

## Analysis of Microbial Community during *Astragalus membranaceus* (Hwanggi) Cultivation Period

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**Purpose:** Hwanggi was a major herb in Gangwon Province. Hwanggi increased its efficacy in 3 year cultivation, but the incidence of root rot and wilt disease was also increased. It was known that the causative fungi of the root rot disease were *Phytophthora* sp., And the causative fungi of wilt disease was *Fusarium* sp. Until now, the causative fungi of Hwanggi has been identified by cultivating the bacteria isolated from infected individuals or soil. However, microorganisms that did not grow in a specific medium were difficult to identify.

**Methods:** Microbial community analysis is a new technology to identify microorganisms that are difficult to separate by conventional culture method using next generation sequencing method. Therefore, microbial community analysis was used to analyze the microbial diversity and the causative microorganisms distribution in the Hwanggi field.

**Results:** In the 1-year-old and 2-year-old field of Hwanggi, there was no difference in the distribution of *Fusarium* sp. between the diseased and non-diseased sites. However, in the 3-year-old Hwanggi field, the distribution of *Fusarium* sp. was 8.3 times higher than that of the non-diseased sites. Microbial diversity was found in various species in the non-diseased sites. When the disease occurred, the causative organisms dominated and the microbial diversity was lowered.

**Conclusions:** Using the microbial community analysis method, it is possible to secure a healthy field when selecting the Hwanggi field. If the database was complementary, further studies of the *Phytophthora* sp. were required.

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