AbstractID: 9585 Title: Equivalent uniform dose calculation for I-131 tositumomab therapy including the cold protein effect

Purpose: Individualized treatment planning may benefit from equivalent uniform dose (EUD) techniques to help correlate 'dose' with objective patient outcome such as time to recurrence or response rate.   Our objective is to illustrate methods used to perform EUD calculations, specifically to incorporate the cold protein effect for non-Hodgkins lymphoma (NHL) patients treated with I-131 tositumomab.

Methods: Data from NHL patients treated with I-131 tositumomab were imaged multiple times for tracer and therapy studies using a SPECT/CT system. Dose rate calculations were performed by Monte Carlo technique for each image set. A 3D time dependent dose rate description was developed using measured uptake curves for the whole body and tumor volume(s). Tumor subunits were connected between time points using center-of-mass alignment and radial deformation. The EUD = $-1/\alpha$ [ln ($<S>$min)], where $<S>$min is the minimum average relative cell survival. S = exp$\{-\alpha$ BED$\}$, where the biological equivalent dose BED(v,t) = D(v,t) $+\lambda_t/\alpha$ *t $+\lambda_p/\alpha$ *P(v,t) for each subvolume; D is the dose; and the λ_t and λ_p represent the effects of proliferation and cold protein (P).

Results: Parameter fits were performed to match changes in tumor size. The tracer study was used to set λ_p based on patient-specific tumor response. The λ_t parameter was set by typical time to progression-free recurrence rates. The linear-quadratic parameters were set consistent with hypersensitivity at low dose rates (α=0.7 Gy^{-1}). EUD was calculated contrasting patients for which there was no cold protein effect with substantial cold protein effect. A common parameter set was used to fit the data, only varying by the cold effect parameter.

Conclusions: The cold protein effect can be substantial and is being included in the EUD calculation to help correlate delivered dose with patient outcome.