

Biological target volume based on DTI-MRI in postoperative chemoradiotherapy for glioblastoma

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Introduction Treating glioblastoma (GBM) effectively by surgery and postoperative radiotherapy (RT) is challenged by infiltrative growth preferentially along white matter tracts (WMT). Diffusion tensor imaging (DTI)-MRI can be used to model tumor probability along the WMTs. The aim of this phase 1 study is to evaluate a biological target definition based on DTI. **Material/methods** Forty-two GBM patients referred for postoperative RT were included between 10/2016 and 06/2018, and treated according to ESTRO-ACROP guidelines (CTV is isotropic 2 cm expansion around GTV). Treatment response was assessed using RANO criteria. Patients with new satellites (separate localisation outside GTV) were identified. An additional pre-radiotherapy DTI-MRI was performed to create two biological CTVs, isovolumetric to the treated CTV. Anisotropic margins were based on tensor directionality of γ_0 and 20 (CTV γ_0 _20; higher γ means a higher presumed probability of tumor spread along WMTs). Dice similarity coefficient (DSC) was used for volumetric comparison of the target volumes. Overlap and Hausdorff distance 95% (HD) between the CTVs and the satellites were analysed to assess if the biological target volumes better predict for recurrence sites (2-sided paired Student's t-test). **Results** At a median follow-up of 11.7 (range 4-23) months, 30 patients had radiologic progression. In 10 of these, 19 satellites were identified. The respective mean (range) DSC of CTV vs. CTV γ_0 , CTV vs. CTV γ_{20} and CTV γ_0 vs. CTV γ_{20} was 0.76 (0.58-0.9), 0.73 (0.59-0.9) and 0.9 (0.77-0.97). The CTV (partially) overlapped 8 satellites with a mean HD of 19.6 mm; the CTV γ_0 and CTV γ_{20} both (partially) overlapped 11 satellites with a respective mean HD of 17.4 and 16.9 mm. This was significantly closer for CTV γ_0 vs. CTV, $p=0.048$ (CTV γ_{20} vs. CTV $p=0.058$, CTV γ_0 vs. CTV γ_{20} $p=0.48$). **Conclusion** DTI improved prediction of satellite localisations, and shows potential for an individualised biological target definition in GBM.