

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.

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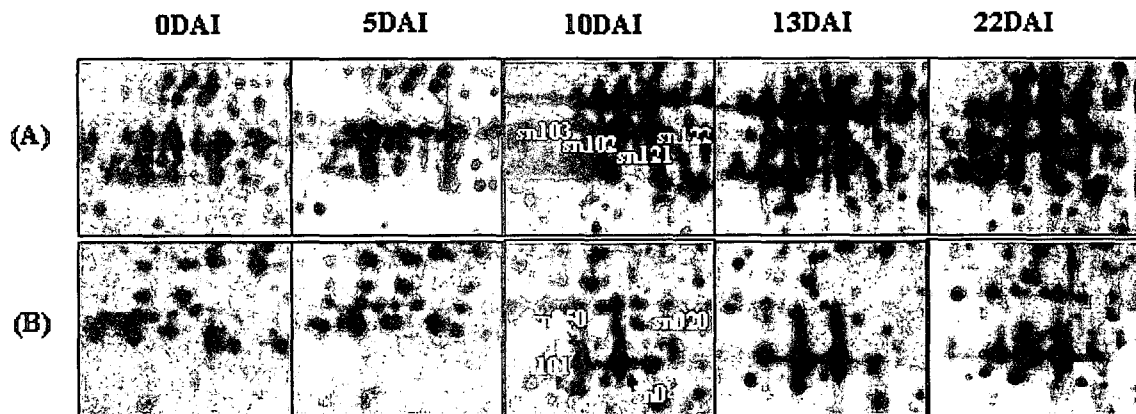


Fig.1. Proteins were regulated differentially during nodule development in SPD. (A) Charperone, (B) Nitrogenase iron protein appeared initially at 10DAI. Red arrows and arrowheads indicate newly induced or up-regulated proteins, blue circles and dotted circle indicate disappeared or down-regulated proteins.

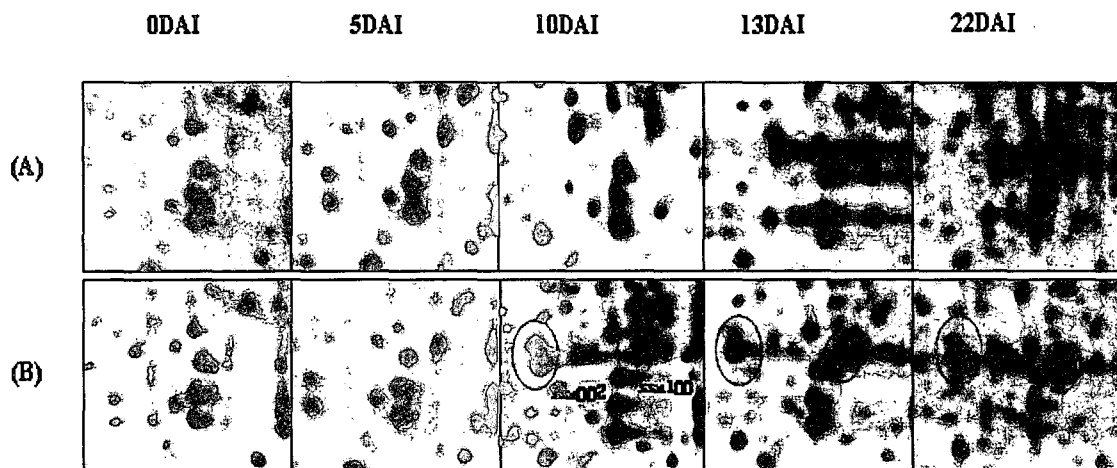


Fig.2. Proteins regulated differentially in between SPD(A) and SS2-2(B) during nodule development. ssn002, malate dehydrogenase, and ssn100, unknown protein were up-regulated in SS2-2 rather than SPD