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Fungal Induced Regulation of the Biosynthesis of Sesquiterpene Phytoalexin (Capsidiol) in Pepper Fruits

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Objectives

To get some insight into the regulatory mechanism controlling the sesquiterpene branch (capsidiol) of isoprenoid pathway, the expression pattern of the isoprenoid pathway genes was compared between susceptible and resistance reactions of pepper fruits infected with anthracnose fungus. Depending on the fruit ripening, quantitative assay of the sesquiterpene phytoalexin, capsidiol, was also conducted in the infected fruits.

Materials and Methods

1. Material : pepper (*Capsicum annuum*), anthracnose fungus (*Colletotrichum gloeosporioides*)

2. Methods: To determine whether capsidiol biosynthesis was induced from pepper by anthracnose fungus , we inoculated 10 μl of spores ($5X10^5$ spores/ml) on the pepper fruits, harvest the treated parts of the fruit and analyze fungal induced accumulation of capsidiol of samples by TLC (developing condition, cyclohexane : EtoAc= 1:1; visualizing reagent, 3.5% vanillin and 0.6% H_2SO_4 in MeOH). The capsidiol biosynthesis related genes were cloned by RT-PCR.

Results and Discussion

Capsidiol, which is known as an antifungal compound, is the principal phytoalexin in the fruits of *Capsicum annuum*. Several non-fungal agents have been tested previously as potential elicitors of phytoalexin accumulation in pepper fruits. In this experiment, the biosynthesis of capsidiol was investigated in pepper fruits infected with anthracnose fungus. The ripe fruits, showing the resistant reaction against the fungus, accumulate high amount of capsidiol in infected area. To understand the regulation of capsidiol biosynthesis in infected fruits, expressed transcripts of isoprenoid pathway genes, such as HMGR, IPPI, FPP synthase, STC and SS, were cloned by reverse transcriptase-polymerase chain reaction using degenerate primers. Then, semiquantitative RT-PCR analysis was conducted to clarify their expression patterns between susceptible and resistant reaction of the pepper fruits. The correlation between STC transcript level and the amounts of capsidiol in the ripe pepper fruits suggests that transcriptional regulation plays an important role in controlling capsidiol biosynthesis.

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