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Measurement of modulation power using porcine lung tissue

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Introduction

The modulation power (P-mod) quantifies the degradation of Bragg-peaks due to submillimeter structures in target materials. However, such structures are not visible in clinical CTs. In this work, we present our measurement of P-mod in porcine lungs and for several proton beam energies.

Materials and methods

A phantom out of RW3 and Plexiglas® with a trachea connector was used to fix the lungs. Radiopaque markers were placed on the lung surfaces and evaluated using repeated CT scans.

The phantom was scanned using a Philips BigBore CT (Philips, the Netherlands) at the start of the experiment and at its end. Furthermore , the measurements were simulated retrospectively (see **Fig.1**) using the CT images of the phantom and the Monte-Carlo dose engine of the RayStation planning system (Raysearch Labs, Stockholm, Sweden)**.**

The CTs were registered using deformable registration and 3D displacement vectors were calculated (see **Fig.2**).

Proton depth dose measurements of pristine Bragg-peaks with different energies and at different locations in the lungs were carried out using the "Giraffe" multi-layer ionization chamber (IBA Dosimetry GmbH, Schwarzenbruck). The measurement were performed under image guidance (see **Fig. 4 & 4**).

The degradation of Bragg-peaks was calculated by convolving the simulated peaks with a Gaussian function until the degradation in measured Bragg-peaks was reached. Afterwards, the additional broadening (assumed to be due to submillimeter structures) was analyzed and P-mod was calculated (see **Eq.1**.).

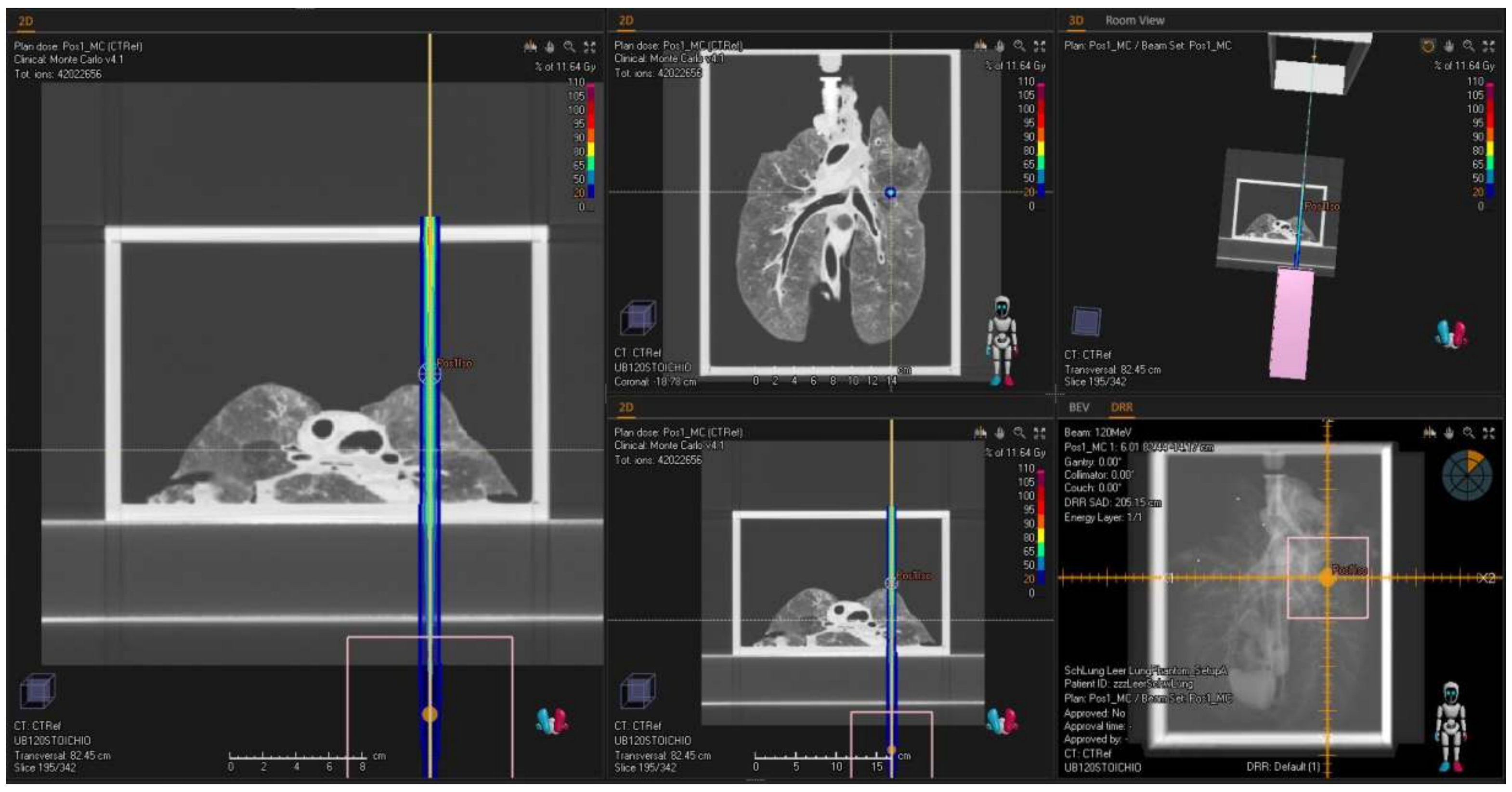


Fig.1: Simulation of measurement using the Raysearch treatment planning system and CT of lung phantom . CT images of the phantom in sagittal, transversal, and coronary section are displayed. The simulation was performed for several positions and energy in the lung sample.

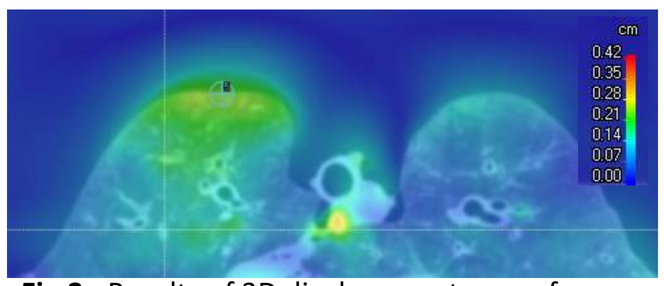


Fig.2: Results of 3D displacement map of deformable registration between CTs pre and post Proton measurements (4hrs). The maximum displacement vector was 0.42 cm.

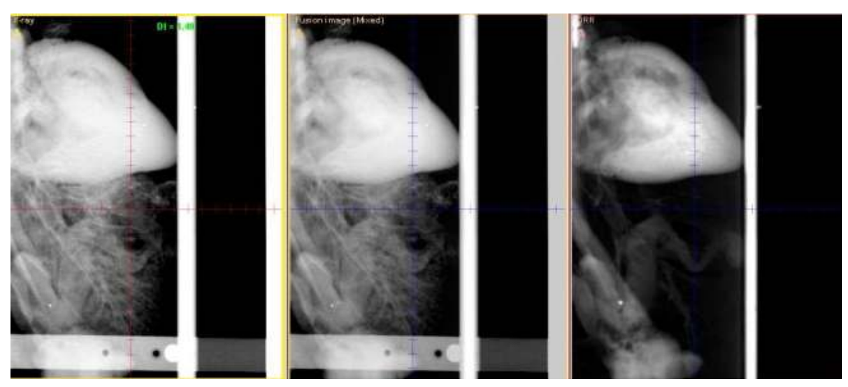
$$t = D.\rho_{mean}$$

$$P_{mod} \equiv \frac{\sigma^2}{t} = d\,(\rho_{mat} - \rho_{mean})$$

Eq.1 The degraded Bragg-Peak can be described by convolution of initial peak with a normal distribution. The mean water equivalent thickness of the material (t) is the mean density of material (ρ_{mean}) divided by thickness of sample (D). The modulation power (P_{mod}) is related to the density difference between material composites and size of pores (d) [1].

Fig.3: Image guidance was performed using the clinical Patient Positioning Verification System (PPVS). Portal X-rays were used to align the phantom relative to the predefined isocenter which is marked on the phantom.

Fig.4: The DRRs from planning are compared to isocenter position using the PPVS. seen below.



Results and conclusion

P-mod quantifies the degradation of Bragg-peaks due to submillimeter structures in target materials. The P-mod (Eq.1). An example of the measured , simulated , and convoluted peaks is shown in **Fig.5.** to evaluate the accuracy of the analysis, the position of measured peaks is compared to the position of simulated then convoluted peaks. The average shift in position was -0.1±1.0 mm .

The measured P-mod values are 98±39 µm which are relatively smaller than the values reported in literature [1] . In **Fig.6**, the data is grouped per Energy of incident protons.

The main advantage of this setup is the ability to use CT data which in-turn allows distinguishing between macro- and micro- structures in the lung system.

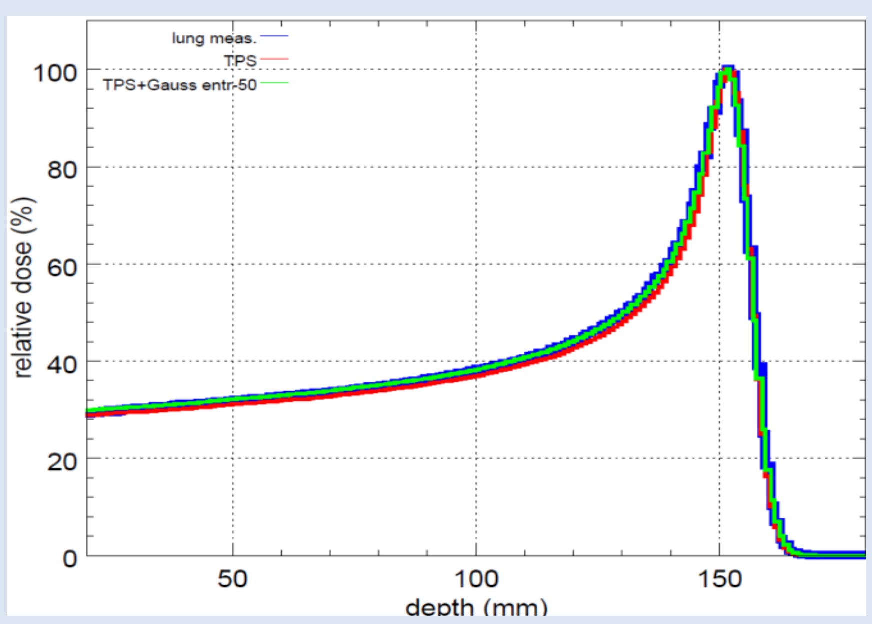


Fig.5: Depth-dose curve measured using the Giraffe (IBA Dosimetry GmbH, Schwarzenbruck) and 170 MeV protons. Measurements were compared to TPS simulated depth dose curves at the point of the measurements.

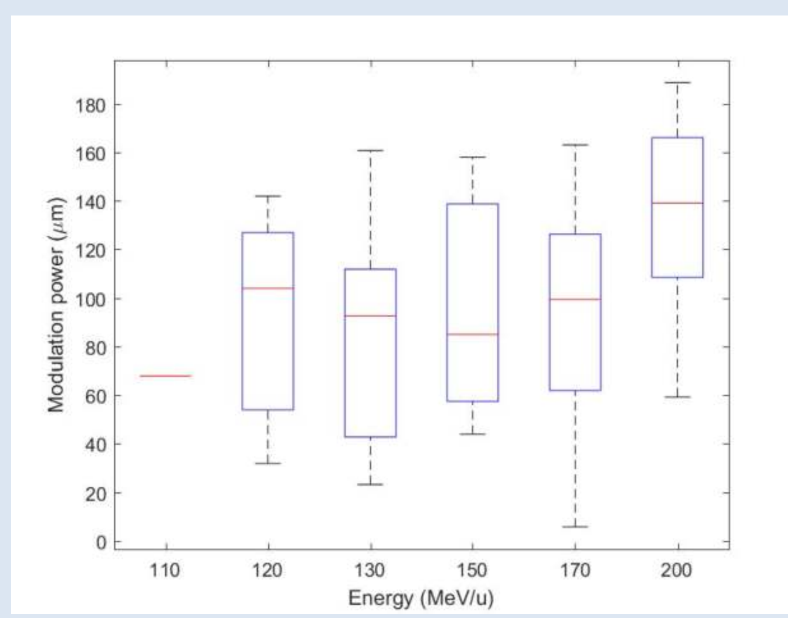


Fig.6: The Modulation power in the peak position of the pristine Bragg-Peak. The data is grouped per energy as several positions were measured. Average value is 98±39 µm

References

[1] Ringbæk, T.P. et al, Phys. Med. Biol. 2017; 62(7): 2892–2909.

[2] Titt, U et al, Med Phys. 2015; 42(11):6425-32.