# CHAPTER I

# INTRODUCTION

Actinomycetes are well known as the antibiotic producers. They have been described as the greatest source of antibiotics since Waksman introduced *Streptomyces* into his systematic screening program for new antibiotics in early 1940s (Okami and Hotta, 1988). Approximately 53 % of them and 29 % of fungi could produce antibiotics and a few (18%) that produced by bacteria (Berdy, 2005). Actinomycetes have provided many naturally occurring antibiotics discovered, including many of those important in medicine, such as aminoglycosides, macrolides, tetracyclines, anthracyclines, polyenes and quinones (Goodfellow, 1988). They are very common inhabitants of soil (Tortora *et al.*, 1995). Organisms belonging to the groups of actinomycetes such as *Streptomyces, Kitasatospora, Amycolatopsis, Micromonospora, Nocardia, Dactylosporangium*, *Streptosporangium*, *Microbispora, Actinomadura*, *Kibdelosporangium* and others, have been searched for antibiotic production (Oki, 1994; Cross *et al.*, 1994; Kim *et al.*, 2003).

The best known actinomycetes is *Streptomyces* which could produce many antibiotics such as Amphotericin B produced by *Streptomyces nodosus*, Nystatin produced by *Streptomyces noursei* (Glasby, 1993; Tortora *et al.*, 1995). Among antibiotic produced from actinomycetes, *Streptomyces* strains could produce approximately 74% antibiotics (Berdy, 2005). Nowadays *Streptomyces* contain about 527 species. This strains have substrate mycelium and aerial mycelium. Spore chain morphology is spirales, rectiflexibiles, retinaculiaperti. Cell walls contain LL-diaminopimelic acid. Optimal pH averaging 6.5-8.0. Growth occurs normally between 25-30 $^{o}$C. Major menaquinones are MK-9 ($H_6$) and MK-9 ($H_8$). DNA G+C content is 69-78 mol % (Goodfellow, 1988; Cross *et al.*, 1994; Collin *et al.*, 1977).

The genus *Kitasatospora* has phenotypically similar to *Streptomyces* strains but contained major amounts of the *meso* isomers of diaminopimelic acid (DAP) (Omura *et al*, 1982). *Kitasatospora* can be readily distinguished from the genus *Streptomyces* by using genotypic characteristic such as specific nucleotide signatures in the sequences of 16S rDNA (Omura *et al.*, 1982; Zang *et al.*, 1997; Wellington *et al.*, 1992). Nowadays *Kitasatospora* contain about 20 species. They have been known to produce antimicrobial agents such as Setamycin, an antifungal

activity from *Kitasatospora Griseola* (Takahashi *et al.*, 1984), Cystargin, an antifungal activity from *K. cystarginea* (Kusakabe and Isono, 1988), and Bafilomycin an antifungal activity from *K. cheerisanensis* (Chung *et al.*, 1999). The data about antibiotics produced from *Kitasatospora* seem to be a little amount when compare with the antibiotics produced from *Streptomyces*, it may be that the study in this genus is still limited.

The genus *Amycolatopsis* was established by Lechevalier *et al.*, (1986) and was assigned to family Pseudonocardiaceae (Embley *et al.*, 1988; Warwick *et al.*, 1994). They contain about 33 species. Recently, increasing interest has been shown in genus *Amycolatopsis* because they are a very important genus in the antibiotics industry. They produce some of the most widely used antibiotics such as Rifamycin, an antimicrobial activity from *A. mediterranei* (Mejia *et al.*, 1997), Vancomycin, an antimicrobial activity from *A. orientalis* (Pittenger and Brigham, 1956).

The discovery of a novel actinomycetes species may lead to produce the new bioactive compounds (Takahashi and Omura, 2003), therefore the study attempts to search natural substances produced from *Streptomyces*, *Amycolatopsis*, and *Kitasatospora* strains from soils are still interesting. This study deals with the identification and antimicrobial activity of *Streptomyces*, *Amycolatopsis*, and *Kitasatospora* strains isolated from soils. The objectives of this study are

1. To isolate and screen the *Streptomyces*, *Amycolatopsis*, and *Kitasatospora* strains which exhibit the antimicrobial activity from soils.
2. To identify and characterize the selected strains based on the phenotypic and chemotaxonomic characteristics including 16S rDNA sequence analysis.
3. To determine antimicrobial activity of fermented extracts from the selected strains.