AbstractID: 1668 Title: Modeling gene expression following the local injection of adenovirus to guide improvement in gene therapy

Two recently completed clinical trials using replication-competent adenovirus-medicated suicide gene therapy (Adenovirus serum type 5 incorporating cytosine deaminase and thymidine kinase) demonstrated tumor destruction and suggested that the effectiveness of the approach was not limited by a lack of biological activity, but rather by the delivery of the virus. Our long rang goal is to optimize the gene therapy treatment to deliver a therapeutic gene expression to the entire prostate with the minimal amount of virus possible.

The purpose of this study is to develop a reliable model to estimate gene expression, which can be used in optimization. In this study the reporter gene, the sodium-iodide symporter was utilized to measure gene expression magnitude and volume in canine prostate following virus injection. A Gaussian-like function ($y=\alpha*\exp(-\beta*x^2) + \gamma$ where y was the gene expression intensity level, x was the spatial distance, and α, β and γ were constants) was used to fit the spatial distribution based on the coverage distribution of measured gene expression. This fitting model in the transverse direction showed good agreement (0.97 to 0.99 of correlation coefficient) with the coverage-based measured gene expression.

The preliminary result provides a potential basis for the gene expression model, which represents the first step in optimizing placement of virus injections for gene therapy.