Novel Design and Optimization of an EGFRvIII-based Cancer Peptide Vaccine

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Cancer vaccines are a revolutionary, new field of cancer therapeutics that aim to utilize the body's natural defenses to treat cancer. Through my research, I designed and optimized an effective anti-cancer vaccine based on the existing EGFRvIII vaccine by computationally and experimentally evaluating optimal proteasome processing, MHC reception, and ultimately malignant cell death. Mass Spectrometry (MS) was conducted on five separate variations of the LEEKKGNYVVTDHC (LEEK) peptide that were fed to the human proteasome. Normalization offset was calculated, and a (Screen Pixel)/Dalton ratio was used to normalize the data. Effective and ineffective peptides were compared with other effective and ineffective variations, respectively. I designed a Java-based algorithm to evaluate the MS data in order to validate graphical analysis. Based on existing mouse survival data, variations A and B consistently performed poorly, while survival rates for variations C, D, and E averaged above 50%. Several repetitions of MS that I conducted demonstrated large amounts of processing in the effective peptides at 2606 Daltons, which was then fully characterized using graphical and computational methods I created. This vaccine complex, as validated computationally, biologically, and graphically, was prevalent in effective peptides, but not present in ineffective peptides. The cancer vaccine variations show significantly improved survival data, which correlates with the increased production of the larger processed peptide at 2606 Da. In summary, my research discovered the optimal EGFRvIII-based cancer vaccine for glioblastoma through characterizing its processing in the proteasome using the experiments and novel analysis methods I developed.