

MOLECULAR CHARACTERIZATION OF
BACTERIA FROM SPONGES

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MOLECULAR CHARACTERIZATION OF BACTERIA FROM SPONGES

By
Shazani Bin Sarijan

Research Report submitted in partial fulfillment of
the requirements of the award of the degree of
Bachelor of Science (Biological Sciences)

**DEPARTMENT OF BIOLOGICAL SCIENCES
FACULTY OF SCIENCE AND TECHNOLOGY
UNIVERSITI MALAYSIA TERENGGANU
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**JABATAN SAINS BIOLOGI
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PENGAKUAN DAN PENGESAHAN LAPORAN PITA I DAN II

Adalah ini diakui dan disahkan bahawa laporan penyelidikan bertajuk:

Molecular Characterization of Bacteria from Sponges.

Oleh: Shazani Bin Sarijan

No. Matrik: UK11601

telah diperiksa dan semua pembetulan yang disarankan telah dilakukan. Laporan ini dikemukakan kepada Jabatan Sains Biologi sebagai memenuhi sebahagian daripada keperluan memperoleh ijazah Sarjana Muda Sains (Sains Biologi), Fakulti Sains dan Teknologi, Universiti Malaysia Terengganu.

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DECLARATION

I hereby declare that this thesis entitled Molecular Characterization of Bacteria from Sponges is the result of my own research except as cited in the references.

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ABSTRACT

The bacteria associated within sponges mostly are uncultured bacteria. The molecular biological techniques have been employed to investigate the bacterial community associated with sponges especially the uncultured bacteria. The aims of this study are to identify the bacteria-associated with sponges and investigate the total bacteria community within sponges using molecular techniques. Sponges within Karah Island ocean region at the northern part of Terengganu had been focused at depths of 5 to 10 meters off the island. The Random Amplified Polymorphic DNA (RAPD) and 16S rDNA clone library were applied in order to investigate the diversity of bacteria on sponges thus identify the uncultured bacteria. The RAPD profiles shows monomorphic pattern for each Operon Primers. This indicated that the small sample size will influence the diversity of bacteria community. However the closest match of each strain indicated 100% uncultured bacteria have been identified from the sponge. Sequences of bacterial strains were access using BLAST (Basic Local Alignment Search Tool) and revealed the four bacteria phyla; Proteobacterium, Bacteriodetes, Bacterium, and Cyanobacterium. In this study, the community of Proteobacterium was majority and perhaps in close relationship with sponges. This study revealed that the predominant bacteria diversity within sponges were similar even from the different geographic region. The similarity of the strains sequence were more than 90% and showing the 16S rDNA clone library analysis can be applied to obtain precise results in term of the bacterial community.

ABSTRAK

Bakteria yang mempunyai hubungan dengan span kebanyakan adalah bakteria yang tidak boleh dikulturkan. Teknik biologi molekul telah digunakan untuk mengetahui komuniti bakteria yang mempunyai hubungan dengan span terutamanya bakteria yang tidak boleh dikulturkan melalui teknik calitan. Oleh itu, kajian ini adalah bertujuan untuk mengenalpasti bakteria yang mempunyai hubungan dengan span dan menyiasat jumlah komuniti bakteria pada span dengan menggunakan pendekatan teknik molekular. Dalam kajian ini, span-span dalam lingkungan perairan Pulau Karah di bahagian utara Terengganu telah ditumpukan pada kedalaman 5 hingga 10 meter dari aras laut. Pembesaran Rawak Polimorfik DNA (RAPD) dan perpustakaan klon 16S rDNA telah diaplikasi untuk menyiasat kepelbagaian bakteria pada span seterusnya mengenalpasti bakteria yang tidak boleh dikultur. Profil RAPD menunjukkan corak monomorfik bagi setiap Primer Operon. Ini menunjukkan saiz sampel yang kecil akan mempengaruhi kepelbagaian komuniti bakteria. Walaubagaimanapun, kepadatan jujukan strain menunjukkan 100% bakteria yang tidak boleh dikulturkan pada span. Jujukan ini telah diakses dengan menggunakan BLAST (Basic Local Alignment Search Tool) dan menunjukkan empat Filum bakteria; Proteobacterium, Bacterioidetes, Bacterium, and Cyanobacterium. Dalam kajian ini juga, komuniti Proteobacterium adalah majoriti dan berkemungkinan mempunyai hubungan rapat dengan span. Kajian ini juga menunjukkan bahawa kepelbagaian bakteria predominan pada span-span adalah lebih kurang sama walaupun daripada bahagian geografi yang berbeza. Persamaan jujukan strain adalah lebih daripada 90% seterusnya menunjukkan bahawa analisis perpustakaan klon 16S rDNA boleh diaplikasikan untuk menerangkan komuniti bakteria secara tepat.