

## Diversity and DMS(P)-related Genes in Culturable Bacterial Communities in Malaysian Coastal Waters

(Kepelbagaian dan Gen berkaitan-DMS(P) dalam Komuniti Kultur Bakteria di Perairan Pantai Malaysia)

FELICITY W.I. KUEK\*, AAZANI MUJAHID, PO-TEEN LIM, CHUI-PIN LEAW & MORITZ MÜLLER

### ABSTRACT

*Little is known about the diversity and roles of microbial communities in the South China Sea, especially the eastern region. This study aimed to expand our knowledge on the diversity of these communities in Malaysian waters, as well as their potential involvement in the breakdown or osmoregulation of dimethylsulphoniopropionate (DMSP). Water samples were collected during local cruises (Kuching, Kota Kinabalu, and Semporna) from the SHIVA expedition and the diversity of bacterial communities were analysed through the isolation and identification of 176 strains of cultured bacteria. The bacteria were further screened for the existence of two key genes (dmdA, dddP) which were involved in competing, enzymatically-mediated DMSP degradation pathways. The composition of bacterial communities in the three areas varied and changes were mirrored in physico-chemical parameters. Riverine input was highest in Kuching, which was mirrored by dominance of potentially pathogenic *Vibrio* sp., whereas the Kota Kinabalu community was more indicative of an open ocean environment. Isolates obtained from Kota Kinabalu and Semporna showed that the communities in these areas have potential roles in bioremediation, nitrogen fixing and sulphate reduction. Bacteria isolated from Kuching displayed the highest abundance (44%) of both DMSP-degrading genes, while the bacterial community in Kota Kinabalu had the highest percentage (28%) of dmdA gene occurrence and the dddP gene responsible for DMS production most abundant (33%) within the community in Semporna. To the best of our knowledge, this is the first study looking at the diversity of culturable bacteria in coastal waters of East Malaysia and also their potential roles in the DMS(P) cycle.*

*Keywords: Culturable bacterial communities; dimethylsulphide; dimethylsulphoniopropionate; diversity*

### ABSTRAK

*Kepelbagaian dan peranan yang dimainkan oleh komuniti mikrob di Laut China Selatan, khususnya di Wilayah Timur, adalah kurang diketahui. Kajian ini bertujuan untuk mengembangkan pengetahuan tentang kepelbagaian komuniti ini di perairan Malaysia, serta potensi penglibatan mereka dalam penguraian atau pengawalan osmosis dimetilsulfoniopropionat (DMSP). Sampel air diperolehi semasa pelayaran tempatan (Kuching, Kota Kinabalu dan Semporna) daripada ekspedisi SHIVA dan kepelbagaian komuniti bakteria telah dianalisis melalui pengasingan dan pengenalpastian 176 strain kultur bakteria. Bakteria ini seterusnya disaring untuk menentukan kehadiran dua gen utama (dmdA, dddP) yang terlibat dalam dua laluan bersaing degradasi DMSP secara berenzim. Komposisi komuniti bakteria dalam tiga kawasan ini berbeza dan perbezaan ini boleh dilihat dalam parameter fisiko-kimia. Input sungai paling tinggi di Kuching dan ini ditunjukkan melalui dominasi *Vibrio* sp., yang berpotensi untuk menjadi patogenik, manakala komuniti Kota Kinabalu adalah petunjuk untuk persekitaran lautan terbuka. Bakteria yang diasingkan dari Kota Kinabalu dan Semporna menunjukkan bahawa komuniti dalam dua kawasan ini berpotensi memainkan peranan dalam bioremediasi, pengikatan nitrogen dan penurunan sulfat. Bakteria yang diasingkan dari Kuching menunjukkan kebanyakan tertinggi (44%) untuk kedua-dua gen pengurai DMSP, manakala komuniti bakteria di Kota Kinabalu menunjukkan peratusan tertinggi (28%) kejadian gen dmdA dan gen dddP yang bertanggungjawab untuk pengeluaran DMS adalah paling banyak (33%) dalam komuniti di Semporna. Sepanjang pengetahuan kami, ini merupakan penyelidikan pertama yang melihat kepelbagaian bakteria yang boleh dikultur di perairan pantai Malaysia timur dan juga potensi penglibatan mereka dalam kitaran DMS(P).*

*Kata kunci: Dimetilsulfida; dimetilsulfoniopropionat; kepelbagaian; komuniti kultur bakteria*

### INTRODUCTION

The South China Sea is a marginal sea that is part of the Pacific Ocean, encompassing an area from the Karimata Straits in the south, to the Straits of Taiwan and Luzon in the North (Morton & Blackmore 2001). The Celebes Sea is connected to the South China Sea through the Sulu Sea (Yoshida et al. 2007). While the bacterial communities in

the Celebes and Sulu Seas have been reported to display some similarities (Yoshida et al. 2007), not much is known about the diversity and function of the microbial communities in South China Sea, especially regarding the eastern region (Kuching and Kota Kinabalu). Most studies about bacterial communities focused on regions near China (Jiang et al. 2007; Liao et al. 2009; Li et