Whole body multi-parametric MRI; A comparison of the diagnostic performance of different sequences

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Target Audience: Radiologists and Oncologists with an interest in Multiple Myeloma.

Purpose:
Whole body magnetic resonance imaging (WBMRI) is gaining ground for initial staging [1] and monitoring treatment response [2] of patients with multiple myeloma. The superiority of WBMRI compared to other imaging modalities such as CT and PET-CT scans has been established [3,4]. However, most of the reported WBMRI protocols are based on anatomical MRI sequences such as pre-contrast T1 weighted, T2-weighted and short tau inversion recovery (STIR). In this study we investigate the diagnostic performance of additional MRI sequences (diffusion weighted and contrast enhanced) for detection of bone marrow involvement in patients with multiple myeloma.

Material and Methods:
Twenty-three patients (15 female, 8 male)(mean age 52.2 years, range 31-69) with biopsy confirmed multiple myeloma underwent a multi-parametric WBMRI. All imaging was performed on a 3.0T MRI (Ingenia, Phillips, Best, Netherland) with the patient supine, using 2 anterior surface coils, head coil and integrated posterior coils. Total scanning time was 75 minutes and involved free breathing axial T2-weighted turbo spin echo (TSE) sequence (TR 1228ms, TE 80ms, slice thickness 5mm, pixel bandwidth 537Hz, acquisition matrix 500*497, SENSE factor 2, number of slices 40); free breathing axial diffusion weighted echo planar imaging (DWI-EPI) with spectral attenuated inversion recovery (SPAIR) plus slice selective gradient reversal (SSGR) fat suppression (TR 6371ms, TE 71ms, slice thickness 5mm, pixel bandwidth 3369Hz, acquisition matrix 124*118, SENSE factor 2.5, number of slices 40, 4 b-values; 0, 100, 300 and 1000 s/mm^2); and pre- and post-contrast 2 points modified Dixon sequences (TR 3.0ms, TE 1.02-1.8, flip angle 15°, slice thickness 5mm, pixel bandwidth 1992Hz, acquisition matrix 196*238, SENSE factor 2, number of slices 120) covering vertex to toe.

MRI images were reviewed by two radiologists in consensus using a locked sequential read paradigm. In phase pre-contrast mDixon images were reviewed first, followed by T2 TSE, b1000 DWI and finally post-contrast water only mDixon images. The body was divided into 10 anatomical stations (cervical, thoracic and lumbar spine, shoulder girdle, humerus, chest wall, pelvis, femur, skull and tibia, fibula and foot as one station). Images were reviewed prospectively for different patterns of bone marrow involvement as previously described [5]. Four patterns of involvement; normal, focal, diffuse and diffuse and focal were allocated. Any focal lesion greater than 5mm seen on any sequence was considered suspicious for disease [6]. When present, a confidence score (1 highly unlikely, 2 Unlikely, 3 Indeterminate, 4 Likely and 5 highly likely) was assigned for likelihood of myelomatous involvement. Confidence scores of 4 and 5 were considered as positive for bone marrow involvement. The number of positive focal lesions (confidence score 4 and 5) for each patient was recorded for each component of the locked sequential read and used to derive the Durie-Salmon PLUS staging [1]. A repeated measure ANOVA with Turkey's multiple comparison post test was used to compare median value of number of positive focal lesions on different sequences.

Results:
There were 15 IgG, 5 IgA and 3 light chain (LC) multiple myeloma patients. Sixteen patients had a focal only pattern of involvement, 6 had diffuse and focal pattern and one patient had a normal marrow on all sequences. Using anatomical MRI (pre-contrast in-phase mDixon and T2 TSE) for Durie-Salmon PLUS staging, 3, 5, 8 and 7 patients were assigned to MGUS, stage 1, stage 2 and stage 3, respectively. The addition of DWI upstaged 12 patients and resulted in 1, 1, 2 and 19 patients being assigned to MGUS, stage 1, stage 2 and stage 3, respectively. The addition of post-contrast water only mDixon did not change staging any further. The median number of focal lesions detected for each patient was significantly lower for pre-contrast in phase mDixon (median 8; interquartile range (IQR) 1-18) and T2 TSE (median 11, IQR 1-29) compared to DWI (median 34, range 22-68) and post contrast water only mDixon (median 22, range 8-42) ($p<0.05$) (figure 1 and figure 2).

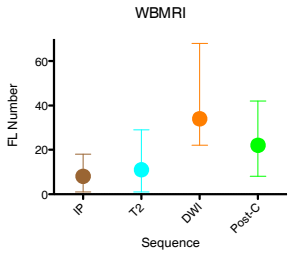

Figure 1: Median (interquartile range) for focal lesion (FL) detection with different sequences

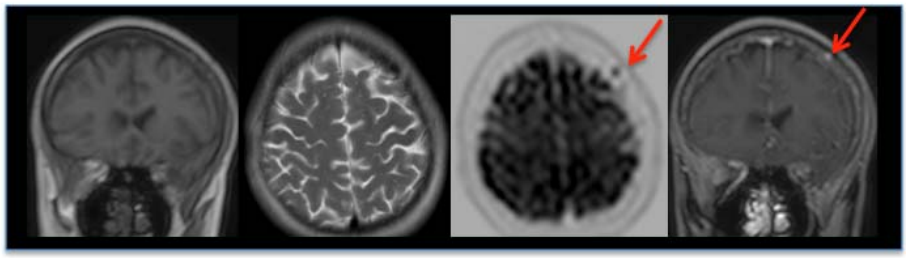

Figure 2: Example of focal multiple myeloma skull involvement. From left to right: Pre-contrast in phase mDixon, T2-TSE, inverted b1000 DWI and post-contrast water only mDixon showing a focal lesion in skull not visible on anatomical MRI, but apparent on additional MR sequences (DWI + Post-contrast) (red arrows).

Discussion and Conclusion:
In this study, we demonstrated that imaging using DWI and post-contrast images increased the detection rate of focal lesions and resulted in upstaging of patients on Durie-Salmon PLUS staging. Furthermore, multiple focal lesions at a given site on DWI were often demonstrated as diffuse enhancement on contrast enhanced imaging, hence fewer focal lesions were demonstrated on contrast enhanced images compared with DWI. Whilst DWI reflects the cellular nidus of each lesion, contrast enhanced imaging likely reflects enhancement of the lesion and the surrounding oedema.

References:
[1] Fechtner et al, 2010. Radiology 257:195-204 [2] Giles et al, 2014. Radiology 271:785-794 [3] Baur-Melnyk et al, 2008. AJR 190:1097-1104 [4] Shortt et al, 2009. AJR 192:980-986 [5] Dimopoulos et al, 2009. Leukemia 23:1545-1556 [6] Hillengass et al, 2010. J Clin Oncol 20:1606-1610