Journal of Animal Science*.

Calibration of dual-energy X-ray absorptiometry estimating pig body composition

ABSTRACT: Eighty-eight barrows were used to evaluate the agreement between composition determined by chemical analyses or dissection and those estimated by DXA and, in addition, to understand in which condition DXA better estimate the reference composition. Thirty animal were raised for chemical analyses purpose only, being slaughtered at three different weights during the growing period. The others fifty-eight pigs were raised until slaughter weight (129.3 kg) for dissection and chemical purposes. Pigs were scanned using a DXA device before slaughtering to estimate BMC, and fat and lean masses. Carcasses were prepared to have standard Canadian commercial presentation and, then, the left sides were scanned again. After, primal cuts (shoulder, loin, belly, and ham) were scanned and dissected to measure adipose tissue, skin, muscles, and bone weights. Finally, carcasses were prepared for chemical analyses to measure lipids, protein, ashes, and water contents. The relationship between dissection and chemical analyses with DXA measurements was performed by comparison of means and regression analyses. All measurements obtained by the two reference methods were different from those obtained by DXA, except of total weight assessed by dissection. However, even with different means, the three methods were able to measure similar range of variability (CV) in most of the samples. The inclusion of a second independent variable was more important for increasing the accuracy of the models that estimate total weight in comparison to those estimating dissected tissues (adipose, muscle, and bone). Fat mass was the DXA measurement that better assessed the dissected adipose tissue. In the other hand, lean mass better estimated muscle of the left carcass and primal cuts. Measurements obtained by DXA in live animals could be used to predict chemical composition of entire animals and left carcass. However,

when DXA measurements from live animal were used to estimate carcass composition, the results were in average 1.7% less accurate than using data collected in the carcasse. In conclusion, measurements obtained by chemical analyses or dissection were different from those obtained by DXA. Regression generated to correct the difference between dissection and DXA were able to estimate properly the dissected tissues of pig left carcasses, as well of the primal cuts.

Key-words: accuracy, carcass, chemical, dissection, live animal, primal cuts.

INTRODUCTION

The interest in using indirect methods to estimate body composition is increasing in animal science. Those methods allow studying the same animal through its growth, which improve the accuracy of the models developed to understand growth or physiological processes (Suster et al., 2006; Ryan et al., 2011). There is also the possibility of reducing the number of animals in the experimental designs, because the slaughter during the course of the projects could be avoided.

Dual energy X-ray absorptiometry (DXA) has its use increased in the last years. Two X-ray beam are emitted in this method, estimating the composition of a subject by determining how much energy is absorbed in the process (Goodsitt, 1992; Pietrobelli et al., 1996). However, DXA uses reference values to determine the composition of the subject, which means that its measurements are interpreted responses (Pietrobelli et al., 1996). Therefore, these reference values can be changed depending on the interpretation of what should be fat or lean masses and then DXA measurements will change as well.

Measurements provided by DXA present great correlation with chemical analyses and dissection, but they are not similar (Scholz et al., 2007). It was demonstrated that linear regressions could be used to adjust DXA measurements. However, these regressions are in

general specific to a group of subject (genetic) and a DXA device (brand and version) (Mitchell et al., 1997; Marcoux et al., 2005). Therefore, improvements in the technology or genetic should be evaluated time-to-time verifying if the method is still accurate. For this reason, this project was developed: (1) to verify the agreement between composition determined by chemical analyses or dissection and those estimated by DXA; (2) to understand in which condition DXA provide measurements that better estimate dissection and chemical composition.

MATERIAL AND METHOD

Animals

This study was carried out using two group of barrows (Fertilis 25 × G-Performer 8.0, Genetiporc Inc., Saint-Bernard, QC, Canada). Thirty animals were raised for chemical analyses purpose only, being 13 pigs slaughtered at 40.5 kg, seven at 66.2 kg, and 10 animals at 80.3 kg. Other 58 barrows were raised until slaughter weight (129.3 kg) for dissection and chemical analyses purposes. Animals received *ad libitum* feed and fresh water throughout the growing period and were cared for in accordance with the recommended code of practice (AAFC, 1993) and the guidelines of the Canadian Council on Animal Care (CCAC, 2009). Diets were formulated to reach nutrient requirement and were provided with an automated feeding system (Andretta et al. 2014).

DXA device

The Lunar Prodigy Advance (GE Healthcare, Madison, WI, USA) device equipped with enCORE package of softwares (version 13.40.038; GE Healthcare, Madison, WI, USA) was used in this study. This device generates two-dimensional projected images with pixels that are identified as bone or soft tissue based on the coefficient of attenuation. Finally, the composition

of the soft tissue within bone pixels is extrapolated according to the composition of soft tissue pixels around it (Pietrobelli et al., 1996).

Data collection

Live animal scanning and slaughter. Pigs were fasted 16 h before slaughter. For scanning, anesthesia was induced with sevoflurane (5%) and maintained with xylazine (2 mg kg^{-1}) and ketamine (20 mg kg^{-1}). Pigs were scanned in prone position with legs extended backward.

Animals were slaughtered after scanning still under anesthesia. Blood and viscera were collected for chemical analyses and the intestines were free of digesta. Carcasses were split in two, being left half carcasses prepared to have standard Canadian commercial presentation including the removal of kidney and leaf fat. Head and tail were retained with the right half carcass for chemical analyses purposes. Carcasses and viscera were refrigerated under 4 ºC during 24 hours, and then frozen and stored under -20 ºC.

Dissection and scanning of carcasses and primal cuts. Dissection and scanning of carcass and primal cuts were carried out simultaneously. The weight of samples were measured before all scanning. The first scan was performed with the entire left carcass skin side up. Then, primal cuts (shoulder, loin, belly, and ham) were obtained using standard Canadian cutting procedures as previously described by Marcoux et al. (2005). Each cut was scanned individually. Dissection method was used as reference to determine the weight of adipose tissue (including jowl), skin, muscle, and bones (including cartilage and the entire feet).

Image analyses. Images of live animals were analyzed using a standard grid for human body. Images of half carcasses and primal cuts were analysed using the arm region of interest (Kipper et al., unpublished data – Capítulo 4 deste documento). Results provided by DXA and

used in this study included DXA weight (kg), bone mineral content (BMC, kg), and fat and lean masses (kg).

Chemical analyses. Chemical analyses were conducted in duplicate and according to the procedure described by Association of Official Analytical Chemists (AOAC, 1990). Standard methods for lyophilization (Method 938.18), for determination of total protein (Method 992.15), lipid (Method 991.36), dry matter (Method 950.46), and ash (Method 920.153) were performed. The study with 58 pigs was performed on two different situations: left carcass and entire animal. Chemical composition of left carcass, and right carcass plus viscera and head were obtained. Finally, entire animal chemical composition was archived by adding the composition of left and right carcasses expressed in kg. The study with the 30 pigs were conducted exclusively to determine entire animal chemical composition. Values from these animals were included in the data set to increase the range of measurement variation.

Statistical analyses

Comparison of means. Comparisons between measurements obtained by dissection or chemical analyses and DXA measurements were performed through PROC GLM (SAS version 9.3; SAS Institute Inc., Cary, NC, USA). In the comparison of dissection and DXA, it was assumed that adipose tissue is represented by fat mass, bone by BMC, and muscle should be the same that lean mass. In the comparison of chemical analyses and DXA, it was considered that lipid denote fat mass, while ash should be the same that BMC. It was also verified if protein, water, or protein plus water were similar to lean mass.

Study of dissected composition. Stepwise procedures using PROC REG (SAS version 9.3; SAS Institute Inc., Cary, NC, USA) were performed to estimate dissection composition from values provided by DXA. Weights of bones, muscles, adipose tissue, and adipose tissue plus skin were considered as dependent variables. Fat and lean masses, and BMC measured by

DXA were used as independent variables. In this study, it was considered the hypothesis that DXA measurement from one sample-condition could be used to estimate dissection composition in other sample-condition. To reach this goal, DXA measurements from left carcass were used to estimate dissection composition of left carcass as well as to estimate primal cut composition. Models were compared in terms of adjusted coefficient of determination ($\mathbf{R^2}$), coefficient of variation (**CV**), and residual standard deviation (**RSD**).

Study of chemical composition. The same approach used to study dissection composition was used to study the data for chemical composition from the 58 animals raised until slaughter weight. In addition, regressions were generated combining data from the two groups of animals (the 58 and the 30 animals). Water, lipid, protein, and ash masses obtained by chemical methods were considered as dependent variable. Fat and lean masses, and BMC measured by DXA were used as independent variables.

RESULTS AND DISCUSSION

Descriptive analyses

The 58 animals presented great variability in terms of body weight at slaughter, with a range of 45 kg between the lightest and the heaviest animal. In the entire group (88 pigs) the range was 115 kg. Dual energy X-ray absorptiometry showed good accuracy in determining the weight of the animals, being the range between the lightest and the heaviest estimated in 45 kg for the population of 58 pigs and 118 kg for the group of 88 animals. This result is similar (P <0.05) to those obtained by scale (Table 1) and it is an important information since DXA should be able to determine the weight with very good accuracy (Goodsitt, 1992).

A great variability (CV) among animals in the composition of primal cuts was observed using dissection and DXA. In general, belly presented the most heterogeneous composition (among pigs) of dissected tissues, while ham and shoulder presented the most homogeneous

composition. The distribution of tissues in the carcass and primal cuts were similar to those presented in previous publication (Marcoux et al., 2003).

Comparison of dissection and DXA measurements were performed for left carcass and primal cuts. The weights provided by both methods were similar ($P < 0.05$). Belly was the only primal cut where the weight was not well estimated by DXA. An overestimation of 4.3% in relation to scale weight was found in this cut, with the problem probably being related with its low thickness (average of 5.4 cm). The DXA devices were developed for human assessment and, for this reason, it has difficulty estimating the true mass of thin samples since the X-rays beam can pass easily through the material (Roubenoff et al., 1993; Barthe et al., 1997).

The correct estimation of the weight is not an attribute that ensure that other DXA measurements are true (Mitchell et al., 1998c). In the current study, DXA underestimated ($P < 0.05$) adipose tissue (in average 68%) and bone weights (23%), as well overestimated ($P < 0.05$) muscle weight (73%) in left carcass, shoulder, loin, and ham, in relation to dissection. This same pattern was observed in belly with a greater disagreement between the techniques in comparison to the previous cuts, which is probably due to the thickness of the cut. Although the techniques did not provided the same values, a great correlation was observed between the methods. Fat and lean masses are estimated by DXA in each pixel considering the triglycerides and the skeletal muscle as references in a linear relation (Pietrobelli et al., 1996). On the other hand, dissection take into account just anatomical concepts and each dissected tissue comprise a mix of chemical elements. Therefore, adipose tissue is not free of protein, as well as muscle is not free of lipid, or bone is not just mineral content.

Chemical body composition analyses of the 30 young animals combined or not with the 58 finished pigs and left carcasses are presented in the Table 2. Combining the 88 pigs increased the variability of the body amount of water, lipid, protein, and ash in 20, 37, 23, and 25%,

respectively. Increasing the range of age or body weight is an efficient procedure to improve the range of variability in chemical measurements (Mitchell et al., 1998a, 2000). A wide variability is important in this kind of study since it helps understanding DXA technology in different contexts.

Similar variability were observed in the composition of the bodies or carcasses of the 58 finished pigs. A small difference between these two conditions is expected because entire animal measurements included viscera and head, which were not accounted in left carcass. Since there were minor variation between entire animal and left carcass compositions, it could be also expected that viscera present small variability among animals. So, DXA measurements from live animals could be used to estimate chemical composition of the carcasses.

Chemical analyses differed (P <0.05) from DXA measurements in all studied responses. In average, the DXA underestimated lipid and ash by 19 and 26% comparing to fat mass and BMC, while it overestimated protein, water, and protein + water by 79, 30, and 9%, respectively, compared to lean mass. Lean is defined by DXA as the mass that is not BMC nor fat mass (no-bone and no-fat tissue), so it is expected that this result should be similar to protein + water. In fact, the correlations of lean mass with protein, water, and protein + water were in average 0.930, 0.943, and 0.971, with greater values being observed in the whole group (88 animals) comparing to finished pigs (58 animals) or left carcasses. Previous study found similar result for fat and lean masses in pigs of 25 kg (Losel et al., 2007). However, the fat was overestimated by DXA in pigs of 8.5 kg in another trial (Koo et al., 2004). The relationship between chemical and DXA results is not static, and it is influenced by the commercial brand of the device and also by the body weight of the animals (Mitchell et al., 1998b; Suster et al., 2003). Therefore, regressions should be developed for a better understanding of this relationship.

Regressions to predict dissected composition

Regression analyses were performed to study the relationship between DXA measurements and dissection. The inclusion of a second independent variable increased the accuracy of some regressions, which was also found in previous studies (Marcoux et al., 2003, 2005; Suster et al., 2004; Losel et al., 2007).

In the current trial, two different conditions were studied: (1) DXA measurements of half carcasses were used to estimate the dissected composition of left carcasses and primal cuts; and (2) DXA measurements of primal cuts were used to estimate the respective cut dissected composition. To avoid misunderstanding, the first condition is referred in this paper as left carcass scan and the second as primal cut scan.

Left carcass scan. Half carcass weight was very precisely estimated when including the BMC as well as fat and lean masses in the regression (Table 3). Previous studies estimated the weight of carcasses or primal cuts using the total weight provided by DXA, which is the sum of BMC, fat and lean masses (Marcoux et al., 2003; Suster et al., 2004). Although the inclusion of these three compartments (BMC, fat, and lean) separately in the model should generate the same accuracy obtained when included just total DXA weight, this procedure allowed studying further the relationship between the composition of total DXA weight and the scale weight.

Most of the variability of carcass weight was explained by lean mass. The inclusion of fat mass increased 54% the R^2 and reduced 95% the RSD. In addition, the inclusion of BMC in the model increased 0.1% the R^2 and represented just 38 g in the error, which is probably lower than the losses during the carcass manipulation for dissection (Mercier et al., 2006). Therefore, the inclusion of BMC in the model can be performed but it is not required. The total weights were the most accurately (lowest RSD values) estimated responses in all studied cases.

Fat mass was the DXA measurement that better estimate the dissected adipose tissue (R^2 of 96.6%). Previous study found lower values of R^2 for the same relationship, probably due

to differences in the dissection methodology (Marcoux et al., 2003). It seems that the more extensive is the dissection, the greater is the expected correlation between adipose tissue and fat mass. In the same way, models to predict the adipose tissue were more accurate than the models to predict adipose tissue plus skin, changing up to 32% the RSD in the total adipose tissue of the left carcass.

The amounts of dissected muscle in left carcass and primal cuts were better explained by lean mass, which is in agreement with previous publications (Marcoux et al., 2003; Suster et al., 2004). Equations estimating muscle showed lower CV of error compared to those estimating bone and adipose tissue in left carcass and all primal cuts.

The lower R^2 were obtained estimating the bone weight of left carcasses and primal cuts, in agreement with previous publications (Marcoux et al., 2003). Best results were obtained by the combination of lean mass and BMC in left carcass, shoulder, and ham. Lean mass was used alone in belly; while just BMC was used in the loin. The inclusion of a second variable increased the R^2 by 18, 14, and 15%; and reduced the RSD by 25, 14, and 18% for half carcass, shoulder, and ham, respectively. In a previous study, bone weight was estimated using lean mass with half of the accuracy and with a 40 g greater RSD than in the current trial (Marcoux et al., 2003).

Primal cut scans. Scans performed in the primal cuts individually were used to estimate its own dissection composition (Table 4). The lean mass explained most of the variability in primal cut weights, except for the loin, which was explained better by the fat mass. The second variable included in the models was the other measurement related with no-bone mass, so BMC was not included in the regressions to estimate cut scale weights. In average, the inclusion of the second variable increased the R^2 by 36, 46, 29, and 26% and decreased the RSD by 93, 95, 86, and 93% for shoulder, loin, belly, and ham, respectively. Data from scans performed individually in the primal cuts allowed to estimate more accurately the cut composition in

comparison to the equations generated using data from scans of the left carcasses. The loin composition was estimated with the same accuracy using data from cut or carcass scan, possibly due to the decades of genetic selection and payment systems based in the standardization of this cut.

In the same way as in left carcass scans, models to predict the adipose tissue were more accurate than the models to predict adipose tissue plus skin, changing up to 14% the RSD in the belly. For the loin cut, the inclusion of a second DXA measurement in the model decreased by 15 and 20% the RSD for adipose tissue and adipose tissue + skin, respectively. The skin classification as adipose tissue was not important in the models with two independent variables estimating loin adipose tissue, since their accuracies were similars.

Muscle weights were well predicted using lean mass in the primal cuts. Fat mass was also included as a second variable in the belly evaluation, increasing 14% the R^2 and reducing 23% the RSD. This relation is probably due to the presence of cartilage in the belly, which is considered as bone in the dissection but is a non-mineralized tissue recognized by DXA as a mix of fat and lean masses. Belly is also a difficult cut to be separated into muscle and adipose tissues during the dissection procedure (Marcoux et al., 2005; Mercier et al., 2006).

The lowest R^2 were obtained estimating the bone weight of the primal cuts, in agreement with previous publications (Marcoux et al., 2003). In shoulder and loin, the best results were obtained by the combination of lean mass (that explained most of the variability) and BMC (that increased the R^2 by 16% for shoulder and by 25% for loin). On the other hand, belly bone weight was predicted better using BMC, lean mass (that increased 10% the R^2), and fat mass (that further increased 10% the R^2). Ham bone weight was predicted using BMC and lean mass (that increased 12% the R^2). In previous study using a Lunar DPX-L device, the carcass bone

weight was estimated using lean mass with half of the present accuracy and with a 40 g greater RSD (Marcoux et al., 2003).

Regressions to predict chemical composition

Measurements obtained by DXA in live animals were used to predict chemical composition of entire animals and left carcasses (Table 5). The inclusion of a second variable in the model increased in average 2.9% the R^2 and reduced 40 g in the RSD for chemical composition estimation, while the third variable increased in average 3.3% the R^2 and reduced 50 g in the RSD. These results were disregarded because did not represent a great improvement in the estimation of chemical composition. Regressions for the relationship of chemical analyses and DXA measurements were linear, except for body weight.

Dual energy X-ray absorptiometry were used to estimate chemical composition of the populations with great accuracy. The most accurate regressions were obtained for protein + water, followed by water and protein. The accuracy were greater in the regressions generated using the data of the whole population (88 pigs) compared to those generated using just the finished pigs (58 animals). It was verified by stepwise that the lipid was better estimated by fat mass, ash by BMC, while protein, water and protein + water were better estimated by lean mass. In general, lipid expressed in grams or in percentage is better estimated using DXA fat expressed in the same unit (Koo et al., 2004; Losel et al., 2007).

It was also possible to use DXA to estimate the left carcass chemical composition using data of live animal scans, but using data of left carcass scans produced best models. The only exception was the ash estimation, in which using live animal measurements was better. This relationship can be easily explained for fat and lean, because DXA measurements in live animals included leaf fat and all visceral adipose tissues, while these tissues are not included in left carcass (Nielsen, 1973). Therefore, DXA measurements in live animals included some

source of variability that was not presented in left carcass. For ash, the problem could be probably related to the methodology (because splitting carcass is not a perfect procedure) or to the DXA ability in evaluating thin samples (Goodsitt, 1992).

In conclusion, regressions generated to correct the difference between dissection and DXA are able to estimate properly the dissected tissues and the chemical composition of pig carcasses and primal cuts. The DXA provide precise result in the evaluation of body compositions and should be further studied, particularly in terms of calibrating other devices and using animals of different genetic lines.

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Table 1 – Description, comparison of means, and correlation between measurements obtained in pork by dissection and dual-energy X-ray absorptiometry (DXA).

Dissection and DXA, kg	*n*	Dissection		DXA		*P*[1]	SEM	*r*[2]
		Mean	CV	Mean	CV			
Entire animal								
Scale weight and DXA weight	88	105.55	33.8	105.54	34.2	1.000	3.82	1.00
Scale weight and DXA weight	58	129.27	6.6	129.60	6.7	0.833	1.13	1.00
Left carcass								
Scale weight and DXA weight	58	48.82	6.8	48.83	6.8	0.989	0.44	1.00
Adipose tissue and Fat mass	58	17.12	15.5	11.93	19.8	<0.001	0.32	0.97
Bone and BMC[3]	58	5.00	8.8	1.04	9.6	<0.001	0.04	0.71
Muscle and Lean mass	58	24.64	7.8	35.86	7.2	<0.001	0.30	0.95
Shoulder								
Scale weight and DXA weight	58	12.27	7.5	12.27	7.5	0.984	0.12	1.00
Adipose tissue and Fat mass	58	4.00	14.9	2.52	20.2	<0.001	0.07	0.92
Bone and BMC	58	1.38	10.0	0.33	11.2	<0.001	0.01	0.65
Muscle and Lean mass	58	6.72	9.0	9.41	8.4	<0.001	0.09	0.94
Loin								
Scale weight and DXA weight	58	13.94	9.1	13.86	9.1	0.719	0.17	1.00
Adipose tissue and Fat mass	58	5.37	20.6	3.75	24.5	<0.001	0.13	0.93
Bone and BMC	58	1.23	11.8	0.25	12.5	<0.001	0.01	0.60
Muscle and Lean mass	58	7.10	8.6	9.86	8.6	<0.001	0.10	0.84
Belly								
Scale weight and DXA weight	58	8.18	9.8	7.82	10.3	0.019	0.11	1.00
Adipose tissue and Fat mass	58	4.26	17.3	2.02	23.3	<0.001	0.08	0.96
Bone and BMC	58	0.40	12.3	0.02	28.2	<0.001	0.00	0.63
Muscle and Lean mass	58	3.44	10.8	5.78	8.7	<0.001	0.06	0.81
Ham								
Scale weight and DXA weight	58	11.91	6.7	11.91	6.6	0.983	0.10	1.00
Adipose tissue and Fat mass	58	3.49	13.9	2.44	15.2	<0.001	0.05	0.95
Bone and BMC	58	0.92	10.5	0.23	10.9	<0.001	0.01	0.80
Muscle and Lean mass	58	7.38	7.8	9.24	7.6	<0.001	0.08	0.98

[1] Probability.
[2] Person correlation.
[3] Bone mineral content.

Table 2 – Description, comparison of means, and correlation between measurements obtained in pork by chemical analyses and dual-energy X-ray absorptiometry (DXA).

Chemical and DXA, kg	n	Chemical		DXA		*P*[1]	SEM	*r*[2]
		Mean	CV	Mean	CV			
Entire animal								
Lipid and Fat mass	88	28.14	51.2	22.20	57.7	0.004	1.45	0.99
Ash and BMC[3]	88	2.98	32.7	2.05	39.4	<0.001	0.10	0.99
Protein and Lean mass	88	16.88	30.6	81.30	28.9	<0.001	1.81	0.99
Water and Lean mass	88	57.14	27.8	81.30	28.9	<0.001	2.14	1.00
Protein + Water and Lean mass	88	74.02	28.4	81.30	28.9	0.040	2.38	1.00
Entire animal								
Lipid and Fat mass	58	37.59	14.5	30.67	16.9	<0.001	0.70	0.95
Ash and BMC	58	3.61	8.1	2.59	10.2	<0.001	0.04	0.88
Protein and Lean mass	58	20.20	7.1	96.35	7.3	<0.001	0.67	0.92
Water and Lean mass	58	67.87	7.6	96.35	7.3	<0.001	0.81	0.96
Protein + Water and Lean mass	58	88.07	7.5	96.35	7.3	<0.001	0.89	0.97
Left carcass								
Lipid and Fat mass	58	14.64	15.3	11.93	19.8	<0.001	0.30	0.96
Ash and BMC	58	1.29	9.3	1.04	9.6	<0.001	0.01	0.78
Protein and Lean mass	58	7.70	8.2	35.86	7.2	<0.001	0.25	0.88
Water and Lean mass	58	24.55	7.8	35.86	7.2	<0.001	0.30	0.87
Protein + Water and Lean mass	58	32.25	7.9	35.86	7.2	<0.001	0.33	0.95

[1] Probability;
[2] Person correlation;
[3] Bone mineral content.

Table 3 – Prediction of the dissected tissues weights, based on the measurements obtained by dual-energy X-ray absorptiometry (DXA) in entire left pork carcasses.

Dependent variable (Dissection), kg	Independent variable (DXA)	*n*	R^2	CV	RSD[1]
	Left carcass				
Scale weight	Lean mass from left carcass	58	45.7	5.0	2.43
Scale weight	Lean mass and fat mass from left carcass	58	99.8	0.3	0.13
Scale weight	Lean mass, fat mass and BMC[2] from left carcass	58	99.9	0.2	0.09
Skin plus adipose tissue	Fat mass from left carcass	58	94.5	3.5	0.60
Adipose tissue	Fat mass from left carcass	58	96.6	3.0	0.45
Muscle	Lean mass from left carcass	58	90.8	2.4	0.58
Bone	Lean mass from left carcass	58	59.3	5.6	0.28
Bone	Lean mass and BMC from left carcass	58	77.2	4.2	0.21
	Shoulder				
Scale weight	Lean mass from left carcass	58	49.0	5.3	0.65
Scale weight	Lean mass and fat mass from left carcass	58	70.0	4.1	0.50
Skin plus adipose tissue	Fat mass from left carcass	58	75.4	6.6	0.27
Adipose tissue	Fat mass from left carcass	58	76.8	7.3	0.26
Muscle	Lean mass from left carcass	58	68.2	5.1	0.34
Bone	Lean mass from left carcass	58	45.4	7.4	0.10
Bone	Lean mass and BMC from left carcass	58	59.3	6.4	0.09
	Loin				
Scale weight	Fat mass from left carcass	58	54.1	6.2	0.86
Scale weight	Fat mass and lean mass from left carcass	58	82.8	3.8	0.53
Skin plus adipose tissue	Fat mass from left carcass	58	87.7	6.9	0.37
Adipose tissue	Fat mass from left carcass	58	88.9	7.1	0.35
Muscle	Lean mass from left carcass	58	78.3	4.0	0.29
Bone	BMC from left carcass	58	33.0	9.7	0.12
	Belly				
Scale weight	Fat mass from left carcass	58	45.9	7.2	0.59
Scale weight	Fat mass and lean mass from left carcass	58	67.5	5.6	0.46
Skin plus adipose tissue	Fat mass from left carcass	58	74.6	8.2	0.35
Adipose tissue	Fat mass from left carcass	58	77.5	8.4	0.32
Muscle	Lean mass from left carcass	58	57.6	7.0	0.24
Bone	Lean mass from left carcass	58	44.4	9.2	0.04
	Ham				
Scale weight	Lean mass from left carcass	58	67.5	3.8	0.45
Scale weight	Lean mass and fat mass from left carcass	58	79.2	3.0	0.36
Skin plus adipose tissue	Fat mass from left carcass	58	68.2	6.7	0.23
Adipose tissue	Fat mass from left carcass	58	72.2	7.3	0.22
Muscle	Lean mass from left carcass	58	77.9	3.7	0.27
Bone	Lean mass from left carcass	58	53.6	7.2	0.07
Bone	Lean mass and BMC from left carcass	58	68.4	5.9	0.05

[1] Residual standard deviation.
[2] Bone mineral content.

Table 4 – Prediction of the dissected tissues weights, based on the measurements obtained by dual-energy X-ray absorptiometry (DXA) in the same cut.

Dependent variable (Dissection), kg	Independent variable (DXA)	*n*	R^2	CV	RSD[1]
	Shoulder				
Scale weight	Lean mass from shoulder	58	64.3	4.5	0.55
Scale weight	Lean mass and fat mass from shoulder	58	99.9	0.3	0.04
Skin plus adipose tissue	Fat mass from shoulder	58	84.2	5.3	0.21
Adipose tissue	Fat mass from shoulder	58	86.3	5.6	0.20
Muscle	Lean mass from shoulder	58	88.5	3.0	0.21
Bone	Lean mass from shoulder	58	52.8	6.9	0.09
Bone	Lean mass and BMC[2] from shoulder	58	68.8	5.6	0.08
	Loin				
Scale weight	Fat mass from loin	58	54.2	6.1	0.86
Scale weight	Fat mass and lean mass from loin	58	99.9	0.3	0.04
Skin plus adipose tissue	Fat mass from loin	58	86.7	7.2	0.39
Skin plus adipose tissue	Fat mass and lean mass from loin	58	91.6	5.7	0.31
Adipose tissue	Fat mass from loin	58	88.0	7.4	0.36
Adipose tissue	Fat mass and lean mass from loin	58	91.3	6.3	0.31
Muscle	Lean mass from loin	58	69.8	4.7	0.34
Bone	Lean mass from loin	58	35.6	9.4	0.12
Bone	Lean mass and BMC from loin	58	60.8	7.4	0.09
	Belly				
Scale weight	Lean mass from belly	58	70.4	5.3	0.43
Scale weight	Lean mass and fat mass from belly	58	99.4	0.7	0.06
Skin plus adipose tissue	Fat mass from belly	58	91.7	4.7	0.20
Adipose tissue	Fat mass from belly	58	93.3	4.6	0.18
Muscle	Lean mass from belly	58	64.2	6.5	0.22
Muscle	Lean mass and fat mass from belly	58	78.6	5.0	0.17
Bone	BMC from belly	58	39.0	9.6	0.04
Bone	BMC and lean mass from belly	58	48.8	8.8	0.04
Bone	BMC, lean mass and fat mass from belly	58	58.7	7.9	0.03
	Ham				
Scale weight	Lean mass from ham	58	73.8	3.4	0.41
Scale weight	Lean mass and fat mass from ham	58	99.9	0.2	0.03
Skin plus adipose tissue	Fat mass from ham	58	89.7	3.8	0.13
Adipose tissue	Fat mass from ham	58	90.8	4.2	0.13
Muscle	Lean mass from ham	58	95.7	1.6	0.12
Bone	BMC from ham	58	63.1	6.4	0.06
Bone	BMC and lean mass from ham	58	75.3	5.2	0.05

[1] Residual standard deviation.
[2] Bone mineral content.

Table 5 – Prediction of the chemical component weights, based on the measurements obtained by dual-energy X-ray absorptiometry (DXA) in different conditions.

Dependent variable (Chemical), kg	**Independent variable (DXA)**	***n***	**R^2**	**CV**	**RSD[1]**
	Entire animal				
Scale weight	Lean mass from live animal	88	97.1	6.3	6.10
Scale weight	Lean and fat masses from live animal	88	99.9	1.1	1.12
Lipid	Fat mass from live animal	88	98.5	1.8	1.77
Ash	BMC[2] from live animal	88	97.0	0.2	0.17
Protein	Lean mass from live animal	88	98.9	0.6	0.54
Water	Lean mass from live animal	88	99.2	1.5	1.47
Protein plus water	Lean mass from live animal	88	99.4	1.6	1.60
	Entire animal				
Lipid	Fat mass from live animal	58	90.7	4.4	1.65
Ash	BMC from live animal	58	76.6	3.9	0.14
Protein	Lean mass from live animal	58	84.4	2.8	0.57
Water	Lean mass from live animal	58	91.8	2.2	1.49
Protein plus water	Lean mass from live animal	58	93.4	1.9	1.68
	Left carcass				
Lipid	Fat mass from live animal	58	83.3	6.3	0.92
Ash	BMC from live animal	58	65.0	5.5	0.07
Protein	Lean mass from live animal	58	64.6	4.9	0.38
Water	Lean mass from live animal	58	71.1	4.2	1.03
Protein plus water	Lean mass from live animal	58	82.3	3.1	0.99
	Left carcass				
Lipid	Fat mass from left carcass	58	91.0	4.6	0.67
Ash	BMC from left carcass	58	60.3	5.8	0.08
Protein	Lean mass from left carcass	58	76.3	4.0	0.31
Water	Lean mass from left carcass	58	75.8	2.6	0.65
Protein plus water	Lean mass from left carcass	58	90.0	2.3	0.75

[1] Residual standard deviation.
[2] Bone mineral content.

8 DISCUSSÃO GERAL

Uma busca rápida em bancos de dados científicos ajuda a mostrar a importância crescente que a tecnologia DXA vem adquirindo em diversas áreas da ciência. Com os resultados de uma pesquisa utilizando as palavras indexadoras DEXA ou DXA em títulos, resumos e palavras-chave de artigos publicados no banco de dados da *Science Direct* (www.sciencedirect.com) foi criada a Figura 7.1. Houve um aumento linear no número de publicações nos últimos 30 anos. Este crescimento ocorreu principalmente após 1992, sendo que a média anual de publicações envolvendo a temática DXA era de apenas dois artigos antes desta data. É importante ressaltar, no entanto, que os dados apresentados neste gráfico englobam todas as áreas de conhecimento, incluindo a medicina humana.

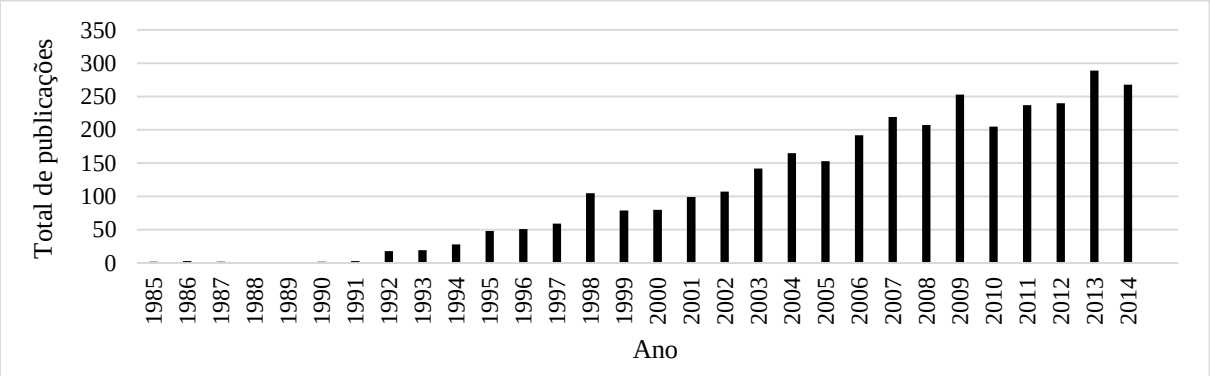

Figura 7.1 – Número total de publicações nos últimos 30 anos em todas as áreas de conhecimento e que continham os termos DXA ou DEXA em títulos, resumos e palavras-chave (n: 3.219).

Fonte: Site da *Science Direct* em 03/09/2014.

Um novo gráfico foi gerado incluindo somente dados das áreas de "ciências agrícolas e biológicas" e de "ciências veterinárias e medicina veterinária" (Figura 7.2). A primeira publicação nestas áreas ocorreu em 1993 e, desde então, vem apresentando uma média de três artigos publicados por ano. É possível observar, portanto, que as pesquisas focadas nesta tecnologia ainda são escassas e recentes em áreas relacionadas com zootecnia. Porém, assim como na medicina humana, a tecnologia DXA apresenta muitas aplicabilidades, tais como

estudos de crescimento, nutrição, desordens metabólicas, desafios sanitários, dentre outros fatores que podem alterar a composição corporal ou a densidade de tecidos nos animais.

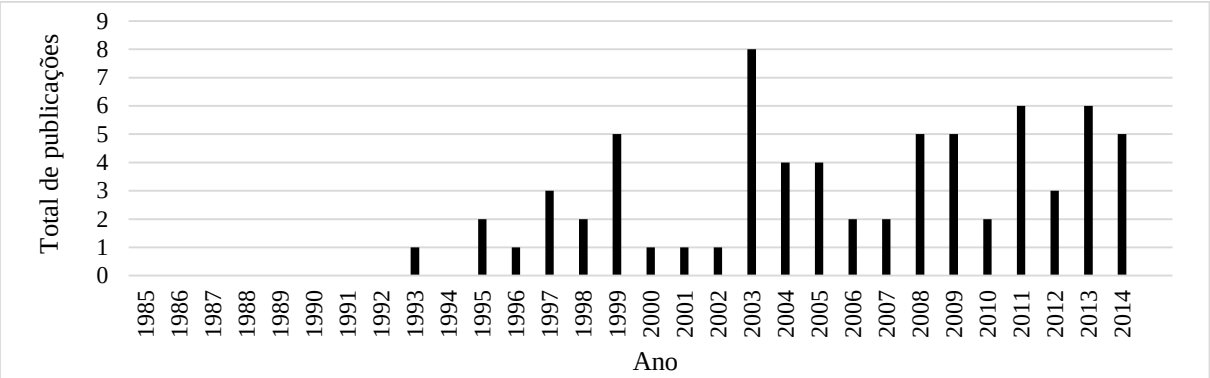

Figura 7.2 – Número total de publicações nos últimos 30 anos nas áreas "ciências agrícolas e biológicas" e "ciências veterinárias e medicina veterinária" que continham os termos DXA ou DEXA em títulos, resumos e palavras-chave (n: 69).

Fonte: Site da *Science Direct* em 03/09/2014.

As dificuldades enfrentadas durante a realização dos projetos que compões esta tese foram das mais diversas ordens. Uma vez que a tecnologia foi desenvolvida para avaliação de pessoas, diversas questões relativas a como enquadrar corretamente o corpo de um suíno, a carcaça ou até mesmo alguns cortes de carne vieram à tona. Poucas modificações ou ajustes na técnica de digitalização são possíveis quando se está avaliando o animal vivo, restando apenas ajustes no método para avaliar as imagens. Estudos prévios já avaliaram alguns destes ajustes (HUNTER et al., 2011; SUSTER et al., 2006). No entanto, muitas questões ainda continuam pendentes porque as diferentes versões e marcas de softwares podem trazer algoritmos distintos. O estudo completo da tecnologia envolveria, portanto, uma análise de todos os softwares e equipamentos DXA nas mesmas condições de ambiente utilizando um conjunto muito bem definido de fantasmas (peças artificiais que simulam porções do corpo). Na inviabilidade de um estudo deste porte, a calibração dos resultados para características da população de interesse, tal como realizado neste estudo, colabora para uma visão global da tecnologia. Neste sentido, as dificuldades que são interpretadas em um primeiro momento como grandes entraves para a utilização dos equipamentos DXA, devem ser vistas como possibilidades para novos estudos.

Assim, com a identificação de falhas e dificuldades, o pesquisador pode propor alternativas, provando-as com o ajuste. Esta última linha de raciocínio possui interesse científico através da sugestão de soluções para pesquisas futuras.

A maioria dos efeitos de interferência para a DXA foram passíveis de ajuste, e quando não, um novo método foi desenvolvido através de reflexão e novos testes. O senso crítico foi uma das principais questões para a correta aplicação da DXA, visto que a representação de algo tridimensional (como um animal) em formato bidimensional pode gerar muitos questionamentos. A maioria das dúvidas puderam ser exauridas através dos protocolos experimentais propostos. No entanto, outras eram relacionadas com fatores intrínsecos do equipamento e tiveram que ser testadas e mensuradas.

Outra abordagem interessante para o uso da tecnologia é a geração de novos protocolos metodológicos. Apesar de seu desenvolvimento inicial para avaliação de pessoas, existe uma infinidade de possibilidades para seu uso. Logicamente, o pesquisador deve possuir amplo conhecimento da tecnologia para explorar adequadamente tal gama de alternativas, principalmente no que se refere a interpretação criteriosa dos resultados, ou em outras palavras, no entendimento correto do que é representado pelos resultados. Embora a interpretação dos resultados seja limitada pelas características intrínsecas da tecnologia, a relação deles com o padrão de uma população bem definida aumenta em muito a sua utilidade. Assim, a variação de uma amostra (desvio padrão) em relação a normalidade da população pode ajudar na interpretação dos resultados (WATTS, 2004). Esta metodologia é chamada de escore T. Quando além destes fatores, também for considerado o efeito da idade (ou outro fator) sobre o valor normal da população, o escore é chamado de Z (BLAKE e FOGELMAN, 2010). A utilização destes escores foi um grande avanço para a medicina humana, uma vez que trouxe resultados mais ajustados a variabilidade populacional. Abordagens como essa podem ser desenvolvidas no contexto da suinocultura, trazendo ainda mais importância e aplicabilidade para a tecnologia na produção animal.

A ferramenta DXA provou ser eficiente para todos os fins propostos, mostrando-se um importante instrumento para avaliação animal. Ela poderá ser utilizada futuramente para estudo de estratégias nutricionais em relação às curvas de crescimento. Outro aspecto é sua aplicação para visualização da relação custo benefício na suinocultura, uma vez que permite determinar a composição de tecidos como músculo ou até mesmo o peso de um corte cárneo de alto interesse econômico em animais vivos.

CONCLUSÕES E PERSPECTIVAS

De forma geral a tecnologia DXA foi adequada para os fins propostos. Resultados precisos foram alcançados depois de pequenos ajustes metodológicos, uma vez que os fatores de influência sobre os resultados foram quantificados e eram de fácil correção através de padronização dos métodos. Além disso, a maior parte dos vieses inseridos nos modelos eram sistemáticos. Por fim, a referida tecnologia provou ser de grande utilidade para estudos de composição corporal em animais vivos ou abatidos e, portanto, a DXA deve ser considerada em futuras pesquisas.

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