RESEARCH COMMUNICATION

Finding a T-cell Epitope for a Melanoma Vaccine by an Immunomics Technique

Viroj Wiwanitkit

Abstract

The identification of tumor-associated T cell epitopes has contributed significantly to the understanding of the interrelationship of tumor and immune system and is instrumental in the development of therapeutic vaccines for the treatment of cancer. Here, the author reports preliminary data from the computation analysis of available Homo sapiens melanoma associate antigen to find potential T-cell epitopes using bioinformatics tool namely MHCPred. Using computational algorithm, we predicted the most potential T cell epitope from known melanoma associated antigen. This data are useful for further vaccine development because these promiscuous peptide binders allows to minimize the total number of predicted epitopes without compromising the population coverage required in the design of multi-epitope vaccines.

Key Words: Epitope - T cell - melanoma - vaccine

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Introduction

During recent years, cancer vaccines have made encouraging progress toward becoming a clinically relevant form of biologic therapy (Doherty et al., 2006). However, current vaccine approaches have shown only limited success in the patients with cancer because of inadequate immune activation. Immune responses to cancer are also probably restricted to the neoplasm's 'immunome', although the set of antigens that drive successful immune response to cancer cells has proven more difficult to uncover (Anonamous, 2005). Researchers now use several bioinformatic tools including sequence analysis tools, epitope mapping tools, microarrays and high-throughput immunology assays to discover the components of the immunome, which are then used to compose these new vaccines.

The identification of tumor-associated T cell epitopes has contributed significantly to the understanding of the interrelationship of tumors and immune system and has been instrumental in the development of therapeutic vaccines for treatment purposes (Braga-Neto and Marques, 2006). Here, the author reports preliminary data from a computation analysis of available *Homo sapiens* melanoma associate antigens to find potential T-cell epitopes using a bioinformatics tool, namely MHCPred (Boon et al., 2004).

Materials and Methods

In this work, prediction of potential T-cell epitopes was performed by bioinformatics tool namely MHCPred (Boon et al., 2004). This system bases on a partial least squares-based, robust multivariate statistical method for the quantitative prediction of peptide binding to major histocompatibility complexes (MHCs), the principal checkpoint on the antigen presentation pathway (Boon et al., 2004). The input nucleotide is *Homo sapiens* melanoma nucleotide, which is derived from PubMed (www.pubmed.com).

Results

The analysis shows that amino acid sequence "430AGATCCTAA438(Predicted IC50 Value = 131.52 nM)" poses the highest epitope property (IC50 Value).

Discussion

Based on advances in bioinformatics, the immunomics becomes a new alternative in vaccine development (Braga-Neto and Marques, 2006). Prediction of peptide binding to MHC molecules is a basis for epitope discovery-driven vaccine development. a partial least squares-based, robust multivariate statistical method for the quantitative prediction of peptide binding to MHCs, the principal checkpoint on the antigen presentation pathway (Brinkman et al., 2004).

No satisfactory treatment currently exists for melanoma once it has spread beyond its original site. At present, the only FDA-approved treatment for advanced melanoma is

Department of Laboratory Medicine, Faculty of Medicine, Chulalongkorn University, Bangkok Thailand 10330 Email: wviroj@yahoo.com, Tel 662-2564136

IFN-alpha2b (Bystryn and Rudolph, 2005). For melanoma, HLA-A*0201 and HLA-DRB1*0405 alleles are preferentially used in the melanoma associated antigen-specific T lymphocyte response (Damico et al., 2005; Lucchese et al., 2005; Ge et al., 2006). Vaccines are an experimental therapy intended to stimulate the immune system to react more strongly against patients' own melanoma cells, thereby destroying the tumour or slowing its progression (Bystryn and Rudolph, 2005). In this work, the author reports the results from prediction of potential T-cell epitopes for human melanoma associated antigen.

Using computational algorithm, we predicted the most potential T cell epitope from known melanoma associated antigen. These data may be useful for further vaccine development because these promiscuous peptide binders allows to minimize the total number of predicted epitopes without compromising the population coverage required in the design of multi-epitope vaccines.

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