

# LIPIDOMIC CHARACTERIZATION OF BACTERIAL COMMUNITIES OF THE SHALLOW-WATER HYDROTHERMAL VENT SYSTEM OF KUEISHANTAO (TAIWAN)

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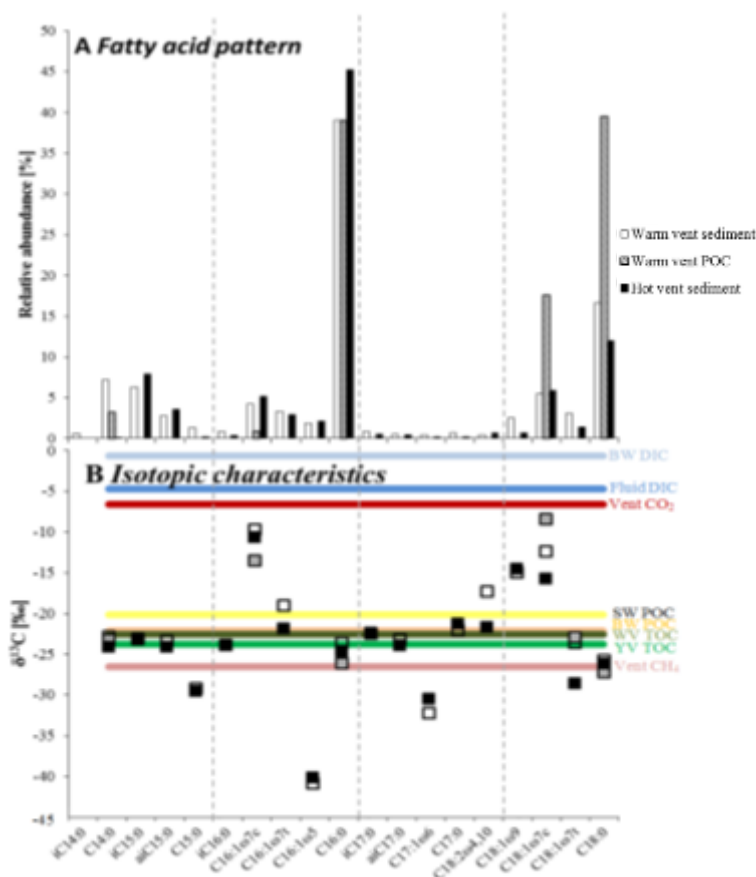
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Hydrothermal vent systems are one of the oldest continuously existing ecosystems on Earth (Rasmussen, 2000), even considered as possible origin of life habitats (Guzman and Martin, 2009). The Kueishantao shallow-water hydrothermal vent system located off NE Taiwan's coast (121°57' E, 24°50' N) is characterized by world-record low pH conditions (pH < 1) and fluid temperatures of up to 116 °C with gas discharges dominated by CO<sub>2</sub> (Chen et al., 2005). In 2015, sediment cores were collected and hydrothermal fluids taken from a hot temperature vent (116 °C, pH = 2.88) and a warm temperature vent (58 °C, pH = 4.51) in order to characterize the difference in the lipidome (i.e., intact polar lipids and fatty acids thereof) of the active bacterial communities.

First results indicated that the fatty acid pattern of both vent sediments consists of 19 different fatty acids, ranging in chain length from C<sub>14</sub> to C<sub>18</sub> (Fig.1A). The fatty acids' stable isotopic ratios ( $\delta^{13}\text{C}$ ) mostly ranged between -20 to -30 ‰, but with C<sub>16:1 $\omega$ 7c</sub>, C<sub>18:1 $\omega$ 9</sub> and C<sub>18:1 $\omega$ 7c</sub> being most positive with  $\delta^{13}\text{C}$ -values of -9 ‰, -14 ‰, and -12 ‰, respectively, in the warm sediments and of -10 ‰, -14 ‰, and -15 ‰, respectively, in the hot sediments (Fig.1B). Hence, both vent types' sediments had a similar fatty acid distribution but the hot vent sediments were mostly characterized by 1 to 5 ‰ more negative  $\delta^{13}\text{C}$  values (Fig.1B). For both vent sites the positive  $\delta^{13}\text{C}$  values of C<sub>16:1 $\omega$ 7c</sub>, C<sub>18:1 $\omega$ 9</sub> and C<sub>18:1 $\omega$ 7c</sub> might be explained by the occurrence of Epsilonproteobacteria, which have been identified metagenomically in the warm vent sediments and fluids of our study site (Tang et al., 2013). These bacteria possess the reverse tricarboxylic acid cycle (rTCA) for carbon fixation, a metabolic pathway that discriminates less against <sup>13</sup>C than the Calvin-Benson-Bassham Cycle and is usually conducted in response to carbon dioxide being highly enriched in the environment (Tang et al., 2013). Accordingly, the DIC was enriched in <sup>13</sup>C ( $\delta^{13}\text{C} = -4.4$  ‰; Fig.1B). Respective discriminations relative to the CO<sub>2</sub> source ranged from 4.6 to 11 ‰ for C<sub>16:1 $\omega$ 7c</sub>, C<sub>18:1 $\omega$ 9</sub> and C<sub>18:1 $\omega$ 7c</sub>, in accordance with the overall isotope fractionation of organisms using the rTCA pathway (2-13 ‰; Pearson, 2010). The rTCA is a more energy-efficient alternative to the Calvin-Benson-Bassham cycle, a clear advantage in the potentially energy-limited environments of shallow-water hydrothermal vent systems (Campbell and Cary, 2004).

The corresponding fatty acid analysis of the warm vent fluid showed the presence of only five fatty acids (Fig.1A) but C<sub>16:1 $\omega$ 7c</sub> and C<sub>18:1 $\omega$ 7c</sub> were enriched in <sup>13</sup>C with  $\delta^{13}\text{C}$  values of -13 ‰ and -8 ‰, respectively. Accordingly, hydrothermal fluids and vent sediments may harbor slightly different microbial communities as already suggested in metagenomic studies (Wang et al., 2015). Nonetheless, not only may identical Epsilonproteobacteria in the fluid fractionate differently against <sup>13</sup>C because of diverging small-scale pH values, metagenomic studies revealed that different genera of Epsilonproteobacteria are contained in warm vent sediments vs. fluid (Tang et al., 2013). Complementing analyses of intact polar lipids (IPLs) as indicators of bacterial community changes are under progress right now and will be presented alongside this study.



**Figure 1** Pattern (A) and  $\delta^{13}\text{C}$  values (B) of fatty acids in emanating fluid particles of the warm vent and the sediment surrounding the warm and hot vents. The  $\delta^{13}\text{C}$  values of the major carbon pools are plotted for comparison. (BW: bottom water; SW: surface water; Sed: sediment; POC: particulate organic carbon; TOC: total organic carbon).

## References

- Campbell, B.J.**, Cary, S.C., 2004. Abundance of reverse tricarboxylic acid cycle genes in free-living microorganisms at deep-sea hydrothermal vents. *Appl. Environ. Microbiol.* 70, 6282–89.
- Chen C.T.A.**, Zeng, Z., Kuo F.W., Yang, T.K., Wang, B.J., Tu, Y.Y., 2005. Tide-influenced acidic hydrothermal system offshore NE Taiwan. *Chemical Geology* 224, 69-81.
- Guzman, M.I., and Martin, S.T.**, 2009. Prebiotic Metabolism: Production by Mineral Photoelectrochemistry of alpha-Ketocarboxylic Acids in the Reductive Tricarboxylic Acid Cycle. *Astrobiology* 9, 833-842
- Pearson, A.**, 2010. Pathways of Carbon Assimilation and Their Impact on Organic Matter Values  $\delta^{13}\text{C}$ , In: Timmis, K. N. (Ed.), *Handbook of Hydrocarbon and Lipid Microbiology*. Springer, Berlin Heidelberg, pp 143-156.
- Rasmussen, B.**, 2000. Filamentous microfossils in a 3,235-million-year-old volcanogenic massive sulphide deposit. *Nature* 405, 676-679.
- Tang, K.**, Liu, K., Jiao, N., Zhang, Y., Chen, C.T.A., 2013. Functional Metagenomic Investigations of Microbial Communities in a Shallow-Sea Hydrothermal System. *PLoS One* 8, 1-11.
- Wang, L.**, Cheung, M.K, Kwan, H.S., Hwang, J., Wong, C.K., 2015. Microbial diversity in shallow-water hydrothermal sediments of Kueishan Island, Taiwan as revealed by pyrosequencing. *Journal of basic microbiology* 55, 1-11.