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Resting-State Functional Connectivity Changes in Aging apoE4 and apoE-KO Mice

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It is well established that the cholesterol-transporter apolipoprotein e (APOE) genotype is associated with the risk of developing neurodegenerative diseases. Recently, brain functional connectivity (FC) in apoE-e4 carriers has been investigated by means of resting-state fMRI, showing a marked differentiation in several functional networks at different ages compared with carriers of other apoE isoforms. The causes of such hampered FC are not understood. We hypothesize that vascular function and synaptic repair processes, which are both impaired in carriers of e4, are the major contributors to the loss of FC during aging. To test this hypothesis, we integrated several different MRI techniques with immunohistochemistry and investigated FC changes in relation with perfusion, diffusion, and synaptic density in apoE4 and apoE-knock-out (KO) mice at 12 (adult) and 18 months of age.

Compared with wild-type mice, we detected FC deficits in both adult and old apoE4 and apoE-KO mice. In apoE4 mice, these changes occurred concomitant with increased mean diffusivity in the hippocampus, whereas perfusion deficits appear only later in life, together with reduced postsynaptic density levels. Instead, in apoE-KO mice FC deficits were mirrored by strongly reduced brain perfusion since adulthood. In conclusion, we provide new evidence for a relation between apoE and brain connectivity, possibly mediated by vascular risk factors and by the efficiency of APOE as synaptic modulator in the brain. Our results show that multimodal MR neuroimaging is an excellent tool to assess brain function and to investigate early neuropathology and aging effects in translational research.

Key words: apoE; apoE4 mice; cerebral blood flow; diffusion tensor imaging; functional connectivity; resting-state fMRI

Introduction
The only gene currently associated to sporadic Alzheimer’s disease (AD) is the e4 allele of the apolipoprotein E (APOE) gene (Mahley and Rall, 2000). Several mechanisms by which APOE-e4 promotes AD have been proposed; after brain injury, apoE is produced by astrocytes to transport cholesterol to the damaged neuronal and synaptic membranes; however, the repair and remodelling of damaged synapses appears to be less effective by apoE-e4 than other isoforms (Mahley et al., 2006; Verghese et al., 2011). Moreover, APOE-e4 carriers are more susceptible to vascular brain damages (e.g., stroke, brain hemorrhage; Zlokovic, 2011, 2013; Liu et al., 2013). This, in the end, can result in a permanent loss of synaptic contacts, with gradual loss of neuronal connectivity (Bu, 2009; Verghese et al., 2011).

Investigating functional connectivity is nowadays possible by resting-state functional MRI (rsfMRI). rsfMRI examines the temporal correlations of blood oxygen level-dependent (BOLD) fluctuations between brain regions at rest, which is thought to reflect resting neuronal activity and is often referred to functional connectivity (FC; Biswal et al., 1995; Damoiseaux et al., 2006; De Luca et al., 2006). This MR technique has generated a great deal of interest among neuroscientists and has been widely used to investigate neurological disorders (Greicius, 2008).

Many studies have reported a correlation between APOE-e4, AD, and abnormalities in functional connectivity measured with rsfMRI or task-based fMRI (Trachtenberg et al., 2012); cognitively normal young APOE-e4 carriers showed elevated resting-state activity in the default mode network (DMN) and high hippocampal activation during memory tasks; both areas that are preferentially affected in early AD (Bookheimer et al., 2000; Filippini et al., 2009). This hippocampal hyperactivation is thought to represent a compensatory response, in which increased cognitive effort is required to achieve an equal level of performance to that of non-e4 carriers (Bondi et al., 2005). Such hyperactivation is followed by a decline in FC and structural interconnectivity between cortical regions at older age (O’Brien et al., 2010; Brown et al., 2011; Machulda et al., 2011). This is in-line with studies.
showing that elderly APOE-e4 carriers have reduced FC compared with APOE-e3 carriers, even in absence of amyloid-β plaques (Sheline et al., 2010). Alterations in the DMN have also been reported in e4-carriers (Fleisher et al., 2009), and similarly in AD patients (Greicius et al., 2004).

Despite an increasing amount of evidence for an association between apoE genotype and FC changes, the mechanisms underlying this relationship remain elusive (Vergiose et al., 2011). Specifically, it is not clear whether changes in FC in APOE-e4 carriers have neural origins or are driven by other copathologies, such as impaired neurovascular coupling.

To determine the underlying neural or vascular origin of such changes, we investigate the relation between functional connectivity, cerebral perfusion, brain tissue microstructure, and postsynaptic density in target-replacement apoE4- and apoE-deficient mice; these mice represent mild and severe AD and postsynaptic density in target-replacement apoE4- and apoE-deficient mice, respectively, and may provide insights on the role of APOE genotype on FC changes, with or without the presence of vascular deficits.

Materials and Methods

Animals

The apoE4 founder mice were originally obtained from Taconic Transgenic Models and a colony was established at the Radboud University Medical Center (Radboud UMC). ApoE4 mice were created by targeting the murine APOE gene for replacement with the human APOE-e4 alleles cultured in E14TG2a embryonic stem (ES) cells as described previously (Sullivan et al., 1997). Resulting chimeras were backcrossed to C57BL/6j (B6) mice for eight generations. The line was derived by embryo transfer and is maintained by increasing homozygous mice. For the present study, male and female apoE4 breeder mice were used to generate homozygous apoE4 offspring (third generation).

The apoE-deficient (B6.129P2-Apoemtm1/J) founders were originally obtained from Jackson Laboratories and a colony was established at the Radboud UMC. In apoE-knock-out (KO) mice the APOE fragment was targeted with an apoE-specific probe (a SacI/BglII fragment) isolated from a mouse APOE cDNA clone. The strongly hybridizing phage clones obtained in this screening, a 7.8 kilobase (kb) EcoRI fragment was isolated and compared with the restriction map. Subsequently these targeted cells were cultured in E14TG2a ES and injected into C57BL/6j (B6) mice. Resultant chimeras were backcrossed for 11 generations and intercrossed to homozygosity. The line was derived by embryo transfer and is maintained by increasing homozygous mice (Piedrahita et al., 1992). For the present work, male and female apoE-KO breeder mice were used to generate homozygous apoE-KO offspring (third generation).

C57BL/6j wild-type mice, obtained from our colony at the Radboud UMC were used as controls. Throughout the experiment animals were housed in groups of two to seven mice per cage in a controlled environment, homogenously illuminated by normal fluorescent room light at 60 lux, with room temperature at 21°C, and an artificial 12 h light/dark cycle (lights on at 7:00 A.M.). Food and water were available ad libitum.

The experiments were performed according to Dutch federal regulations for animal protection. The Veterinary Authority of the Radboud University Nijmegen Medical Centre, the Netherlands, approved all the protocols within this study.

MRI

Two cohorts of apoE4, apoE-KO, and wild-type male mice of 12 months of age (number of animals for each genotype: n = 8, 10, and 9, respectively) and of 18 months of age (n = 9, 9, and 10, respectively) were used for this cross-sectional study. To study genotype and aging related differences in brain function and structure, rsfMRI, cerebral blood flow (CBF), and diffusion tensor imaging (DT-MRI) were measured in each cohort.

MRI measurements were performed on an 11.7 T BioSpec Avance III small animal MR system (Bruker BioSpin) equipped with an actively shielded gradient set of 600 mT/m and operated by Paravision 5.1 software. We used a circular polarized volume resonator for signal transmission and an actively decoupled mouse brain quadrature surface coil for signal reception (Bruker BioSpin). During the MR experiments, low-dose isoflurane was used (3.5% for induction and 1–1.5% for maintenance), slightly adjusted throughout the experiment to maintain a fast and stable breathing frequency (>130 bpm). The mice were placed in a stereotactic device with earbars and toothholder to immobilize the head. Great care was taken to fix the mouse head, as this is important to avoid movement-related artifacts, particularly when applying multishot fast acquisition MR sequences. As we did not detect movement artifacts in the EPI images, we decided not to use further methodologies to limit artifacts from movements, such as the respiratory gating, that would have increased the acquisition time.

Body temperature was measured with a rectal thermometer and maintained at 37°C by a heated airflow device.

Gradient echo (GE) T2*-weighted images covering the entire mouse brain were acquired in three directions for anatomical reference. Subsequently, rsfMRI datasets were acquired using a single-shot spin-echo sequence combined with echo-planar imaging (SE-EPI) sequence. Although its sensitivity to image the BOLD effect is slightly reduced, SE-EPI has less susceptibility artifacts compared with GE-EPI; in addition, it is less sensitive to geometric distortion and physiological noise, which are known to generate confounding results in resting-state FC, also in rodents (Kalthoff et al., 2011). Six hundred repetitions with a repetition time (TR) of 1.8 s and echo time of 16.9 ms were recorded for a total acquisition time of 18 min.

To study brain perfusion under resting conditions, a flow-sensitive alternating inversion recovery arterial spin labeling (FAIR ASL) technique was used (Kim, 1995; Zerbi et al., 2014). Fifteen images with increasing inversion times (TIs; 40–3000 ms) were obtained for the T1 calculations, amounting to a total scan time of 12 min. Inversion recovery data from the imaging slice were acquired after selective inversion interleaved with nonselective inversion.

Diffusion of water was imaged as described previously (Harsan et al., 2010; Zerbi et al., 2013). In short, 22 axial slices covering the whole brain were acquired with a four-shot SE-EPI protocol. B0 shift compensation, navigator echoes, and an automatic correction algorithm to limit the occurrence of ghosts and artifacts were implemented. Encoding b factors of 0 s/mm² (five b = 0 images) and 1000 s/mm² were used and diffusion-sensitizing gradients were applied along 30 non-collinear directions in three-dimensional space. All other imaging parameters are listed in Table 1. Before each sequence, a whole-brain automatic shim protocol was applied; this includes the adjustment of field homogeneity, the adjustment of the basic resonance frequency and the adjustment of the reference pulse gain. The FWHM achieved for a square box of 6 × 6 × 6 mm³ was <35 Hz, in-line with other studies (Nsarrallah et al., 2014).

FC measurements

The rsfMRI datasets were first realigned using a least-squares method and rigid-body transformation with Statistical Parametric Mapping (SPM) mouse toolbox (SPM5, University College London; http://www.fil.ion.ucl.ac.uk/spm/; Saviak et al., 2009). Mean and maximum displacement across the six degrees of freedom (along the x-, y-, and z-axes and on three rotation parameters pitch, roll, and yaw) were measured in each mouse. The mean SE-EPI images of each mouse were then used to generate a study-specific template through linear affine and nonlinear diffeomorphic transformation (ANTS). v1.9; http://pial.upenn.edu/ANTS/). Visual inspection of the normalized dataset was performed to screen for possible normalization biases. On the template, 15 areas were selected in left and right hemisphere and back-transformed in each subject space using the inverse of the affine and diffeomorphic transformations. The selected regions were based on previous work in functional connectivity in mice (Jonkers et al., 2011), and includes: dorsal hippocampus (DH), ventral hippocampus (VH), auditory cortex (AU), motor cortex (M1), somatosensory cortex (S1), visual cortex (V1), and retrosplenial cortex (RS). All cortical ROI were selected 1–2 voxels away from the edge of the cortex, to minimize the impact of susceptibility-
weighted artifacts, which are more prominent in areas of different tissues interface (e.g., near the skull or near the ear canals).

In-plane spatial smoothing (0.4 × 0.4 mm), linear detrending, and temporal high-pass filtering (cutoff at 0.01 Hz) were applied to compensate for small across-mouse misregistration and temporal low-frequency noise. Head movement components detected from the rigid-body transformation were regressed using FSL (the FMRIB software library; Jenkinson et al., 2012). In VH, S1, and AU, voxelwise FC maps were computed using the REST MATLAB toolkit (Song et al., 2011) and group comparisons were assessed voxelwise using SPM5 with the SPMMouse toolbox. In both 12- and 18-month-old mice, two t tests were performed to identify genotype differences in the framework of the general linear model. Statistical significance for voxels exceeding a minimum cluster size of 4, to achieve cluster size $>0.05$ mm³ as by Dubois et al. (2008), was established at $p < 0.05$, uncorrected for multiple comparisons.

For each mouse, the FAIR images with different TIs were realigned over the first TI using a rigid-body model, implemented in SPM. Determination of $T_1$ selective, and $T_1$ non-selective was performed by fitting the averaged signal intensities in each ROI with a three-parameters monoexponential T1 relaxation curve. CBF was determined in cortex, hippocampus, and thalamus using the following equation:

$$ CBF = \frac{T_1 \text{ non-selective}}{T_1 \text{ selective}} \left( \frac{1}{T_1 \text{ selective}} - \frac{1}{T_1 \text{ non-selective}} \right), $$

where A is the blood/tissue partition coefficient for water, assumed to be 0.9 ml/g (Herscovitch and Raichle, 1985; Leithner et al., 2010) and T1 blood was assumed to be 2.75 s at 11.7T (Lin et al., 2012).

### Diffusion tensor MRI parameter estimation and group comparisons

The calculation of four commonly used DT-MRI parameters, mean diffusivity (MD), fractional anisotropy (FA), radial diffusivity (RD), and parallel diffusivity (A1), was performed following a protocol as described previously (Zerbi et al., 2013). Briefly, the diffusion tensor was estimated for every voxel using the PATCH algorithm (Zwiers, 2010). Thereafter, FA, MD, RD, and A1 maps were normalized to a study-specific template through linear affine and nonlinear diffeomorphic transformation using ANTs. Regional differences between apoE4 mice and wild-type, and between apoE-KO and wild-type in spatially normalized diffusion maps were assessed voxelwise using SPM5 following the same procedure as described by Zerbi et al. (2013). Statistical significance for an individual voxel was established at $p < 0.05$, with a minimum cluster size of 4 interconnected voxels (to achieve cluster size $>0.05$ mm³ as by Dubois et al. (2008). As we considered the voxel based analysis (VBA) an explorative approach to investigate structural differences in the whole brain, we did not correct for multiple-comparison.

In addition, ROI of several white matter (WM) and gray matter (GM) areas were drawn on the template image based on an anatomical atlas (Paxinos and Franklin, 2004) and the resulting diffusion-related parameters were measured for further statistical analyses.

### Immunohistochemistry

Directly following the MR measurements at 12 and 18 months of age, anesthetized mice were killed by transcardial perfusion with 0.1 × PBS. The perfused brains were collected and postfixed for 15 h at 4°C in 4% paraformaldehyde fixative and thereafter stored in 0.1 × PBS with 0.01% sodium azide at 4°C for immunohistochemical staining. Eight series of 30 μm coronal sections were cut through the brain using a sliding microtome (Microm HM 440 E) equipped with an object table for freeze sectioning at −60°C. The tissue was stained for postsynaptic density with PSD95 antibody using one complete series of brain sections. Immunohistochemistry was performed using standard free-floating labeling procedures, as described previously (Jansen et al., 2013).

### PSD95

Polyclonal rabbit anti-PSD95 (1:2000; Abcam, catalog #ab18258, RRID: AB_444362) was used as a primary antibody. The sections were first pretreated with 0.9% H₂O₂ in PBS to block endogenous peroxidase and then incubated overnight at room temperature on a shaker table. After incubation, the sections were rinsed three times with 0.1 × PBS and incubated with the secondary antibody, donkey anti-rabbit biotin (1:1500; Biotin-SP-AffiniPure Donkey Anti-Rabbit IgG (H + L), Jackson ImmunoResearch). After 90 min, the sections were rinsed three times again and transferred to a solution containing Vector ABC-elite (1:800; Vector Laboratories) for 90 min. Thereafter, visualization of postsynaptic density was achieved by incubation with DAB-Ni solution. Stained sections were mounted on gelatin-coated glass slides, dried overnight in a stove at 37°C, dehydrated in alcohol series, cleared with xylol, and mounted in Entellan.

### Quantification

The stained sections were analyzed using a Zeiss Axiostar microscope equipped with hardware and software of Microbrightfield. Brain regions were based on the mouse brain atlas of Paxinos and Franklin (2004) and quantified in five regions of the hippocampus: the inner molecular layer (IML), outer molecular layer (OML), cornus ammonis 1 (CA1), CA2, and CA3. Additionally, two regions in the cortex corresponding to the visual and somatosensory cortex were analyzed. The relevant regions were digitized at 100 times magnification with immersion oil using Stereo Investigator. The quantification of the photographs was performed using ImageJ (NIH). The contrast was manually

### Table 1. List of parameters used in each MRI scan

<table>
<thead>
<tr>
<th>Imaging sequences</th>
<th>Anatomical T2*</th>
<th>rsfMRI</th>
<th>CBF</th>
<th>Diffusion tensor imaging</th>
</tr>
</thead>
<tbody>
<tr>
<td>Imaging method</td>
<td>GE</td>
<td>Spin-echo EPI</td>
<td>FAIR-ASL</td>
<td>4-shot spin-echo EPI</td>
</tr>
<tr>
<td>Echo time (ms)</td>
<td>5</td>
<td>16.9</td>
<td>11.8</td>
<td>20</td>
</tr>
<tr>
<td>Repetition time</td>
<td>630 ms</td>
<td>1.8 s</td>
<td>13.75 s</td>
<td>7.55 s</td>
</tr>
<tr>
<td>Image matrix</td>
<td>512 × 512</td>
<td>96 × 96</td>
<td>128 × 128</td>
<td>128 × 128</td>
</tr>
<tr>
<td>Field-of-view (mm)</td>
<td>40 × 40</td>
<td>25 × 25</td>
<td>30 × 30</td>
<td>20 × 20</td>
</tr>
<tr>
<td>Spatial resolution (µm/pixel)</td>
<td>78 × 78 × 340</td>
<td>260 × 260 × 500</td>
<td>234 × 234 × 1000</td>
<td>156 × 156 × 500</td>
</tr>
<tr>
<td>No. of slices</td>
<td>20 × 3</td>
<td>9</td>
<td>1</td>
<td>22</td>
</tr>
<tr>
<td>Total acquisition time (min)</td>
<td>~8</td>
<td>~18</td>
<td>~12</td>
<td>~18</td>
</tr>
</tbody>
</table>

For every voxel using the PATCH algorithm (Zwiers, 2010). Thereafter, FA, MD, RD, and A1 maps were normalized to a study-specific template through linear affine and nonlinear diffeomorphic transformation using ANTs. Regional differences between apoE4 mice and wild-type, and between apoE-KO and wild-type in spatially normalized diffusion maps were assessed voxelwise using SPM5 following the same procedure as described by Zerbi et al. (2013). Statistical significance for an individual voxel was established at $p < 0.05$, with a minimum cluster size of 4 interconnected voxels (to achieve cluster size $>0.05$ mm³ as by Dubois et al. (2008). As we considered the voxel based analysis (VBA) an explorative approach to investigate structural differences in the whole brain, we did not correct for multiple-comparison.

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**Table 1. List of parameters used in each MRI scan**

- **Imaging sequences**
  - Anatomical T2*: GE, Spin-echo EPI
  - rsfMRI: FAIR-ASL, 4-shot spin-echo EPI
  - CBF
  - Diffusion tensor imaging

- **Parameters**
  - **Echo time (ms)**: 5, 16.9, 11.8, 20
  - **Repetition time (ms)**: 630, 1.8, 13.75, 7.55
  - **Image matrix**: 512 × 512, 96 × 96, 128 × 128, 128 × 128
  - **Field-of-view (mm)**: 40 × 40, 25 × 25, 30 × 30
  - **Spatial resolution (µm/pixel)**: 78 × 78 × 340, 260 × 260 × 500, 234 × 234 × 1000
  - **No. of slices**: 20 × 3, 9, 1
  - **Total acquisition time (min)**: ~8, ~18, ~12, ~18

**For every voxel using the PATCH algorithm (Zwiers, 2010). Thereafter, FA, MD, RD, and A1 maps were normalized to a study-specific template through linear affine and nonlinear diffeomorphic transformation using ANTs. Regional differences between apoE4 mice and wild-type, and between apoE-KO and wild-type in spatially normalized diffusion maps were assessed voxelwise using SPM5 following the same procedure as described by Zerbi et al. (2013). Statistical significance for an individual voxel was established at $p < 0.05$, with a minimum cluster size of 4 interconnected voxels (to achieve cluster size $>0.05$ mm³ as by Dubois et al. (2008). As we considered the voxel based analysis (VBA) an explorative approach to investigate structural differences in the whole brain, we did not correct for multiple-comparison.**
enhanced, following the same procedure for all digitized images, and the amount of tissue stained was measured with a threshold-based approach.

**Statistics**

For the statistical analysis, IBM SPSS 20 software was used. Because the setup of the current study was designed to determine the effect of aging and the extent to which apoE4 and apoE-KO mice develop neuropathological traits of AD and not to study the effects of the apoE allele itself, statistical analyses were performed separately for the apoE4 and apoE-KO mice (apoE-e4 vs wild-type, and apoE-KO vs wild-type). Multivariate ANOVA (MANOVA) with Bonferroni corrections was conducted with between-group factors genotype and age of the animals. If the Bonferroni post hoc test indicated a significant interaction between genotype and age, the data were split for the concerning factor and thereafter analyzed again with the MANOVA. For the rsfMRI analysis, respiration of the animals was considered as covariate, to remove its confounding effect in the statistical analysis. Statistical significance was set at $p \leq 0.05$. Correlation analyses between perfusion, diffusion parameters, and PSD-95 were performed with the bivariate Spearman’s correlation method in the cortex (averaged value in the S1, AU, and V1 for rsfMRI, DT-MRI, and PSD-95) and hippocampus. To avoid false-positive correlations, the statistical significance for the correlation analyses was set at $p \leq 0.01$. All values used are expressed as mean ± SEM.

**Results**

The breathing of the mice was constantly monitored during the MR acquisition and used as a measure of the level of sedation of each individual mouse. During the rsfMRI and the CBF scans, the averaged respiration rate for all mice was $153 \pm 4$ and $146 \pm 5$ breaths per minutes (BPM), respectively. During the DT-MRI scan, which is the last scan of our protocol after 2 h anesthesia, the averaged respiration rate for all mice was $84 \pm 3$ BPM. No statistical group differences were found in respiration rate between either genotype or age, suggesting that an equal dose of anesthesia was perceived by the mice during the acquisition. Individual breathing rate changes were also uncorrelated with FC strength and CBF levels.

The displacement across the six degrees-of-freedom did not show significant differences between groups, suggesting that all mice were equally influenced by motion artifacts. The higher movements were detected in the up–down direction ($0.23 \pm 0.03$ mm averaged in all mice), whereas the displacement in other directions was lower than the voxel size. No mice were excluded after visual inspection of the normalized rsfMRI and DTI datasets.

**rsfMRI: independent component analysis**

Results of the ICA in 12-month-old wild-type mice are shown in Figure 1. The number of components is arbitrarily chosen based on previous studies in mouse rsfMRI (Jonckers et al., 2011; Zhou et al., 2014). With 30 components, most of the components properly match specific anatomical and functional brain areas on both hemispheres (Fig. 1b); with this analysis, most of the cortical components were found to be mainly unilateral, with the exception of the motor 1 and 2 regions (M1, M2) and the somatosensory-visual cortices (M1, S1, V1), which display a single band across the two hemispheres (Fig. 1b). By reducing the number of components to 20 and 15, more cortical regions are...
covered by one band bilaterally; other brain regions that displayed a highly unilateral pattern in the 30-component analysis, such as the HC, the caudate-putamen (CPu), and the thalamic nuclei (Th), showed more prominent bilateral activity (Fig. 1).

Mean FC patterns in the different mice groups from seeds in VH, S1, and AU are shown in Figure 2. Overall, a strong bilateral connectivity is notable when seeding in hippocampal regions. In the cortex, we detected a strong connectivity covering somatosensory, auditory, and motor cortices, with some extent also in their corresponding contralateral regions.

The VBA of these patterns revealed a widespread FC reduction in both apoE4 and apoE-KO mice compared with wild-type, particularly visible at younger age. No voxels indicated an increased FC in these genotypes.

**Total correlation analyses**
To compare the FC patterns in different genotype and ages, rs-fMRI data were statistically analyzed based on total correlation (Fig. 3) and partial correlation (Fig. 4).

The multivariate ANOVA showed overall significant aging and genotype effects when comparing apoE4 and apoE-KO with wild-type mice (Fig. 3b,c). In both apoE4, apoE-KO, and wild-type mice, 18-month-old animals showed decreased FC levels compared with 12-month-old mice. Most striking aging differ-
ences were located in the connectivity between motor cortices (left and right) and hippocampus, and, specifically for apoE4 and wild-type mice, between motor cortex and retrosplenial cortex (Fig. 3b, c, top-right). Reduced FC between auditory cortices was also detected in apoE-KO and wild-type animals. The pairwise comparison also revealed significant lower FC in apoE4 and apoE-KO mice, independent of age. These reductions in FC commonly affected auditory, motor, and somatosensory cortices and hippocampal areas (Fig. 3b, c, bottom-left). However, stronger reductions of FC were seen in the apoE-KO mice compared with wild-type mice, at both ages. These deficits seem to occur primarily in the hippocampal-cortical connectivity, but also between M1, AU, S1, and RS. Reduced FC due to aging is seen between M1 and DH, and between AU cortices.

Partial correlation analyses
The multivariate ANOVA of the partial correlation values (with Z-value thresholded at $|z| > 1.96$), showed overall significant genotype effects (Fig. 4); the apoE4 had lower FC compared with wild-type in the direct connectivity between auditory cortices although not significant, $p = 0.052$. In the apoE-KO mice, a more severe reduction was found between somatosensory and motor cortices (Fig. 4b). Reduced partial correlation was found in the motor-somatosensory cortices connectivity for apoE-KO and wild-type mice due to aging ($p = 0.034$, data not shown). Also in the partial correlation analyses, the MANOVA, revealed no significant genotype × age interactions.

CBF
To study differences in cerebrovascular health between the mice groups, we measured CBF with a FAIR ASL. Three ROIs on the left and right brain hemispheres were analyzed: cortex, hippocampus, and thalamus. Because no intraindividual differences in CBF between right and left hemispheres were detected between mice groups (data not shown), values from both sides were averaged.

In the comparison of apoE4 with wild-type, the MANOVA revealed a genotype × age interaction in the cortex and in thalamus ($p = 0.027$ and $p = 0.026$, respectively); after splitting the data for age and for genotype, we found that 18-month-old apoE4 mice have significantly lower CBF in these ROIs compared with wild-type at the same age ($p = 0.005$ for the cortex and $p = 0.002$ for the thalamus), and also compared with 12-month-old apoE4 animals ($p = 0.005$ and $p = 0.002$, respectively; Fig. 5). Contrarily to what is seen in the FC results, in the 12-month-old mice we did not detect any difference between wild-type and apoE4.
Several differences in diffusion parameters were detected in 18-month-old apoE4 and apoE-KO mice compared with wild-type (Fig. 6a,b). In the apoE4 mice, a reduction in FA is also noticeable in the molecular layer of the hippocampus, and in other cortical regions such as in the retrosplenial and in the piriform cortices. In the apoE-KO mice, an increased FA in the external capsule is seen in 12-month-old mice. In both apoE4 and apoE-KO mice, differences in FA and MD were seen near to the ventricle area, possibly due to partial volume effects.

With the ROI-based approach, we measured a higher MD in the DH in apoE4 mice ($p = 0.038$), reflected by increases (not significant) in both RD ($p = 0.056$) and $\lambda_1$ ($p = 0.231$). An increased MD in the apoE4 mice was also found in the corpus callosum (CC) at $-1.7$ from bregma ($p = 0.016$), driven by a higher $\lambda_1$ ($p = 0.001$); similar differences were seen also in the external capsule (EC; higher MD; $p = 0.035$; higher $\lambda_1$; $p = 0.015$); however, no FA changes were measured in these WM regions. The FA differences found by VBA, but not confirmed by the ROI-based approach could therefore be: (1) indicative for a minor change in diffusion proprieties, and (2) true only for a limited part of the structure of interest.

Few other differences were found, such as an increase MD in the DH in apoE-KO mice and an increased MD in the MECtx in apoE4 mice, although were not significant ($p = 0.08$). No significant aging effect or genotype × age interactions were seen in the MANOVA.

PSD-95

Levels of postsynaptic density were visualized and quantified with polyclonal rabbit anti-PSD95 and are shown as relative values compared with wild-type mice (Fig. 8). In the 12-month-old animal group, we found a significant reduction of PSD-95 staining in apoE4 mice compared with wild-type in the IML ($p = 0.005$) and in the CA3 ($p = 0.046$; Fig. 8c). In 18-month-old animals, reduced PSD-95 levels in both apoE-KO and apoE4 mice compared with wild-type was seen in the IML and OML; however, these differences were only significant in the apoE4 group ($p = 0.043$ and $p = 0.039$, respectively; Fig. 8d). Because the staining of the two groups was not performed at the same time, we could not assess aging effects on the different genotypes.

The two-tailed Spearman’s correlation test revealed a strong positive correlation between PSD-95 levels and CBF in both the hippocampal region ($p = 0.003$) and in the cortex ($p = 0.006$). When we split the data for genotype and age, we detected a similar positive correlation for all groups, but smaller in magnitude. The correlation in the cortex was nearly significant at both 12 and 18 months of age ($p = 0.072$ and $p = 0.043$), and more pronounced in the apoE4 mice ($p = 0.014$) than in apoE-KO ($p = 0.087$) and wild-type ($p = 0.033$).

No correlations were found between PSD-95 and DT-MRI parameters, neither a significant correlation between DT-MRI and CBF for the same regions.

**Discussion**

Target-replacement apoE4 and apoE-KO mice are attractive models to investigate the role of apoE and vascular risk factors in relationship with AD-like pathology, such as changes in brain FC. However, the technical challenges to obtain good-quality MR images and the lack of knowledge of murine brain network systems have been strong limiting factors for these studies. Recently, new dedicated hardware and methods for acquisition and data analysis enabled the analysis of rsfMRI in mice, resulting in a growing number of publications (Jonnkers et al., 2011, 2014; Guilfoyle et al., 2013; Nasrallah et al., 2014).
The strongest potential confounding factor when performing FC analysis in animals, still remains the impact of anesthetics. Some studies in rats have used analgesic muscle relaxants, such as dexmedetomidine (Lu et al., 2012) or medetomidine (Zhao et al., 2008), to limit the sedation level of the animals. However, maintaining a stable dose of these anesthetics for prolonged experiments is barely reliable. More recently, it has been demonstrated that robust FC measures in rats and mice could be detected using a regime of low-dose isoflurane (Guilfoyle et al., 2013; Zhou et al., 2014). Compared with other anesthetic regimes, low-dose isoflurane seems to preserve resting-state networks in mice, with similar results to those obtained in awake animals (Jonckers et al., 2014). Isoflurane is also known to increase the resting blood flow, due to its moderate systemic vasodilator effect (Iida et al., 1998). In a separate experiment, we confirmed that both CBF and FC are dependent on isoflurane level, and they both rapidly decline with concentrations of anesthetic >2.2%, comparable to previous findings (Liu et al., 2011). We also measured an increased CBF and a reduced FC by stimulating the maximum vessel vasodilation using a higher percentage of N₂O in the gas composition (Drummond et al., 1987). However, the connectivity patterns, particularly between hippocampus and cortical structures, and the CBF were restored by switching the gas concentration to the standard experimental condition; together, these data indicate that the methodology used for this study is replicable and valid to measure functional connectivity, without reaching the condition of maximum vasodilation and without disrupting the neurovascular coupling. Furthermore, there are no reports on a possible effect of isoflurane on apoE-signaling, suggesting that this anesthetic does not interfere with the outcome of this study, as all animals were kept under the same conditions.
Resting-state FC and perfusion changes in the aging mouse brain

In this study, we found a reduced total FC in apoE4 and apoE-KO mice, at both 12 and 18 months, compared with age-matched wild-type mice. In all animals, CBF was also measured, to test whether changes in vascular performance interfered with the FC results. Changes in cerebrovascular dynamics, such as impaired coupling between neural activity and hemodynamic response, might have directly influenced BOLD signal fluctuations and consequently FC changes (Liu, 2013).

ApoE4

Cross-sectional studies in young, middle-aged, and elderly human apoE-e4 carriers have reported reduced regional CBF and cerebral glucose metabolism over time, particularly in brain regions susceptible to pathological changes in AD (Scarmeas and Stern, 2006). In apoE-e4 subjects, a faster decline of regional CBF during aging has been shown compared with apoE-e3, suggesting its contribution to the increased risk of developing AD (Wierenga et al., 2013). In accordance, we demonstrated that apoE4 mice suffer from decreased cortical CBF at 18 months of age, whereas no differences were found at 12 months of age. Similar to the FC results, we showed a rapid decline of cerebral perfusion in these mice during aging, suggesting a strong aging effect. However, our data also highlight that changes in FC in apoE4 animals are measurable before CBF deficits. This finding suggests that the early FC decline in these mice is more likely attributable to the neural component on the BOLD signal, rather than to the possible interference of the vascular contribution.
In apoE-KO mice we found a concomitant reduction in CBF and resting-state connectivity at both ages. These mice are commonly used as models for vascular pathologies, as they develop aortic aneurysms, atherosclerotic plaques, and endothelial dysfunction throughout their life (Crauwels et al., 2003; Trollope et al., 2011). No investigations on resting-state fMRI were previously performed in apoE-KO mice; however, it is known that, together with vascular deficits, these mice also develop compromised synaptic plasticity (Masliah et al., 1995; Blain et al., 2006) and cognitive performance (Gordon et al., 1995; Masliah et al., 1995; Oitzl et al., 1997; Krzywkowski et al., 1999). Our results suggest that the FC decline observed in these animals reflects the contribution of both impaired neurovascular coupling and damaged neural activity; we hypothesize that the severe vascular pathology, which develop spontaneously in these mice at early age, could have accelerated the occurrence of brain injury by overexposure to stress factors, like cerebral hypoperfusion; the absence of apoE could have further aggravated the synaptic repair processes, leading to loss of neuronal connectivity. Supportively, we found a positive correlation between CBF and postsynaptic density (in sampled regions). Although the correlation of these two measures do not imply a cause–effect mechanism, it does support an association between neuronal and vascular health. It is also interesting to note that the changes in adult apoE-KO mice mirror the observations in the old apoE4 mice; this underlines a certain degree of similarity between these models, although demonstrating a more severe pathology in the KO mice.

**Structural changes and postsynaptic density in the aging mouse brain**

DT-MRI studies in apoE4 and apoE-KO mice are lacking, but changes in diffusion parameters have been reported in human studies: FA reductions in WM of APOE-ε4 carriers have been shown (Nierenberg et al., 2005; Honea et al., 2009; Heise et al., 2011); two studies also reported diffusion differences in hippocampal structures (Nierenberg et al., 2005; Persson et al., 2006). Nevertheless, these dissimilarities were consistent across different ages, suggesting that APOE affects WM and GM microstructure properties from early adulthood, without directly reflecting the associated risk of developing AD (Westlye et al., 2012).

With our exploratory voxel-based analyses, we detected similar changes in WM and GM microstructure in apoE4 mice. However, the only significant results confirmed by MANOVA were an age-independent increased MD in the CC, EC, and DH of the apoE4 mice. It is interesting to note that the changes in MD in WM were reflected by increased parallel and radial diffusivity, but without changes in tensor shape; this could indicate a different structural density of the fibers, resulting in more space for the water molecules to move. Brain atrophy and WM loss could have also increased the partial volume effect in these relatively thin areas, explaining these results. The association between an increased MD (and RD) in the CC and myelin degradation of the axonal bundles has been proposed by previous studies (Song et al., 2005). To verify this hypothesis and directly measure brain atrophy in vivo, voxel-based morphometry (Ellegood et al.,...
2012) or electron microscopy methods could be applied in future studies. Higher hippocampal MD has been consistently associated with neurodegenerative processes in both AD patients and animal models for AD (Zerbi et al., 2013; Zhang et al., 2014). These structural modifications in apoE4 mice are likely not related to neurodegeneration, as neural loss is not expected in this model at a young age. It is possible instead that increased inflammation processes could have driven structural alterations and hippocampal atrophy (Yin et al., 2011).

Furthermore, we did not find differences between apoE-KO and wild-type mice in DT-MRI parameters, suggesting that for these models, water diffusion changes are mild even in presence of severe functional deficits. The structural changes found in these mice were also not related to vascular or synaptic deficits, suggesting a link to the role of apoE in synaptic development, dendrite formation, and axonal guidance.

Synaptic loss and disconnection are strongly related with cognitive decline in AD and may influence FC (dendrite formation, and axonal guidance, suggesting a link to the role of apoE in synaptic development, and axonal guidance). In conclusion, with this study we provide evidence for a relation between apoE genotype, vascular risk factors and functional connectivity. Despite the technical challenges, we demonstrate that rsfMRI, combined with other MR neuroimaging techniques, can be used as powerful tool to investigate early neuropathology and aging effects in translational research.

Notes
Supplemental material for this article is available at https://www.radboudumc.nl/Zorg/Afdeling/anatomic/SectieAnatomic/Documents/20140818%20Supplementary%20Material%20Valerio%20Zerbi.pdf. This material has not been peer reviewed.

References

Zerbi et al. • Connectivity in apoE4 and apoE-KO Mice

synaptic and neural pathway in aging wild-type and AβPPsw-PS1ΔE9 mice. PLoS One 8:e63643. CrossRef Medline
Lin AL, Qin Q, Zhao X, Duong TQ (2012) Blood longitudinal (T 1) and transverse (T 2) relaxation time constants at 11.7 Tesla. MAGMA 25:245–249. CrossRef Medline


