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Whole-Heart Coronary MR Angiography Using a 3D Cones Phyllotaxis Trajectory

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Abstract

Purpose: To develop a 3D cones steady state free precession sequence with improved robustness to respiratory motion while mitigating eddy current artifacts for free-breathing whole-heart coronary magnetic resonance angiography.

Method: The proposed sequence collects cone interleaves using a phyllotaxis pattern, which allows for more distributed k-space sampling for each heartbeat compared to a typical sequential collection pattern. A Fibonacci number of segments is chosen to minimize eddy current effects with the trade-off of an increased number of acquisition heartbeats. For verification, phyllotaxis-cones is compared to sequential-cones through simulations, phantom studies and *in vivo* coronary scans with eight subjects using 2D image-based navigators for retrospective motion correction.

Results: Simulated point spread functions and moving phantom results show less coherent motion artifacts for phyllotaxis-cones compared to sequential-cones. Assessment of the right and left coronary arteries using reader scores and the image edge profile acutance vessel sharpness metric indicate superior image quality and sharpness for phyllotaxis-cones.

Conclusion: Phyllotaxis 3D cones results in improved qualitative image scores and coronary vessel sharpness for free-breathing whole-heart CMRA compared to standard sequential ordering when using a steady state free precession sequence.

Keywords

coronary MRA; 3D cones trajectory; phyllotaxis; motion artifacts; free-breathing

Introduction

Respiratory motion is one of the primary challenges for coronary magnetic resonance angiography (CMRA). Motion of the heart and surrounding structures due to respiration can result in ghosting, diffuse streaking and blurring artifacts. Many techniques for respiratory motion compensation exist and continue to be improved (1). These techniques include using respiratory bellows (1), breath-holding (2, 3), acquisition based respiratory gating (4), and retrospective motion correction (5–14). However, for any retrospective motion compensation technique, a k-space trajectory that is more robust to motion can improve image quality because it can help reduce the effects of imperfections in the correction algorithm. Also, if the imaging data is used for navigation, motion extraction can be more accurate because of reduced artifacts on the signal used for displacement measurements.

In the presence of motion, view ordering techniques that acquire spread out k-space data for each heartbeat can make the artifacts less coherent and overall improve image quality (15). However, for a steady state free precession (SSFP) sequence, which is the standard for CMRA, eddy currents and associated artifacts are introduced when k-space position is varied drastically between excitations (16). This behavior reveals a trade-off between motion robustness and sensitivity to eddy current artifacts for SSFP-based CMRA. A “pairing” approach has been demonstrated that allows distributed k-space coverage with cancellation of eddy current dephasing, which preserved image quality (16). In addition, a phyllotaxis design has been shown to mitigate eddy current artifacts for SSFP with 3D projection reconstruction (3DPR) (17). In this approach, interleaving with a Fibonacci number of segments (i.e., heartbeats) results in a distributed k-space coverage with only small k-space changes between each excitation.

Multiple k-space sampling techniques have been developed for whole-heart coronary MRA which include both Cartesian (18, 19) and non-Cartesian methods (e.g., 3D spiral (19–21), 3DPR (17, 18, 22, 23), 3D cones (7, 24)). Like 3DPR, the 3D cones trajectory offers more robustness to motion and flow artifacts compared to conventional Cartesian sampling due to oversampling near the k-space origin (7, 25). In addition, 3D cones is more efficient compared to 3DPR because it requires fewer readouts to be fully sampled and demonstrates improved SNR when undersampling (24). For CMRA, the segmented 3D cones acquisition uses a sequential ordering scheme to collect cone interleaves, with minimal trajectory change between excitations. While this provides maximal robustness to eddy currents, sequential ordering results in a clustered k-space coverage for each heartbeat that detracts from its overall robustness to motion.

An ordering method based on golden-angles has been recently applied to 3D cones to improve robustness to motion (26); however, this work used a gradient echo acquisition, and with SSFP, large changes in k-space location between excitations cause eddy current artifacts (16, 27), and require a different approach to minimize these effects. In this work, the phyllotaxis (17) design is adapted for the 3D cones trajectory to sample a more distributed region of k-space locations during each heartbeat while minimizing eddy current artifacts. For verification, the phyllotaxis design is compared to the sequential-cones design with point spread function (PSF) analysis, phantom studies, and *in vivo* studies.

Methods

Trajectory Design:

Each 3D cones readout is parameterized using a polar angle defined by an azimuthal angle (ϕ) and elevation angle (θ). Following an initial radial path from the origin of k-space, the cone readout then traverses in a spiral-like fashion along a conic surface (Fig. 1a). The standard design uniformly interleaves multiple spirals on each conic surface to satisfy Nyquist sampling criteria and fills each cone before moving to the next conic surface during the scan. While this approach gives the minimum possible trajectory change between excitations, it results in clumped regions of k-space being acquired every heartbeat (Fig. 1b, 1d).

For a phyllotaxis collection pattern, each successive segment is separated by the golden angle (28) in the azimuthal dimension, which ensures a well-distributed sampling pattern in k-space with minimal gaps. A phyllotaxis 2D fast cardiac sequence was originally proposed in (29) and was expanded to 3D in (17) for the reduction of eddy current effects with 3DPR. When a Fibonacci number of segments (i.e., heartbeats) is used, the changes in trajectory between successive excitations are minimized, which mitigates eddy current artifacts. The total number of phyllotaxis readouts is calculated by multiplying the number of interleaves per segment (readouts per heartbeat) by the number of segments (Fibonacci number).

The elevation function for phyllotaxis-cones is defined by first considering elevation angles derived from the sequential design (24). The distribution of cone readouts at different elevation angles in k-space can be represented using a theta histogram (Fig. 2a). The theta histogram is scaled to match the desired number of total cone readouts that is required for a Fibonacci number of segments by fitting the elevation function of the sequential design with a polynomial. In contrast, for 3DPR the elevation function is defined in Piccini et al. (17) using a square root function. In essence, our approach chooses elevation angles that most closely match the basic 3D cones design and does not have a simple closed-form representation. For phyllotaxis-cones, basing the elevation function on the sequential elevation function ensures uniform coverage, specifically correcting for undersampling in the equatorial region and oversampling in the poles.

The first 200 readout angles of the elevation functions for sequential (containing multiple readouts within each elevation angle) and phyllotaxis (containing a single readout at each elevation angle) can be seen in Fig. 2b. The full elevation function for phyllotaxis is shown in Fig. 2c. Indexes for each heartbeat are chosen by interleaving readout indices spaced by the total number of acquired heartbeats (Fig. 2c). Rather than a uniformly distributed ϕ , as done in the sequential method, golden angle increments are used for the phyllotaxis pattern. The polar angles (all θ and ϕ) are then used to redesign the cones trajectory. A top view of the polar angles for the sequential and phyllotaxis designs is shown in Fig. 3. For sequential (Fig. 3a), ϕ is evenly distributed (within each elevation angle), and for phyllotaxis (Fig. 3b), ϕ is incremented by the golden angle. The phyllotaxis pattern starts at the bottom of the spherical k-space volume and contains multiple segments that traverse towards the top (Fig. 3b). Axial and coronal slices of the k-space sampling density for each pattern are shown in the Supporting Information Figure S1. Finally, the density compensation function for

gridding is recalculated (30) as it is slightly different from the sequential design. When this cones design is segmented by the number of heartbeats, a distributed region of k-space is acquired in each heartbeat (Fig. 1c, 1e). Also, when a Fibonacci number of heartbeats are acquired, the trajectory change between excitations is minimized, as described in Piccini et al. (17). A video showing beat-to-beat 3D cones polar angles and the respective readouts for the sequential and phyllotaxis designs is included as Supporting Information Video S1.

Imaging Experiment:

The 3D cones trajectory was designed with a $28 \times 28 \times 14 \text{ cm}^3$ field of view (FOV), $1.2 \times 1.2 \times 1.25 \text{ mm}^3$ near-isotropic resolution, 18 readouts per heartbeat (segment) for a temporal resolution of 98 ms. To satisfy Nyquist criteria, a minimum of 9,142 readouts were required for standard sequential ordering (508 heartbeats for 18 readouts/heartbeat) (7, 24). For the phyllotaxis method, a Fibonacci number of 610 heartbeats was required, increasing the total number of cone readouts to 10,980. To ensure a fair comparison, the total number of readouts for sequential-cones was increased to 10,980 using the same histogram approach described above, but uniformly spaced ϕ was maintained.

This work is based on free-breathing whole-heart CMRA using alternating-repetition time (ATR) SSFP and 3D cones k-space sampling (7). The timing diagram for the acquisition scheme is shown in Supporting Information Figure S2. Using an ATR-SSFP sequence helps with further fat suppression and to enhance blood-myocardium contrast by using two different repetition times (TR_1 and TR_2) to modify the frequency response profile compared to the conventional balanced SSFP (31). The CMRA sequence acquired leading sagittal and trailing coronal 2D image-based navigators (iNAVs) to track the motion of the heart along all three primary axes. The 2D iNAVs were acquired using a gradient-echo (GRE) sequence with a flip angle = 12° (standard sinc excitation pulse and four dummy TRs for signal preparation), $TE/TR = 1.6/6.3 \text{ ms}$, 8 mm slice thickness, 12 spiral interleaves (75.6 ms per iNAV) to achieve $28 \times 28 \text{ cm}^2$ FOV and 3.1 mm in-plane resolution. After the first 2D iNAV (sagittal) is acquired, a fat saturation module and 10 dummy TRs are played to establish the ATR-SSFP steady-state using a cosine ramp-up for each flip angle. Next, the 3D cones imaging data is acquired for each segment using the following imaging parameters: $TR = 5.4 \text{ ms}$, $TE = 0.6 \text{ ms}$, flip angle = 70° , bandwidth = 125 kHz, and $TR_1/TR_2 = 4.29 \text{ ms}/1.15 \text{ ms}$ (for the ATR-SSFP). The 3D cones acquisition is then followed by a cosine ramp-down to exit the ATR-SSFP to allow for the trailing 2D iNAV (coronal) data collection. Using both iNAVs, estimates for the superior/inferior (S/I), anterior/posterior (A/P) and left/right (L/R) motion estimates were obtained and subsequently used for translational correction of the acquired imaging data as in (7) by using a linear phase modulation term generated using the motion estimates for each heartbeat.

The scan protocol used a three-plane localizer for iNAV slice location planning and to locate and prescribe the appropriate region of interest (ROI) covering the whole heart. Two-chamber and four-chamber 2D CINE scans were used to determine the trigger delay (TD) and duration of the respective mid-diastolic cardiac rest period (7, 14) for a single cardiac phase acquisition (temporal resolution = 98 ms/phase). Scans were performed on a GE Signa

1.5 T EXCITE system (GE Healthcare, Waukesha, WI) (maximum slew rate 150 mT/m/ms and maximum gradient amplitude of 40 mT/m) using an 8-channel cardiac receiver coil.

Simulations:

Robustness to motion was evaluated by comparing the simulated point spread function (PSF) of the different acquisition methods to examine the artifacts. The PSF was calculated by gridding all ones for each trajectory with and without an S/I motion component. The S/I motion data was derived from 2D iNAVs acquired during a separate *in vivo* scan, and subsequently applied by multiplying a linear phase ramp with the k-space data points (all ones) for the portions of the full trajectory acquired in each simulated heartbeat. The S/I motion used for the simulations covered an extent of ~3 mm and is shown in the Supporting Information Figure S3a.

Phantom and *in vivo* Scans:

Phantom scans were performed for both the sequential and phyllotaxis designs using a resolution phantom. The scanner table was automated to oscillate a total of 25 mm in the z-direction at a peak velocity of 13 mm/s and an average period of ~6 seconds. The S/I table motion is shown in the Supporting Information Figure S3b which was also used (after scaling to match the extent of the *in vivo* motion data) for the PSF simulations previously described. Pre and post-rigid-body translational motion-corrected images were reconstructed to examine the resulting artifacts.

In vivo data was collected by scanning eight healthy volunteers (7 male, and 1 female) using the previously described CMRA sequence. The subjects were scanned with the sequential and phyllotaxis trajectories (in randomized order) to image the right coronary artery (RCA) and left coronary artery (LCA). The LCA was analyzed along the left main coronary artery (LMCA) and the left anterior descending (LAD) artery. The left circumflex artery (LCx) was not analyzed in this study. Similar to previous studies (7,12–14), cardiac triggering was implemented using a peripheral plethysmograph (PG) with scan times ranging from 7–10 mins (it was previously found that the PG was closer to the required point of readout (diastole) when triggering compared to a vector electrocardiogram (VCG) and gave better coronary artery depiction (7)). In this study, we did not observe any issues in image quality from using the PG.

Assessment:

To assess the quality of the coronary methods, two metrics were applied, as were similarly used in (12–14).

First, qualitative scores of coronary image quality for the RCA and LCA were obtained through independent blinded reading by two board-certified cardiologists with experience in CMRA. Pairs of images for the sequential and phyllotaxis designs were randomized and displayed together. Image quality of the proximal, mid and distal segments of the RCA and LCA was scored on a 5-point scale: 5-Excellent, 4-Good, 3-Moderate, 2-Poor and 1-Non-diagnostic. For the RCA, proximal, mid and distal was defined (1/3, 1/3, 1/3) from the origin of the RCA to the origin of the posterior descending artery (PDA) at the base of the inferior

septum. For the LCA, proximal, mid and distal was defined (1/3, 1/3, 1/3) from the origin of the left main coronary artery (LMCA) and along the LAD to the apex. A total of 96 segments were scored by each reader.

Second, quantitative measurements of coronary vessel sharpness were obtained using the image edge profile acutance (IEPA) metric (32). The IEPA metric is a gradient-based measurement, defined using eqn. 1 and eqn. 2 (where s = profile line data, n = length of s , and N = number of profile lines in the cross-section), which analyzes the sharpness of multiple cross-sectional profile lines (from one side of the coronary artery to the other) giving values ranging from 0 to 1, where higher values correspond to sharper edges. Eqn. 1 gives the root-mean-squared (RMS) gradient computed along the i^{th} profile line s_i (for $i=1,2,\dots,N$) and $s_i(j)$ is the j^{th} point along the i^{th} profile line. Eqn. 2 then calculates the IEPA score by averaging over all N profile lines and normalizing by the difference between $s_{\max}$ and $s_{\min}$ which represent the maximum and minimum values respectively across all profile lines. This ensures that the IEPA scores range from 0 to 1 which correspond to a constant and a step function respectively. For each method, this was applied to the RCA and LCA using 10 evenly spaced radial profile lines, drawn perpendicular to the lumen axis, located every 1 mm over 50 mm for a total of 500 profiles per segment. A modified CoroEval software (33) was used to extract the amplitude profiles and calculate the IEPA values in MATLAB (The Mathworks, Natick, MA).

$$g_i = \sqrt{\frac{\sum_{j=1}^{n_i-1} [s_i(j) - s_i(j+1)]^2}{n_i - 1}} \quad [1]$$

$$\text{IEPA} = \frac{\sum_{i=1}^N g_i}{N(s_{\max} - s_{\min})} \quad [2]$$

The statistical significance of the results for reader scores and IEPA values was analyzed using the two-tailed Student's t-test for both the RCA and LCA. Example segments with the corresponding scores and IEPA measurements are shown in Supporting Information Figure S4 and Table S1 respectively.

Results

Figures 4 and 5 show the log scale PSF results with and without an introduced S/I motion (in Supporting Information Figure S3a) component (respectively) for the sequential and phyllotaxis designs. In the coronal and sagittal slices of the 3D PSF, the motion introduces some coherent structure to the PSF for sequential ordering, while the effect of motion appeared less coherent for phyllotaxis ordering. The coherent artifacts manifest as blurring/streaking while incoherent artifacts appear as noise and are generally less intrusive. The PSF behavior favors phyllotaxis since the artifacts appear noise-like rather than as coherent aliasing. In the sagittal/coronal profiles for sequential and phyllotaxis (Fig. 5f), the central

lobe full width half maximum (FWHM) increased by 0.963 mm (47%) and 0.875 mm (42%), respectively, in the presence of motion. The wider central lobe for sequential corresponds to a decrease in the effective resolution and more blurring due to the introduced motion compared to phyllotaxis. Additional PSF simulations using the S/I table motion (in Supporting Information Figure S3b) from the phantom study (and after scaling to match the extent of the *in vivo* motion data) are shown in the Supporting Information Figure S5. In the sagittal/coronal profiles for sequential and phyllotaxis (Supporting Information Figure S5f), the corresponding central lobe FWHM increased by 0.575 mm (28%) and 0.513 mm (25%), respectively, in the presence of motion.

Images from the motion phantom study are shown for the sequential and phyllotaxis acquisitions (Fig. 6). Before motion correction, the sequential acquisition demonstrates more coherent artifacts (blurring/streaking) which corrupts the image quality. For phyllotaxis, the motion artifacts manifest more as blurring along with incoherent artifacts. After 2D iNAV-based translational motion correction (Fig. 6c and Fig. 6f), both exhibit minimal residual artifacts. This is expected given that the motion was strictly one-dimensional rigid body motion. Furthermore, no eddy current artifacts are observed for phyllotaxis ordering compared to the sequential ordering. This result is also expected given that the phyllotaxis design ensures that the displacement in k-space locations between consecutive cone readouts within each heartbeat is minimized (16, 17).

Sagittal, coronal and axial slices reconstructed without any respiratory motion correction show that the sequential acquisition exhibits more severe motion artifacts compared to phyllotaxis ordering (Fig. 7(a-f)). The corresponding motion corrected images are also shown in Fig. 7(g-l). With motion correction, images of the RCA and LCA for three of the eight volunteers (Fig. 8 and Fig. 9, respectively) also show improved vessel sharpness for phyllotaxis compared to sequential. Similar results are observed in the other subjects. Also, as previously seen in the phantom dataset, eddy current artifacts are not observed for phyllotaxis ordering compared to the sequential ordering in the *in vivo* images.

Reader scores and IEPA results for the eight volunteer scans are summarized in Fig. 10. Qualitative reader scores are shown in Figs. 10a and 10c. For the proposed phyllotaxis acquisition, higher average reader scores are shown for each subject in the RCA and in the LCA (with the exception of a tie for subject 4). The average reader scores (mean $\pm$ standard deviation) across segments with sequential and phyllotaxis for the RCA are 3.4 ± 1.0 and 4.27 ± 0.96 respectively. The LCA shows similar results as the RCA for sequential and phyllotaxis with 2.8 ± 1.1 and 3.58 ± 0.96 respectively. Additionally, higher average reader scores within each segment (shown in Supporting Information Figure S6 for proximal, mid and distal) are given for the proposed phyllotaxis acquisition compared to sequential in both the RCA and LCA images. For both the RCA and LCA, the differences in reader scores between the sequential and phyllotaxis were statistically significant ($P < 0.001$). The correlation coefficient between each reader for the RCA was 0.70. The Bland-Altman statistics for the RCA gave a mean difference of 0.92, and a 95% confidence interval of $[-0.93, 2.8]$. Furthermore, the correlation coefficient between readers for the LCA was 0.75. The Bland-Altman statistics for the LCA produced a mean difference of 1.2, and a 95% confidence interval of $[-0.31, 2.7]$. Quantitative vessel sharpness measurements are

presented in Figs. 10b and 10d. For each subject, the proposed phyllotaxis technique outperformed sequential after 2D iNAV-based translational motion correction. Larger IEPA measurements are observed for phyllotaxis compared to sequential along the RCA and LCA. This suggests that residual motion artifacts have a larger effect on vessel sharpness for sequential compared to phyllotaxis. Figure 10b showcases these differences in IEPA measurements for each subject using both acquisition schemes. The average IEPA scores (mean $\pm$ standard deviation) across all subjects with sequential and phyllotaxis for the RCA were 0.148 ± 0.020 and 0.159 ± 0.021 , respectively. The LCA shows similar results for sequential and phyllotaxis with 0.134 ± 0.031 and 0.148 ± 0.029 , respectively. For both the RCA and LCA, the differences in IEPA measurements between the sequential and phyllotaxis are statistically significant ($P < 0.001$). Figure 10d visually summarizes these results.

Discussion

This work demonstrates improved motion robustness for phyllotaxis-based 3D cones acquisition compared to sequential ordering. While sequential-cones acquires a clustered region of k-space per heartbeat, phyllotaxis-cones acquires a more distributed region of k-space and introduces less coherent artifacts without introducing noticeable eddy current artifacts for SSFP. Also, for phyllotaxis, the respiratory motion artifacts have less of an impact between heartbeats compared to sequential-cones. Phantom results indicated that highly accurate solutions could be obtained for either approach after motion correction; however, for more complex non-rigid motion (i.e., *in vivo*), artifacts remained for sequential compared to phyllotaxis likely because the non-rigid motion was not completely retrospectively corrected.

To generate the phyllotaxis design, the number of segments must be a Fibonacci number and a redesign is required when changing the number of cones per segment, which is not required for sequential ordering. Limitations include increased scan times and less design flexibility due to the Fibonacci number requirement on the number of segments. This required increasing the total segments by 20% compared to the original sequential design. Also, while sequential was oversampled in this case to match phyllotaxis, another approach would have been to design a trajectory with higher resolution that is Nyquist sampled with the number of readouts required for Fibonacci. For a high number of segments, phyllotaxis results in sweeping polar angles through an approximate longitudinal line (17) (Fig. 1c). Accordingly, it may be possible to design trajectories that have similar behavior, but do not require a Fibonacci number of segments.

When using phyllotaxis, the change in trajectory between successive excitations is slightly greater compared to sequential which may have greater eddy current errors. Analysis and characterization of eddy current effects associated with phyllotaxis-cones compared to sequential-cones when using an SSFP sequence may be merited; however, no increased eddy current errors were observed for stationary phantom scans.

With respect to other work in coronary MRA (7, 12–14, 34–37), the current spatial resolution of 1.2 mm is a comparable choice. When comparing scan times for coronary

MRA, the undersampling factor, gating method, and k-space trajectory can change the scan duration (35–38). For the current phyllotaxis-cones sequence, a scan time of 7–10 mins is comparable to other gated acquisitions (7, 12–14, 36), even with the Fibonacci number (of segments) requirement. Modifications and enhancements to the cones sequence include using 3D iNAVs (12–14) for motion correction and decreasing the scan time (or increasing the resolution) by using variable density sampling with compressed sensing reconstruction (12, 38). These methods are all compatible with a phyllotaxis acquisition ordering. Finally, phyllotaxis-cones has the potential for self-navigation due to its robustness to motion and spread out k-space coverage. For example, when binning the imaging data according to respiratory phases (34, 35), each phase would have a more distributed coverage of k-space for phyllotaxis-cones compared to binning with sequential ordering.

Conclusion

In this work, a 3D cones trajectory based on a phyllotaxis collection pattern is developed for free-breathing whole-heart CMRA. A phyllotaxis design requires a Fibonacci number of segments which, while possibly increasing the acquisition time, provides improved robustness to motion when using SSFP. Simulations, phantom and eight healthy volunteer studies support the notion that phyllotaxis-cones is more robust to motion than sequential-cones. *In vivo* results also demonstrate improved qualitative image scores and coronary vessel sharpness with phyllotaxis-cones.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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FIG 1.

The plots above show how the polar angle (azimuthal angle (φ) and elevation angle (θ)) is defined (a) and the 18 cone polar angles (b, c) on the unit sphere and readouts (d, e) acquired during the 606th heartbeat for both methods: sequential (b, d) and phyllotaxis (c, e) respectively. In plots (e) and (d), phyllotaxis (e) is more distributed in k -space compared to sequential (d) per heartbeat.

FIG 2.

In the histogram plot (a), the readout distributions for both sequential and phyllotaxis are shown (using a bin width of $\pi/250$ radians) which correspond to the elevation functions in (b) and (c). The graph in (b) shows the elevation functions for sequential (blue) and phyllotaxis (red) for readouts 1–200. The graph shows how sequential-cones has coarser sampling in elevation angle while phyllotaxis-cones is more smoothly sampled. The graph in (c) shows the elevation function for all 10,980 readouts and example elevation angles for segments (heartbeats 1 and 305) in the phyllotaxis design.

FIG 3.

The plots above show a top view of the sequential (a) and the phyllotaxis (b) polar angle patterns on the unit sphere corresponding to each cone readout.

FIG 4.

The log scale PSFs without motion. The central axial and sagittal/coronal slices through the 3D PSF are shown for sequential (a, d) and phyllotaxis (b, e) acquisition methods. The central axial and sagittal/coronal profiles for both methods are shown in (c, f) which have similar central and side lobes.

FIG 5.

The log scale PSFs with S/I motion derived from (*in vivo*) 2D iNAVs (Fig. S3a). The central axial and sagittal/coronal slices through the 3D PSF are shown for sequential (a, d) and phyllotaxis (b, e) acquisition methods. In the sagittal and coronal slices, motion artifacts are more concentrated along the vertical axis (motion direction) for sequential whereas the motion is incoherently spread around the center of k-space for phyllotaxis. The central axial and sagittal/coronal profiles for both methods are shown in (c, f). In the sagittal/coronal profile (f), more energy is outside the central lobe for sequential (arrows) which corresponds to more blurring/streaking due to motion compared to phyllotaxis.

FIG 6.

Phantom images acquired on a stationary (a, d) and an oscillating (b, e) scanner table moving 25 mm in the z-direction at a peak velocity of 13 mm/s for both sequential (b, c) and phyllotaxis (e, f). Before motion correction, sequential (b) contains severe streaking artifacts while phyllotaxis (e) contains blurring and incoherent noise artifacts which are highlighted in the corresponding yellow and green boxes. The motion corrected images for sequential and phyllotaxis are shown in (c, f), respectively, after 2D iNAV-based translational motion correction. Small residual motion artifacts with similar structure as (b, e) are shown for sequential (yellow box) and phyllotaxis (green box) in (c, f) respectively.

FIG 7.

The images above show *in vivo* data for central sagittal, coronal, and axial slices when using sequential (a-c) and phyllotaxis (d-f) acquisition methods before correcting for motion. Similar to the PSFs, sagittal and the coronal slices are worse for sequential (a, b) compared to phyllotaxis (d, e). Coherent artifacts for sequential (dotted yellow boxes) are shown compared to less coherent artifacts for phyllotaxis (dotted green boxes). In the images, less streaking and better SNR are apparent for phyllotaxis. The corresponding images for sequential (g-i) and phyllotaxis (j-l) after 2D iNAV-based translational motion correction show improvements, but some coherent artifacts still remain for sequential (solid yellow boxes) while being less severe for phyllotaxis (solid green boxes). The corresponding enlarged regions of interest are shown on the right to highlight these artifacts with yellow and green arrows for sequential and phyllotaxis respectively.

FIG 8.

Reformatted maximum intensity projection images of the RCA for three healthy volunteers (a, b, c) after 2D iNAV-based translational motion correction. The yellow (sequential) and green (phyllotaxis) arrows show proximal (top) and distal (bottom) locations for both methods. The results show improved coronary artery depiction with phyllotaxis for both the proximal and distal regions.

FIG 9.

Reformatted maximum intensity projection images of the LCA for three healthy volunteers (a, b, c) after 2D iNAV-based translational motion correction. The yellow (sequential) and green (phyllotaxis) arrows show proximal (top) and distal (bottom) locations for both methods. Similar to the RCA images, phyllotaxis outperformed sequential for both the proximal and distal regions.

FIG 10.

Results of reader scores (a, c) and IEPA values (b, d) for all eight volunteers. The reader scores for each subject (a) and average scores (c) demonstrate higher values for the phyllotaxis acquisition. Higher reader scores and IEPA values correspond to better coronary image quality and sharper vessels respectively. The IEPA values for every subject (b) and average IEPA value (d) similarly show higher value trends for phyllotaxis. The statistical significance of the results for reader scores and IEPA values was $P < 0.001$ for both the RCA and LCA when using the two-tailed Student's t-test.