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Author Chiung-Yueh Hsu
Author's Email Address No Public.
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Abstract
Pycnogenol (PYC) , whose major components are bioflavonoids, such us oligomeric proanthocyanidins and catechin is extracted with hot water from the bark of French maritime pink (Pinus pinaster solander in aiton) along the coast in the southern French.

The studies on pycnogenol mainly focused on the clinical application in the past years, including treatment for skin pathology、cardiopathy、immune system、cancer、Alzheimer’s disease、high cholesterol、diabetes、arthritis and free radical scavenger etc. However, the references regarding the effect of pycnogenol on the gene expression are very few. Therefore, in this thesis we utilized the proteomics to examine the effect of pycnogenol on the genome-wide gene expression of RAW 264.7 cells.

We used two-dimensional (2-D) gels with high resolution to establish the pH 4-7 11 —cm proteome maps of RAW 264.7 cells either non-treated or with 100 mg/ml pycnogenol for 24 hours. Using PDQUEST software, we detected 713 points on the gels of PYC-treated and 725 points on the non-treated RAW 264.7 cells. The proteome maps of non-treated and treated RAW 264.7 cells were compared with the PDQUEST software. Four statistically significant spots with two-fold or above in the amount proteins were detected. These differentially expressed protein spots were identified are cathepsin D、proteasome a subunit type 1、annexin IV and keratinocyte lipid-binding protein respectively using electrospray ionization mass spectrometry (ESI/MS/MS). These differentially expressed proteins were confirmed by the Western blot .
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