

# Can we make QSI clinically feasible? : A study of short step QSI

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**TARGET AUDIENCE** The neuroradiologists and physicists who are interested  $q$ -space imaging (QSI).

## PURPOSE

With QSI, water molecular displacement can be measured at the micrometer level [1], and several attempts have been made to verify microstructural changes in normal/abnormal human subjects [1-13]. However, QSI requires multiple  $q$ -values for diffusion-weighted image acquisitions with several directions of motion-probing gradients (MPGs). This technique thus requires a long acquisition time, depending on the numbers of  $q$ -values, slices, and MPG directions. Because of this long acquisition time, clinical applications of QSI have remained limited. To apply QSI clinically, the acquisition time needs to be substantially shortened. This study aimed to identify a feasible combination of  $q$  values to shorten QSI acquisition for clinical use. For this evaluation, we employed mean displacement (MD) derived from  $q$ -analysis of water molecular displacement distribution.

## METHODS

**Subject:** This study was approved by the Ethics Committee at Kyoto Prefectural University of Medicine. The subject consisted of one healthy, 46-year-old, male volunteer. **Data acquisition:** All MRI examinations were performed at 3 T using a whole-body scanner (MAGNETOM Skyra 3T, Siemens Healthcare, Erlangen, Germany). For all MRI, the field of view (FOV) was 24 cm. DWI for the QSI was acquired using a single-shot echo-planar imaging (EPI) technique (repetition time, 10,700 ms; echo time, 190 ms), time for applying the MPG pulse / duration time = 143/19.2 ms (effective diffusion time ( $T_{diff}$ ) = 136.6 ms), and a matrix of  $130 \times 130$ . The 11  $q$  values (number of excitations, time) used were  $0 \text{ mm}^{-1}$  (1, 0.72 min),  $3.8 \text{ mm}^{-1}$  (1, 2.68 min),  $7.7 \text{ mm}^{-1}$  (1, 2.68 min),  $11.5 \text{ mm}^{-1}$  (1, 2.68 min),  $15.3 \text{ mm}^{-1}$  (2, 4.82 min),  $19.1 \text{ mm}^{-1}$  (2, 4.82 min),  $23.0 \text{ mm}^{-1}$  (3, 6.95 min),  $26.8 \text{ mm}^{-1}$  (4, 9.1 min),  $30.6 \text{ mm}^{-1}$  (4, 9.1 min),  $34.4 \text{ mm}^{-1}$  (4, 9.1 min), and  $38.3 \text{ mm}^{-1}$  (4, 9.1 min). MPGs were applied in 12 directions. A total of 45 3-mm-thick sections were obtained without intersection gaps. Total acquisition time was 56.35 min. **Short  $q$ -steps combinations:** We considered the probabilistic density function (PDF) with the original 11  $q$  values (described above, including  $q = 0 \text{ mm}^{-1}$ ) as the gold standard. We employed two  $q$ -step-reducing strategies: 1) reducing  $q$ -steps from the original 11 to 6, 4, and 3 steps with equal  $q$ -step width; and 2) eliminating maximum  $q$ -values from the original  $38.3 \text{ mm}^{-1}$  to  $19.1 \text{ mm}^{-1}$  in step-by-step fashion and extrapolating to the original maximum  $q$ -value ( $38.3 \text{ mm}^{-1}$ ) by linear or bi-exponential fitting based on acquired values.  **$q$ -space analysis:** The  $q$ -space analysis was performed on a pixel-by-pixel basis, according to previously described methods [1, 10]. We obtained PDF using Fourier transformation of the signal decay curve at each voxel. From the PDF, the MD was calculated as a full-width at half-maximum  $\times 0.425$  of the PDF. **Evaluations:** Comparisons were performed using paired  $t$  tests (Matlab; The Mathworks, Natick, MA) among the distance from standard MD to reduced  $q$ -step combination-made MD in voxel-by-voxel fashion. The correlation was evaluated as significant for values of  $P < 0.05$ .

## RESULTS AND DISCUSSION

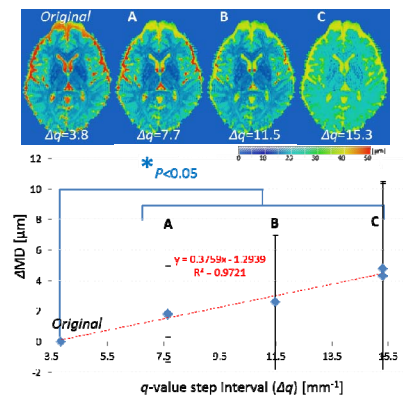
**Effect of  $q$ -step width:** Figure 1 (below) shows the relationship between mean difference from original MD to reduced  $q$ -step MD ( $\Delta$ MD) and  $q$ -step width ( $\Delta q$ ). When  $\Delta q$  was wider than the original,  $\Delta$ MDs increased in a linear manner. Representative slices of MD value (Fig. 1, above) showed clearly different contrast from standard  $q$ -step width. **Effect of interpolation:** Figure 2 (below) shows the relationship between  $\Delta$ MD by reducing strategy 1) with interpolation (linear or bi-exponential fitting) and  $\Delta q$ . When  $\Delta q$  was wider than the original,  $\Delta$ MD was increased. No clear difference was seen between with-interpolation (linear vs. bi-exponential fit in Fig. 2) and without-interpolation (AsIs in Fig. 2). **Effect of extrapolation:** Figure 3 (below) shows the relationship between  $\Delta$ MD by Strategy 2 with extrapolation (linear or bi-exponential fitting, or zero-filling) and maximum  $q$ -value for MD calculation (Max. $q$ ). From the comparisons of gray matter–white matter contrast from representative images (Fig. 3, above), bi-exponential extrapolation might be useful for reducing the number of  $q$ -steps from 11 to 8 (max. $q$ :  $38.3 \text{ mm}^{-1}$  to  $26.8 \text{ mm}^{-1}$ ). This will reduce total acquisition time from 56.35 min to 29.05 min, representing a 48.4% reduction.

## CONCLUSION

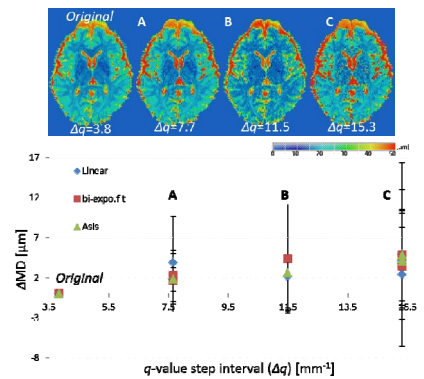
From these results, a larger width of  $q$ -step made a larger difference from original MD to reduced  $q$ -step MD than a smaller width of  $q$ -step. No utility of interpolation was recognized on MD by comparison to without-interpolation. The usefulness of extrapolation with a small number of  $q$ -steps was recognized on MD, and can reduce total acquisition time for QSI.

## References

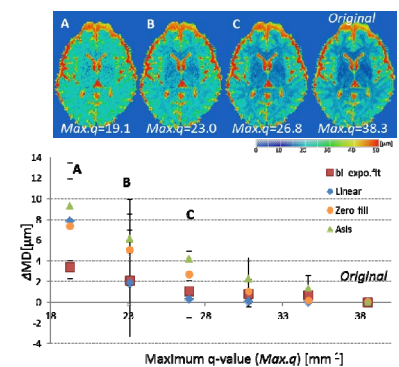
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**Figure 1.** Relationship between  $\Delta$ MD [ $\mu\text{m}$ ] and  $\Delta q$  [ $\text{mm}^{-1}$ ] (below). Representative MD value map (above).



**Figure 2.** Relationship between  $\Delta$ MD [ $\mu\text{m}$ ] by Strategy 1 with interpolation and  $\Delta q$  [ $\text{mm}^{-1}$ ] (below). Representative MD value map (above, bi-exponential fitting).



**Figure 3.** Relationship between  $\Delta$ MD [ $\mu\text{m}$ ] by Strategy 2 with extrapolation and Max. $q$  [ $\text{mm}^{-1}$ ] (below). Representative MD value map (above, bi-exponential fitting).