PHYLOGENETIC ANALYSIS OF BACTERIAL COMMUNITIES IN PANCURAN 7 BATURRADEN HOT SPRING

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ABSTRACT

The diversity of the bacterial communities supported by culturing and capturing through 0.2 m-pore-size filter was studied. The Pancuran 7 hot spring has temperature at around 52°C and pH 7. Community fingerprint analysis by denaturing gradient gel electrophoresis (DGGE) of the PCR-amplified highly variable V9 region of the 16S rRNA gene from the domain *Bacteria* was performed. Three distinct DGGE bands have been analyzed for phylogenetic relationship. The 16S rDNA sequence fragment analysis of these bands revealed a high relationship with *Bacillus* group, two of them have a high similarity with *Anoxybacillus sp*. and one of the single colony that grown at ½ LB medium closely related to *Geobacillus lituanicus*.

Keywords: phylogeny, DGGE, thermophilic

INTRODUCTION

Extremozymes offer new opportunities for biocatalysis and biotransformations as a result of their extreme stability. From recent work, major approaches to extending the range of applications of extremozymes have emerged. Both the discovery of new extremophilic species and the determination of genome sequences provide a route to new enzymes, with the possibility that these will lead to novel applications. Extremophiles are a source of enzymes (extremozymes) with extreme stability, and the application of these enzymes as biocatalysts is attractive because they are stable and active under conditions that were previously regarded as incompatible with biological materials.

Thermophiles, the extremophiles species that survive at high temperature, dominate the deeper branches of the Three Domain Tree of Life. However, they are not limited to these groups and are present throughout both *Archaeal* and *Bacterial* domain. It has been evidence that one of the potential sources of thermophilic bacteria is hot spring. Central of Java, one of province in Indonesia has a lot of hot springs. Unfortunately, the exploration of their thermophilic resource and biodiversity information are very limited.

The key parameters in diversity studies lies on the performance operations of identification and quantification of organisms, but are still difficult tasks in microbial ecology (Brock, 1987). The valuable ecological information has been obtained from bacterial metabolic processes measurements. However, this method could not give any clue about to which species are involved. As a result, our knowledge of the taxonomic compositions of microbial communities and of the factors which control the abundance and distribution of microbial populations is extremely limited.

Over the last 10 years several molecular techniques have been developed in order to study the biodiversity of natural samples (Muyzer, 1998). These techniques could help identify microorganism without isolation (Amann, et al. 1995) and have revealed the enormous extent of microbial diversity (Pace, 1997). Moreover, new molecular approaches have been proposed recently in order to link microbial processes with the organisms involved (Chen, et al. 1997). However, it is very probable that molecular techniques provide a biased view of microbial diversity. For example, many of the procedures rely on PCR, a technique in which biases have been usually shown, and on cloning, which can act in a selective way. Likewise, it is not clear whether bacterial cells in nature exhibit different degrees of resistance to cell disruption, which