URN etd-0407109-183703-174
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Statistics This thesis had been viewed 41 times. Download 27 times.
Department
Year 2005
Semester 1
Degree Master
Type of Document Master's Thesis
Language zh-TW.Big5 Chinese
Title The investigation of the protein profiles of the isolates of Cordyceps spp. by proteomics
Date of Defense 0000-00-00
Page Count 81

Keyword
Cordyceps
proteomics

Abstract
Cordyceps spp. have been used in the traditional Chinese medicine for a long time. Few medicinal Cordyceps spp. possess the curative effects. Therefore it is worth to identify the Cordyceps spp. with the pharmacological activities utilizing the accurate analytical method such as classification by 5.8S rDNA、28S rDNA、5S rDNA and 18S rDNA regions However, the rDNA identification can not distinguish the different pharmacological activities of Cordyceps spp..
In this study, we used two dimensional (2-D) gel electrophoreses to compare the proteomic profiles of 8 related isolates of the genus CordycepsU+BE Cordyceps sinensis BCRC C.S. 、Cordyceps militaries BCRC 32219、Paecilomyces tenuipes IUM077 、IUM067 、Beauveria amorpha ROKI2229、ROKI36、IUM0922 and BCRC35502. The 2-D gels were compared by PDQuest software. The comparative results demonstrated that the proteome map of C.S. was almost totally different from that of BCRC 32219. Among ~731 protein spots in IUM067 only 184 spots were found in IUM077 with the same pI and molecular weight. Compared to ROKI36, 342, 140 and 71 matched protein spots were found in ROKI2229, IUM0922 and BCRC35502 respectively. In order to estimate the similarities between the Cordyceps spp. isolates protein profile similarities were calculated between pairs of isolates using a matching co-efficient. The matching analyses results indicated that BCRC32219 with BCRC C.S similarity 14%, IUM067 with IUM077 similarity 12%, ROKI36 with ROKI2229 similarity 24%, ROKI36 with IUM922 similarity 9% and ROKI36 with BCRC35502 similarity 4%, suggesting that the isolates of a species collected from the different host might have the different protein expressions even though they are supposed to have the same genome.
Advisory Committee Wu-tin fung - advisor

Files etd-0407109-183703-174-001.pdf

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Date of Submission 2006-08-23