

Characterization of Proteins in *Periplaneta americana* L. Active Extract CII-3

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SUMMARY. The emerging technology of proteomics has become an indispensable biological approach for medical and pharmaceutical research nowadays. In recent studies, *Periplaneta americana* L. has attracted increasing attention because of its multiple pharmacological activities. However, little attention has been paid for the exploration of protein profiles. In the present study, proteins of *Periplaneta americana* L. active extract CII-3 were characterized employing high-resolution LC-MS/MS (nanoLC-MS/MS). A total of 83 protein groups were systematically identified in CII-3, and bioinformatic analyses composed of gene ontology (GO) and kyoto encyclopedia of genes and genomes (KEGG) were constructed. It was demonstrated that most of the identified proteins, which were mainly located in the membrane and cytoplasm, were primarily involved in biological processes, including organic substance metabolic process, primary metabolic process and organonitrogen compound metabolic process. KEGG annotation analysis revealed that the proteins in CII-3 were predominantly involved in microbial metabolism in diverse environments, glycolysis/gluconeogenesis and carbon metabolism. These findings provide a new foundation for the medical-pharmaceutical use of CII-3.

RESUMEN. La tecnología emergente de la proteómica se ha convertido en un enfoque biológico indispensable para la investigación médica y farmacéutica en la actualidad. En estudios recientes, *Periplaneta americana* L. ha atraído una atención creciente debido a sus múltiples actividades farmacológicas. Sin embargo, se ha prestado poca atención a la exploración de perfiles de proteínas. En el presente estudio, las proteínas del extracto activo CII-3 de *Periplaneta americana* L. se caracterizaron empleando LC-MS/MS de alta resolución (nanoLC-MS/MS). Se identificaron sistemáticamente un total de 83 grupos de proteínas en CII-3 y se construyeron análisis bioinformáticos compuestos por ontología génica (GO) y enciclopedia de genes y genomas de Kyoto (KEGG). Se demostró que la mayoría de las proteínas identificadas, que se ubicaban principalmente en la membrana y el citoplasma, participaban principalmente en procesos biológicos, incluido el proceso metabólico de sustancias orgánicas, el proceso metabólico primario y el proceso metabólico de compuestos organonitrogenados. El análisis de anotaciones KEGG reveló que las proteínas en CII-3 estaban predominantemente involucradas en el metabolismo microbiano en diversos entornos, la glucólisis/gluconeogénesis y el metabolismo del carbono. Estos hallazgos proporcionan una nueva base para el uso médico-farmacéutico de CII-3.

KEY WORDS: characterization, CII-3, protein, *Periplaneta americana* L.

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