Validation of Random Vessel-Encoded Arterial Spin Labeling as Territorial Perfusion Imaging by Comparison to Conventional VEASL

Yi Dang[1], Jia Guo[2], Jue Zhang[3,4], and Eric Che Wong[5]

[1]Magnetic Resonance Imaging Research Center,Institution of Psychology, Chinese Academy of Sciences, Beijing, Beijing, China, [2]Department of Bioengineering, University of California San Diego, CA, United States, [3]Academy for Advanced Interdisciplinary Studies, Peking University, Beijing, China, [4]College of Enigneering, Peking University, Beijing, China, [5]Department of Radiology and Psychiatry, University of California San Diego, CA, United States

Purpose:

Vessel-encoded arterial spin labeling (VEASL) is a territorial perfusion imaging technique to identify the perfusion territories of cerebral arteries simultaneously [1]. When using conventional VEASL, the collection of an angiogram, and user input of vessel locations in the tagging plane is necessary. In an effort to automate the scan prescription process, random vessel encoded arterial spin labeling (R-VEASL) was proposed to simultaneously measure perfusion territories and detect feeding arteries without prior knowledge of their positions [2-3]. The aim of this study was to validate the output of R-VEASL, by comparison with the perfusion maps acquired with conventional VEASL.

Methods:

Nine healthy subjects were studied in a General Electric MR750 3T scanner, using a commercial 8-channel head RF coil, under a protocol approved by the local IRB, and described in [1, 3]. Firstly, anatomical regions of the anterior circulation, deep gray matter, and posterior circulation were scored by two experienced radiologists (7 years) for their agreement with the R-VEASL perfusion maps as follows using the five-grade marking system : score 5 (agreement both of anatomical regions as well as mixed perfusion), score 4 (anatomical regions agree but mixed perfusion is not detected), score 3(some boundaries are misclassified due to mixed perfusion), score 2 (boundaries of anatomical regions disagree), and score 1 (misclassification of an anatomical region to a wrong feeding artery) [4].

For a quantitative comparison between conventional VEASL and R-VEASL, the Hausdorff distance was calculated between same perfusion regions obtained by two methods as stated in Eq. [1], where $|\cdots|$ is the Euclidean length of the vector between two points [5]. The Hausdorff distance between regions is defined as the maximum distance between two regions and can signify the maximum degree of mismatch between two regions. In our study, the Hausdorff distance measures the maximum distance of any voxel of perfusion region obtained by conventional VEASL that is the farthest away from any voxel of the same perfusion region obtained by R-VEASL and vice versa.

$$d_H = \max\{d(A,B), d(B,A)\} \qquad d(A,B) = \max_{a \in A} \min_{b \in B} |a - b| \qquad [1]$$

In addition, the Dice similarity coefficient (DC) is measured to quantify the overall agreement between same perfusion territories acquired by two methods [6]. The DC as a spatial overlap measure is defined in Eq. [2] as the ratio between the number of voxels in the intersection between two regions, and the mean volume of both regions, where N (…) is the number of voxels in a region. The range of DC between two regions is [0, 1] (0: no agreement, 1: perfect agreement).

$$DC(A,B) = \frac{2N(A \cap B)}{N(A) + N(B)} \qquad [2]$$

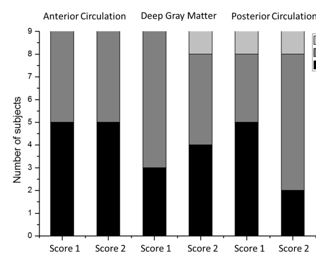

Figure 1. Qualitative agreement of R-VEASL perfusion maps with the anatomical regions of the anterior circulation, deep gray matter, and posterior circulation.

Results:

The qualitative comparison of R-VEASL perfusion images with anatomical regions was shown in Figure 1. Good agreement was found between R-VEASL perfusion territories with anatomical regions. The Hausdorff distance and Dice similarity coefficient of conventional VEASL compared to the images acquired with R-VEASL are summarized for the entire group per territory in Table 1. The Hausdorff distance and DC are both shown for territories of the right and left internal carotid arteries (RICA, and LICA), and the basilar artery (BA). The reported difference in Hausdorff distance between boundaries acquired by conventional VEASL and R-VEASL showed that the overall maximum mismatch for each perfusion territory is about 12 mm (two to three voxels), and the reported Dice similarity coefficient of the same determined regions illustrated a substantial agreement (DC≈0.9).

Conclusion and Discussion:

In this study, the overall good agreement between perfusion images of R-VEASL and anatomical regions has been demonstrated. Moreover, quantitative comparison of perfusion territories between R-VEASL and conventional VEASL has shown that perfusion territories obtained by both methods agree reasonably well. However, by comparing the perfusion images of healthy volunteers obtained by two methods, it seems that R-VEASL performs better than conventional VEASL when detecting perfusion region with mixed perfusion (shown in Figure 2, white arrow).

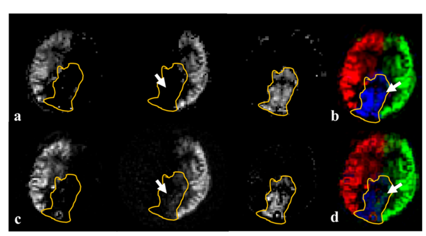

Figure 2. Perfusion maps of the RICA, LICA, and BA of one subject with a normal variant of the circle of Willis generated with conventional VEASL (a) and R-VEASL (c), and the corresponding territorial maps ((b) and (d)). The territory of the BA is outlined in the conventional VEASL images and copied to the other territorial maps. The territorial perfusion images generated with R-VEASL do show the mixed perfusion in the posterior circulation region (white arrow); the mixed perfusion in the posterior circulation (white arrow) is however not visible.

References:

[1]Wong, EC, MRM, 2007. [2]Wong, EC, Guo, J, ISMRM p.294, 2011. [3]Wong, EC, Guo, J, MAGMA, 25(2):95-101, 2012. [4] Hartkamp, NS, et al, MRM, 2014.71(6):2059-2070. [5]Huttenlocher, DP, et al, IEEE Transactions on, 1993. 15(9): 850-863. [6]Dice, LR, Ecology, 1945. 26(3): 297-302.

Table 1. Quantitative Comparison of traditional VEASL with R-VEASL

Method	Territory		
	RICA	LICA	BA
Hausdorff distance (mm)	10.7 ± 2.1	9.9 ± 2.1	9.6 ± 2.3
Dice similarity coefficient	0.90 ± 0.02	0.90 ± 0.02	0.91 ± 0.02