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Root and Nodule Proteome of Grafted Soybeans between Sinpaldalkong and SS2-2

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Objectives

This study was performed to identify proteins associated with autoregulation using proteome analysis of soybeans which were self- and reciprocally grafted between hypernodulating mutant, SS2-2 and its mother line, Sinpaldalkong2.

Materials and Methods

1. Materials

- Plant: SPDK2 (Sinpaldalkong2) and SS2-2 (hypernodulating mutant)
- Bacteria: *Bradyrhizobium japonicum*, USDA110

2. Methods

- Grafting
'straw-band' technique (Bezdicsek et al., 1972)

Two dimensional electrophoresis

2-DE was done following the protocol of BioRad with some modifications especially in sample preparation. The gels were silver-stained and the 2Dimages were analyzed using Melanie III(genebio).

Results and Discussion

- About 1200 protein spots were separated across the pI range of 4-7 in the proteome expression map of roots or nodules (0 or 22 DAI) of both SPDK2 and SS2-2
- Through differential display of proteome maps of root and nodule from each grafts, 3 SPDK2 shoot-regulated proteins and 2 SS2-2 shoot-related proteins were detected, root- regulated proteins and grafting-related proteins were also detected.
- The differentially expressed proteins are being characterized and identified by ESI/QTOF-MS/MS

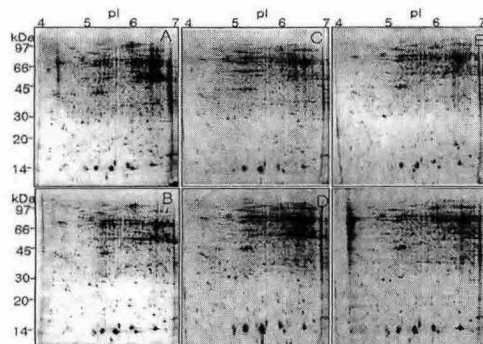


Figure 1. 2D electrophoresis of proteins from nodule at 22day of intact soybean (A, B) of Sinpaldalkong2ho (A, C) and its up-regulated and the Hypernodulating mutant SS2-2 (B, D) and nodule at 22day of self-grafts (C, D) and reciprocal grafts [E, SPD/SS2-2(shoot/root); F, SS2-2/SPD]

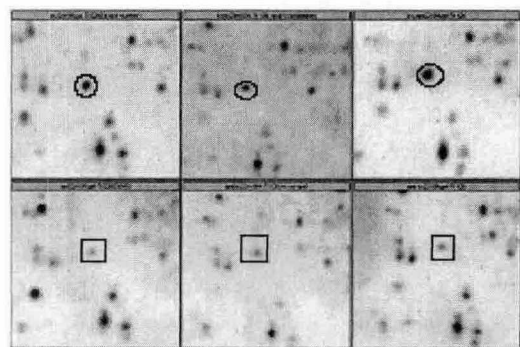


Figure 2. 2D pattern of sn005, ss2-2 shoot-related protein, from each grafts (Figure 1). The circles indicate protein squares indicate proteins down-regulated