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Structural Determinants of Neoantigen Immunogenicity for Cancer Therapy

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OBJECTIVES/SPECIFIC AIMS: We are exploring the structure of the interaction between an immunogenic neoantigen and a T cell receptor (TCR) that recognizes the neoantigen while tolerating the counterpart self antigen. No structural example exists to date of how a TCR can discriminate between a neoantigen and the self antigen. We aim to determine the structural and biophysical features that underlie the immunogenicity for this neoantigen, and the features we determine are likely to be present in other immunogenic neoantigens. Algorithms to predict the immunogenicity of neoantigens are available, but do not incorporate structural or biophysical factors. We aim to improve these methods for immunogenic neoantigen prediction by determining structural and biophysical factors that result in recognition by the immune system. METHODS/STUDY POPULATION: Recombinant protein expression, production, and purification. Protein x-ray crystallography. Biophysical protein-protein binding experiments RESULTS/ANTICIPATED RESULTS: The T cell receptor (TCR) bound to the neoantigen with an affinity 15-fold higher than the self antigen. The leucine to phenylalanine mutation occurs at position 8 of a 9-amino acid long peptide antigen. This position is typically in the interface bound by the T cell receptor. The structures of the unbound neoantigen and self antigen showed that the mutated residue was in the TCR interface. Additionally we noted a change in the side chain position of a proximal tryptophan, potentially due to clashes with the larger phenylalanine residue. The structure of the TCR bound to the neoantigen showed that the TCR interacted with the tryptophan in the mutation-induced conformation and with the phenylalanine residue. Thus the mutation may be altering TCR binding affinity by interactions of the residue itself with the TCR, and by locking the proximal tryptophan residue in an optimal position to interact with the TCR. We are testing the contributions of each of these factors to the overall affinity change. Hydrophobicity has been linked to immunogenicity, so mutations that increase hydrophobicity compared to the self antigen are likely to be immunogenic. However, leucine and phenylalanine are similar on hydrophobicity scales. On the other hand, a side chain rotation is unlikely to represent a large energy barrier. Therefore, we hypothesize that another property of the phenylalanine, such as size or aromaticity, is driving the affinity difference. DISCUSSION/SIGNIFICANCE OF IMPACT: Traditional forms of cancer therapy do not specifically target cancer cells, and their toxicity to healthy cells limits their effectiveness. Immunotherapy, which involves orchestrating a specific anti-cancer immune response, is now an established cancer therapy. Several forms of immunotherapy target "neoantigens," which are derived from mutated proteins in cancer, and are therefore are cancer-specific. Neoantigens represent a foothold that can allow the immune system to distinguish between cancer cells and healthy cells, and thus specifically target cancer cells for destruction while imparting no activity toward healthy cells that lack the neoantigen. Most cancer mutations that result in neoantigens arise from random passenger mutations in cancer and will be different among patients. Neoantigen-based cancer therapies are thus a precision medicine technique. The quality of neoantigens to induce an immune response (immunogenicity), which relates to how likely they are to be presented to the immune system and recognized as foreign, has been shown to be a critical factor in predicting the outcome of immunotherapy treatment. We are investigating, on a structural and biophysical level, features that may increase the likelihood of a neoantigen being recognized as foreign by the immune system. The structural insight we gain can be incorporated into algorithms that predict neoantigens from cancer exome sequencing for patient-specific identification of immunogenic neoantigens for immunotherapeutic intervention.

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TGFbeta, Early Cytokine Dysregulation, and Airway Smooth Muscle Dysfunction in Cystic Fibrosis

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OBJECTIVES/SPECIFIC AIMS: This study aims to first describe the unique cytokine profile and TGFbeta levels of young children with CF, then understand the pathologic effects of TGFbeta on lung function in a CF animal model. These powerful translational studies linking observations in clinical disease with a transgenic mouse model allow us a unique opportunity to investigate the role of TGFbeta in early CF lung disease. METHODS/STUDY POPULATION: Cytokine levels (TGFbeta, TNFalpha, IL-8, IL-6, HNE, and IL-1beta) in bronchoalveolar lavage fluid (BALF) from CF patients ($n = 15$) and non-CF control patients ($n = 21$) under 6 years old were determined by ELISA and Luminex assay. Tracheotomized patients without significant underlying lung disease were chosen as non-CF inflamed control patients, as they had similar levels of neutrophilic inflammation and infection as CF patients. The percentage of BAL neutrophils (% PMNs) in each sample was assessed. The relationships between cytokines were analyzed using linear regression and principal components analysis. In animal studies, CF and non-CF mice ($n = 4$-5 per group) were treated with intratracheal adenoviral TGFbeta1 vector, an empty vector control, or PBS. After one week, animals were collected; lung function, response to the bronchoconstrictor methacholine, and rescue with albuterol were measured utilizing a FlexiVent machine. Lungs were collected for histology. Immunohistochemistry for alpha-SMA was performed and pictures of all cross-sectional airways were obtained. Burden of ASM was assessed by dividing the square root of alpha-SMA stained airway smooth muscle by the basement membrane perimeter length of each airway. RESULTS/ANTICIPATED RESULTS: Patient characteristics of CF and non-CF inflamed control patients were similar in terms of age (3.6 yrs vs 3.3 yrs respectively, $p = 0.49$), positive BAL culture (13% vs 14%, $p = 0.94$), and % PMNs (65% vs 56%, $p = 0.64$). Despite these similarities, TGFbeta levels were 2-fold higher in CF versus non-CF BAL ($p = 0.034$). Analysis of BAL cytokines from both patient groups showed that three principal components describe 86% of total variance across the cytokine variables. These components represent different contributions from the cytokines, with TGFbeta, IL6, and % PMNs comprising one component of similarly regulated inflammatory markers. These components can distinguish CF versus non-CF patients with 77% accuracy (area under the curve: 0.77). TGFbeta concentrations were uniquely associated with increased IL-6 in CF samples ($r = 0.74$; $p = 0.0015$) but did not demonstrate association with other cytokines. After TGFbeta exposure, CF mice demonstrated greater abnormalities

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