Proteomic tool

R&D RESULT

Patent

Knowledge Area

- Biomedicine
- Proteomics
- Histones

Collaboration

- Technology available for licensing
- Other collaborations

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Procedure for the identification of carbonylated histones

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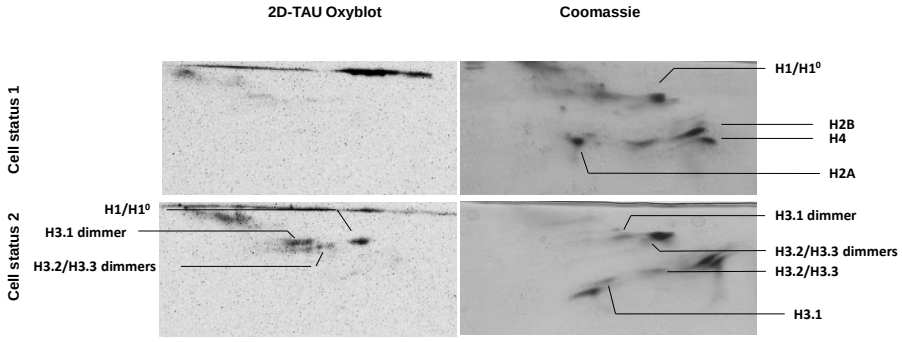
Background: Histones are proteins responsible for packaging the DNA and thereby regulate the compaction of chromatin, the expression of genes and protect the DNA. Different post-translational modifications (PTMs) in histones (produced by chemical amino acid specific histone modifications) constitute the "histone code" involved in the control and regulation of different cellular physiologic processes. An interesting modification is the carbonylation of histones, among other processes involved in the removal of excess amounts of histones. Existing techniques for the analysis of protein carbonylation do not allow analyzing carbonylation of histone variants. It is therefore necessary to develop methods, in the area of clinical diagnostics and research, of analyzing the carbonylation of histone variants.

The invention: Researchers at the Center for Biomedical Network Research on Rare Diseases (CIBERER) and the University of Valencia have developed a method and a kit for identifying carbonylated histone variants in a two-dimensional electrophoretic system without chemical derivatization affecting its electrophoretic path. This procedure allows identifying the carbonylation of specific histone variants and correlates their levels with changes in gene expression, DNA protection and histone detoxification, pathophysiology of disease and aging.

Applications: The main application of the invention is in the **biotechnology sector**, as a method for identifying carbonylated histones. The study of histone carbonylation provides valuable information about cellular physiological processes. This technique can be used to study mechanisms of DNA protection and recycling or disposal of histones. It can also be used for studies related to the pathophysiology of diseases (cancer, inflammatory processes, etc ...). Furthermore, through the characterization of histone carbonylation levels, it can be evaluated if certain drugs are involved in cell proliferation inhibition and nuclear proteasome activity inhibition (of great interest in the pharmaceutical industry dedicated to the evaluation of new compounds with inhibitory activity of the proteasome).

Advantages: The main advantages provided by the invention are:

- Simple and rapid method for the study of histone carbonylation.
- Differentiation in the carbonylation of histone variants.
- Indirect and inexpensive assessment of chemotherapeutic drugs that inhibit proteasome nuclear activity.



Histone carbonylation analysis in two different cellular conditions following the method of the present invention.

OTRI oficina de transferència de resultats d'investigació

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