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Proteome Analysis of Nodule Development in both Sinpaldalkong2 and SS2-2

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Objectives

This study was performed to understand the molecular processes of nodule development using proteome analysis of hypernodulating mutant, SS2-2 and its mother line, Sinpaldalkong2 and identified proteins expressed differentially between two soybeans.

Materials and Methods

Materials- Plant: SPD(Sinpladalkong2) and SS2-2(hypernodulating mutant)

Bacteria: *Bradyrhizobium japonicum*, USDA110

Methods- 1) Two dimensional electrophoresis
2) Image analysis- Melanie III(genebio)
3) MALDI-TOF and MS/MS

Results and Discussion

- Proteome expression maps of roots(0, 5DAI) or nodules(10, 13, 22DAI) of both SPD and SS2-2 were established and characterized.
- Among proteins that expressed differentially during nodule development, about 130 proteins were identified using MALDI-TOF and MS/MS and classified with its function.
- Chaperone and nodulin, such as nitrogenase iron protein, leghemoglobin were important responsible to nitrogen fixation were expressed significantly in nodule proteome map.

- Malate dehydrogenase was up-regulated in SS2-2 than SPD during nodule development, but it is still unknown how its function is responsible to hypernodulation.

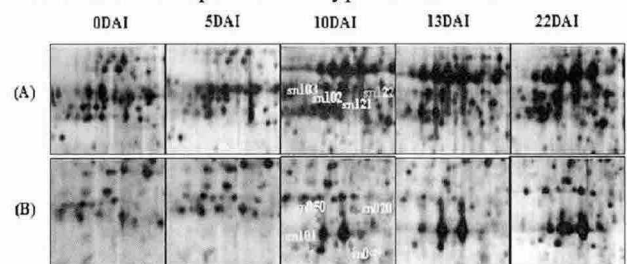
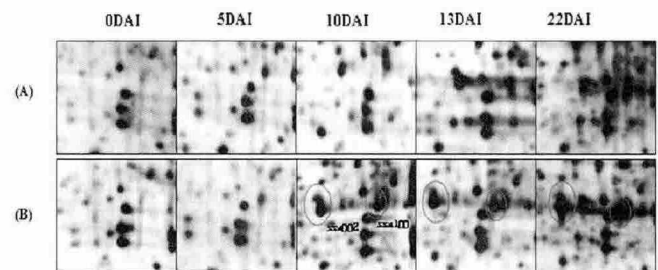


Fig.1. Proteins were regulated differentially during nodule development in SPD. (A) Charperone, (B) Nitrogenase iron protein appeared initially at 10DAI. Red arrows and arrowheads indicate newly induced or up-regulated proteins, blue circles and dotted circle indicate disappeared or down-



regulated proteins.

Fig.2. Proteins regulated differentially in between SPD(A) and SS2-2(B) during nodule development. *ssn002*, malate dehydrogenase, and *ssn100*, unknown protein were up-regulated in SS2-2 rather than SPD.