Mechanisms and Clinical Significance of Particle RBE

Variable RBE (vRBE) Models are the Future of Particle Therapy Treatment Planning

Robert D. Stewart, Ph.D.

Associate Professor of Radiation Oncology and Medical Physicist Leader, Clinical Radiation Biology University of Washington School of Medicine Department of Radiation Oncology 1959 NE Pacific Street Seattle, WA 98195-6043 206-598-7951 office 206-598-6218 fax trawets@uw.edu



Presented: 2020 Joint AAPM/COMP Meeting (July 12-16) **Date and Time:** Tuesday July 14 from 3:30 PM - 4:30 PM **Location:** Virtual



Disclaimer

- Co-investigator on a Research Collaboration Agreement with RaySearch Inc.
- Have an unapologetic bias towards the use of vRBE models for outcome assessment and plan optimization



Learning Objectives

- Understand the relationship between the RBE for DNA double strand break (DSB) induction (RBE_{DSB}) and the RBE for reproductive cell survival
- Gain an appreciation for the strengths and weaknesses of RBE modeling as useful predictive tools for the analysis of laboratory and clinical studies
 - Do mechanism-inspired RBE models **capture** <u>more</u> **biology** than LET-based models? From a clinical perspective, do we care more about LET or biology?
- Provoke discussion and <u>debate</u> on forward-looking strategies to more fully exploit the potential of hadron therapy using RBE-based plan optimization
 - Is plan optimization based on LET more accurate and less risky than **robust planning** using a mechanistic RBE model?



RBE for DSB Induction (RBE_{DSB})

DSB are the most critical form of initial molecular damage created by ionizing radiation

Pairs of mis-rejoined DSB create chromosome aberrations that are often lethal or highly mutagenic.

 RBE_{DSB} closely related to the RBE for cell survival.

Monte Carlo models reflect and synthesis a large body of measurements, i.e., they are the "gold standard" for RBE_{DSB}

Figure adapted from data presented in Stewart *et al.* (2011, 2015, and 2018). Open and filled symbols are published data from *track structure simulations*. **Solid lines** are for the Monte Carlo Damage Simulation (MCDS).

Published models for RBE_{DSB} are in good agreement with each other for a wide range of particle types and energies.



Track-end radiobiology and RBE_{DSB}

Monte Carlo models are in very good agreement for ¹H⁺ and ⁴He²⁺ ions with even a sub-millimeter range.

RBE_{DSB} only exceeds 1.1 in the last 2 mm of a proton track-track-end effects only have an impact on a few tens or hundreds of cells per proton (*i.e.*, *it's a small volume effect*)!

For the rapeutic protons, RBE_{DSB} only exceeds 1.4 well beyond the tip of a pristine Bragg peak (range ~ 1-2 mm).





Is *RBE_{DSB}* Predictive of Trends in Cell Survival with LET?



Repair-Misrepair-Fixation (RMF) Model (Carlson et al. 2008, Stewart et al. 2018)

1. Estimate α_{R} and $(\alpha/\beta)_{R}$ from a fit to kV x-ray data (red filled circles) 2. Use MCDS to compute ion- and energy-specific value for RBE_{DSB}

3. Compute ion-specific value for α_{ion} and β_{ion} using RMF formula

$$\alpha_{ion} = \alpha_{R} \cdot RBE_{DSB} \left(1 + \frac{2\overline{z}_{F}RBE_{DSB}}{(\alpha / \beta)_{R}} \right)$$
$$\beta_{ion} = \beta_{R} \cdot RBE_{DSB} \cdot RBE_{DSB}.$$

$$\overline{z}_F \cong LET / \rho d^2$$

d is effective diameter of cell nucleus (~ few μm)

4. Compute cell survival: $S(D) = \exp(-\alpha_{ion}D - \beta_{ion}D^2)$

(dashed lines in figure are *predictions* and not fits!)



$RBE_{DSB} \rightarrow RBE$ for Reproductive Cell Survival

In the MCDS + RMF system of models, the RBE for cell survival is always greater than or equal to the RBE for DSB induction.

Low dose RBE:
$$RBE_{LD} \equiv \frac{\alpha_{ion}}{\alpha_R} = RBE_{DSB} \left(1 + \frac{2\overline{z}_F RBE_{DSB}}{(\alpha / \beta)_R} \right) \ge RBE_{DSB}$$

High dose RBE: $RBE_{HD} \equiv \sqrt{\frac{\beta_{ion}}{\beta_R}} = RBE_{DSB} \ge 1.$

For ion dose *D*, RBE for cell survival only depends on $(\alpha/\beta)_R$ and the asymptotic value for RBE_{LD} and RBE_{HD}.

$$RBE(D) = \frac{(\alpha / \beta)_{R}}{2D} \left\{ -1 + \sqrt{1 + \frac{4D}{(\alpha / \beta)_{R}} \left(1 + \frac{D}{(\alpha / \beta)_{R}} \frac{\left(RBE_{HD}\right)^{2}}{RBE_{LD}}\right) RBE_{LD}} \right\}$$

Reviewed in Stewart et al. Med Phys. 45(11):e925-e952. doi: 10.1002/mp.13207 (2018). PMID: 30421808



For protons, the RBE for cell survival is in good agreement with RBE_{DSB} (red squares and yellow triangles are with n few %). For ${}^{4}\text{He}^{2+}$ and other massive ions, RBE_{LD} can be much larger than RBE_{DSB} .

Is LET an effective alternative to RBE modeling?

Laboratory studies provide overwhelming evidence that molecular and cellular damage tends to (1) increase with increasing LET, (2) decreases with increasing dose, and (3) increases with decreasing tumor and tissue (α/β)

- LET-based approach of Unkelback *et al.* (2016) is effectively the same as plan optimization using a Monte Carlo model (Stewart *et al.* 2011, 2015) for proton RBE_{DSB}
- Optimization based on LET and RBE_{DSB} does not capture the dose-dependence nor the tissue-specific aspects of particle RBE
 - Parameter "k" depends on (α/β) and dose.
- Neglecting the dose- and tissue-specific aspects of particle RBE is potentially more risky than robust planning (e.g., Kamp presentation) using RBE models that capture fundamental molecular and cellular mechanisms.



Representative plan optimized for dose (RBE = 1.1), track-end avoidance in a critical OAR, and RWD (= dose \times RBE_{DSB})



Conclusions

- Mechanism-inspired RBE models for the endpoint of cell survival may not capture all of the relevant biology. *But...* they do capture <u>more</u> fundamental molecular and cellular biology than LET-based methods
 - LET-based approach of Unkelback *et al.* (2016) is effectively the same as using RBE_{DSB} for plan optimization, <u>if</u> selective applied to contoured (*critical*) OAR
 - Track-end based optimization is *much more aggressive* about pushing biological hot spots out of **contoured** critical OAR and into adjacent (**non-specific**) tissue than global RBE-based optimization. Which approach is more risky?
- RBE modeling has been effective for high LET carbon ions and fast neutron therapy Why not use it for proton plan optimization too?
 - Uncertainties in vRBE modeling can be mitigated through robust planning (e.g., Kamp presentation). Plans could also be rescaled to ensure tumor coverage is not compromised.
- RBE-based plan optimization is no more risky than LET-based optimization and, regardless, arguably superior to a constant clinical RBE = 1.1 for plan optimization.