

Isolation and Characterization of Tn5 Insertion Mutants of *Pseudomonas fluorescens* Antagonistic to *Rhizoctonia solani*

Seur Kee Park*, Ki Beum Park¹ and Ki Chung Kim¹

Department of Agricultural Biology, College of Agriculture, Suncheon National University, Chonnam 540-070, Korea

¹Departemnt of Agricultural Biology, College of Agriculture, Chonnam National University, Kwangju 500-757, Korea

Rhizoctonia solani 길항세균 *Pseudomonas fluorescens*의 Tn5 삽입 돌연변이주 분리 및 특성

박서기* · 박기범¹ · 김기청¹

순천대학교 농과대학 농생물학과, ¹전남대학교 농과대학 농생물학과

ABSTRACT : *Pseudomonas fluorescens* Biovar III strain S-2 antagonistic to *Rhizoctonia solani* was subjected to Tn5 mutagenesis by the transposon vector pGS9. Ampicillin and kanamycin resistant (Amp^r, Km^r) transconjugants were recovered at a frequency of 1.3×10^{-7} per initial recipient cell, when recipient cells were washed twice in TE buffer before conjugation. Of the ca. 3000 transconjugants, a frequency of noninhibitory (Inh⁻), nonfluorescent (Flu⁻) and auxotrophic (Pro⁻) mutants were 0.27%, 0.47% and 0.40%, respectively. In these mutants, all Inh⁻ mutants showed the same colony morphology as wild type, whereas all Flu⁻ and Pro⁻ mutants inhibited the growth of *R. solani*. These mutants were also susceptible to chloramphenicol, indicating only the Tn5 element, except for parts of pGS9, was integrated into the recipient genome. In a Southern blot analysis, the Tn5 element inserted into one site on the chromosome for each of the chosen mutants. However, Tn5 insertion sites of Inh⁻, Flu⁻, and Pro⁻ mutants were differed in each other. These indicate that the genes essential for *R. solani* inhibition, fluorescent production and auxotrophic are chromosomally located, but not linked to each other.

Key words : *Pseudomonas fluorescens* Biovar III, Tn5 mutagenesis, Inh⁻, Flu⁻, Pro⁻ mutants, Southern blot analysis.

Rhizoctonia solani causes damping-off of many crops especially at seedling stage. Its biological control has been extensively studied worldwide (8, 16, 19, 38). A variety of *Pseudomonas* species have been reported to be associated with disease suppression of *R. solani* (3, 11, 12, 16, 18, 19, 24, 28).

Certain pseudomonads produce siderophore that has high affinity to iron and thereby outcompetes other organisms when iron is limited in the environment (8, 21, 22, 25, 27). Some produce secondary metabolites such as antibiotics (7~9, 11~14, 17, 18, 20, 30, 31, 35, 36) and hydrogen cyanide (37) that serve to actively antagonize other organisms. The cor-

relations between bacterial inhibition of pathogens *in vitro* and disease suppression in the soil have supported for the role of these compounds in biological control.

Recent advances in recombinant DNA technology have accerlated genetic analysis of the mechanism of disease suppression (8, 10, 14, 22, 34). An important and versatile tool in this approach is the transposon, Tn5 (2, 22, 26, 32). Its transposition into bacterial genome is random, results in single-site nonleaky polar mutations, and usually leads to inactivation of the gene (5). Therefore, Tn5 insertion mutants defective in fungal inhibition can be used to find the compounds associated with the inhibition as well as to clarify the role of the compounds

*Corresponding author.

in the disease suppression as compared with wild type for their characteristics. A Tn5 insertion mutation also represents a new physical marker at the site of insertion (5). Therefore, the mutants can be also used to facilitate cloning of genes for which direction is not possible (29,31,41).

Recently, we isolated *Pseudomonas fluorescens* Biovar III that inhibited growth of *R. solani* *in vitro* and suppressed damping-off of eggplant in green house (28). We have tried to clone genes from the bacterium for the antagonism. Here, we report isolation and partial characterization of Tn5 insertion mutants defective in *R. solani* inhibition, fluorescent production, and Tn5-induced auxotrophs.

MATERIALS AND METHODS

Organisms and plasmids. The organisms and plasmids used in this study are listed in Table 1. Plasmid vector pGS9 (30.5 kb) was composed of p15 A replicon that functions in *Escherichia coli* but not in other bacteria, tra genes encoding the N type of bacterial conjugation system, and Tn5 (32). The plasmid vector was carried in *E. coli* WA803.

Media and culture conditions. *P. fluorescens* strains were grown on nutrient broth yeast extract medium (NBY)(6) or Kings medium B (KMB)(6) supplemented with ampicillin (50 µg/ml) at 28°C. *E. coli* was cultured at 37°C on Luria-Bertani (LB) broth or plates (23) supplemented with kanamycin (50 µg/ml) and chloramphenicol (50 µg/ml). *R. solani* was grown on potato dextrose agar (PDA) at 28°C.

Transposon mutagenesis. The 5.7 kb transposon Tn5 that contains for kanamycin resistance gene (5) was transferred into *P. fluorescens* using the pGS9 that harbors Tn5 (32). *E. coli* donor strain WA803 was grown overnight at 37°C with shaking in LB broth supplemented with kanamycin. *P. fluorescens* recipient strain S-2 was grown at 28°C with shaking in KMB broth supplemented with ampicillin for 24 hrs. Approximately 10⁹ donor cells were sedimented and suspend in 50 µl of sterile distilled water. Approximately 10⁹ recipient cells were not washed, or washed twice in sterile distilled water or TE buffer, and then suspended in 50 µl of sterile distilled water. The mixtures of donor and recipient suspensions (1:1) were transferred onto yeast extract-dextrose-CaCO₃ (YDC) (6), LB or KMB plates, and in-

Table 1. Organisms and plasmids used in this study

| Organisms | Relevant characteristics ^a | Source or reference |
|---|---|----------------------|
| <i>P. fluorescens</i> biovar III S-2 | Wild type antagonistic to <i>R. solani</i> , inhibition, Amp ^r , Nal ^r Km ^s , Rif ^s | This laboratory (28) |
| <i>E. coli</i> WA803 | <i>met thi supE hsdR hsdM</i> | 39 |
| Plasmid pGS9 | Cm ^r Km ^r , p15A replicon N-tra, Tn5 | 33 |
| <i>R. solani</i> | Wild type, isolated from eggplant and pathogenic | This laboratory (28) |
| Tn5 mutants | | |
| S2-1050, S2-1083 | Inh ⁻ , Flu ⁺ , Pro ⁺ ^b | This study |
| S2-1102, S2-1568 | Inh ⁻ Flu ⁺ , Pro ⁺ | This study |
| S2-1574, S2-1651 | Inh ⁻ Flu ⁺ , Pro ⁺ | This study |
| S2-2620 | Inh ⁻ Flu ⁺ , Pro ⁺ | This study |
| S2-1979, S2-2014 | Inh ⁺ , Flu ⁻ , Pro ⁺ | This study |
| S2-2033, S2-2161 | Inh ⁺ , Flu ⁻ , Pro ⁺ | This study |
| S2-2430, S2-2460 | Inh ⁺ , Flu ⁻ , Pro ⁺ | This study |
| S2-2820 | Inh ⁺ , Flu ⁻ , Pro ⁺ | This study |
| S2- 12, S2-2168 | Inh ⁺ , Flu ⁺ Pro ⁻ | This study |
| S2-2326, S2-2355 | Inh ⁺ , Flu ⁺ Pro ⁻ | This study |
| S2-2478, S2-2651 | Inh ⁺ , Flu ⁺ Pro ⁻ | This study |

^aAmp^r, Nal^r, Km^r, Rif^s and Cm^r indicate resistance (r) or susceptible (s) to ampicillin, nalidixic acid, kanamycin, rifampicin, and chloramphenicol, respectively.

^bInh⁺, *R. solani* inhibition on KM-PDA; Inh⁻, *R. solani* noninhibition on KM-PDA; Flu⁺, fluorescent pigment production on KMB; Flu⁻, nonfluorescent pigment production on KMB; Pro⁺, prototrophic on Vogel-Bonner minimal medium; Pro⁻, auxotrophic on Vogel-Bonner minimal medium.

cupated for 24 hrs at 28°C. Transconjugants were selected on mannitol-glutamate(MG) (15) or KMB plates containing ampicillin and kanamycin.

Isolation of noninhibitory, nonfluorescent and auxotrophic mutants. *R. solani*-noninhibitory mutants were selected on kanner minimal medium with one-fifth strength potato (KM-PDA) plates (34). Amp^r, Km^r transconjugants were spotted on the edge of petri plates using toothpicks and a 0.5 cm plug of *R. solani* was placed in the center of the plate. Noninhibitory and nonfluorescent mutants were selected after 5 and 3 days culture at 28°C on KMB agar, respectively. Auxotrophic mutants were selected after 2 days culture at 28°C on Vogel-Bonner minimal medium (4).

Isolation of DNA. Total genomic DNA was isolated from strain S-2 and mutants as described by Maniatis (23). Plasmid DNA from strain S-2 and mutants were isolated by the alkaline lysate procedure of Portnoy and White (1) and Boiling method (23). pGS9::Tn5 plasmid was isolated by the alkaline lysate procedure of Crosa and Falkow (1), purified by the polyethylene glycol treatment described by Maniatis (23) and used as a probe in southern blot analysis.

Restriction endonuclease digests and electrophoresis.

Restriction endonucleases purchased from Boehringer Mannheim Biochemicals (BMB, Germany) and Kosco (Korea) were used according to the instructions of the manufacturer. 1 µg of genomic DNA was digested at 37°C for 1.5 hrs after adding 2 units of *EcoRI* or *PstI*. Electrophoresis was performed in 0.8% agarose gels with Tris-borate buffer (25 v/cm for 8 hrs). *PstI*-digested 1.2 kb and *HpaI*-digested 5.4 kb in Tn5 DNA (5) were purified by gene clean kit (Gene clean II kit, Bio 101, Inc. USA) after electrophoresis. The 1.2 kb and 5.4 kb DNA fragments were used as a probe for *EcoRI*- and *PstI*- digested genomic DNA, respectively.

Southern blot hybridization. Labeling of probe DNA and detection were conducted using Dig DNA Labeling and Detection Kit (BMB, Germany). After electrophoresis, agarose gels were depurinated in 0.25 M HCl for 10 min to facilitate transfer to large fragments, denatured in 1.5 M NaCl and 0.5 M NaOH for 45 min, and neutralized in 1 M Tris-HCl (pH 8.0) and 1.5 M NaCl for 45 min. DNA fragments then transferred to nitricellulose (Hybond™-N, Amersham, USA) by the method of Southern (23).

The blotted nitrocellulose filters were prehybridized, hybridized, washed and detected according to the instructions of the manufacturer.

RESULTS

Frequency of transconjugation. Amp^r, Km^r transconjugants of strain S-2 were little recovered when recipient cells were not washed or washed twice in distilled water. However, the transconjugants were recovered at a frequency of 1.3×10^7 per initial recipient, when recipient cells were washed twice in TE buffer before mating, and then spread on KMB. Although the recipient cells were washed twice in TE buffer, its frequency was very low when they were mated on LB and YDC plates, or spread on MG plates (Table 2).

Characterization of Tn5 mutants. Approximately 3,000 Amp^r, Km^r transconjugants from 9 independent matings were screened. Of these, 8 mutants (ca. 0.27%) were defective in *R. solani* inhibition on KM-PDA plates (Inh⁻), 14 mutants (ca. 0.47%) were nonfluorescent on KMB, and 12 mutants (ca. 0.40%) were auxotrophic on Vogel-Bonner minimal medium (Table 3). All the mutants defective in *R. solani* inhibition produced fluorescent pigment (Flu⁺), whereas all of the nonfluorescent mutants (Flu⁻)

Table 2. Frequency of *Pseudomonas fluorescens* transconjugants from different mating methods^x

| Preparation of recipient cells | Mating plate | Frequency on | |
|--------------------------------|--------------|-----------------------|-----------------------|
| | | MG ^y | KB |
| Non washing | YDC | <10 ^{-9ez} | <10 ^{-9e} |
| | KB | <10 ^{-9e} | <10 ^{-9e} |
| Washing twice-water | YDC | <10 ^{-8d} | <10 ^{-8e} |
| | KB | 1.2×10^{-8d} | 1.5×10^{-8c} |
| Washing twice-TE buffer | LB | <10 ^{-8d} | <10 ^{-8d} |
| | YDC | 1.5×10^{-8c} | 1.4×10^{-8c} |
| | KB | 2.7×10^{-8b} | 1.3×10^{-7a} |

^x*P. fluorescens* was mated with *E. coli* WA803 (pGS9::Tn5) and spontaneous mutation frequency of recipient cells to Km^r was less than 10⁻⁹.

^yMG and KB, mannitol-glutamate and Kings medium B, respectively, supplemented with ampicillin (50 µg/ml) and kanamycin (50 µg/ml); YDC, yeast extract-dextrose-CaCO₃, LB, Luria-Bertani plate.

^zMeans within a column followed by the same letter are not significantly different at 5% level by Duncan's Multiple Range Test.

inhibited growth of the *R. solani*. Also, all of the auxotrophic mutants inhibited growth of the *R. solani* and produced fluorescent pigment (Table 3. Fig. 1).

Physical analysis of the chosen mutants. Wild type and all of the chosen mutants (7 Inh⁻, 7 Flu⁻ and 6 Pro⁻ mutants) did not have an indigenous plasmid and pGS9. All of the mutants were resistant to kanamycin (Km) but susceptible to chloramphenicol (Cm), indicating that the vector portion of

the plasmid pGS9 except for Tn5 element was not integrated into the host genome.

The distribution and number of Tn5 elements in the DNAs of these mutants were determined by southern blot analysis. The total DNA from each mutant and parental strain S-2 were digested with *EcoRI*, and then hybridized with digoxigenin-labe-

Table 3. Characteristics of *Pseudomonas fluorescens* strains selected from 3000 transconjugants

| Strain | Inhibition of <i>R. solani</i> ^a | Characteristics ^b | No (Percent) of isolation |
|---------------------|---|------------------------------|---------------------------|
| 554 1050 1083 1102 | - | Flu ⁺ | 8 (0.27%) |
| 1568 1574 1651 2620 | - | Pro ⁺ | |
| 287 460 475 1724 | + | Flu ⁻ | 14 (0.47%) |
| 1979 2012 2014 2033 | | Pro ⁺ | |
| 2161 2430 2455 2460 | | | |
| 2677 2820 | | | |
| 12 684 720 764 | + | Flu ⁺ | 12 (0.40%) |
| 964 1509 1924 2169 | | Pro ⁻ | |
| 2326 2478 2355 2651 | | | |

^a - and + indicate mutants noninhibitory to and inhibitory to *R. solani*, respectively.

^b Flu⁺ and Pro⁺ indicate fluorescent pigment production and prototrophs, respectively.

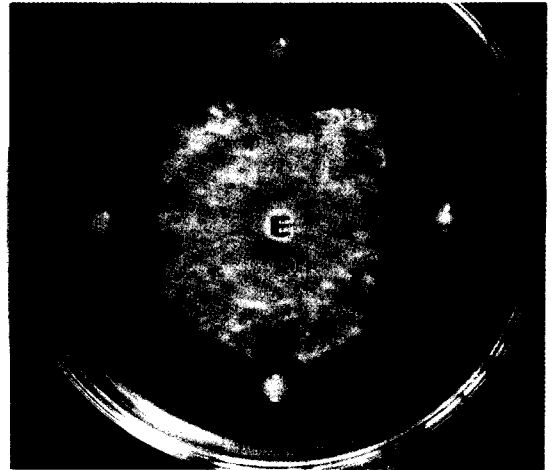


Fig. 1. Characteristics of wild type (A) and Tn5-induced mutants (B, C, D) of *P. fluorescens* inhibitory to *R. solani* (E). Noninhibitory mutants (B) produce a fluorescent pigment, while nonfluorescent mutants (D) inhibit *R. solani* growth. Auxotrophic mutants (C) inhibit *R. solani* growth and produce a fluorescent pigment.

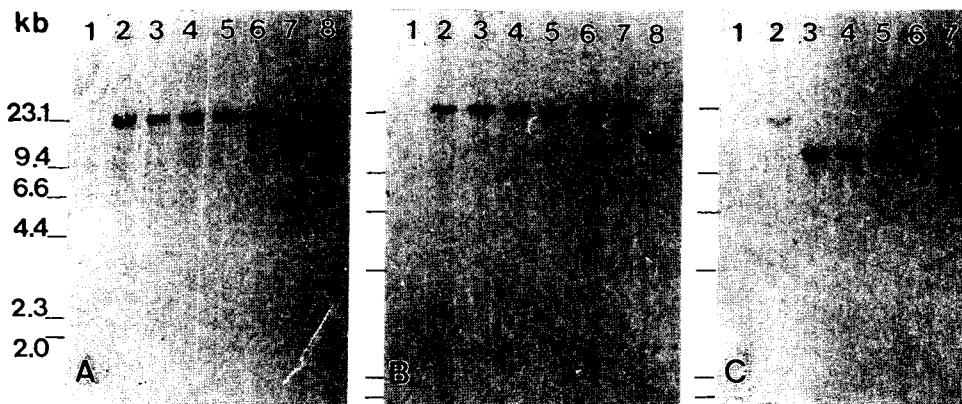


Fig. 2. Southern blot analysis of *EcoRI*-digested total genomic DNA from Tn5-induced noninhibitory mutants (A), nonfluorescent mutants (B) and auxotrophic mutants (C) of *Pseudomonas fluorescens*. Blots of digested DNA were hybridized with digoxigenin-labeled 1.2 kb *PstI* fragment of Tn5. Lane 1, wild type S-2; lanes A2 to 8, noninhibitory mutants S2-1050, S2-1083, S2-1102, S2-1568, S2-1574, S2-1651, S2-2620; lanes B2 to 8, nonfluorescent mutants S2-1979, S2-2014, S2-2033, S2-2161, S2-2430, S2-2460, S2-2820; lanes C2 to 7, auxotrophic mutants S2-12, S2-2169, S2-2326, S2-2355, S2-2478, S2-2651.

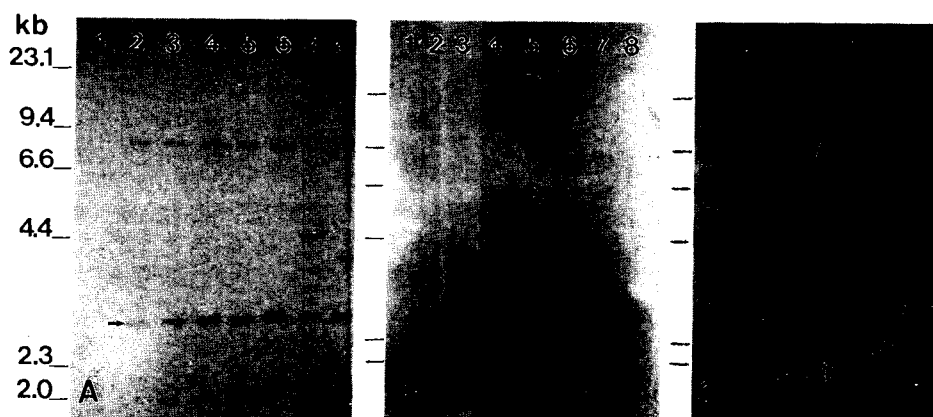


Fig. 3. Southern blot analysis of *Pst*I-digested total genomic DNA from Tn5-induced noninhibitory mutants (A), nonfluorescent mutants (B) and auxotrophic mutants (C) of *Pseudomonas fluorescens*. Blots of digested DNA were hybridized with digoxigenin-labeled 5.4 kb *Hpa*I fragment of Tn5. Lane 1, wild type S-2; lanes 2 to 8, the same mutants as Fig. 2. Bands of an arrow indicate ca. 2.5 kb *Pst*I fragment of Tn5, and also two bands besides it indicate two boundary fragments adjacent to Tn5.

led 1.2 kb *Pst*I fragment of Tn5. The DNA from parental strain S-2 was not hybridized, but all of the mutants was hybridized to one fragment (Fig. 2). These results suggest that the mutants have a single insertion of Tn5 in a genome. In addition, Tn5 insertions of *Inh*⁻ mutants (Fig. 2A) and *Flu*⁻ mutants (Fig. 2B) appeared in a fragment more than 23 kb in six out of seven strains. Also, three out of six *Pro*⁻ mutants contained Tn5 insertions in a same size and three strains in different size fragments (Fig. 2C).

To further determine whether the Tn5 insertion was at the same sites or not, the DNAs from these strains were digested with *Pst*I and hybridized with digoxigenin-labeled 5.4 kb *Hpa*I fragment of Tn5 (5). Three internal fragments of set size in Tn5 and two boundary fragments adjacent to Tn5 should be hybridized, because *Pst*I cleave Tn5 four times (6). In this experiment, however, bands of one internal fragment (ca. 2.5 kb) and two boundary fragments were hybridized, and those of two internal fragments less than 1.2 kb were not appeared (Fig. 3). Among them, the two boundary fragments of seven *Inh*⁻ mutants were 8.5 kb and 2.0 kb in five strains, 4.4 kb and 3.5 kb in one strain, and 8.5 kb and 4.0 kb in one strain (Fig. 3A). The boundary fragments of seven *Flu*⁻ mutants were 2.4 kb and 2.1 kb in six strains, and 7.0 kb and less than 1.2 kb in one strain (Fig. 3B). Also, the boundary fragments of six *Pro*⁻ mutants were the same site in three strains

and the different sites in three strains (Fig. 3C). However, Tn5 insertion sites among *Inh*⁻, *Flu*⁻, and *Pro*⁻ mutants were differed in each other.

DISCUSSION

Amp^r, *Km*^r transconjugants in matings between *E. coli* WA803(pGS9) and *P. fluorescens* strain S-2 were not obtained by the general methods, which were conducted in several *Pseudomonas* spp. (2, 22, 26). Thomashow and Weller (34) used an antibiotic phenazine-resistant spontaneous mutant of *E. coli* WA803 in Tn5 mutagenesis of *P. fluorescens* because antibiotics produced from recipient cells inhibited donor cells. Pierson (unpublished data) also mated them on agar plates supplied with 100 µg/ml iron ammonium citrate or 10 mM p-aminobenzoic acid to suppress the phenazine production. However, strain S-2 used in this study did not inhibit *E. coli* WA803 and were not conjugated by methods described above. The conjugants were obtained only when recipient cells were washed in TE buffer before mating. Therefore, the conjugation is thought to be not affected by certain antibiotics produced from strain S-2. Additional works are needed to understand the reasons that conjugation of strain S-2 did not occurred.

In this study, the frequency of Tn5-induced mutants defective in *R. solani* inhibition, fluorescent production and the auxotrophic mutants were 0.27%,

0.47% and 0.40%, respectively. In *P. fluorescens* strain 2-79RN₁₀ antagonistic to *Gaeumannomyces graminis* var. *tritici*, the frequency of Tn5-induced mutants defective in phenazine antibiotic production, fluorescent production and the auxotrophic mutants were reported as 0.3%, 0.25% and 0.3%, respectively. While, in *P. aureofaciens* strain 30~84 the frequency of Tn5-induced mutants defective in phenazine production, siderophore production and the auxotrophic mutants were reported as 0.4%, 0.5% and 1.0%, respectively (Pierson, unpublished data). As described above, the frequency of Tn5 mutants reported on *Pseudomonas* spp. had various ranges according to strains or characteristics.

Several reports suggested that *P. fluorescens* affect biological control by producing certain substances related to fluorescent pigment (7, 20~22, 25, 27, 34, 36). However, in this study, all of nonfluorescent (Flu⁻) mutants inhibited growth of *R. solani*, similar to those of wild type strain S-2. This result suggests that *R. solani* inhibition by strain S-2 are not due to substances related to fluorescent pigments.

All of the wild type and mutants do not contain an indigenous plasmid. Therefore, total DNA from their strains is chromosomal DNA and the Tn5 element of the all mutants inserted into the chromosome. We, therefore, conclude that the genes essential for *R. solani* inhibition, fluorescent production and auxotrophic are chromosomally located. Also, vector portion of the plasmid pGS9 except for Tn5 element was coded for chloramphenicol (Cm) resistance (32). Therefore, the mutants should be resistant to Cm, if the vector pGS9 has been integrated into the chromosome. However, all chosen mutants were susceptible to Cm, indicating only Tn5 element, except for part of vector pGS9, was integrated into the chromosome.

The Tn5 element was inserted into one site on the chromosome for each of the all chosen mutants. Similar observations were made in Tn5 mutagenesis of several *Pseudomonas* spp. (2, 22, 26, 34). However, five of seven strains in Inh⁻ mutants, six of seven strains in Flu⁻ mutants and three of six strains in Pro⁻ mutants were inserted Tn5 element at the same site. These results differ from those of DeBrijin and Lupski (5), who reported that Tn5 insertions in cloned DNA sequences appeared a completely random pattern. Therefore, the mutants that Tn5 element inserted into the same site are

thought to be the same strains. However, Tn5 insertions sites among Inh⁻, Flu⁻ and Pro⁻ mutants were clearly differed in the all chosen strains. All of Inh⁻, Flu⁻ and Pro⁻ mutants were also not overlapped for their ability to fungal inhibition, fluorescent production and auxotrophic. These results suggest that the genes essential for *R. solani* inhibition, fluorescent production and auxotrophic are not linked to each other.

It needs much additional work to understand the *R. solani* inhibition mechanism and the genetics of substances related to the fungal inhibition in *P. fluorescens*. Using Tn5 mutants reported here, we should now be able to isolate, identify and characterize the genes related to the fungal inhibition and to learn more about their role in the disease suppression.

요 약

*Rhizoctonia solani*의 길항세균인 *Pseudomonas fluorescens* Biovar III strain S-2를 transposon vector pGS9으로 Tn5 삽입 돌연변이 시켰다. 변이체들은 수용세포를 TE buffer로 2번 세척후 KMB배지에서 집합, 도말하였을 경우에만, 1.3×10^{-7} 의 빈도로 분리되었다. 약 3000개의 변이체 중에서, *R. solani* 억제력을 상실한 균주는 0.27%, 형광색소를 상실한 균주는 0.47%, 영양요구성 균주는 0.40%이었다. 이들 돌연변이주들 중에서, *R. solani* 억제력을 상실한 균주는 모두 야생형 균주와 동일한 균총을 형성한 반면, 형광색소를 상실한 균주와 영양요구성 균주 모두는 *R. solani*를 억제하였다. 또한, 이들 돌연변이주들은 모두 chloramphenicol에 감수성을 나타냈기 때문에, pGS9의 vector 부위를 제외한 Tn5 부위만 수용세포의 genome에 삽입되었음을 알 수 있다. southern blot 분석결과, 선발된 돌연변이주 모두에서 Tn5가 염색체에 하나씩 삽입되었는데, 그들의 삽입부위는 *R. solani* 억제력을 상실한 균주, 형광색소를 상실한 균주, 그리고 영양요구성 균주사이에 차이가 있었다. 이것은 *R. solani* 억제, 형광색소 형성, 영양요구에 필요한 유전자가 모두 염색체에 있지만, 서로 연결되어 있지 않다는 것을 나타낸다.

ACKNOWLEDGEMENT

This paper was supported by NON DIRECTED RESEARCH FUND, Korea Research Foundation, 1992.

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