

Process For Discovering Validating And Personalizing Transposable Cancer Vaccines

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INVENTORS

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OTHER INFORMATION

KEYWORDS

Transposable elements, Cancer vaccine, Tumor antigens, MHC-1 expression, Differential Expression

CATEGORIZED AS

- **Biotechnology**
- Bioinformatics

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BACKGROUND

Cancer inununotherapy heightens the immune system's ability to recognize a cancer and destroy the cancer cells, as opposed to more traditional compounds that directly inhibit the cancer's ability to proliferate. Cancer immunotherapy can provide good responses, even in advanced stages of cancer. Some current immunotherapies include cancer vaccines, antibodies, T cell infusions, and checkpoint blockade therapy. Malignant tumors often co-opt immune suppression and tolerance mechanisms to avoid immune destruction.

Immune checkpoint blockade removes inhibitory signals of T-cell activation, which enables tumorreactive T cells to overcome regulatory mechanisms and mount an effective antitumor response. Accordingly, immune checkpoint blockade inhibits T cell-negative costimulation in order to unleash antitumor T-cell responses that recognize tumor antigens.

However, only a subset of patients respond to current cancer immunotherapies, and it is difficult to predict which patients will respond. To increase the number of patients who benefit, combination therapies are being used. Cancer vaccine in combination with checkpoint blockade therapy is a promising approach to increasing the antitumor immune response. But, cancers typically have specific mutations (private mutations) in a person or individual tumor and cancer vaccines based on private mutations may be prohibitively expensive and inhibit widespread adoption of this approach.

TECHNOLOGY DESCRIPTION

This technology involves the identification of personalized cancer vaccines that use public antigens that are shared across individuals.

Genomewide

dysregulation of transcription and translation in cancer leads to overexpression of non-canonical protein coding genes, including transposable elements (TEs). TEs are strongly repressed in healthy cells to prevent genomic instability but can become dysregulated in cancer.

The technology further involves a computational framework for identifying potential cancer antigens within transposable elements, using e.g. RNA-seq, mass spectrometry, or other data. Some embodiments use autonomous transposable elements in the hmnan genome, e.g., L1HS.

Candidate cancer antigens are identified from expressed transposable elements. Differential expression levels are determined for proteins using baseline expression levels (using measurements of healthy tissue) and tumor expression levels (using measurements of tumor tissue). Protein(s) having a differential expression level greater than a threshold are selected.

Cancer vaccine(s) can then be generated for the selected cancer antigens. Particular cancer vaccines are selected for a patient based on differential expression levels for proteins using baseline expression levels of the patient and tumor expression levels of the patient. A vaccine for protein(s) having a differential expression level greater than a threshold can be selected.

APPLICATIONS

Identification of potential tumor vaccine antigens, particularly those from transposable elements.

Identification of potential tumor vaccine antigens based on differential expression.

Generation of personalized tumor vaccines matched to, for example, MHC-I haplotype.

ADVANTAGES

Makes use of overlooked cancer antigens such as transposable elements.

INTELLECTUAL PROPERTY INFORMATION

Country	Type	Number	Dated	Case
United States Of America	Published Application	20240142436	05/02/2024	2020-263

RELATED MATERIALS