ABSTRACT

The anti microbial activities were determined by agar diffusion modified method by using Nutrient agar medium and *Staphylococcus aureus* ATCC 25923, *Pseudomonas aeruginosa* ATCC 27853, *Escherichia coli* ATCC 25922, *Bacillus subtilis, Salmonella typhimurium* as test microorganisms. Six spesies were showed anti microbial activity expressed as clear zone around the colonies agar (diameter 0,8 cm, height 3 mm). Diameters of the clear zone were observed each 24 hours for 10 days in order to establish diversity of the anti microbial activities.

The profile of antimicrobial power of four *Streptomyces* sp. isolates reveal different activities. *Streptomyces* sp. 2 has the highest activity in inhibiting *Staphylococcus aureus* ATCC 25923 at day 2 with inhibitory zone diameter as much as 27.6 mm, *Escherichia coli* ATCC 25922 at day 5 with inhibitory zone diameter as much as 29.2 mm, and *Salmonella typhimurium* at day 7 with inhibitory zone diameter as much as 27.5 mm, *Streptomyces* sp.-3 has the highest activity in inhibiting *Pseudomonas aeruginosa* ATCC 27853 at day 6 with inhibitory zone diameter of 42.4 mm. *Streptomyces* sp. 4 has the highest activity in inhibiting *Bacillus subtilis* at day 5 with inhibitory zone diameter of 20.7 mm.

Phylogenetic analyses based on PCR showed that they formed distinct phyletic band. Three isolates (sp.-1, sp.-3, and sp.-4) were determined based on their 16S rRNA sequences. These isolates were assigned to genus *Streptomyces*. It is evident that by an partial 16S rRNA gene sequence of the strain that it formed a distinct phyletic line within the range of variation encompassed by the genus *Streptomycetes* and the sharp separation of the organism from representatives of the genus *Streptomyces* was strengthened by the fact that is sequencing 16S rRNA differed from those of 1489 recognized *Streptomyces* spesies.

Key words : *Streptomyces*, mangrove, 16S rRNA gene, antibiotic

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