**PAA-14**

**Microbial response to antibiotics in community level in seawater microcosm**

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**Key word:** bacteria, antibiotics, growth rate, community composition

Pharmaceuticals are a group of emerging chemicals of environmental concern. Antibiotics (AB) are chemical agents which inhibit the growth of bacteria. Recent studies evidenced a potential of trace concentration of AB that can select AB resistant bacteria in the environment. Our aim in this study is to know effect of AB on both bacterial growth and community composition in seawater. We examined the effect of three different antibiotics Sulfamethoxazole (SMX), Oxytetracycline (OTC), and Erythromycin (ERY) with different concentration on bacterial growth in seawater microcosms. After 48 hours of incubation, microcosms with addition of antibiotics showed changes in total cell abundance and growth rate. Growth rate in the microcosm without antibiotics was 0.5 day⁻¹ whereas those in microcosms with lower concentration of AB (0.1μg ml⁻¹) were SMX 0.4 day⁻¹, OTC 0.2 day⁻¹ and ERY 0.1 day⁻¹, whilst high concentration (10μg ml⁻¹) were SMX 0.2 day⁻¹, OTC 0.1 day⁻¹ and ERY -0.1 day⁻¹. These results showed growth inhibition of natural bacterial assemblage with dose dependent manner and the susceptibility to each AB is different. The shift of community composition with AB will also be reported using catalyzed reporter deposition fluorescence in situ hybridization (CARD-FISH).

**PAA-15**

**Dynamics of marine bacterial abundance and sulfonamide resistance genes in a microcosm with sulfamethoxazole addition**

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**Key word:** sulfamethoxazole, bacterial community, resistance gene, marine bacteria

Antibiotic inflow to aquatic environments is of concern to affect on bacterial community. Sulfamethoxazole(SMX) has been used for human and animal clinics in Asian countries and found to be higher concentration than ppb level in river to coastal ocean. The aim of this study is to determine effect of SMX on bacterial cell abundance and fate of SMX resistance genes (sul1, sul2 and sul3). SMX were added at 10 ng ml⁻¹, 100 ng ml⁻¹, 500 ng ml⁻¹ and 1000 ng ml⁻¹ to natural seawater microcosms. The concentrations, used this experiment, were one to two orders of magnitude below minimal inhibitory concentration in clinical standard. After 48 hours of incubation at 26°C, cell growth was inhibited along with the SMX concentrations. The increases of cell abundance in the SMX treatments were from 0.8 to 0.6 times compared with the control (without SMX). SMX resistance genes, sul2 and sul3 were quantified in bacterial assemblage. The sul1 was detected in seawater whereas sul2 and 3 were not, suggesting that only sul1 is present in the original seawater as detectable amount. Since detected amount of sul1 was not changed at 0 and 48 hours of incubation, sul1 is evidenced to be maintained among bacterial assemblage, at which SMX resistant bacteria would be selected.

**PAA-16**

**Symbionts influence on the fatty acids of clam Mesolina solidissima**

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**Key word:** symbionts, deep-sea, hydrothermal vent, bivalve, chemosynthesis

The lipids and fatty acids of the Lucinid clam, Mesolina solidissima, collected from deep-sea cold-seep vents, were examined to assess its lipid physiology and nutritional relationship with its symbionts. The vent clam obtained many of its lipids from symbiotic chemosynthetic bacteria. The fatty acids in a vent bivalve were determined by using gas chromatography - mass spectrometry analysis of the 4,4-dimethylxalamin derivatives. The major polyunsaturated fatty acids (PUFA) in the clam muscle and visceral phospholipids consisted of a limited number of n-4 and n-7 (n-4 family) PUFA. Noticeable levels of various n-4 family PUFA were observed in the phospholipids. These findings indicate that the clam utilizes n-4 family PUFA, which were assimilated from the symbionts. This fatty acid composition is unusual for a marine animal in the grazing or detrital food chain because many marine animal lipids contain high levels of n-3 PUFA. Similar to other vent clams, such as Calyptogena phaseoliformis, the lack of 22:6n-3 with significant levels of n-4 family PUFA in this species indicates its selective assimilation of specific sulfur-oxidizing bacteria. Both the bivalve and its symbionts maintain their membrane fluidities by using these various PUFA in cold deep-sea.