In vivo cerebral perfusion territory and watershed zone delineation in healthy volunteers using ASL, DSC-, and DCE-MRI.

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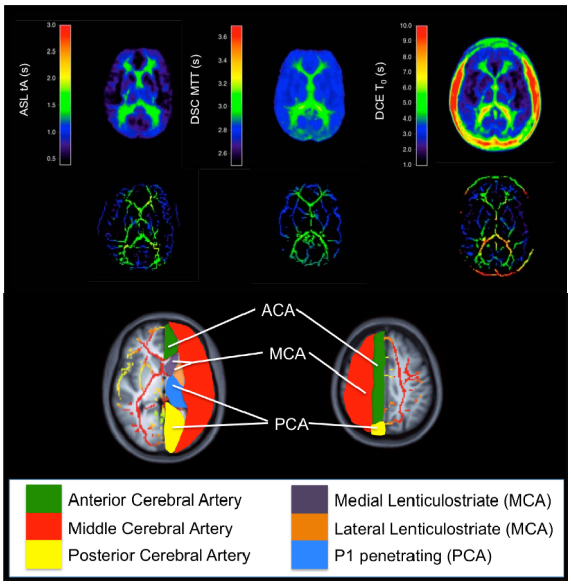
Target Audience: Neuroradiologists, neurophysiologists, anatomists, and researchers with an interest in neurovascular disease and analysis of conditions with a potential underlying neurovascular component or risk.

Purpose: Knowledge of arterial perfusion and watershed regions in the brain is used to identify tissues which may be at risk during times of cerebral perfusion autoregulatory failure, or metabolic stress in the brain parenchyma[1]. This applies to acute insults during systemic hypoperfusion and stroke, and longer-term insults through chronic metabolic or autoregulatory change implicated in neurodegenerative diseases such as multi-infarct or Alzheimer's dementia. While many hard-copy atlases exist depicting watershed regions in the brain, and these areas are well known empirically among neuroradiologists from cadaveric injection studies and patho-anatomical correlations, no atlases are available in commonly-used template space for group-wise analysis of disease with respect to watershed zones, and this is the first time to the authors' knowledge that fine detail of perfusion and watershed territories has been determined in vivo. Vessel-selective ASL can identify gross regional perfusion but it can be difficult to implement. We wished to identify methods to interrogate watershed regions from the timing parameters derived form perfusion-weighted imaging (PWI) that could be used individually, and in a template or atlas format in MNI space.

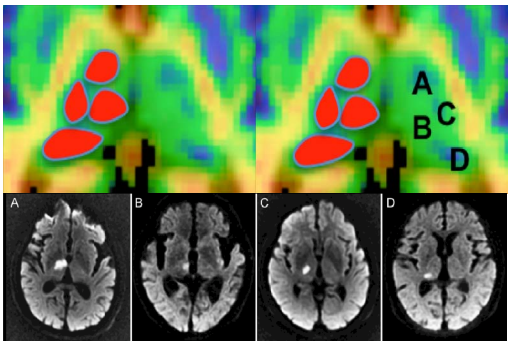
Methods: 14 young, healthy volunteers (5M:9F, mean 29.2 (29-48) years) underwent ASL, and DSC-MRI, and DCE-MRI imaging at 3 T on two separate occasions. Strict criteria on time and conditions of scan, recent exercise, and caffeine intake were imposed to minimize inter-visit variation. Phase contrast angiography was used to ensure all participants had a non-variant circle of Willis anatomy, with normal flow characteristics in the internal carotid and vertebrobasilar arteries, and structurally normal brains. Arrival time (tA) was derived from multi-inversion ASL, mean transit time (MTT) was derived from DSC using gamma-variate fitting[2,3], and arrival time (T_0) was derived from DCE-MRI using standard Tofts' kinetic modeling. These maps were constructed into templates in MNI space using FSL and skeletonized using a local tangential surface mapping tool based on confluent local signal maxima to identify border zones of delayed or prolonged perfusion timing parameters.

Results: The timing parameters from perfusion-weighted MR provide a probabilistic identification of major arterial territory watershed zones, in addition to perforating watershed zones in subcortical tissues. When constructed into a template in MNI space, there is good subjective correlation between the watershed zones identified here, and current literature hard copy atlases in proprietary space, and probabilistic MCA flow territory in MNI space derived from a recent nuclear medicine study[4]. The left figure demonstrates the anterior, posterior, middle, thalamic and lenticulostriate perfusion territories and respective intervening borderzones in MNI space as defined by these methods, based on skeletonization of the timing templates. The right figure demonstrates the sensitivity of this technique, with identification of the separate canonical thalamic perfusion territories, with patho-anatomical correlations from diffusion-weighted imaging in acute ischemic infarctions[5]. Cerebellar perfusion territories were also faithfully reproduced (not shown here for brevity). An MNI space atlas was constructed showing the perfusion territories.

Discussion: We have demonstrated the use of PWI (ASL, DSC-, and DCE-MRI) timing parameters for the identification of watershed regions in the brain, and used them to create a template in MNI space. While this is currently limited to those with normal cerebrovascular anatomy and flow, it may be useful in the group-wise analysis of imaging data in which subjective anatomical delineations of watershed or perfusion regions are currently employed. While the template provides a continuous description of perfusion timing parameters in the brain, skeletonization and hard segmentation allow an atlas to be defined.



Conclusion: Presented here is the first demonstration of all major recognized hemispheric, subcortical, and cerebellar perfusion territories and watershed zones in vivo in healthy subjects using physiological MR perfusion imaging techniques. This data furthers the understanding of neurovascular physiology and hemodynamics, and provides a key novel tool in the investigation of population-based studies of diseases with a neurovascular association or risk.



References:
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