

Improved Precision of Hip Structure Analysis Using Optimized Projection Images From Segmented 3D CT Scans of the Hip

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Introduction

The hip structure analysis (HSA) method was developed to derive cross-sectional properties at certain locations in the proximal femur from 2D DXA scans to permit a mechanical interpretation. A major limitation on HSA precision is that inconsistent femur position alters projected dimensions so that real dimensional differences cannot be distinguished from projection error. CTXA™ (Mindways Software, Inc.) is a commercial quantitative computed tomography (QCT) application that generates DXA-like projection images from 3D QCT data sets. CTXA projection images are analyzed and used clinically in the same manner as DXA projection images and are compatible with the HSA method.

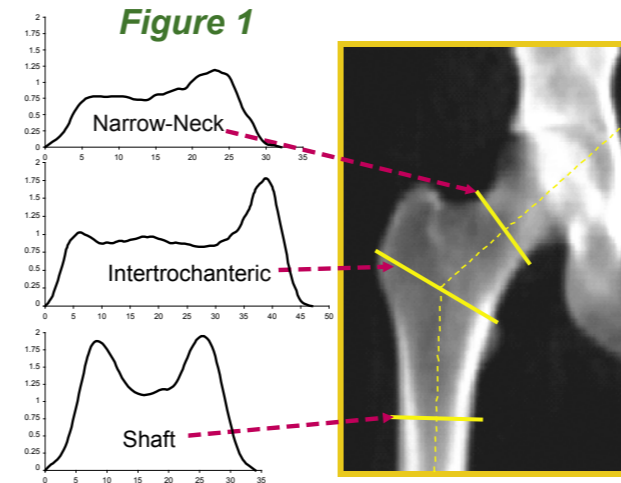
In DXA scans the projection view of the hip is determined by the way that the femur is positioned at scan time but femur shape is highly variable and it has few bony landmarks that aid in proper positioning. The CTXA software extracts the femur from the obscuring soft-tissue, finds the correct frontal plane and automatically generates the appropriate projection. We hypothesized that ability to control the projection plane in software should improve femur position consistency and produce better HSA precision than observed with DXA. We present here comparisons of HSA measurement precision estimates based on paired-scan CTXA projection images and compared to previously published precision estimates using DXA scans from two large clinical trials [1]

Methods

The CT data were acquired as part of a study to estimate the operational precision of CTXA at a single clinical site. Data were acquired with an unaltered CT scan protocol for measuring proximal femur BMD with the CTXA software. Paired CT scans on 24 adult subjects with repositioning between them were done at a single visit using a GE NX/i helical CT scanner at 100 mAs, 120 kVp and a 3 mm section spacing. The CTXA software segmented bone from soft tissue and generated a frontal projection of the femur as used for a DXA-equivalent bone mineral analysis of the hip. Resulting CTXA projection images with a pixel spacing of 0.7 mm in both directions were converted to DICOM format then exported to the HSA program. The DXA precision study was generated from two large clinical trials conducted by Eli Lilly & Co. where study designs used screening DXA scans of the hip followed later with a second scan at the start of the trial. DXA precision was measured with 936 scan pairs averaged over various Hologic DXA scanner models (Hologic Inc., Waltham MA, USA). For both CTXA and DXA, coefficients of variation were computed from paired scan data using the method of Gluer et al. [2]

Hip Structure Analysis (HSA)

The HSA method uses the principle of Martin and Burr[3] that in a bone mass image acquired so that the bone axis is parallel to the image plane, a line of pixels orthogonal to the bone axis is a projection of the corresponding cross-section and can partially describe its geometry. As in Figure 1, three cross-sections are acquired from the proximal femur image.

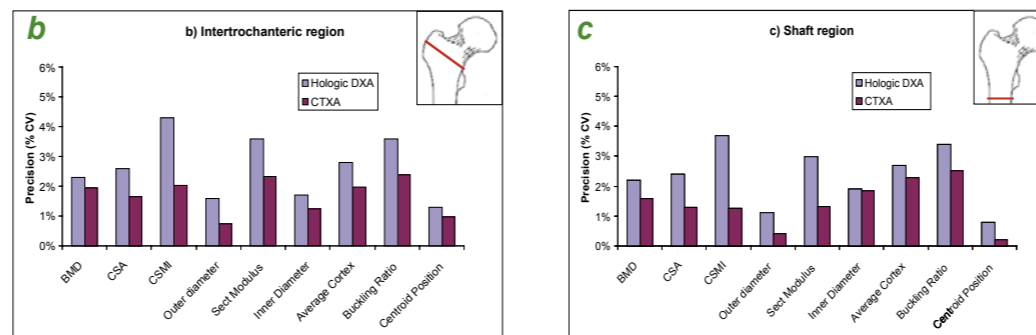


In addition to femoral neck length and the neck-shaft-angle, BMD, outer diameter, bone cross-sectional area (CSA), cross-sectional moment of inertia (CSMI), centroid position and section modulus were derived from the mass profiles using algorithms described previously.[4]. Estimates of buckling ratio and cortical thickness used simple concentric annulus models of the cross-sections assuming fixed proportions of mass in the cortex. [4]

Results

Coefficients of variations for the three HSA regions are compared between CTXA and DXA in Figure 2a-c.

Figure 2 (a-c)



References

- (1) Khoo, B., et al. 2005 Bone, 37: p. 112-21. (2) Gluer, C., et al. 1995 Osteoporosis International, 5: p. 262-269. (3) Martin, R.B. and D.B. Burr, 1984, J Biomech, 17(3): p. 195-201. (4) Beck, T.J., et al., 2001, J Bone Miner Res, 16(6): p. 1108-19.

Discussion and Conclusion

As we had hypothesized, the ability of the CTXA algorithm to control the HSA projection plane produced a marked improvement in precision, compared to what is typically achieved with DXA in the clinical setting. The precision improvement was greatest at regions where the DXA precision was the worst i.e., where positioning uncertainties are greatest. For the critical parameters CSA, CSMI, section modulus and buckling ratio precision improved by a factor of ~3 at the NN region and by a factor of ~2 at the IT and shaft regions. Results were remarkable given that an existing CTXA data set was used without modification for optimal HSA results. For example, precision at the shaft was somewhat constrained since only 15 of the 28 CT data sets scanned sufficiently distal on the shaft to incorporate the standard HSA shaft region. While the 3 mm slice thickness and reconstruction interval used are suitable for quantitative bone mineral density estimates, a smaller, overlapping slice thickness should provide more accurate and/or precise HAS estimates. This is especially true in the femoral neck region where the oblique angle of the femoral neck relative to the scan direction may significantly degrade bone border definition and cortical/trabecular bone delineation relative to what may be achieved in the femoral shaft that runs essentially orthogonal to the scan planes.

The HSA algorithms were also not modified for this study to take advantage of the 3D volumetric data from which the CTXA is derived. Importantly, a number of HSA assumptions required by the 2D limitations of DXA data are no longer necessary since they can be measured directly. For example buckling ratio and cortical thickness estimates require assumptions of cross-sectional shape and of the proportion of bone in the cross-section that is cortical. Also the cross-sectional moments of inertia and section moduli in DXA are only relevant to bending in the projection plane while 3D data should provide derivation of these properties relevant to bending in any direction so that more realistic stress analyses can be performed. Improvements of the HSA algorithms to take full advantage of the 3D volumetric data set from CTXA are currently under development.

Overall, the results of this preliminary analysis indicate HSA measurement precision accuracy is considerably better with CTXA than with DXA. While these results do not directly indicate the basis for the improved precision, it is plausible that the post-acquisition-processing methods used within CTXA result in more consistent femur positioning than may be commonly achieved with DXA. It is also likely that some further improvement in HSA measurement precision can be obtained by optimization of the HSA algorithm and the CT scan protocols.