INTRODUCTION

Bacterial blight (BB) is a destructive disease to *Oryza sativa* resulting in severe losses in rice production, ranging from 10 to 20% and up to 50 to 70% in severely infected fields in Asian countries (Mew et al. 1993; Adhikari et al. 1994). BB is a vascular disease resulting in tanish grey to white lesions along the veins in leaf. Under field conditions, BB occurs at the tillering stage, progress steadily with plant growth and peaking at the flowering stage (Mew et al. 1993). Severely infected leaves tend to dry quickly, and many farmers attribute the symptoms of the disease to drought, thus leading to invocatable losses (Mew 1987). The causative agent of BB is *Xanthomonas*...
oryzae pv. oryzae (Xoo), a Gram-negative and waterborne bacteria, which exhibit genetic variation among isolates. (Nino-Liu et al. 2006).

BB management tactics, such as resistant cultivars, are the most economical strategy for disease management. However, it has only been partially successful because of the enormous diversity in the pathogens. While others, such as agro-chemicals, are harmful to the environment. Moreover, the overuse of chemical fungicides has decreased the efficacy of host-plant resistance due to the occurrence of resistant pathogens (Mew et al. 1992; Ji et al. 2008; Chung et al. 2015). In contrast, biocontrol deserved a special significance as an eco-friendly, cost-effective alternative strategy for bacterial blight management without the negative effect of synthetic chemical agents that can cause environmental pollution and may induce pathogen resistance.

Biological control of crops diseases using microbial antagonists are an eco-friendly alternative to chemical pesticides and is being studied extensively on several different plant diseases with a variety of microbial antagonists (Palaniyandi et al. 2013b). Biocontrol of bacterial blight using Bacillus species, Pseudomonas species, Delftia species and Lyso bacter species have been reported (Vasudevan et al. 2002; Han et al. 2005; Ji et al. 2008). Delftia tsuruhatensis strain HR4, a novel plant growth-promoting bacterium was isolated from the rhizoplane of rice. This strain showed antagonistic activity against three main rice pathogens (X. oryzae pv. oryzae, Rhizoctonia solani and Pyricularia oryzae Cavara) and suppresses BB infestation in greenhouse condition. Furthermore, the nitrogen-fixing activity was studied which may contribute to the plant health (Han et al. 2005). Another bacteria isolated from rice rhizosphere is Lyso bacter antib ioticus, which can significantly inhibit the growth of various phytopathogenic bacteria and fungi, especially BB pathogen Xoo. In greenhouse experiments, whole bacterial broth culture showed significant biocontrol efficacy up to 69-7%. However, bacterial cells re-suspended in water, cell-free culture extracts and heat-inactivated cultures also significantly reduced BB severity, which suggested that not only antibiotics but density of colonization on leaves may be involved for biological control of rice BB (Ji et al. 2008).

Actinomycetes are abundant in soil environment, especially in root rhizosphere (Palaniyandi et al. 2013b). It is reported that Actinomycetes do benefit to plant, thus have a long history of being used for biological control of plant disease caused by Fusarium, Rhizoctonia, Alternaria, Pythium and Streptomyces scabiei (El-Tarabily et al. 1997; Boukaew et al. 2013; Palaniyandi et al. 2013b). Compared with other bacteria, Actinomycetes is more suitable to adapt to soil environment because of spore production (El-Tarabily and Sivasithamparam 2006). More importantly, Actinomycetes can produce many secondary metabolites which were reported to be involved in direct or indirect biocontrol mechanism. Secondary metabolites from Streptomyces include antibiotics (Yamaguchi 1982; Lee et al. 2012), hydrolytic enzymes (Lee et al. 2012), volatile compounds (direct mechanism) and some compounds that can regulate plant defence system (indirect mechanism) (Palaniyandi et al. 2013b). Direct mechanism, like antibiotic production from Streptomyces are well studied, and some of the antibiotics have been successfully developed for commercialization (Zhou et al. 2014). Although several studies have been focused on induction of plant defence mechanism for biocontrol of fungal disease (Zhao et al. 2012; Palaniyandi et al. 2013b), none has been reported in biological control of Xoo by indirect mechanism. Recently, an endophytic Streptomyces strain showed its biocontrol ability against rice bacterial leaf blight by inhibition of Xoo growth, but the active compound was not characterized (Hastuti et al. 2012). Moreover, Streptomyces toxytricini VN08-A-12 was selected from 2690 Actinomycetes strains by strong inhibitory activities against the growth of different races of Xoo. In field test, strain VN08-A-12 was not only able to reduce the Xoo lesion lengths but also increased the rice yield in two different rice cultivars (Duong et al. 2014).

Currently, most screening method are based on the antagonistic assay against the phytopathogen Xoo, however, strong inhibition activity against Xoo do not ensure the high biocontrol efficacy. Moreover, this method may omit some biocontrol agent that can trigger plant defence system. Compare with them, we have developed a screening method (Park et al. 2012), using the target plant’s explant to screen a compound that can protect rice from BB disease directly. In this study, crude extract from Streptomyces sp. MJM4426 was found to significantly protect rice leaf explant from BB infection, and the active compound was isolated and identified. Furthermore, the biocontrol ability in greenhouse condition were evaluated and the potential biocontrol mechanism was also discussed.

Materials and methods

Plant material and bacterium

Seed of O. sativa L. cv. Milyang 23, a rice cultivar susceptible to BB disease, was obtained from the National Academy of Agricultural Science, Rural Development Administration (RDA), Jeonju, Republic of Korea. Xanthomonas oryzae pv. oryzae KACC 10331 was obtained from the Korean Agricultural Culture Collection (KACC), National Institute of Agricultural Biotechnology (NIAB),
Republic of Korea. *Xoo* was cultured by streaking on YGC medium (Glucose 10 g l\(^{-1}\), Yeast extract 5 g l\(^{-1}\), CaCO\(_3\) 30 g l\(^{-1}\), agar 15 g l\(^{-1}\), pH 7.0) and incubating at 28°C for 24 h. A single colony was inoculated into 3 ml of M210 liquid medium in a 13 ml tube and further incubated at 28°C with shaking at 150 rev min\(^{-1}\) for 24 h.

Assessment of inhibitory activity against bacterial blight disease by using rice leaf explants

Inhibitory activity against bacterial blight disease followed the description in the previous research (Park et al. 2012). *Xanthomonas oryzae* KACC 10331 were precultured and diluted in distilled water, and 200 μl of *Xoo* culture media was then pipetted separately into individual well on a 96-well plate. Whole rice leaves were cut into 15-cm length and their surface was sterilized with a diluted antiseptic solution and the leaves were rinsed in sterilized distilled water three times. The leaves were rinsed three times in distilled water. Subsequently, rice leaf explants (4 × 4 mm\(^2\)) were placed in 96-well plates. Crude extracts or purified compound treatment ranged from 50 to 0.78125 μmol l\(^{-1}\) with twofold serial dilution. The plate was incubated at 30°C for a week, similar to the seasonal temperature in the field. A quadruple treatment set was repeated three times.

Evaluation of diseased leaf area

The calculation of the diseased leaf area percent (DLA %) followed the method as described in the previous research (Park et al. 2012). DLA % was evaluated after 1 week incubation by converting the lesion on the explants into black and white mode using Adobe Photoshop CS6 (Adobe Systems Incorporated, San Jose, CA, USA). An image-analysing program on the web (http://chemist.hosting.param.com/imgarea/) was used to calculate the white coloured area, corresponding to *Xoo* infection. The least concentration inhibiting infection was determined by the diseased area ratio less than 10%.

Characterization of *Streptomyces* sp. MJM4426

Genomic DNA was isolated from strain MJM4426 using a bacterial genomic DNA isolation kit (Promega, Madison, WI, USA), according to the manufacturer’s protocol. The 16S rRNA gene was amplified by PCR using a universal primer set, 27F (5' AGA GTT TGA TCA TGG CTC AG-3') and 1492R (5' GGA TAC CTT GTT AGC ACT T-3') (Mao et al. 2012). The 16S rDNA sequence was searched for similarities to known sequences in the GenBank database (National Center for Biotechnology Information, National library of medicine) using the BLAST search program. The sequence was aligned with the reference strains using CLUSTALX ver. 1.8 (Thompson et al. 1997). A phylogenetic tree was constructed by the neighbour-joining method (Saitou and Nei 1987) using MEGA 6.0 software (Tamura et al. 2013).

Morphological characteristics of strain MJM4426 were assessed on International Streptomyces project (ISP) medium for its growth, spore formation and pigmentation as described previously (Shirling and Gottlieb 1966). Physiological characteristics were studied by degradation of casein, starch, xanthine and tyrosine, growth in the presence of sodium chloride, utilization of different sole carbon sources, sensitivity to different antibiotics, requirements for temperature and pH and were also studied (Palaniyandi et al. 2011).

Fermentation and preparation of crude extracts of *Streptomyces* sp. MJM4426

*Streptomyces* sp. MJM4426 was precultured in a 250-ml baffled flask containing 40 ml modified Bennett’s medium (glucose 10 g l\(^{-1}\), yeast extract 1 g l\(^{-1}\), peptone 2 g l\(^{-1}\), beef extract 1 g l\(^{-1}\), pH 7.2) and incubated at 28°C for 2 days with constantly shaking at 200 rev min\(^{-1}\). Then the seed culture was inoculated in 500 ml of DYMC medium (dextrin 25 g l\(^{-1}\), dry yeast 12 g l\(^{-1}\), corn starch liquor 20 g l\(^{-1}\), NaBr 1 g l\(^{-1}\), CoCl\(_2\) 1 g l\(^{-1}\), pH 7.0) at 1% inoculum size in 2-l baffled Erlenmeyer flasks. The flasks were incubated at 28°C in a shaking incubator set to 200 rev min\(^{-1}\) for 7 days. Totally, 10 l of culture broth was harvested, the supernatant was extracted with three times volume of ethyl acetate and concentrated in vacuum for further study.

Isolation and purification of an active compound

Isolation of the active compounds was performed as previously described with some modification (Park et al. 2011). The crude extract was eluted on a Sephadex LH-20 column (110 × 2.2 cm) in 80% aqueous methanol (Fig. S1). Compound A was isolated from the active fraction protecting rice leaf explants from infection of *Xoo*, and purified by preparative HPLC with a YMC-Pack Pro C18 column (250 × 4.6 mm). The HPLC system (HITACHI, Chiyoda, Tokyo, Japan) was equipped with diode array detector L-2455 and binary pumps of L-2130. For the mobile phase, water with 5% acetonitrile (A) and 100% acetonitrile (B) were used at flow rate of 0.25 ml min\(^{-1}\). B was flowed with gradient elution from 0 to 95% over 50 min.
LC-ESI/MS analysis

The analytical condition followed the previously described method (Park et al. 2011). Compound A was analysed using an LC-MS system (Varian, Palo Alto, CA, USA) consisting of a 212-LC binary solvent delivery system, a MetaTherm HPLC column heater, a Prostar 410 auto sampler, a Prostar 335 photodiode array detector and a 500-ion trap mass spectrometer. A Chromsop C18 column (150 × 2.0 mm) was coupled with the system. The mobile phase was composed of water with 0.1% formic acid (v/v) (A) and acetonitrile with 0.1% formic acid (B) at flow rate 0.2 ml min⁻¹. B was fixed at 10% for 2 min, and then flowed with gradient elution from 10 to 100% over 28 min. Mass spectra were obtained under negative and positive ionization modes at the range of m/z 100–1000.

UPLC-Q-TOF/MS analysis

The accurate mass value of the purified compound was compared with the staurosporine standard using ultra performance liquid chromatography-quadrupole time-of-flight (UPLC-Q-TOF) mass spectrometry (Waters Corp., Milford, MA, USA). The system was equipped with a Waters micromass Q-TOF premier, UPLC Acuity System and a Acquity UPLC BEH C18 column (100 × 2.1 mm, 1.7 μm, Waters). The mobile phase consisted of water (A) and acetonitrile (B) with 0.1% formic acid (v/v) at flow rate 0.3 ml min⁻¹. B was maintained at 5% for the first 1 min and then gradually flowed from 5 to 100% over 9 min. Ionization was conducted under positive mode within a range of m/z 50–1000. The procedure was performed with the following conditions: ion source temperature at 200°C; desolvation gas flow at 700 l h⁻¹; cone gas flow at 50 l h⁻¹; cone voltage at 40 V; and capillary voltage 3000 V.

Antibacterial activity assay against Xanthomonas oryzae pv. oryzae KACC 10331

The OD value of X. oryzae pv. oryzae KACC 10331 culture broth was adjusted to 0.5 at 600 nm by a GENESYS 6 UV-Vis Spectrophotometer (Thermo Scientific, Madison, WI, USA) and diluted 1 : 20 (v/v) in Mueller–Hinton broth medium. Two hundred microlitres of medium was placed into a 96-well plate and compound A was treated with the serial dilution method from 50 to 3.125 μmol l⁻¹, as recommended by the National Committee for Clinical Laboratory Standards (NCCLS) (Park et al. 2011). The plates were incubated at 28°C for 24 h. The MIC value was the lowest concentration that shows an increase in bacterial growth under 2% when measured by the OD600 on an EL808 Microplate Reader (BioTek Ins., Winooski, VT, USA). 2,4-diacycteylphloroglucinol (DAPG) was used as a positive control, treated with twofold serial dilution method from 5000 to 312.5 μmol l⁻¹. The MIC value was calculated using the following formula.

\[
\text{Increase in bacterial growth (\%)} = \left[1 - \frac{(C_{24}^a - C_{0}^b) - (T_{24}^a - T_{0}^b)}{(C_{24}^a - C_{0}^b)} \right] \times 100
\]

C_{24}^a, OD600 for control (not treated) incubated after 24 h, C_{0}^b, OD600 for control (not treated) at 0 h; T_{24}^a, OD600 for treatment incubated after 24 h, T_{0}^d, OD600 for treatment at 0 h.

Greenhouse experiments

Streptomyces sp. MJ4426 was inoculated into DYC medium and incubated at 28°C for 7 days with constant shaking at 200 rev min⁻¹. The culture broth was centrifuged and the supernatant was extracted with ethyl acetate, and concentrated in vacuum. The crude extract was dissolved in 50% DMSO and diluted with H2O to the concentration of 10 000, 5000 and 1000 μg ml⁻¹ for treatment. Staurosporine was dissolved in 50% DMSO to the treatment concentration of 200, 100 and 50 μg ml⁻¹. Xanthomonas oryzae KACC 10331 was inoculated in M210 medium and incubated at 28°C for 3 days. The bacterial cells collected from plates were suspended in distilled water and the cell density was adjusted to OD600 at 0.5.

A susceptible rice cultivar Millang were planted for 6 weeks in 40 × 40 cm² pots with six plants per pot. Each treatment was replicated three times. The crude extracts and staurosporine solution was daubed on the leaf surface by using a brush. On the second day post inoculation, the treated pots were inoculated with Xoo pathogen by dipping a pair of scissors into the Xoo suspension (OD600 = 0.5) and cutting off the tip of the leaves. Treated pots placed in a randomized complete block design were kept in the greenhouse for 7 days before harvest. Lesion length of bacterial blight symptom was measured.

Statistical analysis of data

All the experiments were performed at least three times. Significant differences in treatments were analysed by SPSS ver. 22 (IBM SPSS statistics, New York, NY) by one-way analysis of variance (ANOVA) for data comparison. The Tukey’s test was used to compare means.
Results

Identification of Streptomyces sp. MJM4426

Strain MJM4426 was selected for its suppressive activity against Xoo by using rice leaf explants. This strain was isolated from soil in Jeju island, Republic of Korea and maintained in glycerol (20%, v/v) at the Extract Collection of Useful Micro-organisms (ECUM) library (http://www.ecum.or.kr) at Myongji University.

Strain MJM4426 was also analysed for its relatedness to known genera based on 16S rRNA sequence. A BLAST search for sequences related to the MJM4426 showed 99% similarity to Streptomyces species. CLUSTAL analysis of the 16S rRNA and subsequent phylogenetic tree construction showed that strain MJM4426 was closely related to Streptomyces fradiae and Streptomyces rubrolavendulae (Fig. 1).

Strain MJM4426 grew on a range of agar medium, showing typical morphology of Streptomyces (Table S1). The colour of substrate mycelium was either yellow or greyish orange, the aerial mycelium was either white or grey and the spore was grey in ISP4 medium. Strain MJM4426 can utilize glucose, sucrose, arabinose and inositol, but not mannose and mannitol. Enzymatic degradation was observed in starch and casein, but not in tyrosine and xanthine. Other physiological characteristics were shown in Table S2.

Characterization of an active compound against Xoo

The fourteenth fraction by Sephadex LH-20 column chromatography represented suppressing activity against bacterial blight in rice leaf explants. The active fraction was purified by preparative C18 RP-HPLC and compound A was detected at 41 min on HPLC (Fig. S1). The m/z value of compound A was at 467 by LC-ESI/MS under a positive ion mode. Compound A exhibited an m/z value at [M+H]+ 467-2086 using a high resolution UPLC-Q-TOF/MS and its molecular formula were estimated as C28H26N4O3 that corresponds to staurosporine (Fig. 2c). The lowest concentration to suppress the growth of more than 98% of X. oryzae pv. oryzae KACC 10331 was represented as MIC value. Staurosporine isolated from Streptomyces sp. MJM4426 exhibited an MIC value of 256 μg ml−1, while the positive control DAPG presented an MIC value at 4 μg ml−1 (Table 1).

Rice leaf explants test by using staurosporine and DAPG

The change in colour from green to yellow when rice leaf explants infected with Xoo was used to estimate the severity of plant disease. The activity to suppress bacterial invasion into rice leaf explants was calculated by imaging diseased leaf area % (DLA %). Staurosporine showed the least concentration at 12.5 μmol l−1 for a protective effect of >90% leaf area, as compared to DAPG inhibited the infection at 2500 μmol l−1 (Fig. 3a,b).

Disease suppression efficacy of crude extracts and staurosporine in greenhouse conditions

Compared with healthy rice leaves (Fig. 4a), white lesion developed from the cutting edge when infected with Xoo (Fig. 4b). Significant reduction in white lesion was observed after treatment with crude extract at the concentration of 10 000 μg ml−1 (Fig. 4c) and staurosporine at the concentration of 200 μg ml−1 (Fig. 4d). Crude extracts and staurosporine suppressed the lesion length of BB in a dose dependent manner. At a concentration of 10 000 μg ml−1, the lesion length was decreased from 1-1 to 0.5 mm (Fig. 4e). BB disease was also suppressed by staurosporine at the concentration of 200 μg ml−1, lesion length was decreased from 1-1 to 0.2 mm (Fig. 4f). However, there was no effect at the concentration of 50 μg ml−1.

Discussion

Mechanisms of biocontrol were currently recognized as competition with pathogens for nutrients and space in and around the host plant (Siddikee et al. 2010), iron acquisition by production of siderophore (Macagnan et al. 2008), suppression of pathogens by antagonistic microbes through direct production of antibiotics (Yamaguchi 1982; Lee et al. 2012), cell wall-degrading enzymes (Lee et al. 2012), and parasitism (Palaniyandi et al. 2013a) or indirectly by induction of host resistance (Zhao et al. 2012).

Until now, biological control of bacterial blight disease have been focused on the isolation of antibiotic-producing bacteria. Velusamy et al. (2006) isolated DAPG-producing Pseudomonas fluorescence and demonstrated the suppressive effect on rice bacterial blight disease in net-house and field experiment. DAPG-producing defective mutant were much less effective in the suppressive
activity, which proved the important role of antibiosis on the biocontrol efficacy. Although Xoo inhibitory compounds were also isolated from *Phomopsis longicolla* and *Streptomyces bottropensis* (Lim et al. 2010; Park et al. 2011), the biocontrol efficacy were not determined.

In our study, staurosporine was newly isolated from *Streptomyces* sp. MJM4426 and showed strong suppressive activity against BB disease in rice explant assay. More than 90% area of rice leaf explants remained green without serious lesions by Xoo when treated with staurosporine in the concentration of 12.5 μmol l⁻¹. This is 200-fold higher than DAPG (the positive control) which is active at the concentration of 2500 μmol l⁻¹ (Fig. 3). However, direct treatment of staurosporine to *X. oryzae*

![Phylogenetic analysis of *Streptomyces* sp. MJM4426 based on the 16S rDNA sequence. The tree was constructed using the neighbour-joining method using MEGA 6.0 program. Kimura-2 parameter was used as the nucleotide substitution model. The bootstrap values (%) presented at the branches were calculated from 1000 replications. Scale bar indicates 0.002 substitutions per nucleotide position.](image-url)
Figure 2 Spectrometric analysis of compound A and staurosporine. Compound A was determined as staurosporine with their identical m/z values at [M+H]^+ 467.2081 (a) and [M+FA−H]^− 511.1963 (b) on a high resolution UPLC-Q-TOF/MS. (c) Structure of staurosporine.
pv. oryzae KACC 10331 did not show any remarkable inhibitory activity. The MIC value of staurosporine and DAPG against Xoo were 256 and 4 \( \mu \text{g ml}^{-1} \) respectively (Table 1). These results suggested that staurosporine might modulate some plant defence system to protect rice from BB infection rather than a bactericidal effect against Xoo.

We give two hypothesis to the rice BB inhibitory activity by staurosporine: Preventing plant cell death or disturbing the pathogen’s virulence. Staurosporine is an indolo[2,3-a]carbazole alkaloid compound which was previously isolated from Streptomyces staurosporeus and Streptomyces roseoflavus strains (Omura et al. 1977; Park et al. 2006), and its anti-fungal and anti-hypertensive biological activities are already reported (Rüegg and Burgess 1989). Staurosporine is a protein kinases inhibitor that controls ATP binding to the kinases (Karaman et al. 2008) and affects cell viability by participating in apoptotic pathway (Chae et al. 2000; Stepczynska et al. 2001). It is reported that the hypersensitive cell death of tobacco induced by Trichoderma viride was decreased with the treatment of staurosporine through inhibiting the TvX-induced activation of p47 protein kinase (Suzuki et al. 1999). In our research, staurosporine was newly found to inhibit Xoo’s infection only in the presence of plant tissue (Figs 3 and 4), which imply the staurosporine may involve in the plant defence mechanism. It is necessary to explore in the future study if there is any protein kinase which regulate the hypersensitive cell death in rice, can interact with staurosporine.

Furthermore, Xoo is reported to produce a range of virulence factors, including adhesin, polysaccharides, lipopolysaccharide, extracellular enzyme, iron-chelating siderophores and type III-secretion-dependent effectors, which are collectively essential for virulence (He et al. 2010). These virulence factors contribute to the Xoo’s attachment, invasion to the host tissue and regulation of the plant cell death. The expression of these factors were regulated by quorum-sensing pathways, multiple two-component system and transcriptional regulators such as Clp, Zur, FhrR, and post-transcriptional factors like RNA-binding proteins (Büttner and Bonas 2010).

<table>
<thead>
<tr>
<th>MIC (( \mu \text{g ml}^{-1} ))</th>
<th>Staurosporine (compound A)</th>
<th>256</th>
</tr>
</thead>
<tbody>
<tr>
<td>DAPG†</td>
<td>4</td>
<td></td>
</tr>
</tbody>
</table>

*The Minimum inhibitory concentration (MIC) value was the lowest concentration that shows an increase in bacterial growth under 2% when measured by the OD600.
† 2, 4-diacetyphloroglucinol as a positive control.

Figure 3 Suppression of bacterial blight by staurosporine and DAPG. (a) Staurosporine and DAPG were treated to observe their anti-rice bacterial blight activity following twofold dilution from the maximum concentration 50 \( \mu \text{mol l}^{-1} \) for staurosporine and 5000 \( \mu \text{mol l}^{-1} \) for DAPG respectively. A1–H1: Blank infected with Xoo, A6–D6: 5000 \( \mu \text{mol l}^{-1} \) for treatment of DAPG, and E6–H6: 50 \( \mu \text{mol l}^{-1} \) for treatment of staurosporine. (b) Computation of bacterial blight suppressing activity with diseased leaf area %. The damaged area on the rice explants by Xoo was evaluated under the treatments of staurosporine (●) and DAPG (♦). The experiment was performed with 12 replicates.
Recently, two antibiotics difficidin and bacilysin which suppress BB disease were isolated from *Bacillus amyloliquefaciens*. These compounds can downregulate the expression of genes involved in cell division, and protein and cell wall synthesis, as well as *Xanthomonas* virulence (Wu et al. 2015). In contrast to them, staurosporine have no bactericidal activity which indicated the suppressive effect were not related with *Xoo*’s cell division or growth. Therefore, it can be suggested that staurosporine potentially modulate rice resistance to *Xoo* and controls certain genes responsible for inducing programmed cell death, or synthesis of defence factors in the host. They may also protect rice from bacterial blight infection by directly regulating *Xoo* pathogenesis. DNA microarray analyses are currently underway to determine the mechanisms involved in staurosporine-mediated protection against BB in rice. The actual mechanism will be elaborated with more details in further study.
Acknowledgements

This work was carried out with the support of “Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01132401)” Rural Development Administration, Republic of Korea, ‘Agenda Research Program (PJ010085032015)’ RDA and Microbial Genomics and applications Center, Republic of Korea.

Conflict of Interest

The authors declare that no conflict of interest exists.

References


Staurosporine suppress BB disease in rice

Supporting Information

Additional Supporting Information may be found in the online version of this article:

Figure S1. Experimental scheme to isolate compound A from Streptomyces sp. MJM4426.

Table S1. Growth and cultural characteristics of MJM4426.

Table S2. Physiological properties of MJM4426.