To compare with blankgroup：$^{\Delta}P<0.05$，$^{\Delta\Delta}P<0.01$

Table 3 shows： The positive group, 1:2, 1:1 group can significantly prolong the time of myocardial ischemia mice's hypoxia,which can protect the myocardial ischemia mice clearly.

Myocardial ischemia is the basic pathophysiological process of coronary heart disease, myocardial ischemia due to reduced blood flow, oxygen cannot get enough can lead myocardial ischemia. Myocardial ischemia and hypoxia can cause myocardial cell metabolism disorder, particularly sharp drop in energy generation materials, which is hard to maintain normal heart function, reduced myocardial contractility and the diastolic dysfunction. Because of the blood flow interruption, the product is difficult to remove harmful [5]. H.attenuatum Choisy and Salvia miltiorrhiza can clear the ischemic parts of the free radicals, prevention and treatment of atherosclerosis, which can enhance myocardial contractility, heart rate; which can relieve acute ischemia and myocardial ischemia reperfusion injury and improve Ischemic myocardial hypoxia, reduced myocardial infarct; myocardial ischemia and damage can be repaired, preserved cardiac function.Therefore, compatibility of H.attenuatum Choisy and Salvia miltiorrhiza effect from the multi-channel, multi-target interference, although each division, but may help solve the problem for the use and enhance the efficacy of the original.

Conclusions

In this study, mice with Isoprenaline hydrochloride copy myocardial ischemia, H.attenuatum Choisy and Salvia miltiorrhiza compatibility of its protective effect in each group. The results showed that: H.attenuatum Choisy and Salvia miltiorrhiza compatibility 2:1 group can significantly reduce the LDH, CK levels, increased SOD activity and decreased MDA content, extend the time of myocardial ischemia and hypoxia. So, under the same condition of compatibility does myocardial ischemia has protective effect in mice.

It is based on the special effects of the H.attenuatum Choisy and Salvia miltiorrhiza on the Myocardial Ischemia. On the tradition Chinese medicine compatibility theory, It remedy the Myocardial Ischemia with two medicine, which have broad prospects for development. We will consider the studies of exact dose, the formulations and clinical in the future.

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The Summary of Proteomics Technology Apply to Ischemic Stroke Research

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Abstract：Proteomics is one part of the molecular biology, which have been widely used in medical research and have important role in guiding disease prevention, diagnosis , treatment and discovery of new drug targets. Ischemic stroke is high incidence of cerebrovascular disease right

now, including the characteristics of high incidence, mutilation rate and recurrence rate, which is one of the three diseases cause human death. Proteomics technology is now used in ischemic stroke clinical studies and animal studies, through the experiments found related protein, which provide the basis for the disease etiology, pathogenesis and mechanisms. In this paper, a brief overview of proteomics apply to ischemic stroke will be given.

Key Words: Proteomics; ischemic stroke; application technology

1.The necessity of proteomics applied tostudy of ischemic stroke

Stroke, also known as 'Zhong-feng' , from the nature of the lesions can be divided into ischemic stroke and hemorrhagic types. Ischemic stroke is an important lethal and debilitating disease,which accounts for about 60% -80 % and serious harm to human life and health[1], it mostly due thrombosis or emboli blocking the brain blood vessels. In recent years proteomics technology as a popular means for disease research, which methods and techniques of continuous development and improvement of traditional Chinese medicine treatment of disease research has opened up a new areas ,and also for ischemic stroke research provides a new idea .

Proteins are the direct executors of life activities, and the protein group is all proteins in a cell or tissue collection. Proteomics is the study of protein levels in large features , including protein expression level, post-translational modification, protein-protein interactions , whereby the protein level of the diseases , cell metabolic processes such as the overall and comprehensive understanding of its significance in guiding the disease. This concept was first used by Wilkins and Williams Australia in 1994, at the first session of the International Conference for the first time put forward two-dimensional electrophoresis, and first seen in the literature in July 1995 of the "Electrophoresis" magazine. Proteomics research in the field of medicine has been more widely applied, including pathogenesis research, clinical diagnosis, drug screening and drug targets and prognostic assessment and personalized medicine and so on. Therefore, the application of proteomics technology for ischemic stroke prevention, diagnosis and pathogenesis studies to elucidate its mechanism of protein molecular level also has a certain necessity.

2. Theoverview and application of proteomics technologyin study of ischemic stroke

With the completion of the Human Genome Project, proteomics as a part of molecular biology have become a hotspot for biomedical research, and two-dimensional gel electrophoresis, mass spectrometry and bioinformatics are the three pillars of proteomics research[2]. Proteomics is technically more complex, including protein separation and identification, detection and information analysis, etc.

2.1 Isolation and identification of proteins

Protein separation mainly base on two-dimensional electrophoresis (2-DE), two-dimensional liquid chromatography analysis, fluorescence difference gel electrophoresis protein separation bidirectional technology (DIGE), that separate and detect proteins in complex mixtures, and creating proteome map[3]. Commonly used in the proteins identification with electrospray ionization tandem mass spectrometry (ESI-MS/MS), matrixassisted laser desorption ionization time-of-flight mass spectrometry(MALDI-TOF-MS), surface-enhanced laser de-sorption and ionization time-of-flight mass spectrometry technology(SELDI-TOF-MS). By the mass spectrometry techniques to further the development of protein fingerprints (SELDI-TOF-MS) technology, microarray and mass spectrometry techniques combine the advantages of both , including chromatography with mass spectrometry is a special protein chip technology, the protein chips, flight mass spectrometry and analysis software 3 parts[4].Protein chips have insight into tumor cells, tissues and organisms subtle changes in protein content, samples with less, high-throughput analysis of a particular advantage of the physicochemical properties of proteins[5].

Two-dimensional electrophoresis protein separation technology is the core technology[6], "soft ionization" The emergence of mass spectrometry technology as the core technology for protein identification, and the two-dimensional electrophoresis combined mass spectrometry techniques were internationally recognized as the current proteomics technology standard methods[7-8]. Animal experiments Lieutenant Rats lymphocyte separation protein was extracted , for two-way gel

electrophoresis separation , software analysis obtained after target protein,and the use of matrix-assisted laser desorption ionization mass spectrometry peptide mass fingerprinting , the result shows multiple proteins in cerebral hemorrhage and cerebral ischemia model group up-regulated[9].

2.2 Detection of protein

Western blotting(WB) is a component of the electrophoretic separation of proteins from the gel to one solid support through the antibody attached to a solid phase support of the target protein epitopes presented with specificity reactions were detected. It can be used to verify whether there is protein, WB is now considered as the most ideal method applied to verify protein expression in proteomics, which re-examination for protein determination ultimately provide the basis for the protein , making proteomics technology to better serve the development of medicine[10].

2.3 Analysis of protein informatics

Biological sciences, computer science, applied mathematics and other disciplines intersect forming a new discipline that bioinformatics. It mainly includes proteome database and related software tools[11]. Protein database is proteomics bioinformatics core, which SWISS-PROT and TrEMBL most representative[12]. Search through a database to determine whether the unknown protein known novel protein. Protein data on the Internet have a series of bioinformatics tools, suitable for different types of experimental data obtained for identification and characterization of proteins.

3. Conclusion

Proteomics technology to find ischemic stroke patients and normal differences in protein expression and through animal models related protein expression in rat, It have some significance in ischemic stroke pathogenesis and differences in protein expression after treatment with a certain sense , and the study of ischemic stroke down to the level of molecular biology. For ischemic stroke, as an indicator of protein expression, changes in regulation and function of protein modification as the research direction provide a new method for the prevention and treatment of this disease, which for clinical prevention, diagnosis and treatment has very important significance.

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