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Meeting Abstract

Immune monitoring of T-cell responses to full-length tumor antigens

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Abstract

The ultimate goal of vaccination trials in cancer patients using tumor antigen derived immunogens is to achieve clinical responses either in the form of tumor regression or stabilization. As potential clinical responses observed in these trials are expected to result from the elicitation of tumor antigen specific immune responses, the rigorous monitoring of vaccine elicited immune responses, including T-cell responses, is a key element for the implementation of efficient vaccination protocols in cancer patients, as well as for the interpretation of clinical correlates.

This, however, has been limited by the lack of relatively simple but efficient general methods for the immune monitoring of antigen specific T-cell responses to full-length antigens, that are directed against multiple epitopes and may considerably vary in individuals of heterogeneous genetic background. The need of simplifying the immune monitoring protocols, among other reasons, has led to early clinical trials using simple immunogens encoding single epitopes, often the ones recognized in association with MHC alleles frequently expressed in the population, limiting both the patients eligible for these trials and the immunogenicity of these candidate vaccines. As the field is rapidly moving towards the use of more complex immunogens including full-length tumor antigen encoding viruses and recombinant proteins, the need for developing appropriate immune monitoring approaches has become imperative. In addition, our increasing awareness of the existence of tumor antigen specific populations exerting suppressor/immunoregulatory functions, has created the need of incorporating the evaluation of these populations into current immune monitoring protocols. I will review our recent progresses in the development of approaches for the immune monitoring of T-cell responses to full-length tumor antigens. Furthermore I will describe future developments and discuss the implications of these findings for vaccine design.