



## Bacterial populations concomitant with *Sclerotium rolfsii* sclerotia in flooded soil, as estimated by 16S rRNA gene, PCR-DGGE and sequence analyses

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### ABSTRACT

**Objective:** The bacterial communities concomitant with sclerotia of *Sclerotium rolfsii*, the causal agent of soybean stem rot, were examined by using PCR-DGGE.

**Methodology and results:** Fungal sclerotia were buried in soil amended with organic matter and incubated under flooded conditions for 15 or 30 days in a greenhouse and in the field. The recovered sclerotia were examined for their viability and their concomitant bacterial communities. The DGGE band patterns showed the largest bacterial diversity in samples from soil amended with rice straw or wheat bran and flooded for 30 days. In the greenhouse for instance, the diversity index from organic amendment under 30 day flooding was higher than 1.80, while for other treatments the index was less than 1.5. This trend was similar in the field experiment. There was a negative relationship between the diversity index from DGGE band patterns and sclerotial viability or disease incidence. Examination of the nucleotide sequences of the DGGE bands revealed that members of Clostridiaceae were dominant in the samples flooded for 30 days, whereas Oxalobacteraceae, Nocardiaceae, and Actinomycetaceae were major groups under unflooded conditions.

**Conclusion:** This is the first report of the soil bacterial flora concomitant with sclerotia of *S. rolfsii* under flooded conditions.

**Keywords:** bacterial community, diversity, PCR-DGGE, *Sclerotium rolfsii*, sequencing, soybean