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**ABSTRACT**

Polyphasic taxonomy approach (base on properties of morphology, physiology and 16S rRNA gene sequence analysis) was investigation for identification of Streptomyces spp., antagonist to Acidovorax avenae subsp. citrulli (Aac). Total 16 isolates of Streptomyces were retested for inhibition the growth of bacteria Aac by biological assay method. The results showed that 12 isolates of Streptomyces were stable and strong inhibited the growth of Aac. Selected 7 isolates as follows Strep.-13, Strep.-15, Strep.-22, Strep.-33, Strep.-78, Strep.-84 and Strep.-87 were tested to control bacterial fruit blotch disease of watermelon in greenhouse condition by seed coating and spraying method, All tested, Streptomyces isolate did not induce disease symptoms on watermelon seedlings or reduce germination percentage of watermelon seeds. Ability to control target disease was difference between isolation of Streptomyces spp. And application method. For seed coating method the result showed that Streptomyces.-84 was decreased number of seedling disease significantly. For spraying method, the Streptomyces.-84 and -87 were highly significant reduced disease severity on watermelon plants.

Investigation on morphological and chemical properties revealed that all selected Streptomyces spp. isolate were Gram-positive bacteria, which have no fragmentation of substrate mycelium. Colony characteristic and spore chain type were diversified. The growth characteristics on tree media namely Arginine-glycerol-mineral salt agar, Czapek’s solution agar and Yeast extract-malt extract agar of selected 7 of Streptomyces spp. were different. They showed distinctively in ability to utilization of carbon source and 1 isolate (Strep.-33) showed ability to produce melanin pigment and growth on medium containing 4% sodium chloride. However, all Streptomyces spp. isolate produced catalase, amylase, chitinase, avicellase and cellulose, reduce nitrate and no resistance to streptomycin (100 μg/ml).

Study on nucleotide sequence of 16S rRNA gene was analysis. An obtained full length of 16S rRNA gene from Strep.-13, Strep.-15, Strep.-22, Strep.-33, Strep.-78, Strep.-84 and Strep.-87 were 1,551, 1,507, 1,519, 1,519, 1,503, 1,509 and 1,511 nucleotides, respectively. Nucleotide sequence alignment was done with Streptomyces nucleotide sequences retrieved from the Ribosomal Database Project and EMBL-GenBank databases. Results revealed that they were not completely similar with any Streptomyces species in databases, but belonged to the Streptomycesetaceae.
Classification of antagonistic *Streptomyces* spp. by polyphasic taxonomy approach,(based on properties of morphology, physiology and 16S rRNA gene sequence analysis) all seven antagonistic *Streptomyces* strains were identified as new and distinctively species of *Streptomyces*. The most closely related with *Streptomyces*-84 was *Streptomyces aureofaciens* with similarity coefficient 0.89.