Polyphasic taxonomy approach (base on properties of morphology, physiology and DNA fingerprint) was investigated for identification of Streptomyces spp., antagonistic to phytopathogenic bacteria. Total 97 samples of composts and plant residues were collected from Khon Kaen, Chaiyaphum, Udon Thani, Maha Sarakham, Roi Et, Kalasin and Petchabum provinces. The Streptomyces spp. was isolated from these samples by serial dilution plating technique. Total 386 isolates of Streptomyces spp. were obtained. The antibiotics activity against important phytopathogenic bacteria for solanaceae and cucurbitaceae was carried out by bioassay. Only 13 isolates of antagonistic Streptomyces spp. were selected and divided into 4 groups according to the species of tested phytopathogenic bacteria as follows. Group 1 consisted of 5 isolates (PR1, PR7, PR9, PR10 and PR11) inhibited the growth of Acidovorax avenae subsp. citrulli. Group 2 consisted of 4 isolates (PR1, PR10, PR11 and PR12) inhibited the growth of Pseudomonas syringae pv. lachrymans. Group 3 consisted of 8 isolates (PR2, PR4, PR5, PR6, PR8, PR10, PR11 and PR13) inhibited the growth of Xanthomonas campestris pv. vesicatoria. Group 4 consisted of 7 isolates (PR1, PR2, PR3, PR7, PR10, PR11 and PR12) inhibited the growth ofRalstonia solanacearum. Therefore, the isolate PR 10 and PR11 showed high potential broad-spectrum antagonists against 4 species of economic important phytopathogenic bacteria. Preliminary test for biological control efficacy in greenhouse condition was investigated with Streptomyces-PR10 and PR11. Result showed that the PR10 and PR11 reduced the bacterial wilt and bacterial fruit blotch diseases.

Investigation of morphological and chemical properties revealed that all selected Streptomyces spp. isolates were Gram-positive bacteria, which have no fragmentation of substrate mycelium. Colony characteristic and spore chain type were diversified. The growth characteristics on three media namely Arginine-glycerol mineral salt agar, Czapek's solution agar and Yeast extract-malt extract agar of selected 13 of Streptomyces spp. were different. They showed distinctively in ability to produce melanin pigment, nitrate reduction, growth on medium containing sodium chloride, utilization of carbon sources, production of chitinases and cellulases and antifungal. However, all 13 Streptomyces spp. isolates produced catalase and no resistance to streptomycin (100 \( \mu g/ml \)).

Study on genotypic information of antagonistic Streptomyces spp. by pulse field gel electrophoresis technique was not successfully. However, the suitable condition for lyses cells of Streptomyces embedded in
agarose gel (plug) could be pointed out as follows; treating plugs with sucTE buffer containing lysozyme (2 mg/ml) and follow by buffer B (0.5 M EDTA pH 9.5, 0.5% SDS and 1% lauroyl sarcosine) containing proteinase K (1mg/ml). The restriction enzymes BamHI produced many pieces of DNA fragments from genomic DNA of selected Streptomyces spp. Using repetitive sequence-PCR (rep-PCR) technique with BOXA1R primer, the DNA fingerprint of 13 selected Streptomyces spp. showed clearly distinctively at level of Streptomyces species. The Streptomyces-PR8 and PR9 are highly closed relationship with similarity coefficient of 0.90.

Classification of antagonistic Streptomyces spp. by polyphasic taxonomy approach (based upon their morphology, physiology and genomic DNA fingerprint) resulted that the 6 isolates consisted of PR1, PR6, PR7, PR10, PR12 and PR13 were identified as *S. baarnensis, S. neyagawaensis, S. nojiriensis, S. chrysomallus* subsp. *fumigatus, S. nobortoensis* and *S. nigrescens*, respectively. The PR8 and PR9 were identified as the same species as *S. sioyaensis*. The isolate PR2, PR3, PR4, PR5 and PR11 were identified as distinct species but could not designated their species names so far.