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PROTEOMIC PROFILING OF HEART IN RATS TREATED WITH SALUSIN- β

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Aims Salusins are newly found endogenous polypeptides, which consist of 28 or 20 amino acids designated Salusin- α and Salusin- β , respectively. Recent research revealed that they play an important role in heart. However, the mechanism is not clear. This study aims to investigate proteomic profiling of heart in rats treated with Salusin- β .

Methods Ten adult male Wistar rats were randomly divided into control group (n=5) and Salusin- β group (n=5). The rats in Salusin- β group were injected Salusin- β (5 nmol/kg) via the femoral vein, while the rats in control group were injected equal amount of saline before total protein preparation. After 24 h, the heart samples of all rats were collected for proteomic analysis, including two-dimensional gel electrophoresis (2-DE) combined with mass spectrometry (MS). Finally, to obtain an overview of the differential proteins, the GO (gene ontology) analysis was performed by Gominer software.

Results There were approximately 1828.33 ± 29.14 protein spots in each 2-DE gel of the heart samples of control group visualised by silver staining, while 1851.33 ± 23.01 protein spots in that of Salusin- β group. Further, 13 differential proteins were identified by MS, among which 10 were down-regulated and 3 were up-regulated in heart after the treatment with Salusin- β . These proteins were mainly located in mitochondria and involved in many biological processes, such as biological oxidation, energy metabolism, stress, development and binding.

Conclusions The characterisation of these proteins may help us come closer to understanding the mechanism about the effects of Salusin- β on heart.