

The Prospect of the Application of Differential Proteomics in Kinesiology

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Abstract: The application of differential proteomics in kinesiology is common. This paper mainly analyzes the application of differential proteomics and summarizes the application prospect of differential proteomics in kinesiology in the future, as follows.

1. Introduction

Protein is the basis of cellular biogenic activities. Researchers can judge the state of the cells according to the differences in proteome of individual cells, and even find the reasons for the differences. At present, Chinese scholars have made some achievements in proteome research. Proteome has been effectively applied in biological, medical and health and other life science fields, and achieved remarkable research results.

2. Analysis on the Application of Differential Proteomics

2.1 Application in Exploring Biomarkers

The exploration of biomarkers can be used as a marker for clinical diagnosis and treatment, providing a powerful tool for people to further understand the development mechanism of diseases. In addition, differential proteomics can also be used as therapeutic targets and drug development targets. For example, Edwards used two-dimensional electrophoresis technology to detect prostate cancer antigen-1 in urine samples of 17 patients with prostate cancer and other patients with bladder cancer, benign prostatic hyperplasia, testicular cancer and so on. The results showed that prostate cancer antigen-1 was detected in the urine of 16 patients with prostate cancer in the study, and prostate cancer antigen 1 was not detected in the urine of patients with other diseases. This indicates that prostate cancer antigen-1 in urine may be a marker of prostate cancer progression. Wulfuhe used differential proteomics technology to compare breast ductal carcinoma in situ and normal breast ductal / lobular tissues. Under this technology, the scholar found that some proteins related to cytoskeleton, apoptosis and microenvironment were different, and proteins not related to breast cancer also showed high expression in cancer tissues. The results of differential proteomics technology can be further studied, which provides a strong support for the early diagnosis of breast cancer. In addition, some scholars chose the female nipple suction liquid as a sample and analyzed the 5-40ku protein by differential proteomics technology. It was found that the specific protein with a molecular weight of 6.5-15.9ku accounted for more than 75% of the breast cancer patients, and there was specific proteins in their milk. For normal women, there was no more than 9% specific protein in the milk. It can be concluded that there is a certain difference in the protein expression of nipple aspirate between breast cancer patients and normal female patients, and this difference can be used to explain that breast cancer has appeared^[1].

2.2 Application in Signal Transduction

The signal transduction system mainly appears in eukaryotic cells, and it is through signal transduction that eukaryotic cells adjust themselves to the external and internal environment. Protein receptors on cell membrane or in cell are typical representatives of signal transduction system, which mainly plays the role of signal receptor. Signal transduction involves the interaction

between cellular proteins and receptors. In addition, it also includes the post-translational modification of the receptor itself, which mainly refers to phosphorylation. Pandey scholar used EGF in HeLa cell processing, then immunized and subcloned the tyrosine phosphorylated protein by phosphorylation tyrosine antibody, and identified by MALDI-TOF-MS after gel electrophoresis, not only discovered the known EGFR signal transduction pathway information molecules, but also discovered other new signal molecules.

3. Application Prospect of Differential Proteome in Kinesiology

3.1 Application in the Research of Exercise Signal Transduction Pathway

Exercise signal transduction pathway can change the structure and function of the body after exercise. Protein is the main component of signal transduction pathway system. The process of signal transduction is closely related to protein translation and interaction. At this stage, experimental technology restricts the development of sports medicine. At present, there are few researches on sports signal transduction pathway in China, and the research content is also shallow. For example, in the study of exercise-induced myocardial hypertrophy signal transduction pathway, although a lot of information about the signal transduction pathway of exercise-induced myocardial hypertrophy has been mentioned, it can't explain the types of myocardial hypertrophy caused by different sports. Many factors are usually between pathological myocardial hypertrophy and exercise-induced myocardial hypertrophy, but the difference between them is not clear. For another example, there are still some problems in the information transduction pathway of exercise metabolism and apoptosis induced by exercise. Thus, differential proteomics can find all the proteins related to signal transduction according to the changes of total intracellular proteins before and after receptor activation, so that researchers can start from different proteins and further search for long downstream signal transduction molecules. This multi-directional and bidirectional method can further accelerate the research process of signal transduction^[2].

3.2 Application in Exploring Biomarkers of Sports Fatigue

Sports fatigue is one of the hot issues in the field of sports medicine. According to the relevant data, the research on sports fatigue has a history of 100 years. There are many theories about sports fatigue, such as lactic acid theory, energy exhaustion theory, metabolism accumulation theory and so on. Under the background of the continuous development of science and technology, the research methods, research means and research equipment of sports fatigue have been significantly improved. With the influence of physiology, sports medicine and biochemistry, people gradually realize that the occurrence of sports fatigue has obvious complexity. Chinese scholar Feng Weiquan put forward the theory of neural--endocrine--immune and metabolic regulation network. Under this theory, it is believed that the network interaction among molecules, cells and tissues promotes the body to produce exercise-induced fatigue. It can be seen that sports fatigue is closely related to tissues, organs and systems. The body will change the expression and function of protein in the state of fatigue. Previous studies on exercise-induced fatigue caused by myocardial protein are more, but with a high degree of singleness, mainly refers to the study of known and single protein. For example, Tian Zhenjun, a scholar, has studied that the activity of CK and isoenzyme in myocardium of rats after overtraining will decrease. Deirel scholar research showed that after treadmill endurance training, the myocardial heat shock protein showed a significant upward trend. Guo Lin studied the effect of different exercise intensity on the protein expression of adrenal oncogene C-fos. The results showed that the protein expression of adrenal oncogene C-fos was positively correlated with exercise intensity. The protein expression of adrenal oncogene C-fos increased with the increase of exercise intensity. And the longer the recovery time after exercise, the greater the protein expression of adrenal oncogene C-fos. Hashimoto scholar studied the effect of exercise on the activity of myocardial calcium pump in rats, and found that the ability of myocardial sarcoplasmic reticulum to absorb Ca²⁺ decreased significantly after exercise, which indicated that the activity of myocardial calcium pump decreased significantly. Therefore, differential proteomics can play a

very important role in the exploration of biomarkers of exercise-induced fatigue. Differential proteomics can provide a comprehensive understanding of the changes of known and unknown proteins in the development of exercise-induced fatigue, and can help researchers find biomarkers that lead to exercise-induced fatigue. It is very important to diagnose the occurrence and development of exercise-induced fatigue in differential proteomics. In addition, researchers can also make scientific and reasonable exercise training plan for human body with the help of differential proteomics, which plays an important role in ensuring the training effect and avoiding the occurrence of overtraining. For example, Rogers scholar used differential proteomics to study the left ventricular muscle protein of 8 rats in the quiet group and 8 rats in the exercise training group. The results showed that the proteome of the two groups showed great differences, among which the most different proteome was 20kDa heat shock protein and 3 α - hydroxysteroid dehydrogenase. At present, the research technology of human differential proteomics has been further developed, and the project of plasma protein separation and purification has been gradually launched. In particular, great achievements have been made in the study of proteome in pancreatic juice, saliva and cerebrospinal fluid. The above technologies provide strong support for minimally invasive diagnosis of sports fatigue and non-invasive diagnosis of sports fatigue ^[3-4].

3.3 Application in Nutrition Intervention

The nutritional status of the body will affect human health, exercise ability and physiological function. Reasonable nutrition supplement can eliminate sports fatigue in the shortest time, which is of great significance to strengthen the body immunity. Differential proteomics can be applied to the study of nutritional supplements and nutritional targets, which is of great significance to further explain the mechanism of action and adverse reactions of nutrients. At present, the application of proteomics in nutritional intervention has achieved certain results. Among them, Eberini scholar carried out observation on mice with adjuvant arthritis, analyzed the changes of blood protein expression profile before and after taking NSAIDs, and quantified the protein. The results showed that indomethacin had a significant inhibitory effect on serum protein expression of AA mice model. For another example, Steiner scholar studied the effect of cyclosporine on the kidney of mice, and found that calcium binding protein appeared in the protein two-dimensional electrophoresis map after the kidney of mice was affected by cyclosporine A. The protein exists in renal tubules and is related to the binding and transport of calcium ions. This indicates that cyclosporine A can calcify renal tubules ^[5-6].

4. Conclusion

To sum up, differential proteomics plays an important role in kinesiology research. The above is the application of differential proteomics and its development prospect in kinesiology, hoping to be helpful to the research in this field.

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