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30-second Bound and Pore Water Concentration Mapping of Cortical Bone using 2D UTE with Optimized Half-Pulses

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Abstract

Purpose—MRI of cortical bone has the potential to offer new information about fracture risk. Current methods are typically performed with 3D acquisitions, which suffer from long scan times and are generally limited to extremities. This work proposes using 2D UTE with half pulses for quantitatively mapping bound and pore water in cortical bone.

Methods—Half-pulse 2D UTE methods were implemented on a 3T Philips Achieva scanner using an optimized slice-select gradient waveform, with preparation pulses to selectively image bound or pore water. The 2D methods were quantitatively compared with previously implemented 3D methods in the tibia in five volunteers.

Results—The mean difference between bound and pore water concentration acquired from 3D and 2D sequences was 0.6 and 0.9 mol ¹H/L_{bone} (3 and 12 % respectively). While 2D pore water methods tended to slightly overestimate concentrations relative to 3D methods, differences were less than scan-rescan uncertainty and expected differences between healthy and fracture-prone bones.

Conclusion—Quantitative bound and pore water concentration mapping in cortical bone can be accelerated by 2 orders of magnitude using 2D protocols with optimized half-pulse excitation.

Keywords

MRI; ultrashort echo time; cortical bone; bound water; pore water

Introduction

Cortical bone has two main water components that can be imaged using MRI—the water bound to the collagen matrix (bound water) and the water residing in the pore space (pore water) (1). Because the majority of the signal (from bound water) has a $T_2 \approx 400 \mu\text{s}$, ultra-short echo time (UTE) or zero echo time (ZTE) imaging has been used to image cortical bone (2–5). Most UTE and all ZTE methods use 3D acquisitions, which puts a lower limit on the scan time for a given field of view and resolution. In particular, pulse sequences for bound or pore water imaging that use adiabatic pulses require long scan times due to specific absorption rate (SAR) constraints. Even with fast bi-component analysis (6), a scan time on the order of 10 min is required. Thus, despite the potential of bound-/pore-water imaging to evaluate bone fracture risk (7–9), the translation of such methods into clinical practice has been hampered by relatively long scan times.

One way to overcome the scan time limitations of 3D UTE is to use a slice selective acquisition and 2D readout. The number of radial k-space spokes required for Nyquist sampling of a single 2D slice is approximately two orders of magnitude lower than the number required for a 3D acquisition. However, slice selective excitation with UTE-MRI is technically challenging. Using a conventional slice selective excitation, the time needed to rephase spins across the slice following the RF pulse limits the shortest achievable echo time. The solution to this problem is to break the RF pulse into two half-pulses and add the complex signals resulting from each (10). Ideally, the signals from inside the slice add constructively, while the signals outside the slice cancel. With this approach, no spin rephasing is needed and so effective echo times of $\sim 100 \mu\text{s}$ are achievable. However, the efficacy of half-pulse excitation is known to be highly sensitive to gradient waveform inaccuracies, potentially caused by eddy currents, propagation delay, or the response characteristics of the gradient amplifier.

Several techniques have been proposed to overcome the sensitivity of half-pulse excitation to gradient imperfections, including double half-pulses (11), out-of-slice magnetization saturation (12, 13), a dedicated pre-scan to estimate imperfections (14), and direct improvement of gradient waveform accuracy (15). While 2D UTE with half-pulses has been used for quantitative imaging (12, 16, 17), the challenges associated with its use has limited translation. To date, limited quantitative in vivo 2D UTE studies of bound and pore water imaging have been reported.

Here we report the implementation of optimized half-pulse excitation with T_2 -selective magnetization preparations (5, 18, 19) for fast, quantitative bound and pore water imaging of human cortical bone in vivo. We employed the direct approach of improving half-pulse performance by using an iterative method to pre-distort the slice select gradient to minimize gradient waveform error (20). This pre-distortion method is fast and simple, and has been implemented as a software tool on our scanner, permitting real-time optimization for any given slice prescription.

Methods

Five volunteers (24M, 42M, 27M, 35M, 59F) underwent tibia scans on a 3T Philips Achieva scanner, with IRB approval and written informed consent. The adiabatic inversion recovery (AIR) and double adiabatic fast passage (DAFP) methods (5, 18, 19) were used to selectively image bound and pore water, respectively, of the tibia. An 8-channel knee coil was used for signal reception and a short- T_2 reference marker with a known proton concentration was placed in the field of view (FOV) to allow maps of bound and pore water concentration to be converted to absolute units of mol $^1\text{H}/\text{L}_{\text{bone}}$. Both 2D and 3D protocols were run on all subjects.

The 3D sequences were similar to those previously reported (5, 19). Briefly, every TR period, an AIR or DAFP preparation was implemented using 10-msec, 3.5-kHz HS8 adiabatic pulses, followed by 16 non-selective excitations and acquisitions along center-out radial trajectories in k-space at 3.2 ms spacing. A variable flip angle excitation scheme was used to maintain constant signal amplitude across each of the 16 acquisitions per TR period. Images were acquired with isotropic FOV/resolution = 200 mm/1.5 mm, and were reconstructed using k-space trajectories that were measured for x-, y-, and z-directions and then interpolated to describe all readout directions. Both 3D AIR and DAFP scans required 33,792 radial acquisitions with TR = 400 ms, resulting in a scan time $\approx$ 14 min each.

In contrast, the 2D scans used two half-pulse excitations to select a 5-mm slice and 256 radial acquisitions to encode a 200×200 mm FOV with 1.5 mm in-plane resolution, which reduced the scan time to $\approx$ 14 s each (including 1.3 s of fixed dummy scan time). Aside from the slice selective excitation, the 2D protocols were otherwise essentially identical to the 3D protocols, using the same AIR and DAFP preparations, 16 radial acquisitions per TR, and images were reconstructed using measured read-out trajectories. Golden angle spacing of the radial spokes was added to minimize coherent streaking artifacts. Also, in order to evaluate the signal-to-noise ratio (SNR) needed for accurate signal quantification, scans were repeated 8 $\times$ and images were reconstructed using either 1 (14 s) or 8 (104 s) averages.

The slice selective excitation was implemented using a 550 μs -duration variable rate (21) half-gauss pulse (10). The slice-select gradient was a bipolar, smoothly varying waveform with a maximum gradient strength of 23 mT/m, maximum slew rate of 125 mT/m/ms, and maximum acceleration of 1000 mT/m/ms². To make the half-pulse excitation robust to gradient imperfections the slice-select gradient waveform was optimized for each subject during the scan session using the iterative pre-distortion method described by Harkins et al (20) and illustrated in Fig 1. Briefly, using a modified Duyn's method to measure the gradient waveform (22, 23), the input waveform was iteratively adjusted to minimize the error between the measured and desired waveforms. The process converged in 3 to 5 iterations, requiring less than one minute per iteration, and resulted in 0.2% average root-mean-squared-error between the ideal and measured waveforms. Recent studies showed that this optimization improved slice profiles for 2D UTE across a range of echo times (24). Also, to further suppress out-of-slice signal in the DAFP scans, saturation slabs—the REigonal Saturation Technique (REST) in Philips software—were implemented once per TR immediately prior to the excitation train. These were not added in the AIR scans because

1) out-of-slice signal contamination was less of an issue, as the bone signal intensity was similar or greater to the surrounding muscle and fat, and 2) to avoid potential unwanted magnetization transfer effects between bound water signal and macromolecular content. The 2D slice profiles, with and without gradient optimization and saturation slabs, were measured in a CuSO₄ phantom by combining the 2D excitation scheme with the full 3D UTE readout.

Bound and pore water concentration maps were calculated from both 2D and 3D AIR and DAFP images using previously defined signal equations (19). With the 3D scans, TE was defined as the time from the center of the RF pulse to the start of acquisition (25). For the 2D scans, the TE was defined from the end of the pulse to the start of acquisition, because signal loss due to T_2 during the RF pulse is negated by the concomitant broadening of the slice profile (25, 26). To compare similar volumes of tissue, a slab of 3D data corresponding to the location and thickness of the 2D slice was extracted. From there, mean concentration was tabulated from each map by manually defining one large region of interest (ROI) of cortical bone. Because the 2D images had relatively low SNR, the Rician noise bias needed to be accounted for in estimation of each ROI mean value. The mean concentration, μ , was estimated as $\mu = \sqrt{|\mu_B^2 - \sigma^2|}$, where μ_B is the measured mean signal in the bone and σ is an estimate of the standard deviation of the added noise (27). The mean of a background ROI, μ_N was measured and used to estimate σ^2 , as $\sigma^2 = \mu_N^2 / (\pi/2)$.

Differences between 2D and 3D maps were calculated on a subject-by-subject basis, and reported both in units of mol ¹H/L_{bone} and as a percent error. Along with mean differences (d), the standard deviation (s) and limits of agreement ($d \pm 1.96s$) (28) were computed and displayed on Bland Altman plots. The SNR ($\equiv \mu_B/\sigma$) needed for reliable bound and pore water measurement was also evaluated.

Results

Figure 2 shows the effect of gradient waveform optimization and out-of-slice saturation on experimentally measured slice profiles of a CuSO₄ phantom imaged with the 2D sequence without DAFP or AIR preparation. Before gradient optimization or out-of-slice saturation, the total out-of-slice signal per voxel was $\approx 20\%$ of the in-slice signal. Adding out-of-slice saturation alone reduced this value to $\approx 9.2\%$, while the gradient optimization dropped it to $\approx 3.8\%$. When used together, the out-of-slice signal dropped to $\approx 3.3\%$.

Figure 3 shows representative raw 2D AIR and DAFP images of the tibia and corresponding images from the 3D volumes. Qualitatively, the image contrasts look similar, though the 2D images have higher noise variance, as expected. In one subject, RF spiking was present, so the artifacts were removed from k-space using a robust principal component analysis (RPCA) algorithm before reconstruction (29). Figure 4 shows the bound and pore water maps resulting from the AIR and DAFP images in Fig 3. These maps show good qualitative agreement between 2D and 3D acquisitions, and analysis of the SNR values showed approximately the same SNR efficiency for the 2D and 3D acquisitions, as expected. Specifically, the mean SNR values for 3D, single-acquisition 2D (14 s), and 8-average 2D

(104 s) were 23, 3.0, and 5.7, respectively for the bound water maps and 11, 2.4, and 5.2 for the pore water maps.

An overview of differences between 2D and 3D bound and pore water concentration measurements is shown in Fig 5. The left frames show measures from 2D and 3D acquisitions plotted against each other, along with the linear regression line and the line of unity. The right frames show Bland-Altman comparisons of the differences between 2D and 3D measures as a function of the mean. Apparent from both plot types is the generally close correspondence of the 2D and 3D measures. Quantitatively, the mean ($\pm$ standard deviation) across subjects of the difference between 3D and 2D measures was 0.6 ± 0.4 mol $^1\text{H}/\text{L}_{\text{bone}}$ for bound water and -0.9 ± 0.6 mol $^1\text{H}/\text{L}_{\text{bone}}$ for pore water. The corresponding limits of agreement were -0.2 to 1.5 mol $^1\text{H}/\text{L}_{\text{bone}}$ for bound water and -2.1 to 0.2 mol $^1\text{H}/\text{L}_{\text{bone}}$ for pore water. For comparison, the average value of the standard error of each measure (standard error was defined as the mean signal across an ROI divided by the square root of the number of voxels in the ROI), was equal to 0.21 (2D) and 0.06 (3D) $^1\text{H}/\text{L}_{\text{bone}}$ for bound water concentration, and 0.16 (2D) and 0.03 (3D) $^1\text{H}/\text{L}_{\text{bone}}$ for pore water concentration.

These levels of per-subject precision indicate that differences observed between the 2D and 3D maps was due to more than just thermal noise; however, the range of the limits of agreement were still approximately equal to previously reported inter-study standard errors (≈ 2 mol $^1\text{H}/\text{L}_{\text{bone}}$) for 3D imaging of both bound and pore water concentrations (5). Note also that one of the five subjects had clinically diagnosed osteoporosis and exhibited bound and pore water concentrations that differed from the other subjects by much more than the inter-subject standard error or limits of agreement between 2D and 3D measures.

Discussion

The results demonstrate that 2D UTE with suitable half-pulse excitation can provide measures of bound and pore water concentration in bone that are effectively equivalent to those from previously established 3D protocols. The primary benefit of 2D compared with 3D protocols is a substantially reduced scan time, from ≈ 30 min to as low as ≈ 30 sec for both bound and pore water mapping. This comparison may somewhat overstate the speed advantages of 2D, because 3D scans can, in principle, be accelerated by methods such as compressed sensing or by using an anisotropic FOV. Nonetheless, it is unlikely that accelerated 3D scan times will be as short as those of the 2D methods presented here. Also, it remains to be determined if both bound- and pore-water concentrations need to be measured independently. If not, then a factor of $2\times$ acceleration results from using only DAFP or AIR (or through bi-component analysis, which fits only the ratio of the two signals, (6)). In this case though, the relative scan time acceleration of 2D vs 3D remains the same.

Reduced scan times are not only efficient, they also open the door to scanning multiple bone sites in a single session, and are more accommodating to a wider population, particularly patients who may not be capable of handling long scan times. Likewise, the scan time benefits of 2D offer the potential to implement methods that would require impractical scan durations with 3D acquisitions, such as high resolution protocols over a large FOV, as would

be needed to map bound and pore water in the femoral neck or vertebral bodies. In addition to practical benefits, the faster scans will allow for pulse sequence variations and experimental studies that require a longer repetition time or multiple acquisitions. For example, with a longer TR, it may be possible to implement more complicated and effective T_2 -selective preparations. Similarly, with additional scans it may be possible to include patient-specific T_1 measurements to find the optimal inversion time for the AIR scans, or rapidly measure bi-exponential T_2^* signal decay as an alternative approach to characterizing bound and pore water content in cortical bone (8).

The shift from 3D to 2D protocols does not come without costs. Most obviously, 2D UTE protocols acquire image data only over a single slice. However, based on two recent studies, this does not appear to be a significant limitation in long bones, at least. Bound and pore water imaging of the radius and tibia in vivo (5) show little variation of concentrations along the length of the mid-shaft. Likewise, in a study of cadaver radii (9), correlations between bound and pore water concentrations and the bone material properties did not change significantly in measures found from different axial slices between the 25% and 50% locations of the distal mid-shaft.

The other obvious cost of 2D compared to 3D is the loss of SNR, which presents two challenges. First, with the fastest 2D scan times and, therefore, lowest SNR, these methods are applicable only in regions such as the tibia where relatively large voxels and large ROIs can be evaluated. Second, when computing the mean signal over an ROI from a map with relatively low SNR, one must take care to account for the Rician noise characteristics. In the present study, using only simple ROI means (not shown) from the single-average (14 sec) scans resulted in systematic errors of ≈ 15 and 30%, for bound and pore water concentrations, respectively. In scans performed with 8 averages, these errors dropped to ≈ 4 and 19%.

The primary challenge of effectively implementing 2D UTE for quantitative studies is producing robust slice selective excitation in the presence of gradient waveform imperfections, including propagation delay, eddy currents, and transient response characteristics of the gradient amplifiers. In the present study, an iterative pre-distortion method (Fig 1) was used to optimize the gradient waveform (20), and, for pore water imaging, out-of-slice saturation was also used. While these methods reduced out-of-slice signal substantially, it was not reduced to zero and likely remains the primary source of difference between the 2D and 3D measures. This is particularly true for pore water images, because surrounding tissues have relatively long T_2 s and, consequently, high signal intensities in the DAFP sequence. In contrast, the long- T_2 signal suppression of the AIR sequence also reduces signal intensity of other tissues and, consequently, mitigates the effect of out-of-slice signal contamination.

Ultimately, the 2D and 3D scans provided effectively identical results. The 95% limits of agreement are similar in range to the inter-study standard error and small relative to the differences between the measures from the osteoporotic subjects and young healthy controls. For example, previous 3D studies have found mean bound and pore water concentrations of 28 and 7 mol $^1\text{H}/\text{L}_{\text{bone}}$ in young and healthy tibia (5), compared with values of 17 and 14

mol $^1\text{H}/\text{L}_{\text{bone}}$ in tibia of osteoporotic subjects (30). More studies are necessary to translate bound and pore water imaging into clinical practice, but the substantial reduction in scan time demonstrated here removes one significant hurdle.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

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References

1. Horch RA, Nyman JS, Gochberg DF, Dortch RD, Does MD. Characterization of ^1H NMR signal in human cortical bone for magnetic resonance imaging. *Magn Reson Med*. 2010; 64:680–7. [PubMed: 20806375]
2. Techawiboonwong A, Song HK, Leonard MB, Wehrli FW. Cortical Bone Water: in vivo quantification with ultrashort echo-time MR imaging. *Radiology*. 2008; 248:824–833. [PubMed: 18632530]
3. Weiger M, Brunner DO, Dietrich BE, Müller CF, Pruessmann KP. ZTE imaging in humans. *Magn Reson Med*. 2013; 70:328–32. [PubMed: 23776142]
4. Rajapakse CS, BashoorZadeh M, Li C, Sun W, Wright AC, Wehrli FW. Volumetric Cortical Bone Porosity Assessment with MR Imaging: Validation and Clinical Feasibility. *Radiology*. 2015; 276:526–535. [PubMed: 26203710]
5. Manhard MK, Horch RA, Gochberg DF, Nyman JS, Does MD. In Vivo Quantitative MR Imaging of Bound and Pore Water in Cortical Bone. *Radiology*. 2015; 277:221–229. [PubMed: 26020434]
6. Chen J, Carl M, Ma Y, Shao H, Lu X, Chen B, Chang EY, Wu Z, Du J. Fast volumetric imaging of bound and pore water in cortical bone using three-dimensional ultrashort-TE (UTE) and inversion recovery UTE sequences. *NMR Biomed*. 2016:1–8.
7. Horch RA, Gochberg DF, Nyman JS, Does MD. Non-invasive predictors of human cortical bone mechanical properties: T(2)-discriminated H NMR compared with high resolution X-ray. *PloS one*. 2011; 6:e16359. [PubMed: 21283693]
8. Bae WC, Chen PC, Chung CB, Masuda K, D'Lima D, Du J. Quantitative ultrashort echo time (UTE) MRI of human cortical bone: correlation with porosity and biomechanical properties. *J Bone Miner Res*. 2012; 27:848–57. [PubMed: 22190232]
9. Manhard MK, Uppuganti S, Granke M, Gochberg DF, Nyman JS, Does MD. MRI-derived bound and pore water concentrations as predictors of fracture resistance. *Bone*. 2016; 87:1–10. [PubMed: 26993059]
10. Pauly, J., Conolly, S., Nishimura, DG. Slice-selective excitation for very short T2-species. Proceedings of the 8th Annual Meeting of the ISMRM, Amsterdam, The Netherlands; Proceedings of the 8th Annual Meeting of the ISMRM, Amsterdam; The Netherlands. 1989. Abstract #28
11. Josan S, Pauly JM, Daniel BL, Pauly KB. Double half RF pulses for reduced sensitivity to eddy currents in UTE imaging. *Magn Reson Med*. 2009; 61:1083–9. [PubMed: 19235919]
12. Techawiboonwong A, Song HK, Wehrli FW. In vivo MRI of submillisecond T 2 species with two-dimensional and three-dimensional radial sequences and applications to the measurement of cortical bone water. *NMR Biomed*. 2008; 21:59–70. [PubMed: 17506113]
13. Josan S, Kaye E, Pauly JM, Daniel BL, Pauly KB. Improved half RF slice selectivity in the presence of eddy currents with out-of-slice saturation. *Magn Reson Med*. 2009; 61:1090–5. [PubMed: 19319972]
14. Abe T. Half radiofrequency pulse excitation with a dedicated prescan to correct eddy current effect and gradient delay. *Medical Physics*. 2013:40.

15. Fabich HT, Benning M, Sederman AJ, Holland DJ. Ultrashort echo time (UTE) imaging using gradient pre-equalization and compressed sensing. *J Magn Reson.* 2014; 245:116–124. [PubMed: 25036293]
16. Du J, Hamilton G, Takahashi A, Bydder M, Chung CB. Ultrashort echo time spectroscopic imaging (UTESI) of cortical bone. *Magn Reson Med.* 2007; 58:1001–9. [PubMed: 17969110]
17. Diaz E, Chung CB, Bae WC, Statum S, Znamirowski R, Bydder GM, Du J. Ultrashort echo time spectroscopic imaging (UTESI): an efficient method for quantifying bound and free water. *NMR Biomed.* 2012; 25:161–8. [PubMed: 21766381]
18. Horch RA, Gochberg DF, Nyman JS, Does MD. Clinically compatible MRI strategies for discriminating bound and pore water in cortical bone. *Magn Reson Med.* 2012; 68:1774–84. [PubMed: 22294340]
19. Manhard MK, Horch RA, Harkins KD, Gochberg DF, Nyman JS, Does MD. Validation of quantitative bound- and pore-water imaging in cortical bone. *Magn Reson Med.* 2014; 71:2166–2171. [PubMed: 23878027]
20. Harkins KD, Does MD, Grissom WA. Iterative method for predistortion of MRI gradient waveforms. *IEEE T Med Imaging.* 2014; 33:1641–1647.
21. Conolly S, Nishimura D, Macovski A. Variable-Rate Selective Excitation. *J Magn Reson.* 1988; 458:440–458.
22. Duyn JH, Yang Y, Frank Ja, van der Veen JW. Simple correction method for k-space trajectory deviations in MRI. *J Magn Reson.* 1998; 132:150–3. [PubMed: 9615415]
23. Gurney, P., Pauly, J., Nishimura, DG. A simple method for measuring B0 eddy currents. Proceedings of the 13th Annual Meeting of the ISMRM, Miami, USA; Proceedings of the 13th Annual Meeting of the ISMRM; Miami, USA. 2005. Abstract #866
24. Harkins, KD., Manhard, MK., Grissom, WA., Does, MD. Automatic Gradient Predistortion Applied to Clinical 2D-UTE. Proceedings of the 24th Annual Meeting of the ISMRM, Singapore; Proceedings of the 24th Annual Meeting of the ISMRM; Singapore. 2016. Abstract #4289
25. Robson MD, Gatehouse PD. Consequences of T2 relaxation during half-pulse slice selection for ultrashort TE imaging. *Magn Reson Med.* 2010; 64:610–5. [PubMed: 20665804]
26. Harkins KD, Horch RA, Does MD. Simple and Robust Saturation-Based Slice Selection for Ultrashort Echo Time MRI. *Magn Reson Med.* 2015; 73:2204–2211. [PubMed: 25046136]
27. Gudbjartsson H, Patz S. The Rician Distribution of Noisy MRI Data. *Magn Reson Med.* 1995; 34:910–914. [PubMed: 8598820]
28. Bland JM, Altman DG. Statistical Methods for Assessing Agreement Between Two Methods of Clinical Measurement. *Lancet.* 1986; 327:307–310.
29. Campbell Washburn AE, Atkinson D, Nagy Z, Chan RW, Josephs O, Lythgoe MF, Ordidge RJ, Thomas DL. Using the Robust Principal Component Analysis Algorithm to Remove RF Spike Artifacts from MR Images. *Magn Reson Med.* 2016; 2525:2517–25.
30. Manhard, MK., Tanner, SB., Gochberg, DF., Nyman, JS., Does, MD. Bound and Pore Water MRI of Cortical Bone in Osteoporotic Patients. Proceedings of the 24th Annual Meeting of the ISMRM, Singapore; Proceedings of the 24th Annual Meeting of the ISMRM; Singapore. 2016. Abstract #177

Figure 1.

The ideal gradient waveform (G_{nom}) is applied (G_{app}) and measured (G_{obs}). For every iteration i , the gradient error ($\Delta^i = G_{nom} - G_{obs}^i$) and update matrix K are used to find a new G_{app}^{i+1} . Iterations continue until the RMSE converges; error over the first four iterations are shown in the middle graph. The error is minimized within an RMSE of 0.2%.

Figure 2.

Slice profile shown for both unoptimized and optimized gradient waveforms, with and without the saturation slabs. Inset shows zoomed in section of slice profiles where the suppression of out of slice signal from the saturation slabs is apparent.

Figure 3.
Representative images showing 3D (top) AIR and DAFP acquisitions and 2D acquisitions (bottom).

Figure 4. Representative tibia maps from 3D (top) AIR and DAFP acquisitions and 2D acquisitions (bottom). Mean bound (left) and pore (right) water values for the bone are shown below.

Figure 5.

Left: Mean bound and pore water concentrations from 2D and 3D scans are plotted against each other, along with the regression line (solid) and the line of unity (dashed). The uncertainty of the measurements is about the size of the marker for the 2D data and less than the size of the marker for the 3D data. Right: Bland Altman plots show mean 2D and 3D values plotted against the difference between them, with the mean difference (solid line) and limits of agreement (dashed lines) shown.