

## Brain Diffusivity and Neurochemical Changes in Obstructive Sleep Apnea: A Pilot Correlation Study

Manoj Kumar Sarma<sup>1</sup>, Rajakumar Nagarajan<sup>1</sup>, Paul Michael Macey<sup>2</sup>, Ravi Aysola<sup>3</sup>, and M. Albert Thomas<sup>1</sup>

<sup>1</sup>Radiological Sciences, UCLA School of Medicine, Los Angeles, CA, United States, <sup>2</sup>School of Nursing, UCLA School of Medicine, Los Angeles, CA, United States, <sup>3</sup>Division of Pulmonary and Critical Care Medicine, UCLA School of Medicine, Los Angeles, CA, United States

**Target audience:** Researchers interested in obstructive sleep apnea syndrome, spectroscopic imaging and diffusion tensor imaging.

**Purpose/Introduction:** Obstructive sleep apnea (OSA) is a common disorder characterized by repeated hypoxic episodes during sleep. OSA patients demonstrate daytime sleepiness, diurnal fatigue, mood changes, and altered concentration likely leading to cognitive deterioration<sup>1</sup>. Studies have shown that cognitive dysfunction in these patients are associated with chronic exposure to nightly hypoxic periods<sup>2</sup>. Cerebrovascular risk factors such as hypertension, diabetes mellitus, and obesity are common in OSA<sup>3</sup>. Advanced neuroimaging techniques, such as diffusion tensor imaging (DTI) and magnetic resonance spectroscopic imaging (MRSI), enable non-invasive identification of OSA-induced, structural–neurochemical changes<sup>4,6</sup>. DTI is sensitive to the microstructure of brain tissue; various indices derived from DTI data, including fractional anisotropy (FA), and diffusivity (MD), identify cerebral structural changes in OSA. Although MRSI is used in differentiating a variety of brain lesions, there have been only a limited number of MRSI studies on OSA patients, but identification of chemical alterations associated with DTI changes could help identify the nature of the pathology in the sleep condition. The goals of this study were to examine if there is any correlation between FA and MD with metabolite ratios in various brain regions of OSA patients. We also investigated changes in FA and MD between OSA patients and healthy controls in those regions.

**Materials and Methods:** We assessed ten moderate-to-severe OSA patients (54.60±10.81 years) and six age matched healthy volunteers (46.66±8.77 years). OSA patients were recruited following a diagnostic sleep study at the UCLA Sleep Disorders Center, based on full overnight polysomnography scored with standard criteria. Evidence of clinical brain pathology was cause for exclusion. All subjects gave informed consent according to an institutionally approved research protocol. All data were collected on a 3T Trio-Tim MRI scanner (Siemens Medical Solution, Erlangen, Germany) using the Siemens VB17a compiler. DTI was performed using a single-shot multi-section spin-echo echo-planar pulse sequence [repetition time (TR) = 10,000 ms; echo-time (TE) = 87 ms; average = 1] in the axial plane, with a 130 x 130 matrix size, 256 x 256 mm<sup>2</sup> field of view (FOV), 2.0 mm slice thickness, 72 slices. For each slice, diffusion gradients were applied along 30 independent orientations with b = 1000 sec/mm<sup>2</sup> after the acquisition of b = 0 sec/mm<sup>2</sup> (b0) images. MRSI data was collected using a from a compressed sensing based 4D echo planar J-resolved spectroscopic (EP-JRESI) sequence. For this purpose, the standard EP-JRESI sequence was modified to accommodate for the 25% NUS of the fully sampled data<sup>7</sup>. The following parameters were used for CS EP-JRESI: TR/TE = 1.5s/30ms, 1.5x1.5x1.5 cm<sup>3</sup> voxel for VOI localization, 64Δt<sub>i</sub> increments, 256 bipolar echo pair, FOV = 24x24cm<sup>2</sup>, 2 averages, F1 and F2 bandwidths of 1000 Hz and 1190 Hz, respectively. Before applying the NUS based EP-JRESI sequence, 3D high resolution T<sub>1</sub>-weighted images for localization were collected using a MPRAGE pulse sequence. EP-JRESI was performed over an axial slice covering frontal/occipital regions. Modified Profit algorithm<sup>8</sup> was applied to process the extracted data and to calculate metabolite ratio with respect to the 3.0 ppm creatine peak (S/S<sub>Cr</sub>). FA and MD were calculated using the SPM diffusion toolbox<sup>9</sup> and subsequent ROI analysis was done using ImageJ<sup>10</sup>. The FA and MD differences between OSA patients and healthy controls were tested with a two-tailed t-test with statistically significant level p < 0.05. To explore for any relationship between the FA/MD values and metabolite ratios, Pearson correlation was performed on the patient data. A Bonferroni-like correction for multiple comparisons was used to calculate an adjusted alpha level. All statistical analysis was done using the SPSS software (Version 20.0, SPSS Inc, Chicago, IL, USA).

**Results:** Table 1 shows significant correlations between FA/MD values and MRS indices in left frontal white, right frontal white, medial frontal gray/white and medial occipital gray regions. Left frontal FA correlated with choline (Cho) ratio, and MD correlated negatively with glutamine (Gln) ratio. In the right frontal region, MD correlated significantly with myo-inositol (ml) ratio, and in the medial frontal white/gray FA correlated with N-acetylaspartate (NAA) ratio. Other metabolite ratios showed positive but non-significant correlations with FA and MD. Fig. 1 shows FA (a) and MD (b) values of OSA patients and healthy controls in the left frontal white, right frontal white, medial frontal gray/white and medial, occipital gray regions. Reduced FA and increased MD were observed between OSA and healthy controls in all brain regions (p < 0.05).

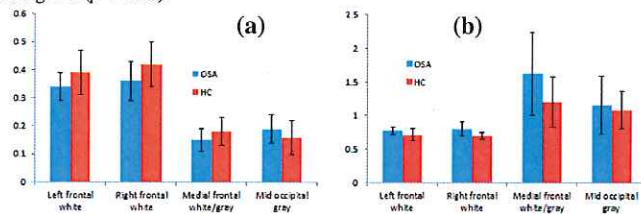


Fig. 1: Bar graphs showing mean (a) FA (±SD), (b) MD (±SD) ( $\times 10^{-3}$  mm<sup>2</sup>/s) value changes in four selected regions of OSA patients compared to healthy controls (HC) (all p < 0.05).

**Discussion and Conclusion:** White matter is extensively altered in OSA patients resulting reduced axonal integrity and changes identified by DTI indicate the underlying pathologies. Our finding of decreased FA and increased MD values are in accordance with earlier studies<sup>4,11</sup>. Lower FA primarily represents axonal groups that are damaged, shrunken, or that have less myelin. Increased MD values can result from subacute processes as well as chronic pathological conditions like chronic ischemia, gliosis, and demyelination. The correlations between FA/MD values and metabolic ratios supports these interpretations of the nature of structural injury in OSA. The use of CS based EP-JRESI sequence has the advantages of acquiring measurements across multiple brain regions, which is important for assessing a condition like OSA as multiple cortical, limbic and lower brains regions show structural and function alterations with other techniques. Future studies with more OSA patients and controls are required to confirm these findings of abnormalities associated with the sleep disorder.

**Acknowledgement:** This research was supported by NINR 013693.

**References:** 1. Malhotra A, White DP. Lancet 2002;360:237–45. 2. Lim DC, Veasey SC. Curr Neurol Neurosci Rep 2010;10: 47–52. 3. Anderson KN, Bradley AJ. Nat Sci Sleep 2013;5:61–75. 4. Macey PM, Kumar R, Woo MA, et al. Sleep 2008;31:967–77. 5. Alchanatis M, Deligiorgis N, Zias N, et al. Eur Respir J 2004;24:980–86. 6. Sarchielli P, Prescitti O, Alberti A, et al. Eur J Neurology 2008;15:1058–64. 7. Furuyama JK, Wilson NE, Burns BL, et al. Magn Reson Med 2012 ;67:1499–505. 8. Schulte, RF and Boesiger, P. NMR Biomed 2006; 19: 225–263. 9. Poldrack R. Project: SPM Toolbox: Summary. 10. <http://rsbweb.nih.gov/ij/plugins/roi-manager-tools/index.html>. 11. Emin Akkoyunlu M, Kart L, Kılıçarslan R, et al. Respiration 2013 [Epub ahead of print].

Region	Metabolite ratios	Correlation Coefficients	p-value	
Left Frontal white	FA	Cho	0.852	0.031*
		tNAA	0.69	0.058
	MD	Gln	-0.756	0.030*
	Glx	-0.676	0.065	
Right Frontal white				
FA	Gln	-0.996	0.056	
	tNAA	0.754	0.083	
MD	ml	0.961	0.002*	
Medial frontal white/gray				
FA	NAA	0.765	0.045*	
Medial occipital gray				
FA	Cho	0.787	0.063	
MD	ml	-0.647	0.116	

Table 1: Pearson Correlation between the FA/MD and metabolite ratios significant at 0.05 level. tNAA = NAA+NAAG, tCho = Cho+PCH+GPC, Glx = Glu+Gln.