BIOMARKERS TO IDENTIFY HIV-SPECIFIC T-CELL SUBSETS

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Technology description

The invention provides a method to determine the immune response in an HIV-infected individual by comparing the expression profile of the subjectΓÇÖs HIV-specific T-cells with that of a chronic progressor (individual exhibiting a very high viral load compared to non-HIV infected individuals) or a controller (individual capable of maintaining very low viral load for upto 12 months). The invention identifies the informative genes that are particularly relevant to classify HIV-infected patients in order to predict patterns related to treatment of HIV, monitoring HIV disease progression, classifying immune response to HIV vaccine and survival in HIV infected subjects. The present invention can be effectively used to analyze proteins, peptides, or nucleic acid molecules isolated from sample sources such as blood, plasma, lymph, urine, tissue, mucus, sputum, saliva or other cell samples. The gene expression levels are obtained by hybridizing the sample with a suitable microarray on which probes specific for all or a subset of the informative genes have been immobilized, and determining the extent of hybridization of the nucleic acid in the sample to the probes on the microarray.

Application area

The information regarding the genes that are important in HIV treatment response provides knowledge of additional targets for diagnosis and therapy. The present invention can further be used to generate databases comprising informative genes which will have many applications in medicine, research and industry, and in particular, in treatment of HIV infection.

Advantages

Immunology

Institution

Dana-Farber Cancer Institute

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