## Separation of Proteins from UV irradiation Stressed Soybean (Glycine max (L.) Merr.) Leaf Tissues by Two-dimensional Polyacrylamide Gel Electrophoresis

Tae-Seon Kim<sup>1</sup>, Seong-Woo Cho<sup>1</sup>, Jae-Eun Lee<sup>2</sup>, Yook-Han Kim<sup>2</sup>, Byoung-Moo Lee<sup>5</sup>, Kun Cho<sup>3</sup>, Jong-Soon Choi<sup>3</sup>, Keun-Yook Chung<sup>4</sup>, Beom-Heon Song<sup>1</sup>, Seung-Keun Jong<sup>1</sup>, Hong-Sig Kim<sup>1</sup> and Sun-Hee Woo<sup>1†</sup>

Dept. of Crop Science, Chungbuk National University, Cheongju 361-763, KOREA
Breeding Resource Development, National Institute of Crop Science, Suwon 441-857, KOREA
Proteomics Analysis Team, Korea Basic Science Institute, Daejeon 305-333, KOREA
Dept. of Agriculture Chemistry, Chungbuk National University, Cheongju 361-763, KOREA
Dept. of Plant Biotechnology, Dongguk University, Seoul 100-715, KOREA

## **Objectives**

We have used soybean leaf UV irradiation stress, to identify protein expression is a major challenge of functional genomics. MALDI-TOF/MS and homology studies on these induced proteins revealed their possible roles in stressed soybean plants, such as cellular protection.

## Material and Methods

Five varieties of soybean (*Glycine max* L.) were used for this experiment. Seed leaf proteins were examined by and two-dimensional gel electrophoresis according to the protocol of O'Farrell (1975). We tried to identify the proteins that formed peptide bands in 2-DE gel by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF/MS).

## **Results and Discussion**

Protein extracts were first prepared from leaf tissue of UV-treated soybean plants, and the proteins were visualized with two-dimensional electrophoresis (2-DE). Matching gels were then run using protein extracts of a soybean treated with soybean leaf UV irradiation. After visual comparison, the proteins spots that were differentially expressed in UV irradiation of soybean tissues were cut from the gels and analyzed by matrix-assisted laser-desorption ionization time of flight mass spectrometry (MALDI-TOF/MS). Using this approach we demonstrated a successful proof-of-concept experiment by identifying UV irradiation proteins present in the total protein extract. Several of the differentially expressed protein spots were identified.

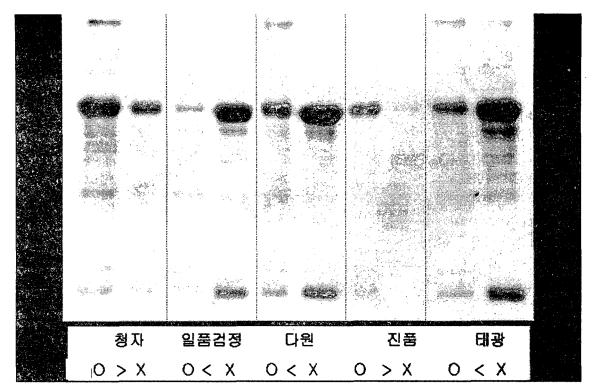


Figure 1. SDS-PAGE을 이용한 품종들간 UV처리와 무처리의 단백질 비교

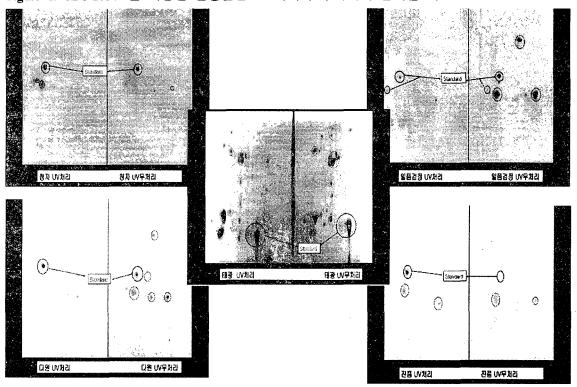


Figure 2. 이차원전기영동(2-DE)을 이용한 청자, 다원, 태광, 일품검정 및 진품 품종들간 단백질 비 $\square$