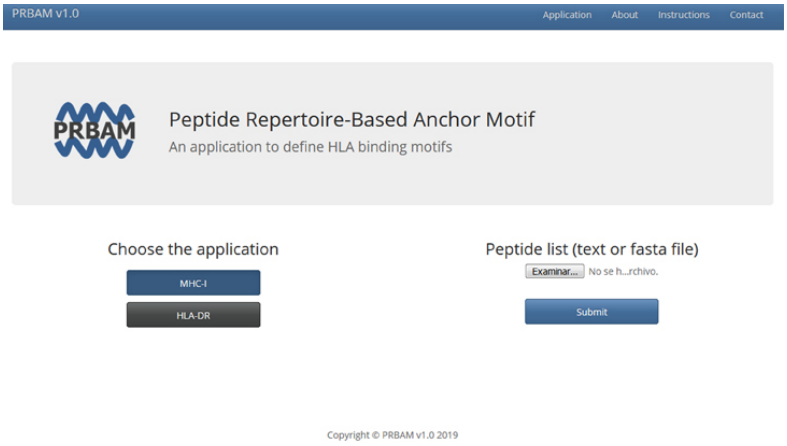
UABDIVULGA
BARCELONA RECERCA I INNOVACIÓ

07/03/2019

New software for the analysis of the antigen presentation to T lymphocytes developed



Researches of the UAB have developed a new software for the identification of the features of the peptide repertoires presented by HLA class I and HLA-DR molecules to T lymphocytes. T lymphocytes recognize protein fragments (peptides) showed in the cell surface by the molecules of the major histocompatibility complex (MHC, HLA in humans). These molecules can present thousands of different peptides with some restrictions. The analysis of these peptide repertoires is essential to elucidate T cell activation in response to infections and during autoimmune diseases and cancer. With this new software, called PRBAM (Peptide Repertoire-Based Anchor Motif), a new powerful tool for the analysis of the peptide repertoires of the MHC molecules is provided. PRBAM uses a new algorithm, making it complementary to other existent programs.

T lymphocytes are cells of the immune system essential to eliminate tumour virus-infected cells and to direct the antibody response and the activation of other cells during the elimination of the pathogens. T cell receptors do not recognize the pathogens directly, but protein fragments

presented by a group of glycoproteins called major histocompatibility complex (MHC, HLA in humans) molecules. There are two types of MHC molecules: class I and class II. Each of them shows in the cell surface a varied pool of peptides derived from proteins located in different cell compartments. In addition, peptides binding MHC class I molecules are different (shorter and anchored in the binding site ends) to those binding MHC class II molecules.

MHC molecules are encoded by some extremely polymorphic genes. These molecules are involved in transplanted tissue and organ rejection. The difficulty to find two compatible individuals for a transplant gives the idea of the degree of polymorphism of these genes. The high variability of these molecules imply the union of different peptide pools to each allotype

The identification of the features of the peptides that bind to each HLA molecule is of a great importance to find peptide ligands which can be recognized by T lymphocytes. Is in this context, a group of researchers led by Dr. Alvarez of the Unitat d´Immunologia of the Departament de Biologia cel·lular, fisiologia i immunologia of the UAB has developed a new computational tool, based in the known interactions between peptides and MHC class I and HLA-DR molecules (HLA-DR is a type of HLA class II molecule). The program determines, using peptide lists obtained by mass spectrometry, the anchor motifs of the peptide repertoire associated to a specific HLA class I or HLA-DR molecule. The software, called PRBAM (Peptide Repertoire-Based Anchor Motif) and described in the scientific journal Immunology, is easy and direct to use and determines with a high efficiency the sequence features of each peptide repertoire.

The algorithm used by PRBAM is different to others developed previously and used in other programs and it is superior, at least for some HLA-DR molecules, to other disposable alternatives. Finally, PRBAM is a new tool useful for the interpretation of the complex peptide repertoires analysed in the field of Immunopeptidomics and it is complementary to other programs reported previously.

Anna Mestre-Ferrer, Erika Scholz, Jepi Humet-Alsius i Iñaki Alvarez
Immunology unit
Department of Celular Biology, Phisiology and Immunology
Universitat Autònoma de Barcelona
Inaki.Alvarez@uab.cat

References

Mestre-Ferrer A, Scholz E, Humet-Alsius J and Alvarez I. (2019). **PRBAM: a new tool to analyze the MHC class I and HLA-DR anchor motifs**. *Immunology*, 156, 187–198.
DOI: 10.1111/imm.13020.

View low-bandwidth version