AbstractID: 5581 Title: Validation of a New Photon Dose Calculation Model Analytical Anisotropic Algorithm

Purpose: To validate a new photon dose calculation model Analytical Anisotropic Algorithm (AAA) on Eclipse^{TM} treatment planning system (TPS). Comparison of AAA dose calculation was performed with measurements and other two conventional algorithms, Pencil Beam Convolution (PBC) algorithm on Eclipse^{TM} and Collapsed Cone Convolution/Superposition (CCC) algorithm on Pinnacle$^{3.0}$ TPS.

Method and Materials: Four phantoms were CT scanned and the image set was imported into both TPS for dose computation and analysis. The four phantoms were: 1) homogenous tissue equivalent phantom, 2) tissue equivalent phantom with infinite lung heterogeneity, 3) tissue equivalent phantom with finite lung, 4) IMRT dose verification phantom. Measurements were made by exposing the phantom using Varian Linac. Point measurement and film measurements were compared with calculated results from the three algorithms. Dose responses for high and low energy photon beams were investigated for several different depths and PDD curves were compared in the phantom for various field sizes. The IMRT plans were generated by both TPS and were performed on the IMRT phantom to compare fluence maps.

Results: AAA dose prediction fits the film measurements well except that there is up to $\pm 6\%$ discrepancy for dose profile perpendicular to the interface of tissue and lung. Point measurements support the AAA algorithm calculations. AAA also accurately predicts the decrease in PDD curves due to the lung inhomogeneity for 6MV energy. For the high energy photon beam and very small field size (2cm*2cm) in lung region, AAA prediction is up to 8% lower than the measurements.

Conclusion: AAA algorithm accounts for attenuation corrections and electron transport, and models the deposited dose in the lung with greater accuracy than PBC. It is also faster than CCC algorithm. AAA algorithm can not accurately model the lateral scattering in tissue heterogeneity, but it can still give a reasonably close (within $\pm 6\%$) prediction.