

Cortical and subcortical changes in Alzheimer's disease: a longitudinal and quantitative MRI study

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29 Abstract

30 Quantitative MRI provides important information about tissue properties in 31 brain both in normal ageing and in degenerative disorders. Although it is well 32 known that those with Alzheimer's disease (AD) show a specific pattern and 33 faster rate of atrophy than controls, the precise spatial and temporal patterns 34 of quantitative MRI in AD are unknown. We aimed to investigate 35 neuroimaging correlates of AD using serial quantitative MRI. In our study, 36 twenty-one subjects with AD and thirty-two similar-aged healthy controls 37 underwent two serial MRI scans at baseline and 12 months. Tissue 38 characteristics were captured using two guantitative MRI parameters: 39 longitudinal relaxation time (qT1) and transverse relaxation time (qT2). The 40 two groups (AD and controls) were statistically compared using a voxel based 41 quantification (VBQ) method based on Matlab and SPM8. At baseline, 42 subjects with AD showed a significant reduction of gT1 and gT2 compared to 43 controls in bilateral temporal and parietal lobes, hippocampus, and basal 44 ganglia. This pattern was also observed at follow-up. Longitudinally, in AD we 45 found a significant increase rather than further reduction of qT1 and qT2 from 46 the baseline in bilateral hippocampus, thalamus and right caudate nucleus. In 47 addition, the longitudinal change of qT1 in left hippocampus was negatively 48 correlated with cognitive decline in AD over the 1-year period, and the general 49 disease severity significantly predicted the amount of increase of gT1 in 50 bilateral hippocampus over 12 months. The longitudinal change of qT2 in left 51 parahippocampus correlated with change in neuropsychiatric features over 52 time. In summary, quantitative MRI parameters were reduced in AD cross-53 sectionally, but increased over time, showing distinct spatiotemporal patterns

54	from the atrophy in AD. We also showed the clinical relevance of quantitative
55	MRI parameters, indicating their potential promise as new imaging markers in
56	AD.
57	
58	(286 words)
59	
60	Keywords quantitative MRI, VBQ, Alzheimer's disease, amyloid, relaxometry,
61	early diagnostics

63 Introduction

64 One of the main current research focuses on Alzheimer's disease (AD) is 65 early intervention, thus, there is a pressing need for reliable biomarkers for 66 early AD detection. Existing biomarkers include cerebrospinal fluid (CSF), 67 PET/SPECT imaging of neural metabolism and β -amyloid binding, as well as 68 structural and functional MRI [1]. Among these techniques, MRI is 69 noninvasive, so provides a powerful and safe tool for research and clinical 70 diagnosis / screening, both of which are important for investigating the 71 underlying neuropathology and early detection [2]. 72 73 It has been shown that MRI not only reveals changes in brain volume and 74 macrostructure, but also microstructural alterations in brain tissue integrity 75 and its biochemical environment [3]. An emerging neuroimaging technique is 76 quantitative MRI (qMRI) based on the physical measurement of longitudinal 77 (qT1) and transverse (qT2) relaxation times. (Here we shall refer to these 78 quantitative measurements as qT1 and qT2 to distinguish them from the more 79 common gualitative radiological T1 or T2 weighted scans). In general, gT1 is 80 correlated with water content and the level of myelination, and qT2 is related 81 to chemically determined brain iron concentration [3].

82

Quantitative MRI provides important information about tissue properties in
brain both in normal ageing [4,5], degenerative disorders such as Parkinson's
disease [6], AD and dementia with Lewy bodies (DLB) [7], and neuronal loss
due to brain and spinal cord injury [8]. In our previous study of DLB using
qMRI, we demonstrated that the spatial pattern in the changes of qT1 and

88	qT2 was different from the pattern of atrophy, thus quantitative MRI may
89	provide incremental benefit over and above that of structural MRI [7]. We also
90	argue that quantitative MRI may indirectly detect neuronal and molecular
91	changes in AD that precede the structural brain damage and clinical
92	impairments decades in time [2]. Although it is well known that those with AD
93	show a specific pattern and faster rate of atrophy than controls, the precise
94	spatial and temporal patterns of quantitative MRI alteration in AD are
95	unknown.

In this study, we aimed to investigate neuroimaging correlates of AD using serial quantitative MRI. In particular, we evaluated maps of qT1 and qT2 in grey matter comparing these parameters between the AD and the similarly aged control groups using the voxel-based quantification (VBQ) approach [4] both cross-sectionally and longitudinally. In addition, we explored the clinical relevance of quantitative MRI changes over a 12-month period.

103

104 Materials and Methods

105 Subjects, assessment and diagnosis

106 Thirty-six subjects with probable AD [9] over the age of 60 were recruited from

107 a community dwelling population of patients referred to local Old Age

108 Psychiatry, Geriatric Medicine or Neurology Services. Thirty-five similarly

aged control subjects were recruited from relatives and friends of subjects

110 with dementia or volunteered via advertisements in local community

111 newsletters. Twenty-one AD subjects and 32 controls underwent MR imaging

at both baseline and follow-up and are included in the analyses reported here.

113 These subjects underwent clinical and neuropsychological evaluations at

baseline and follow-up at 1 year. (The rest of subjects were not scanned at

follow-up, thus excluded from the analysis.)

116

The research was approved by Newcastle & North Tyneside 1 Research 117 118 Ethics Committee (No. 05/Q0905/217). All subjects or, where appropriate, 119 their nearest relative, provided written informed consent. Assessment of 120 global cognitive measures at both baseline and follow-up assessments 121 included the Cambridge Cognitive Examination (CAMCOG) [10], which 122 incorporates the Mini-Mental State Examination (MMSE) [11]. Motor 123 parkinsonism was evaluated with the Unified Parkinson's Disease Rating 124 Scale Part III (UPDRS-III) [12]. For subjects with dementia, neuropsychiatric features were evaluated with the Neuropsychiatric Inventory (NPI) [13]. 125

126

127 MRI data acquisition

128 Participants underwent MRI scanning on a 3T Philips Achieva MRI system 129 with an 8-channel receiver head coil at both baseline and 12-month follow-up. 130 Structural images were acquired using a T1 weighted volumetric sequence 131 (3D MPRAGE, sagittal acquisition aligned with the AC-PC line, 1mm isotropic 132 resolution, matrix 240×240×180, TR=9.6ms, TE=4.6ms, flip angle=8°, SENSE factor 2). In addition, a B0 field-map using a dual echo 3D GRE (2mm 133 isotropic resolution, matrix 128×128×72, TR=27ms, TE=2.6/6.1ms) was 134 135 acquired.

Quantitative mapping of tissue qT1 and qT2 relaxation times was performed
using custom designed MRI sequences developed in-house under a research
agreement with Philips Medical Systems.

140

141 Fast qT1 mapping was based on the inversion recovery (IR) methods 142 originally published by Ordidge et al [14] and expanded by Clare and Jezzard 143 [15]. The sequence imaged 72 axial slices spanning the brain, which were 144 grouped into 5 consecutive slabs each of thickness 24mm. For each slab a 145 slice selective adiabatic (sech) inversion pulse was applied to invert the 146 magnetisation ensuring that the region of full inversion encompassed the 24 147 mm thick section of interest. This inversion was followed by slice selective 148 single shot EPI readout of 12 contiguous slices of 2 mm thickness equally 149 spaced across the slab. The first slice was imaged 250ms post inversion and 150 subsequent slices every 205 ms thereafter. During the repetition time (TR) of 151 15000ms each slab was inverted and imaged with a slab order of 1,3,5,2,4 to 152 minimise interaction between slices. In this way the time between inverting 153 adjacent slabs was 6000ms, sufficient to allow full relaxation of brain tissue. 154 The sequence was repeated 12 times and on each repetition the order of 155 acquired slices within each slab was permuted by one position, for example 156 1,2,3,4,5,6,7,8,9,10,11,12 157 2,3,4,5,6,7,8,9,10,11,12,1 158 3,4,5,6,7,8,9,10,11,12,1,2 159 etc

such that the at the end of acquisitions every slice had been imaged at each

161	of the 12 inversion times. Total scan time was therefore 180s for the
162	complete IR series in 72 slices with isotropic 2mm resolution. This sequence
163	is shown schematically in Figure 1.
164	
165	Insert Figure 1 here
166	
167	Calculation of qT1 maps used a purpose written algorithm in Matlab, which
168	reordered the data into incremental inversion order for each slice and then
169	performed voxel-wise non-linear least squares fitting to the standard 3
170	parameter model for the inversion recovery experiment:
171	

$$S(T_{IR}) = S_o(1 - \alpha e^{\frac{-T_{IR}}{qT_1}})$$

181

173 where T_{IR} is the inversion time, $S(T_{IR})$ is the signal value or the data obtained 174 from the inversion recovery experiment, qT1 is the longitudinal relaxation 175 time, S_o is the proton density and α is the effective inversion efficiency . qT1, 176 S_o and α were computed pixel-wise from the fitting process. Ideally α is 177 expected to be 2 but it was allowed to be a free variable in the fitting in order 178 to increase the accuracy of the computed qT1. The 3D images of proton 179 density S_o , qT1, and the goodness of fit were saved for evaluation. 180

readout based around a Gradient and Spin Echo Imaging sequence. The

183 sequence collected 8 spin echoes with equal spacing of 20ms and 5 gradient

Fast qT2 mapping used a multi-spin echo sequence with segmented EPI

recalled echoes per spin echo (EPI factor 5) to accelerate image collection.

185 Repetition time was set to 4700ms and 72 slices were collected in standard

186 interleaved acquisition (2mm isotropic resolution, matrix 128×128). Total

187 scan time was 120s.

188

189 Calculation of qT2 maps again used a purpose written algorithm in Matlab,

190 which performed voxel-wise non-linear least squares fitting to the standard 2

191 parameter model for transverse relaxation.

192

$$S(TE) = S_o e^{\frac{-TE}{qT2}}$$

193

where *TE* is the echo time, qT2 is the transverse relaxation time and S_o is the proton density. qT2, and S_o were computed pixel-wise from the fitting process. The 3D images of proton density S_o , qT2, and the goodness of fit were saved for evaluation.

198

199 Scans were collected using both sequences in aqueous and gel based test

200 objects of known qT1 and qT2 and compared to data collection using a single

201 slice inversion recovery sequence for qT1 and a single slice Carr-Purcell

202 Meiboom-Gill (CPMG) sequence for qT2 to validate the method.

203

204 Statistical Tests of Demographic, clinical, and cognitive measures.

205 Group characteristics were evaluated with Statistical Toolbox of Matlab

206 (www.mathworks.co.uk/products/statistics). Differences in demographic and

207 clinical data were assessed with use of either t-tests for continuous variables

208 or χ^2 tests for categorical measures. For each test statistic, a probability value 209 of *p*<0.05 was regarded as significant.

210

211 Voxel-based quantification

212 MRI data processing was performed in a combined FSL

213 (fsl.fmrib.ox.ac.uk/fsl/fslwiki) and SPM (www.fil.ion.ucl.ac.uk/spm) based on

214 the previously validated voxel-based quantification (VBQ) procedure [4]. At

both baseline and follow-up, raw qT1 and qT2 imaging datasets were

216 corrected for field inhomogeneities using B0 maps and the PRELUDE/FUGUE

algorithm in FSL [16]. Then, the bias corrected qT1 and qT2 maps were used

for subsequent analysis.

219

220 Volumetric structural T1 weighted images were firstly segmented using

Gaussian mixture model implemented in the VBM toolbox [17], and brain

tissues were classified into grey matter (GM), white matter (WM) and

223 Cerebrospinal fluid (CSF) for both baseline and follow-up. A conjunction GM

brain mask was generated for each individual subject (in both AD and control

groups) by computing the intersection between the GM probability maps at

the baseline and that at the follow-up of the same subject, and then

thresholded at *p*>0.5 in each participant's native space. This mask was used

to select a common area of GM tissue at both baseline and follow-up in order

to ensure there were equal number of voxels tested in both time points, thus

avoiding potential bias in the statistical analysis.

231

232 As in standard longitudinal VBM procedure, only the baseline GM probability 233 maps were non-linearly normalized to standard MNI space 234 (www.mni.mcgill.ca) using the diffeomorphic registration algorithm (DARTEL) [17] in SPM, and the resulting parameters were used to normalize the qT1 235 236 and gT2 maps in both baseline and follow-up. The gT1 and gT2 maps at both 237 time points were firstly co-registered with the GM probability maps derived 238 from structural T1 images at baseline, then the thresholded conjunction GM 239 brain masks were applied to qT1 and qT2 data at both time points. Finally, we 240 transformed the GM maps of qT1 and qT2 MRI parameters into standard MNI 241 space using the participant-specific diffeomorphic parameters estimated from 242 the baseline scans based on the previous DARTEL procedure. However, we 243 did not apply modulation to these quantitative MRI parameters in order to 244 avoid confound of age and disease related GM volume changes. Finally, all 245 normalized quantitative qT1 and qT2 maps were smoothed with an isotropic 246 Gaussian kernel of 6 mm full width at half maximum.

247

For statistical analysis investigating disease induced regional microstructural 248 249 alterations between the AD and control groups, and between the baseline and 250 follow-up, we used the General Linear Model (GLM) with age and gender as 251 covariates. Then, two-tailed t-tests were performed at each voxel to detect 252 voxel-wise difference between the groups or time points. We also tested the 253 group x time interaction using a mixed model ANOVA. The false positive rate 254 was controlled using family-wise error (FWE) correction for multiple 255 comparisons, and thresholded at p < 0.05 at the cluster level.

256

257 *Post-hoc region-of-interest analysis*

258	To explore the clinical relevance of qT1 and qT2, in a post-hoc region-of-
259	interest (ROI) analysis, we extracted the averaged quantitative MRI values
260	from significant clusters found in the longitudinal comparison. Here, we used
261	the unsmoothed maps in order to preserve the original values of the MR
262	parameters. Then, we correlated cognitive and clinical measures with the
263	averaged quantitative MRI values extracted from the significant clusters
264	obtained from the previous group comparisons. These measurements
265	included the CAMCOG, MMSE, UPDRS III and NPI total scores. Multiple
266	comparisons were controlled using Bonferroni correction for the number of
267	ROIs.

268

269 **Results**

270 Demographic clinical and cognitive measures

As shown in Table 1, there were no significant differences between AD and
control groups for age, sex and educational level. However, as expected, the
two groups significantly different at both baseline and follow-up for UPDRS III,
NPI, MMSE and CAMCOG scores with subjects with AD scoring poorer in all
measures compared to the controls.

277

Insert Table 1 here

- 278
- 279 Cross-sectional comparison of qT1: AD vs. controls

280	As shown in Figure 2A and Table 2A, at the baseline, we found a significant
281	decrease in qT1 for the AD group compared to controls (p<0.0001, FWE) in
282	bilateral temporal, parietal and occipital lobes, as well as several subcortical /
283	striatal nuclei. Largest significant clusters were within bilateral hippocampus,
284	parahippocampus, cuneus, precuneus, caudate and putamen. At the follow-
285	up, we found a very similar pattern of qT1 changes comparing between AD
286	and control groups. See Figure 2B and Table 2B. No significant increase in
287	qT1 was found for the AD group compared to controls at either baseline or
288	follow-up.
289	
290	Insert Table 2 here
291	
292	Insert Figure 2 here
293	
294	Cross-sectional comparison of qT2: AD vs. controls
295	For q12 at the baseline, we also found a significant decrease for the AD group
296	compared to controls (p<0.0001, FWE) in left superior and right middle
297	temporal lobes, bilateral hippocampus and left parahippocampus as shown in
298	Figure 3A and Table 3A. At the follow-up, we found a very similar pattern of
299	qT2 changes comparing between AD and control groups except for a cluster
300	covering left caudate, putamen and pallidum, and a right cuneus cluster,

- 301 which were not seen at the baseline. See Figure 3B and Table 3B. No
- 302 significant increase in qT2 was found for the AD group compared to controls
- 303 at either baseline or follow-up.

304	
305	Insert Table 3 here
306	
307	Insert Figure 3 here
308	
309	Longitudinal comparison of qT1: baseline vs. follow-up
310	When comparing qT1 between baseline and follow-up in the AD group, we
311	found a significant increase over 12 months in bilateral hippocampus and
312	parahippocampus (p <0.0001, FWE), thalamus (p <0.0001 for left and p =0.002
313	for right, FWE) and right caudate (<i>p</i> <0.0001, FWE) as shown in Figure 2C
314	and Table 4A. The significant hippocampus clusters in the longitudinal
315	comparison are more medial to the clusters found in the cross-sectional
316	comparisons; see Figure 2. We found no longitudinal change for $qT1$ in the
317	control group and no group (AD and controls) x time (baseline and follow-up)
318	interaction.
319	
320	Insert Table 4 here
321	
322	Longitudinal comparison of qT2: baseline vs. follow-up
323	For qT2, we found a significant increase between the baseline and the follow-
324	up in the AD group as shown in Figure 3C and Table 4B. Significant clusters
325	are located in left parahippocampus (p <0.0001, FWE), right caudate, putamen
326	and insula (p <0.0001, FWE), as well as right middle frontal lobe (p =0.002,
327	FWE). We found a significant group x time interaction in right insula

(*p*<0.0001, FWE) bordering with right putamen and extending to right caudate
at lower threshold (*p*<0.001, uncorrected). We argue that atrophy is unlike the
explanation of this effect because if atrophy were a driver of an increase in
qT2 over time, we would expect AD subjects at baseline to have a greater
qT2 than controls because of their greater atrophy, a result opposite to what
we found here.

334

For the control group, we found a significant longitudinal increase in qT2

336 (*p*<0.0001, FWE) in left superior parietal lobe, caudate head, and

337 supplementary motor area extending to superior medial prefrontal cortex.

338 (See Figure 3D.)

339

340 Correlation between cognitive / clinical measures and quantitative MRI

341 Here, the main focus is on the relationship between longitudinal changes in 342 quantitative MRI parameters and cognitive / clinical measures in the AD group 343 at baseline, follow-up and change over the 1-year period. Thus for qT1, we 344 have defined three region-of-interest (ROIs) based on the results of the 345 longitudinal comparison of gT1, i.e. left / right hippocampus and right caudate. 346 We found a significant negative correlation between the longitudinal changes 347 in gT1 in left hippocampus and the cognitive decline (i.e. change in total 348 MMSE score over the 1-year period) in AD (r=-0.58, p=0.006). We found a 349 significant correlation between baseline CAMCOG score and the changes of 350 qT1 in bilateral hippocampus over the 1-year period. In addition, a significant 351 correlation was found between baseline UPDRS III score and the longitudinal

changes of qT1 in bilateral hippocampus. Both effects were stronger in the
right hemisphere than in the left and only the right hippocampus survived the
correction for multiple comparisons. (See Table 5A.) Nonetheless, this
suggests that baseline CAMCOG and UPDRS scores predict changes in qT1
in these regions, that is, the more severe the dementia in general, the more
qT1 increases.

358

We also found a significant correlation between qT1 in right caudate and

360 UPDRS score cross-sectionally at both baseline (r=0.60, *p*=0.004) and follow-

up (r=0.51, *p*=0.018) in AD. Moreover, qT1 in right hippocampus was

362 significantly correlated with the CAMCOG score only at the follow-up (r=-0.60,

363 *p*=0.004) but not at the baseline. (See Table 5A.) No other correlation

364 survived the correction for multiple comparisons.

365

366

Insert Table 5 here

367

368 For qT2, we have extracted qMRI values from four significant clusters found in

the longitudinal comparison: right insula extending to putamen, left

370 parahippocampus, right caudate and right superior medial frontal cortex

371 (BA8). We found a significant correlation between the longitudinal changes of

372 qT2 in left parahippocampus and the changes in NPI score over time (r=0.54,

373 *p*=0.012) in AD. (See Table 5B.) No other correlation was found.

374

375 Individual analysis in longitudinal comparison

376 Figure 4 shows the individual variability in longitudinal changes in quantitative 377 MRI within the AD group, and how it relates to disease severity. It can be 378 seen in Figure 4A that subjects with AD showed a general increase in qT1 in 379 right hippocampus, and the rate of increase seems to accelerate in moderate 380 and severe cases of AD, i.e. baseline MMSE score lower than 20. The same 381 pattern was observed in other clusters found in the longitudinal analysis. 382 Figure 4B shows the individual changes in qT2 in left parahippocampus over 383 time. We have found a very similar trend as in qT1 with subjects with AD 384 generally showing an increase in qT2 over 12 months. We have also found 385 similar pattern in other significant clusters derived in the longitudinal analysis 386 in the AD group. 387 388 Insert Figure 4 here 389

390 Discussion

391	Using novel longitudinal and quantitative MRI method and voxel-based
392	quantification, we showed that at the cross-sectional level, qT1 and qT2 in AD
393	were significantly decreased in multiple cortical areas in bilateral temporal and
394	parietal lobes with the largest changes in medial temporal structures
395	comparing to similarly aged control subjects at baseline. This pattern is
396	consistent with previous neuroimaging studies with AD showing significant
397	volume reduction in these regions such as hippocampal, enthorinal and
398	parahippocampal cortices [18].

399

At follow-up, we found a very similar pattern of quantitative MRI changes in both qT1 and qT2 comparing AD and control groups with the main affected brain areas in bilateral hippocampus and associated structures. This demonstrates the robustness of qMRI in reproducing a consistent pattern of quantitative MRI parameter changes at two different time points with 12 months gap.

406

407 It is worth noting that both qT1 and qT2 parameters consistently picked up 408 substantial changes in subcortical regions, e.g. bilateral caudate, putamen 409 and thalamus. However, comparing to neocortex, in particular the 410 hippocampus, these basal nuclei and thalamus have received much less 411 attention in previous research, and conventional volumetric MRI showed a 412 mixed picture of atrophy in these subcortical areas. For example, atrophy of 413 putamen was found in DLB but not in AD [19], whereas putamen and thalamic 414 atrophy were both shown in AD in a different study [20] reflecting a relatively 415 high level of noise in volumetric measures in these regions and large interstudy variability. In contrast, quantitative MRI may detect neuronal and 416 417 macromolecular changes in tissue environment, which does not rely on 418 atrophy shown in structural T1 weighted MRI. Based on this, we argue that 419 gMRI provides incremental benefit over and above that of structural MRI. 420 Quantitative MRI also offers a unique opportunity to detect early brain 421 changes in AD before observable brain volume reduction can be reliably 422 shown and cognitive / clinical impairments can be found [2]. 423

424 Although we found that AD was characterized by a reduction in qMRI

425 parameters in cross-sectional comparison, in longitudinal comparison, we 426 found that qT1 was increased rather than decreased in right caudate, bilateral 427 hippocampus and parahippocampus, as well as in thalamus. We also found that qT2 was increased in right caudate, putamen and insula in addition to left 428 429 parahippocampus in AD. Frontal changes in gT2 over time were also notable 430 in AD. This spatial pattern is consistent with the development of atrophy in AD 431 [21]. Increase in qT2 was found in healthy controls in left superior parietal 432 lobe, left caudate head, and bilateral supplementary motor area extending to 433 superior medial prefrontal cortex. However, none of these brain regions 434 overlap with longitudinal qT1 / qT2 changes found in AD suggesting the 435 increase of gT2 in AD and controls may reflect distinct underlying causes. The 436 only significant group x time interaction was found in right insula extending to 437 putamen and caudate nucleus.

438

439 To further understand the increase in qMRI over time in AD, we performed an 440 individual analysis, which showed the changes of gT1 and gT2 over time in 441 hippocampus, caudate and other clusters found in the longitudinal 442 comparison. By sampling individual subjects that were at different stages of 443 the disease indicated by their severity (i.e. baseline MMSE), we have pictured 444 an overall trajectory of gT1 and gT2 in clinically diagnosed AD. It is notable 445 that the rate of gMRI increase was slow at early stages of AD but accelerated 446 at severe stage of AD. Thus, although gT1 and gT2 decreased in AD 447 comparing with controls at the cross-section level, it is possible that qT1 and qT2 may increase over time in AD because plaque burden may stabilize or 448 449 even fall in established stages of AD as the disease progresses. In addition,

450 we found that general disease severity (measured by different but related 451 scales, i.e. CAMCOG and UPDRS) predicts the rate of change in qT1 in 452 hippocampus showing a faster rate of increase at the severe stage of AD.

453

454 These changes in gMRI followed a trend that mirrors the inverted 'U' shape 455 trajectory of brain β -amyloid over time [22] suggesting that at the severe stage 456 of AD the brain β -amyloid (and/or other factors) may undergo a decrease. A 457 more quantitative treatment of the parallels between the current results and 458 the findings by Jack et al will require a deeper analysis of how the very 459 different properties of the two might reflect how brain β-amyloid burden is 460 captured by each imaging method, and the consequences of this for temporal 461 trajectory of these variations. This analysis is outside the scope of the current 462 paper, and the comparisons we provide here should be regarded as 463 preliminary and illustrative. However, it is clear that such a 'U' shaped 464 temporal pattern has not been found in atrophy in AD.

465

466 In addition, we showed the clinical relevance of guantitative MRI parameters 467 in AD, i.e. the change of gT1 at left hippocampus was correlated with 468 cognitive decline (annual changes in MMSE score) in AD. For qT2, the 469 longitudinal change in right parahippocampus was significantly correlated with 470 the annual changes in neuropsychiatry condition (NPI) in AD over time. In 471 addition, we found a significant correlation between gT2 in right caudate 472 nucleus and parkinsonism (UPDRS score) at the cross-sectional level (at both 473 baseline and follow-up), suggesting the AD pathology may be present in basal 474 ganglia structures, therefore causing motor parkinsonism in AD. Here, it is

interesting to see that qT2 in caudate was sensitive to the changes in UPDRS
scores. This finding is also consistent with Wilson et al. [23], which showed
that parkinsonian signs are strong predictors for the progression of AD.

478

479 In our previous cross-sectional study on dementia with Lewy bodies (DLB), 480 we also found a significant reduction of qMRI parameters in DLB compared to 481 controls [7]. In addition, we showed that the spatial pattern of gMRI alteration 482 only partly overlapped with that of atrophy, making the latter an unlikely 483 explanation for the qMRI decreases. In the current study, we have followed 484 the similar analysis procedure in order to avoid partial volume effect due to 485 atrophy. In seeking the possible underlying biochemical interpretation of these 486 quantitative MRI parameters and their evolution over time, qT1 is 487 predominantly influenced by water content but also relates to the degree of 488 myelination [24,25,26]. Both gT1 and gT2 are also sensitive to the level of 489 iron, which is present in amyloid plaques [27] and in microbleeds.

490

491 Although it is not possible to precisely determine the pathological changes 492 associated with alterations in qT1 or qT2 in AD, it has been suggested that 493 decreases in qT1 and qT2 might be associated with increases in amyloid 494 burden and iron load in the brain based on histologically confirmed animal 495 model of AD [28,29]. Consistent with our finding, decreased gT1 was found to 496 be associated with an increase in β -amyloid deposition in 5xFAD transgenic 497 mouse model of Alzheimer's disease compared with wild type mice [30]. In 498 addition, decreased qT2 was found in APP/PS1 transgenic mouse model of

AD [31,32] probably reflecting a complex interaction between β-amyloid and
iron concentration as well as other factors.

501

502 In a longitudinal study of β -amyloid plaque development in Tg2576 transgenic 503 mice using qT2 relaxation time [33], it has been found that qT2 decreases 504 with age (12 - 18 months) following an increase in plaque area, number and 505 size in the brain. Although it is difficult to match the disease stage of the 506 mouse model to humans with AD and it is not common to find atrophy in the 507 animal model of AD, this finding is nonetheless consistent with our results 508 showing decreased qT2 in medial temporal lobes in AD. It has also been 509 shown in a study based on APP/PS1 transgenic mice model that gT2 is 510 modulated by the level of amyloid in subiculum without histochemically 511 detectable iron in the brain [34], providing promises in detecting the 512 pathological process in AD at the earliest stages. 513

514 In addition to our previous findings on gMRI changes in DLB [7], as well as 515 the established literature on animal qMRI correlates, the current data provided 516 convergent evidence for the potential ability of quantitative MRI in detecting 517 early changes of tissue property caused by neurodegenerative disease. Being 518 able to apply this novel technique in human using relatively safe MRI method 519 enables new means for early detection of AD and tracking its progression 520 over time. This approach is also likely to close the gap between animal models of amyloidosis and studies on human AD in the context of drug 521 522 discovery.

523

524 Conclusion

525	In summary, quantitative MRI parameters were reduced in AD cross-
526	sectionally, but increased over time, showing distinct spatiotemporal patterns
527	from the atrophy in AD. Our findings are consistent with animal model of AD
528	showing quantitative MRI can provide information, which may reflect
529	pathology such as amyloid burden and iron load. We also showed the clinical
530	relevance of quantitative MRI, indicating their potential promise as new early
531	imaging markers in AD. With reduced radiation, MRI is more suited for
532	longitudinal studies than PET. Thus, longitudinal and quantitative MRI will be
533	valuable in developing new treatments by tracking brain changes associated
534	AD in vivo.

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