Combined stereoscopic X-ray and MR Imaging ("XMR") for the evaluation of prostate brachytherapy implants with comparison to standard CT-based dosimetry.

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Purpose.

Permanent prostate brachytherapy (PPB) is recognised as a curative treatment option for men with localised prostate cancer. Radioactive sources are implanted directly into the prostate gland in order to deliver as targeted a radiation dose as possible whilst minimizing doses to nearby organs at risk such as the urethra and rectum. Dosimetric evaluation of the implant requires the knowledge of source positions in relation to soft tissue structures including the prostate gland. This is an essential part of the process in order to document the quality of individual implants, predict outcome, provide technical feedback to the operator and allow multicentre studies. If an implant is found to be of poor quality, then additional treatments can be directed. The current standard is to carry out dosimetric evaluation based on information derived from CT imaging [1]. However, CT is limited by similar appearances of soft tissue structures making delineation difficult, and ambiguities concerning source positions particularly when in clusters. XMR imaging combines excellent soft tissue visualisation by MRI with seed visualisation by stereoscopic X-ray imaging [2]. The purpose of this study was to analyse PPB implants using the XMR facility and compare generated dosimetric data with standard CT-derived parameters.

Methods.

With appropriate ethical approval, patients who had undergone PPB implants with EchoSeeds™ (model 6733) presented four weeks later for both a CT scan and an XMR scan (1.5T Intera scanner and BV Pulsera mobile X-ray set, Philips, Best, The Netherlands) within 4 hours of each other. Following the acquisition of T2-weighted turbo spin echo images (TE=120ms, TR=4.9s) with an axial slice-thickness of 3.3mm using a 4-element body array coil, the subject was transferred via a sliding table top to the x-ray system where two oblique radiographs were taken as well as a video sequence between the two views. MR and x-ray images were fused by a registration technique that relied on a combination of prior calibration and real-time optical tracking [3]. Individual seed locations were manually extracted from the two x-ray images with the help of the fluoroscopic video and marked to their nearest MR coordinates. Further optimisation was carried out by a point-to-image registration technique to compensate for any patient motion. Resultant images were transferred to the Varian software package (Variseed 7.1) for outlining of structures and the generation of dosimetric parameters. Dosimetric parameters generated included: volume, the V100 (volume of prostate receiving 100% of the prescribed dose (145Gy)) and the D90 (% of prescription dose to 90% of the prostate). Comparisons were made between the two datasets (CT and XMR) using Bland-Altman analysis as a test of agreement.

Results.

Ten patients were entered into the study. The scanning process was well tolerated and images were successfully transferred onto the planning software. Sources were confidently visualised on the plain radiographs, and the soft tissue structures well outlined on the MR films. Marked seed positions on the MR images corresponded very well with signal voids. The Bland-Altman analysis is shown in table 1. Whilst the means of the dosimetric parameters are similar, the wide limits of agreement suggest little agreement between the methods

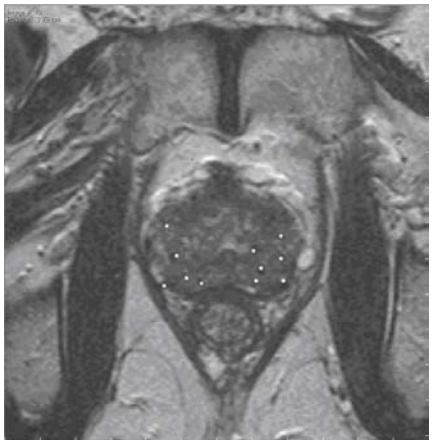
Conclusions

XMR-based dosimetry is feasible. The technique gives different results to those from CT. This may be due to superior soft tissue delineation and confident localisation of sources. Time will tell whether these differences have a clinical impact in the future.

Table 1. Bland-Altman analysis of dosimetry values

Dosimetric parameter	Mean difference (CT to XMR)	Limits of agreement (95% CI)
Vol (cc)	-1.4	-9.6, 6.8
V100 (%)	0.6	-8, 9.2
D90 (%)	1.1	-17.5,19.7

Fig 1. Example MR image showing an axial slice of the prostate with source positions marked as white dots.



References

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