3D Diffusion-Weighted ¹²⁹Xe MRI for Whole Lung Morphometry

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Purpose: To obtain whole lung morphometry measurements from ¹²⁹Xe in a single breath-hold with 3D multiple b-value ¹²⁹Xe diffusion-weighted MRI (DW-MRI) with an empirically optimized diffusion time and compressed sensing for scan acceleration.

Methods: Prospective three-fold undersampled 3D multiple b-value hyperpolarized 129 Xe DW-MRI datasets were acquired, and the diffusion time (Δ) was iterated so as to provide diffusive length scale (Lm_D) estimates from the stretched exponential model (SEM) that are comparable to those from 3 He. The empirically optimized 129 Xe diffusion time was then implemented with a four-fold undersampling scheme and was prospectively benchmarked against 3 He measurements in a cohort of five healthy volunteers, six ex-smokers, and two chronic obstructive pulmonary disease patients using both SEM-derived Lm_D and cylinder model (CM)-derived mean chord length (Lm). **Results:** Good agreement between the mean 129 Xe and 3 He Lm_D (mean difference, 2.2%) and Lm (mean difference, 1.1%) values was obtained in all subjects at an empirically optimized 129 Xe $\Delta=8.5$ ms.

Conclusion: Compressed sensing has facilitated single-breath 3D multiple b-value $^{129}\mbox{Xe}$ DW-MRI acquisitions, and results at $^{129}\mbox{Xe}$ $\Delta=8.5$ ms indicate that $^{129}\mbox{Xe}$ provides a viable alternative to $^{3}\mbox{He}$ for whole lung morphometry mapping with either the SEM or CM. Magn Reson Med 79:2986–2995, 2018. © 2017 The Authors Magnetic Resonance in Medicine published by Wiley Periodicals, Inc. on behalf of International Society for Magnetic Resonance in Medicine. This is an open access article under the terms of the Creative Commons Attribution License, which permits use, distribution and reproduction in any medium, provided the original work is properly cited.

Key words: hyperpolarized ¹²⁹Xe; lung morphometry; compressed sensing; stretched exponential model; hyperpolarized ³He

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INTRODUCTION

The apparent diffusion coefficient (ADC) calculated from hyperpolarized ³He diffusion-weighted MRI (DW-MRI) has been shown to be sensitive to changes in lung microstructure (1,2). The non-Gaussian diffusion behavior of the gas in the lungs results in a non-monoexponential signal attenuation with increasing b-value (3). The signal decay is determined by experimental and physiological factors including gas diffusivity, diffusion gradient strengths and timings, and the complexity of alveolar microstructure, which together influence the measurement of ADC (4,5). Theoretical diffusion models, such as the cylinder model (CM) (6,7), stretched exponential model (SEM) (8), and q-space analysis (9), have been proposed to model this non-Gaussian diffusion behavior and derive estimates of alveolar length scales (i.e., morphometry) from multiple b-value DW-MRI acquisitions. Compressed sensing (CS) has enabled multiple b-value ³He DW-MRI for 3D whole lung morphometry mapping in a single breath-hold (10) for quantitative regional assessment of lung microstructure.

With the limited availability of ³He gas (11), ¹²⁹Xe provides a more cost-effective alternative for pulmonary MRI, and with advancements in polarization levels (12,13), recent studies have shown that comparable ventilation and microstructural information can be obtained using both nuclei (14–17). DW-MRI with ¹²⁹Xe is, however, inherently more challenging due to the lower diffusivity and gyromagnetic ratio of ¹²⁹Xe compared with ³He, resulting in longer diffusion gradient times, longer sequence echo time (TE) and repetition time (TR), and lower image SNR. Despite these challenges, theoretical models have been proposed for interpreting the ¹²⁹Xe DW-MRI signal from multiple b-value acquisitions (18), and estimates of alveolar length scales have been derived from healthy subjects and chronic obstructive pulmonary disease (COPD) patients (19-21). However, the multiple b-value interleaves in previous studies were acquired using noncontiguous, relatively thick 2D slices without whole lung coverage and in some cases in separate breath-holds-due to the associated long scan times. Furthermore, to our knowledge, no direct comparison of alveolar length scales derived from application of theoretical diffusion models of ³He and ¹²⁹Xe in vivo have yet been presented.

In this study, compressed sensing acceleration methods developed for 3He (10) were adapted for 3D multiple b-value $^{129}\mbox{Xe}$ DW-MRI in a single breath-hold, and 3D morphometric maps of mean diffusive length scale (Lm_D) were generated using the SEM. Results were compared against equivalent 3D $^3\mbox{He}$ Lm_D morphometric maps acquired with CS, and an optimal $^{129}\mbox{Xe}$ diffusion time of

Table 1 Summary of Subject Demographics and Pulmonary Function Test Data

			FEV ₁	FEV ₁ /	TLC	RV	T _{LCO}	Smoking
Subjects	Age	Sex	(% pred)	FVC (%)	(% pred)	(% pred)	(% pred)	Pack Years
Healthy volunteers								
HV1	26	Male	102.9	81.2	105.6	107.0	_	_
HV2	31	Male	102.0	82.8	100.3	85.0	_	_
HV3	34	Male	77.0	88.0	91.7	107.2	_	_
HV4	31	Male	105.0	87.0	91.6	70.7	_	_
HV5	33	Male	85.1	76.0	84.0	74.1	_	_
Ex-smokers								
ES1	47	Female	86.7	68.8	108.4	105.3	93.0	30.0
ES2	51	Male	95.2	69.2	106.7	100.9	97.2	30.0
ES3	53	Female	90.1	59.7	130.0	139.2	99.2	4.1
ES4	55	Male	107.7	67.5	132.0	127.0	86.5	10.0
ES5	52	Female	90.9	71.0	101.9	106.6	89.3	25.0
ES6	50	Male	111.6	96.1	109.0	89.4	98.4	22.5
COPD patients								
COPD1	62	Female	39.6	36.5	_	_	37.4	_
COPD2	64	Female	69.7	50.0	-	_	61.0	_

 $\Delta\!=\!8.5$ ms was derived empirically. Prospective acquisitions with the optimal ^{129}Xe diffusion time were then benchmarked in healthy volunteers, ex-smokers, and COPD patients with both SEM-derived Lm_D and CM-derived mean chord length (Lm) measurements.

THEORY

The Stretched Exponential Model

The non-Gaussian signal decay from an imaging voxel can be modeled as the superposition of signals with different apparent diffusivities (*D*):

$$\frac{S_b}{S_0} = \int_0^{D_0} p(D)e^{-bD}dD$$
 [1]

where S_0 is the signal when b=0, S_b is the signal corresponding to a non-zero b-value, D are all possible apparent diffusivities between 0 and D_0 (the free diffusion coefficient of $^3{\rm He}$ or $^{129}{\rm Xe}$ in air/N₂), and p(D) is the probability distribution associated with the apparent diffusivities. The non-Gaussian HP gas diffusion signal decay in the lungs can be well described by an SEM fit (Equation [2]) (22).

$$\frac{S_b}{S_0} = e^{[-b \ DDC]^{\alpha}}$$
 [2]

With ³He DW-MRI, the SEM-derived parameters of distributed diffusivity coefficient (DDC) and heterogeneity index (α) have been shown to be sensitive to changes in lung microstructure and are valid over a range of experimental conditions. DDC is dependent on diffusion time, while α has been demonstrated to be insensitive to lung inflation and experimental diffusion time (23). A numerical expression for p(D) can be estimated from the SEM-derived parameters using the approach developed by Berberan-Santos et al. (24):

$$p(D) = \tau_0 \frac{B}{D\tau_0^{(1-\alpha/2)/(1-\alpha)}} \cdot \exp\left[-\frac{(1-\alpha)\alpha^{\alpha/(1-\alpha)}}{D\tau_0^{\alpha/(1-\alpha)}}\right] \cdot f(D),$$

where τ_0 is 1/DDC, and f(D) is defined by

$$f(D) = \begin{cases} 1/[1 + C(D\tau_0)^{\delta}], & \delta = \alpha(0.5 - \alpha)/(1 - \alpha), & \alpha \le 0.5, \\ [1 + C(D\tau_0)^{\delta}], & \delta = \alpha(\alpha - 0.5)/(1 - \alpha), & \alpha > 0.5, \end{cases}$$
[4]

The parameters B and C are functions related to α , and parameters at specific α values can be found in Table 1 of Berberan-Santos et al. (24). Interpolation can be used to derive the corresponding parameters B and C for other α values. The expression for p(D) can subsequently be related to a distribution of diffusion length scales $p(L_D)$ associated with the different apparent diffusivities through the 1D diffusion equation $L_D = (2D\Delta)^{1/2}$ (i.e., root mean squared displacements, where Δ is the diffusion time). The $p(L_D)$ distributions should then represent the distribution of microscopic dimensions of the airways (i.e., the diffusion-restricting boundaries) contained within a given voxel. These distributions can then be used to calculate the mean diffusion length scale (Lm_D) as a quantitative estimate of the mean acinar airway dimensions within a given voxel. The Lm_D metric should therefore be analogous to the calculation of mean linear intercept length (L_x) from histology.

This method of calculating Lm_D differs from the method used to derive mean chord length (Lm) with the CM. In the CM, the underlying assumptions are that the acinar airways are considered cylindrical objects and thus the HP gas diffusion signal can be described by two anisotropic diffusion coefficients, longitudinal (D_L) and transverse (D_T). Phenomenological expressions were empirically optimized from Monte Carlo simulations to relate D_L and D_T to the cylindrical lung airway parameters, outer airway radii (R) and alveolar sleeve depth (h) (6,25). Lm is subsequently derived from the alveoli surface area and volume based upon the geometrical parameters of R and h (7).

METHODS

All in vivo MRI experiments were performed under the approval of the UK National Research Ethics Committee

and the local National Health Service research office. All CS simulations and lung morphometry calculations were implemented in-house using MATLAB (MathWorks, Natick, Massachusetts, USA) software. The signal-to-noise ratio (SNR) for each dataset was computed in the magnitude images (b = 0) by dividing the mean signal of the entire segmented lung region by a region of background noise corrected for Rician distribution bias. It should be noted that SNR calculated from CS images present a biased measure of SNR, due to the denoising process associated with CS reconstruction.

3D Multiple b-Value 129Xe DW-MRI with CS

A fully sampled 3D 129Xe DW-MRI dataset was acquired from a healthy male volunteer (HV1) on a 1.5 T (GE HDx) MR scanner using a flexible quadrature transmit/receive vest coil (Clinical MR Solutions, Brookfield, Wisconsin, USA) which was tuned to the Larmor frequency of ¹²⁹Xe at 1.5 T (17.66 MHz). All lung imaging was performed at a lung volume of functional residual capacity plus 1L following inhalation of a dose of 800 mL enriched Xe [86% 129 Xe, $\sim 30\%$ polarization (12,13)] mixed with 200 mL of N₂. Image acquisition parameters were: 3D spoiled gradient echo sequence; $2 \times \text{interleaves}$ (b = 0, 12 s/cm²); elliptical-centric phase encoding; in-plane resolution = 64×52 (6.25 mm pixel dimension); 18 effective coronal slices (15 mm slice thickness); field of view = $40 \times 32.5 \times 27 \text{ cm}^3$; TE/TR = 11.2/14.4 ms; diffusion time (Δ) = 5 ms (diffusion gradient strength = 22.7 $mT/m, \ ramp \ time = 0.3 \ ms, \ plateau \ time = 3 \ ms, \ gap$ between lobes = 1.4 ms); flip angle = 2.2° ; bandwidth = ± 6.97 KHz.

 $^{129}\mathrm{Xe}$ $\Delta\!=\!5$ ms was first chosen as it corresponds to the diffusion time originally proposed for $^{129}\mathrm{Xe}$ lung morphometry with the CM (18). This time was derived theoretically such that acinar airway geometrical parameters from the CM for $^{129}\mathrm{Xe}$ would be the same as those obtained with $^3\mathrm{He}$ (18), and these values have been subsequently used in 2D $^{129}\mathrm{Xe}$ DW-MRI experimental studies (20,21). Retrospective CS simulations of the fully sampled dataset with acceleration factors (AF) between 2 and 5 were implemented using the methodology described previously for $^3\mathrm{He}$ (10). The Wilcoxon signed-rank test was employed to assess differences in fully sampled and retrospectively reconstructed ADC maps for each AF on a pixel-by-pixel basis.

The optimum k-space sampling pattern for three-fold undersampling was chosen based on the simulation results and was used for prospective acquisition of 3D ¹²⁹Xe multiple b-value DW-MRI data from four healthy volunteers (HV1, HV2, HV3, HV4). Prospective data were acquired with an inhaled gas mixture of 750 mL 129 Xe and 250 mL nitrogen, with imaging parameters as for the fully sampled acquisition other than the following: four interleaves (b = 0, 12, 20, 30 s/cm²); TE/TR = 11.7/15.0 $\Delta = 5$ (maximum ms diffusion strength = 31.9 mT/m, ramp time = 0.3 ms, plateau time-= 3.5 ms, gap = 0.9 ms); and flip angle $= 2.7^{\circ}$. The AF of 3 reduces the scan time from 57 to 19 s. ¹²⁹Xe Lm_D maps were calculated using the SEM, and results were compared with Lm_D maps derived from the same volunteers'

lungs using 3He DW-MRI as described by Chan et al. (10). 3He Lm $_D$ at 3He $\Delta=1.6$ ms was chosen for comparison because healthy and COPD Lm $_D$ values derived at this diffusion time have been demonstrated to match histologically derived healthy and COPD mean linear intercept values (26).

Empirical Determination of Optimal ¹²⁹Xe Diffusion Time

With the aim of obtaining the best agreement between ^{129}Xe and ^3He lung morphometry results [rather than simply using the $^{129}\text{Xe}~\Delta=5$ ms proposed by Sukstanskii and Yablonskiy (18)], HV1 was imaged at additional diffusion times ($\Delta=5,7,8,$ and 10 ms). $^{129}\text{Xe}~\Delta=10$ ms was chosen as it corresponds to the same 1D characteristic free diffusion length ($\sqrt{2D_0\Delta}\sim530\,\mu\text{m}$) as experienced in the benchmark ^3He experiment (assuming $D_0^{Xe-air}=0.14~\text{cm}^2/\text{s},~D_0^{He-air}=0.88~\text{cm}^2/\text{s},$ and $\Delta^{He}=1.6$ ms). Each additional scan was acquired with the same gas mixture and b-values as the previous prospective CS acquisitions at $^{129}\text{Xe}~\Delta=5$ ms, and Lm_D maps were calculated from each dataset.

Benchmarking of Empirically Optimized ¹²⁹Xe Diffusion Time

The empirically optimized diffusion time (129 Xe $\Delta=8.5$ ms [see Results]) was then benchmarked against 3 He equivalent measurements for lung morphometry mapping over different ranges of acinar length scales that are experienced with smoking-related emphysema. Five healthy volunteers (age, 31.0 ± 3.1 years), six ex-smokers (age, 51.3 ± 2.7 years), and two COPD patients (age, 63.0 ± 1.4 years, GOLD II-IV) were recruited for this preliminary study. Subject demographics and pulmonary function test (PFT) data for each subject are summarized in Table 1.

Each subject was imaged with 3D multiple b-value ¹²⁹Xe DW-MRI, using 750 mL of inhaled ¹²⁹Xe and the following imaging parameters: TE/TR = 14.0/17.3 ms; maximum DW gradient strength = 32.6 mT/m; $\Delta = 8.5$ ms; ramp time = 0.3 ms; plateau time = 2.3 ms; gap = 5.6ms; and flip angle = 3.1°. Using 129 Xe $\Delta = 8.5$ ms, the duration of three-fold undersampled CS scans was increased by 3 s due to the increased diffusion time. Therefore, four-fold undersampling (AF = 4) was now implemented in the subsequent prospective CS acquisitions to further reduce the breath-hold to 16 s, similar to the 15 s acquisition for ³He (10), and to demonstrate the clinical viability of this sequence. 3D ³He DW-MRI was acquired in same-day scan sessions for all subjects (except for HV1-HV3, for whom ³He data were acquired approximately 1 year previously), with experimental parameters described previously (10). 129Xe and He Lm_D maps were derived and compared in each subject.

Finally, the applicability of $^{129}\text{Xe}~\Delta=8.5$ ms to CM derivations of lung morphometry parameters was assessed. The $^{129}\text{Xe-based}$ CM phenomenological expressions are optimized for $^{129}\text{Xe}~\Delta=5$ ms; however, if the same theoretical free diffusion length is probed with both nuclei (i.e., $\Delta_{\text{He}}=1.6$ ms and $\Delta_{\text{Xe}}=10$ ms), the original $^{3}\text{He-based}$ phenomenological expressions should in theory be applicable for derivation of ^{129}Xe lung morphometry parameters (18). Initial CM analysis of ^{129}Xe DW-MRI data in healthy subjects at $^{129}\text{Xe}~\Delta=8.5$ ms and

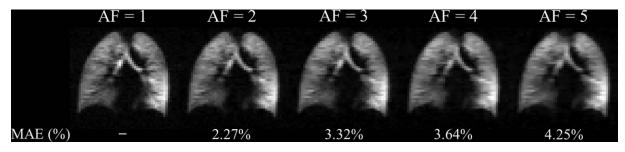


FIG. 1. CS simulation results for 3D ¹²⁹Xe DW-MRI. Reconstructed magnitude image (b = 0) for each AF, with corresponding MAE values (AF = 1; fully sampled dataset [SNR = 25]).

 $^{129}\mathrm{Xe}~\Delta=10$ ms, suggested that, as with the SEM, more consistent $^{129}\mathrm{Xe}$ lung morphometry results were obtained with $^{129}\mathrm{Xe}~\Delta=8.5$ ms (see Discussion). The 3D multiple b-value $^{129}\mathrm{Xe}~\Delta=8.5$ ms was therefore analyzed using the $^3\mathrm{He}\text{-based}$ CM phenomenological expressions (7), and the $^{129}\mathrm{Xe}~\Delta=8.5$ ms was therefore analyzed using the $^3\mathrm{He}$ -based CM phenomenological expressions (7), and the $^{129}\mathrm{Xe}$ mean chord length (Lm) was hence derived and compared with $^3\mathrm{He}\text{-derived}$ Lm for each subject in the preliminary study.

RESULTS

3D Multiple b-Value ¹²⁹Xe DW-MRI with CS

The SNR of the fully sampled 129 Xe DW-MRI dataset was 25. Optimal k-space undersampling patterns for different AFs were determined through CS simulations. Retrospectively reconstructed datasets from each optimal undersampling pattern showed a small increase in mean absolute error (MAE) of normalized signal intensity value for the b=0 data (from 2.27% at AF=2 to 4.25% at AF=5), indicating a good preservation of image details

with increased AF (Fig. 1). Whole lung mean ADC histograms and single slice ADC maps generated from the reconstructed CS datasets also demonstrated a good preservation of quantitative information and low MAE $_{\rm ADC}$ (Fig. 2). Wilcoxon signed-rank tests for each AF found no significant differences (P > 0.05) between CS-reconstructed and fully sampled ADC maps on a pixel-by-pixel basis, confirming preservation of quantitative information and indicating that CS is suitable for 3D 129 Xe multiple b-value DW-MRI.

Prospective 3D 129 Xe multiple b-value DW-MRI was acquired in four healthy volunteers with AF=3 and 129 Xe $\Delta=5$ ms, and resulting ADC and Lm_D maps were compared with previously calculated lung microstructural maps acquired using 3D 3 He multiple b-value DW-MRI. Mean SNR for the four prospective 129 Xe datasets was 40. The prospective CS whole lung mean 129 Xe ADC value for volunteer HV1 (0.0329 cm²/s) was very similar (+1.2% difference) to the fully sampled mean ADC value (0.0325 cm²/s) that was obtained for CS simulations.

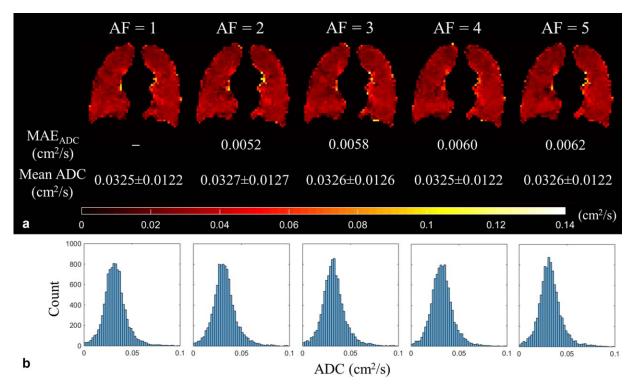


FIG. 2. ADC results for 3D ¹²⁹Xe DW-MRI CS simulations. (a) Single-slice ADC maps with the MAE_{ADC}, and mean global ADC values for each AF. (b) Corresponding whole lung ADC histograms for each AF.

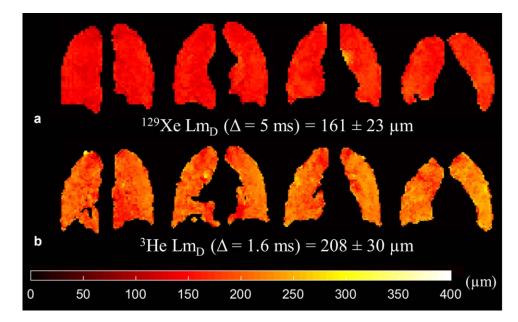


FIG. 3. Prospective CS results for a healthy volunteer (HV1) (SNR = 30). (a) Example ¹²⁹Xe Lm_D maps derived from 3D multiple b-value ¹²⁹Xe DW-MRI. (b) Example ³He Lm_D maps in comparative slices demonstrate the mismatch in Lm_D values between the two nuclei.

Example ^{129}Xe and ^{3}He Lm_D maps from the comparative slices in HV1 are shown in Figure 3 and a summary of mean ADC and Lm_D values for each volunteer is provided in Table 2. At ^{129}Xe $\Delta = 5$ ms, mean ^{129}Xe Lm_D values for all subjects were $\sim\!\!50\,\mu\text{m}$ smaller than the corresponding mean ^{3}He values.

Empirical Determination of Optimal ¹²⁹Xe Diffusion Time

A strong positive linear correlation ($r\!=\!0.998$, $P\!<\!0.001$) was established between ^{129}Xe Lm_D and diffusion times, and at $\Delta\!=\!8.5$ ms the ^{129}Xe Lm_D value best matched the volunteer's ^3He Lm_D value (Fig. 4a). In contrast to Lm_D, mean ^{129}Xe ADC decreased with increasing diffusion time; a 12.5% decrease in mean ^{129}Xe ADC was observed from $\Delta\!=\!5$ ms to 10 ms. The relationship between ^{129}Xe ADC and diffusion time was nonlinear, however, and best fitted a logarithmic function (R $^2\!=\!0.961$) (Fig. 4b).

Benchmarking of Empirically Optimized ¹²⁹Xe Diffusion Time

The mean 3 He and 129 Xe SNR of the b=0 image for all preliminary study subjects was 32 and 65, respectively. A summary of 129 Xe Lm_D and corresponding 3 He Lm_D values are shown in Table 3. An improved matching of mean 129 Xe and 3 He Lm_D was obtained with the empirically optimized diffusion time, and this is visible in example Lm_D maps from three representative subjects (Fig. 5). A difference in Lm_D of less than 7% was

observed in all subjects, with a mean difference (129 Xe 3 He) in all subjects of -2.2%. Figure 6a shows a very strong correlation (r=0.987, P<0.001) between individual lung 3 He and 129 Xe mean Lm_D values in all subjects. Lm_D values fall around the line of equality, and this good agreement was confirmed by Bland-Altman analysis (Fig. 6b) of individual lung Lm_D values, where a mean bias of -2.1% ($-4.8\,\mu$ m) for 129 Xe mean Lm_D with a 95% confidence interval of -6.7% to 2.5% (-14.8 to $5.2\,\mu$ m) was observed.

The mean difference in $^{129}\mathrm{Xe}$ and $^{3}\mathrm{He}$ CM Lm values was +1.1% (Table 3), demonstrating a similar level of agreement in CM-derived Lm at $^{129}\mathrm{Xe}$ $\Delta=8.5$ ms as SEM-derived Lm_D. $^{3}\mathrm{He}$ and $^{129}\mathrm{Xe}$ CM single lung Lm values were also strongly correlated ($r=0.980,\,P<0.001$) (Fig. 6c), and Bland-Altman analysis of mean single lung Lm values indicates a mean bias of +2.3% in $^{129}\mathrm{Xe}$ Lm values with a 95% confidence interval of -15.2% to 19.9% (Fig. 6d).

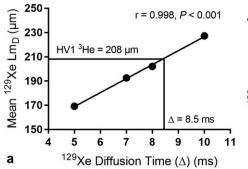
DISCUSSION

3D Multiple b-Value ¹²⁹Xe DW-MRI with CS

CS has enabled the acquisition of 3D multiple b-value ^{129}Xe DW-MRI in a single breath-hold for the generation of whole lung maps of alveolar diffusion length scale with a voxel size of $6.25\times6.25\times15~\text{mm}^3.$ Retrospectively undersampled ^{129}Xe datasets demonstrated good preservation of image details and microstructural information

Table 2 Summary of Whole Lung Mean ADC and Lm_D Values for Four Healthy Volunteers Derived from Prospective 3D Multiple b-Value ¹²⁹Xe and ³He DW-MRI With CS

Subjects	129 Xe ADC (cm 2 /s) ($\Delta = 5$ ms)	129 Xe Lm _D (μ m) (Δ = 5 ms)	3 He ADC (cm 2 /s) ($\Delta = 1.6$ ms)	3 He Lm _D (μ m) (Δ = 1.6 ms)
HV1	0.033 ± 0.012	161 ± 23	0.182 ± 0.085	208 ± 30
HV2	0.039 ± 0.012	176 ± 20	0.196 ± 0.077	223 ± 24
HV3	0.030 ± 0.011	157 ± 19	0.166 ± 0.068	205 ± 23
HV4	0.030 ± 0.011	156 ± 18	0.169 ± 0.065	210 ± 20



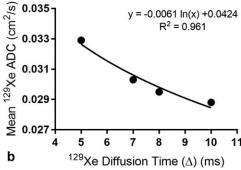


FIG. 4. Global mean 129 Xe Lm_D and ADC results at different 129 Xe diffusion times for one healthy volunteer. (a) A strong linear dependence in 129 Xe diffusion time and mean 129 Xe Lm_D value was observed. At 129 Xe Δ =8.5 ms, the 129 Xe Lm_D matches the volunteer's corresponding 3 He Lm_D value. (b) Mean 129 Xe ADC decreases with increasing diffusion time in a nonlinear logarithmic relationship.

with increased undersampling. MAE and MAE_{ADC} values from ¹²⁹Xe CS simulations were similar to those reported with ³He (10). The presence of image blurring in the fully sampled 129Xe images is likely the result of elliptical-centric phase encode ordering used with ¹²⁹Xe in contrast to sequential encoding used previously with ³He. Elliptical-centric phase encoding maximizes SNR at the consequence of increased image blurring with a RF depolarization k-space filter that originates from the center of k-space (27). The full width at half maximum values of retrospectively undersampled ¹²⁹Xe ADC histograms decreased with AF; this trend matches the results of ³He CS simulations (10) and demonstrates decreased spatial heterogeneity associated with the denoising reconstruction process of CS. However, this loss of spatial heterogeneity did not result in a statistically significant difference between fully sampled ADC and undersampled CS ADC maps.

Prospective three-fold undersampled 3D multiple b-value ^{129}Xe DW-MRI was acquired in four healthy volunteers at $\Delta\!=\!5$ ms. The difference of $\!+\,1.2\%$ between CS

 $(0.0329\,\mathrm{cm^2/s})$ and fully sampled mean $^{129}\mathrm{Xe}$ ADC $(0.0325\,\mathrm{cm^2/s})$ for one volunteer (HV1) was similar to the small differences we reported previously between fully sampled and CS undersampled 2D and 3D $^3\mathrm{He}$ ADC values (10,28). The whole lung mean $^{129}\mathrm{Xe}$ ADC value for all four healthy volunteers ($\sim 0.033\,\mathrm{cm^2/s}$) was also consistent with previously reported healthy subject ADC values, with b=12 s/cm² at 1.5 T (29). The observed mean Lm_D mismatch of approximately 50 µm between $^3\mathrm{He}$ and $^{129}\mathrm{Xe}$ suggests that the $^{129}\mathrm{Xe}$ diffusion time of $\Delta=5$ ms, previously proposed for in vivo lung morphometry with the CM (18), is not applicable for $^{129}\mathrm{Xe}$ lung diffusion length scale measurements derived from the SEM.

Empirical Determination of Optimal ¹²⁹Xe Diffusion Time

Mean 129 Xe ADC values (at b=12 s/cm²) decreased non-linearly with increasing diffusion time; a trend observed previously in 3 He ADC measurements (4,30). The logarithmic relationship observed between 129 Xe ADC and diffusion time also matches the trend observed for 3 He

Table 3 Summary of 129 Xe Whole Lung SEM-Derived Lm_D and CM-Derived Lm Values for Healthy Volunteers, Ex-smokers, and COPD Patients Acquired With AF = 4 and 129 Xe Δ = 8.5 ms and Their Corresponding 3 He Mean Lung Morphometry Values (AF = 3, 3 He Δ = 1.6 ms)

	Stre	etched Exponentia	al Model	Cylinder Model (³ He-based)			
Subjects	129Xe Lm _D (μm)	³ He Lm _D (μm)	Lm _D Difference (%)	129Xe Lm (μm)	³ He Lm (μm)	Lm Difference (%)	
Healthy volunteers							
HV1	205	208	-1.4	183	183	0.0	
HV2	218	224	-2.7	222	210	+5.6	
HV3	206	205	+0.5	196	171	+12.5	
HV4	200	210	-4.8	173	178	-3.1	
HV5	192	205	-6.3	164	170	-3.6	
Mean HV	204	210	-2.9	188	182	+2.3	
Ex-smokers							
ES1	232	234	-0.9	259	222	+14.3	
ES2	230	234	-1.7	254	240	+5.3	
ES3	234	236	-0.8	266	250	+6.0	
ES4	245	246	-0.4	326	335	-2.7	
ES5	221	231	-4.3	222	226	-2.1	
ES6	217	215	+0.9	217	201	+7.2	
Mean ES	230	233	-1.2	257	246	+4.7	
COPD patients							
COPD1	317	323	-1.9	639	671	-5.0	
COPD2	251	263	-4.6	318	381	-19.8	
Mean COPD	284	293	-3.2	478	526	-12.4	
Overall mean	_	_	-2.2	_	_	+1.1	

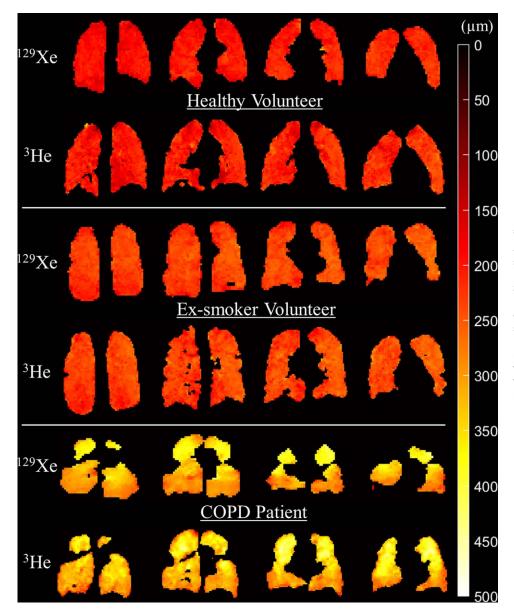


FIG. 5. Comparison of 129 Xe and 3 He example slice Lm_D maps for a representative healthy, exsmoker, and COPD subject. 129 Xe Lm_D maps derived using 3D multiple b-value 129 Xe DW-MRI at an empirically optimized diffusion time $\Delta = 8.5$ ms demonstrate good agreement with 3 He Lm_D maps. 3D 129 Xe DW-MRI mean SNR was 37, 44, 80 for the representative healthy volunteer, ex-smoker, and COPD patient, respectively.

ADC (30). The SEM-derived Lm_D values exhibited a strong positive linear dependence with Δ over the range of 5–10 ms. The dependence of Lm_D on Δ reflects the changes in the theoretical characteristic free diffusion lengths probed for each experiment. At $\Delta=10$ ms, corresponding to the characteristic free diffusion length of 129 Xe ($\sqrt{2D_0\Delta}=530\,\mu\text{m}$) which is identical to the free diffusion length of 3 He in air for the diffusion times used by Chan et al. (10), a mismatch of Lm_D values was still observed in the data from three healthy volunteers (Fig. 7).

This mismatch suggests that even at the same characteristic free diffusion length there may be inherent differences in the specific diffusion dephasing regime of the respective gas in the lung alveoli which makes this assumption of Gaussian relation between diffusion length and diffusion time inexact. The differences in diffusion dephasing regime stems from intrinsic properties (i.e., gyromagnetic ratio and diffusivity) of each gas, and

thus leads to different mechanisms that contribute to non-Gaussian diffusion signal behaviors that are not accounted for in the calculation of characteristic free diffusion length. For example, differences in the diffusional dephasing regime due to microscopic background susceptibility gradients may exist between $^{129}\mathrm{Xe}$ and $^{3}\mathrm{He}$ at the same field strength due to the smaller gyromagnetic ratio of $^{129}\mathrm{Xe}$. These effects on diffusive length scales are similar to the effect of different B_0 field strengths on $^{3}\mathrm{He}$ ADC values (5).

Benchmarking of Empirically Optimized ¹²⁹Xe Diffusion Time

The decision to further accelerate with four-fold undersampling was motivated by the need to reduce the breath-hold duration incurred with 129 Xe diffusion times > 5 ms. To verify that good agreement in Lm_D values was obtained with three- and four-fold undersampling,

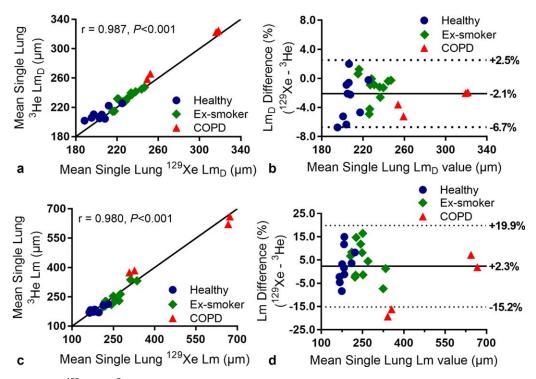


FIG. 6. (a) Comparison of 129 Xe and 3 He mean single (left and right) lung Lm_D values for all subjects. The solid line represents the line of equality. (b) Bland-Altman analysis of mean single lung Lm_D values. The percentage difference (129 Xe - 3 He) between the two nuclei is plotted against the mean single lung Lm_D value of the two nuclei for all subjects. The solid line represents the mean percentage difference, and the two dotted lines indicate the 95% (± 1.96 SD) difference range. (c) Comparison of 129 Xe and 3 He mean single lung Lm values derived from the cylinder model for all subjects. Both 129 Xe and 3 He data were analyzed with the 3 He-based cylinder model. The solid line represents the line of equality. (d) Corresponding Bland-Altman analysis of mean single lung Lm values.

all five healthy volunteers were imaged with an additional AF = 3 129 Xe CS acquisition at 129 Xe Δ = 8.5 ms. A slice-by-slice comparison of mean Lm_D values for the five healthy volunteers was performed, and Bland-Altman analysis confirmed a mean bias of +1.5% $(+2.9 \,\mu\text{m})$ for AF=4. The 95% confidence interval of -6.9% to +10.0% (-13.4 to 19.3 µm) was within typical standard deviation values of lung LmD values in healthy volunteers. This slight increase in mean slice Lm_D values obtained with AF=4 is likely the result of CS reconstruction error associated with increased undersampling. In addition, the broad 95% confidence interval range could also be explained by inexact coregistration of image slices due to slight changes in subject position between the AF = 3 and AF = 4 scan sessions. However, the small increase in LmD justifies that implementation of AF = 4 in prospective acquisitions with 129 Xe $\Delta = 8.5$ ms. The reduction of scan time to within 16 s is more tolerable for a wider range of subjects, therefore AF = 4 will be used in all subsequent 3D multiple b-value ¹²⁹Xe DW-MRI acquisitions.

Using the empirically optimized diffusion time, $^{129}\text{Xe-}$ derived Lm_D values demonstrated improved matching with ^3He Lm_D at ^{129}Xe $\Delta=8.5$ ms than at ^{129}Xe $\Delta=5$ ms. The mean difference between whole lung ^{129}Xe and ^3He Lm_D values across all subjects was -2.2%, and the mean bias in individual lung ^{129}Xe Lm_D values was -2.1%. ^{129}Xe $\Delta=8.5$ ms was derived from preliminary data, and this small bias may suggest that a different optimal diffusion time (slightly longer than $\Delta=8.5$ ms) could be used

to bring the bias toward 0%. Considering $\Delta\!=\!8.5$ ms Lm_D for HV1, a ^{129}Xe $\Delta\!=\!9.1$ ms was found to match the volunteer's ^3He Lm_D value (Fig. 7). Additionally, when the previous ^{129}Xe $\Delta\!=\!5$ and 8.5 ms results for HV2 and HV3 are considered in conjunction with an additional acquisition at ^{129}Xe $\Delta\!=\!10$ ms, a similar optimal diffusion time of around 9 ms was obtained as well (Fig. 7).

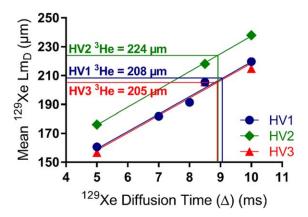


FIG. 7. Mean ^{129}Xe Lm_D results at different ^{129}Xe diffusion times for three healthy volunteers. A strong linear dependence in ^{129}Xe diffusion time and mean ^{129}Xe Lm_D value was obtained for HV1 (r=0.98, P=0.015). When the $\Delta\!=\!8.5$ ms results for HV1 was considered, the diffusion time $\Delta\!=\!9.1$ ms corresponded to the subject's ^3He Lm_D value. A similar diffusion time trend was observed in the other two healthy volunteers (HV2 and HV3).

Nevertheless, the observed bias of -2.1% is equivalent to the same-day reproducibility error (2.1%) (31) of Lm values calculated from multiple b-value $^3{\rm He}$ DW-MRI using the CM. This indicates that any mismatch between $^3{\rm He}$ and $^{129}{\rm Xe}$ Lm_D values at the $^{129}{\rm Xe}$ $\Delta\!=\!8.5$ ms is of the order of same-day reproducibility error, and we conclude that comparable lung morphometry maps can be obtained with $^{129}{\rm Xe}$.

One limitation of this study is that the $^{129}\mathrm{Xe}$ diffusion time was optimized based upon the $\mathrm{Lm_D}$ results from healthy volunteers only. In subjects with emphysematous changes to alveolar length scales, a different relationship between $^{129}\mathrm{Xe}$ $\mathrm{Lm_D}$ and diffusion time may exist. However, the strong agreement between $^{129}\mathrm{Xe}$ and $^{3}\mathrm{He}$ $\mathrm{Lm_D}$ results from the subsequent prospective acquisitions in healthy volunteers, ex-smokers, and COPD patients suggests that $^{129}\mathrm{Xe}$ $\Delta=8.5-9$ ms is valid across a range of alveolar sizes subject to age and smoking-related emphysema.

The empirically optimized ¹²⁹Xe $\Delta = 8.5$ ms used in our study is significantly longer than the diffusion time used in other 129Xe lung morphometry studies. In Sukstanskii and Yablonskiy (18), 129 Xe $\Delta = 5$ ms was chosen and CM phenomenological expressions for acinar airway geometrical parameters were also recalibrated for ¹²⁹Xe such that lung morphometry results matched those of ³He. However, it was noted that if the same theoretical free diffusion length is probed with both nuclei, the ³Hebased phenomenological expressions can be applied to derive ¹²⁹Xe lung morphometry parameters (18). In a small subset of the preliminary study cohort (HV1–HV4), the assumption that, like the SEM, the CM will yield more comparable lung morphometry results at $^{129}\mathrm{Xe}$ $\Delta = 8.5$ ms than with $^{129}\mathrm{Xe}$ $\Delta = 10$ ms was explored. $^{129}\text{Xe}~\Delta\!=\!8.5$ and 10 ms data were analyzed with $^{3}\text{He}\text{-}$ based CM parameters, and derived Lm was compared with ³He-derived Lm values. A mean difference of 4.3% was obtained between 129 Xe $\Delta = 8.5$ ms Lm and 3 He Lm, whereas at 129 Xe $\Delta = 10$ ms the difference was larger (11.5%). These results, albeit in a small subset of subjects, support the implementation of the ³He-based CM with 129 Xe DW-MRI at 129 Xe $\Delta = 8.5$ ms.

The mean ³He Lm values for healthy volunteers $(\sim 180 \,\mu\text{m})$, ex-smokers $(\sim 250 \,\mu\text{m})$, and COPD patients $(\sim 500 \,\mu\text{m})$ were consistent with previously reported ^{3}He Lm values (7,32,33). The mean ¹²⁹Xe Lm for ex-smokers (with $^{129}\text{Xe}\ \Delta = 8.5\ \text{ms}$) are also in agreement with previous ¹²⁹Xe Lm values reported at 3 T obtained with ¹²⁹Xe $\Delta = 5$ ms (20,21). The ¹²⁹Xe Lm for the GOLD II COPD subject (318 µm) is also comparable to the ¹²⁹Xe Lm (~350 μm) reported in COPD patients (GOLD I-III) (20,21). When 129 Xe Lm from the 129 Xe $\Delta = 8.5$ ms data was evaluated with ³He-based CM, an overall mean difference of +1.1% and +2.3% was obtained for whole lung and individual lung 129Xe and 3He Lm values, respectively. This small bias is of a similar magnitude as that observed with SEM-derived Lm_D and therefore suggests that 129Xe lung morphometry results obtained with 129 Xe $\Delta = 8.5$ ms are comparable to 3 He results analyzed with both the cylinder and stretched exponential models.

CONCLUSIONS

With limited availability of ³He, there is a strong motivation to evaluate functional and structural information that can be derived from the readily available and cheaper ¹²⁹Xe gas isotope. Compressed sensing has facilitated acquisition of single-breath 3D multiple b-value ¹²⁹Xe DW-MRI for whole lung morphometry mapping. SEM-derived Lm_D demonstrated a linear dependence with diffusion time, and the best agreement between $^{129}\mbox{Xe}$ and $^{3}\mbox{He}\mbox{ Lm}_{\mbox{\scriptsize D}}$ results was obtained with an empirically optimized 129 Xe $\Delta = 8.5$ ms. Prospective CS acquisitions were used to validate 129 Xe $\Delta = 8.5$ ms in healthy volunteers, ex-smokers, and COPD patients, and a strong agreement (mean Lm_D bias of -2.2%) in ¹²⁹Xe and ³He Lm_D values was obtained. A similar level of agreement (mean Lm bias of +1.1%) was obtained with CM-derived Lm, indicating that ¹²⁹Xe DW-MRI acquired with ¹²⁹Xe $\Delta = 8.5$ ms is a viable alternative to ³He for 3D whole lung morphometry assessment with both cylinder and stretched exponential models.

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