Cortical Bone Segmentation for Accurate Canine Body Composition Quantification using 3 Tesla Fat-Water MRI

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Purpose: Whole-body fat-water MRI (FWMRI) is unique among the available body composition imaging methods in providing true 3D volumetric images without the use of ionizing radiation. However, the inability to detect and therefore account for bone volume leads to discrepancies between MRI-derived and true whole body mass. We describe a whole-body FWMRI acquisition and semi-automated image analysis pipeline, for whole-body FWMRI and body composition quantification that identifies cortical bone voxels as a separate tissue depot. The performance of this pipeline in the estimation of total body mass and body mass change was tested in a dog model.

Methods: This study was approved by the local Institutional Animal Care and Use Committee. Six healthy adult male dogs (27.4 ± 3.4 kg at baseline) were scanned at two time points: baseline (week 0) and after 4 weeks on an obesogenic diet. Five of the six dogs were scanned twice at week 4 to determine test-retest reproducibility. Scans were performed on a 3.0 Tesla Achieva MRI scanner (Philips Healthcare, Best, The Netherlands). The integrated quadrature body coil was used for excitation and reception. FWMRI scans were acquired using a multi-station, multi-slice, multi-echo gradient echo (multiple Fast Field Echo, mFFE) protocol with 12 table positions, 20 axial slices/position, and a slice thickness of 5 mm with zero slice gap. Other protocol parameters were: TR/TE1/TE2/TE3 [ms] = 150/1.34/2.87/4.40, flip angle = 20°, water-fat shift = 0.251 pixels, BW = 1734 Hz/pixel, axial in-plane FOV = 420 mm × 322 mm, acquired matrix size = 232 × 179, and acquired voxel size = 1.8 mm × 1.8 mm × 5 mm. Total scan duration was 5 min 33 sec, with 27.8 second breath holding performed only for table positions including the abdomen. Volumes of total body adipose tissue, lean tissue, and cortical bone (AT, LT, CB) were quantified using a semi-automated approach. Proton density fat fraction images, defined as |fat signal|/(|fat signal| + |water signal|), were calculated, and AT and LT were separated by thresholding at 50% fat fraction. To reduce the effect of fat fractions originating from background and low signal regions in the analysis, the sum image volume (|fat signal| + |water signal|) of the dog was separated from background by clustering into two classes, tissue and background, using a version of a Fuzzy C-means algorithm that incorporates spatial continuity[1]. Fat fractions originating from noise in low signal regions were suppressed by multiplication of the tissue cluster map. CB volume was quantified as low signal regions inside the body not originating from air. The body was segmented by thresholding the "belongingness" (range 0-1) of the Fuzzy C means tissue cluster at an empirically determined level of 0.3. Two-dimensional hole filling (in axial and coronal planes) morphological steps were used to close the body and thereby fill holes from both air and CB inside the body. CB and air inside the body were separated by segmenting air from the sum images using a semi-automated method[2] for the identification of the air pockets. After segmentation, tissue depot volumes were calculated as the sum volume of all voxels in the segmented class. Volumes were converted into mass estimates using literature values for tissue densities: 0.923 kg/L for adipose, 1.100 kg/L for soft lean, and 1.72 kg/L for cortical bone[3]. Once all tissues were segmented, and calculated volumes converted into masses using corresponding densities, the AT, LT and CB masses were summed to form an FWMRI-derived total body mass estimate. FWMRI-derived masses were compared to the masses measured by a scale.

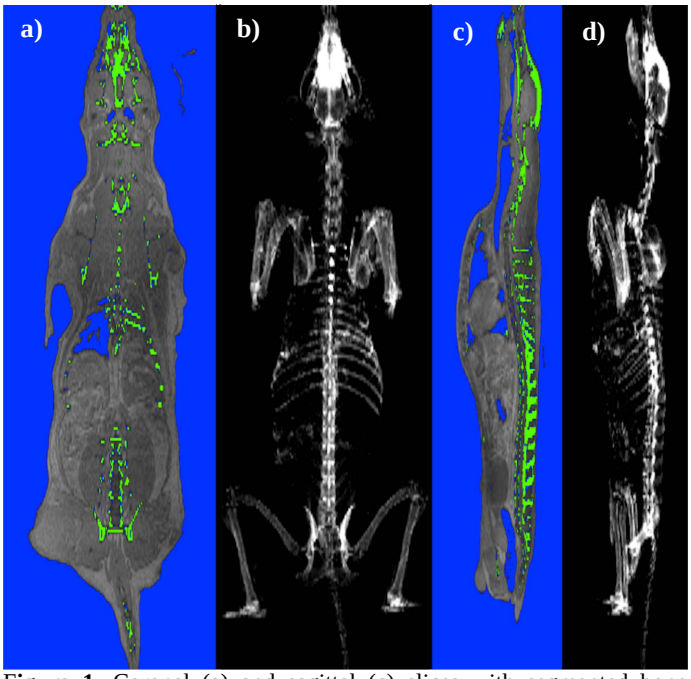

Figure 1. Coronal (a) and sagittal (c) slices with segmented bone (green) and air (blue) overlaid on FWMRI distinguish portions of skull, ribs, and vertebrae, from trachea, lungs, and visceral gas pockets, allowing reconstruction of the underlying skeleton, shown in coronal (b) and (d) sagittal whole body projections.

Results: The acquisition and processing pipeline effectively discriminates CB from air (**Figure 1a,c**), and the segmented CB clearly reconstructs the skeleton (**Figure 1b,d**). Test-retest reproducibility using a one-way analysis of variance (ANOVA) yielded a coefficient of variation (CV) of 0.25%, 0.42%, and 3.08% for AT, LT and CB respectively. When CB fraction was not accounted for, the concordance correlation coefficient (CCC) of the change in mass measured by the scale and FWI-derived mass between week 0 and week 4 was 0.735 (95% CI 0.460 - 0.881), with a coefficient of bias (Cb) of 0.75 (Cb = ratio of CCC to Pearson correlation coefficient). When the CB contribution was accounted for, the CCC improved to 0.931 (95% CI 0.813 - 0.975) with Cb = 0.94.

Discussion: The ability of our FWMRI acquisition / processing pipeline to discriminate between signal voids arising from CB and air significantly improves the quantitative agreement between FWMRI and scale measures of changes in whole body absolute mass, improving the accuracy with which the contributions of individual tissue types to body mass changes can be parsed. This study demonstrates the potential of whole-body FWMRI acquired on human 3T scanners to quantify body composition in a dog model that closely resembles many aspects of obesity and obesity-associated endocrine and metabolic dysregulation in humans. This work reveals the potential for a powerful new imaging modality and body composition measurement method for translational research in the area of obesity and metabolic disease.

References: [1] Liew AW-C, *et al*. IEEE Trans Fuzzy Syst 13(4); 2005. [2] Malmberg F, *et al*. Wiederhold P, Barneva RP, editors. Proceedings of the 13th International Workshop on Combinatorial Image Analysis (IWCIA); 5852 of LNCS, 201–211. Springer, 2009. [3] Chowdhury B, et al. Int J Obes Relat Metab Disord 18(4); 1994.