Hsiu-Chuan Chou et al., Insights in Analytical Electrochemistry, 3:2
DOI: 10.21767/2470-9867-C1-003

Proteomic survey of metabolic pathways in xylose-fermenting yeasts *Scheffersomyces stipitis*

Hsiu-Chuan Chou[4]*, YC Chang[1], PY Hsieh[1], LF Tseng[1], YJ Su[1], YC Chou[2], HL Chan[3], and **CF Lee[4]***
[1]National Tsing Hua University, Taiwan
[2]Chung Hwa University of Medical Technology, Taiwan
[3]National Tsing Hua University, Taiwan
[4]National Tsing Hua University, Taiwan

It is generally regarded that international energy shortages cause energy prices continuing to rise further, that the production of bio-ethanol is indispensable. In the past, glucose was used to produce biofuel. However, it is controversy over using food crops to produce fuel because most alcoholic fermentation of glucose is often obtained from sugar cane, corn and other food crops. Fortunately, the second most abundant sugar, xylose, can be utilized to generate ethanol as well. Moreover, xylose can be obtained from lignocellulosic biomass, which is in the form of forestry, agricultural, and agro-industrial wastes, such as rice rods and other plant fibers. As shown in literatures, *Scheffersomyces stipitis* is most suitable for fermenting xylose in microaerobic environment, whereas *Scheffersomyces stipitis* mutant LC11S02 collected in outdoors is most suitable for fermenting xylose in anaerobic environment. Interestingly, after mutations induced by NTG (N-methyl-N-nitro-N-nitrosoguanidine) for 30 minutes, a yeast strain LC321, similar to wild-type *Scheffersomyces stipitis* that is able to produce a high level of ethanol under microaerobic condition, was selected from mutated 483 strains. Furthermore, protein expression profiles were distinguished among wild-mutant (LC11S02), chemical-mutant (LC321) and standard strain (BCRC21775) by means of two dimensional differential gel electrophoresis (2D-DIGE) and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS). Our results revealed 108 identified proteins that are associated with metabolic pathways in xylose-fermenting yeasts. Taken together, this study has the potential to provide new insights for biofuel production by efficient xylose utilization from plant biomass.

Key words: alcoholic fermentation, xylose, Scheffersomyces stipitis, proteomics

Biography

Hsiu-Chuan Chou is a Professor at National Tsing Hua University in Taiwan since 2016. she received her PhD degree from King's College, University of London in 2005. Her group focuses on studying immune cell migration, podosomes dynamics as well as proteomic approaches for the phenotypic hallmark traits and cellular signaling pathways in targeting toxic effect of environment and drug resistance of cancer treatment.

chouhc@mx.nthu.edu.tw

Notes: