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Effect of bioturbation activities by the grapsid crab (Helice formosensis) on the lipid contents and microbial consortia in tidal flat sediments: fatty acids classes-sources and fate

メタデータ	言語: 出版者: 琉球大学21世紀プログラム 公開日: 2007-07-10 キーワード (Ja): キーワード (En): 作成者: Mchenga, Islam S.S., Tsuchiya, Makoto メールアドレス: 所属:
URL	<a href="http://hdl.handle.net/20.500.12000/847">http://hdl.handle.net/20.500.12000/847</a>

**PE-18 : Effect of bioturbation activities by the grapsid crab (*Helice formosensis*) on the lipid contents and microbial consortia in tidal flat sediments: fatty acids classes-sources and fate**

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**Abstract**

Macro invertebrates directly mediate key processes in the biogeochemical cycle of sediment, by releasing nutrients and consuming oxygen and organic matter. They indirectly mediate processes by redistributing particulate and dissolved substances in the sediment. A field study was conducted to investigate how burrowing activities by the grapsid crab (*Helice formosensis*) affects lipids content, fatty acid composition, and bacterial abundance in tidal flat sediments. Reported findings have shown a significant increase in total lipids in sediments of the crabs' burrow opening shaft and burrow chamber (1567.8 and 5108.2  $\mu\text{g g}^{-1}$  DW respectively, ANOVA,  $p < 0.03$ ). This may be attributed to growth of bacteria, fungi and the product of their metabolic activities. The estimation of total microbial abundance measured by the sum of the extracted microbial derived fatty acids (bacteria and fungi biomarkers), resulted in a higher total abundance in the sediments of burrow shaft and chamber (45.7 and 24.2  $\mu\text{g g}^{-1}$  DW respectively) as compared to the surface sediments (19.9  $\mu\text{g g}^{-1}$  DW). Multivariate analyses based on principal component analysis (PCA) showed a clear separation of fatty acid methyl ester (FAMES) patterns, indicating change in bacteria makers' odd-branch fatty acids  $\text{C}_{15}$ - $\text{C}_{17}$  (common in gram-positive bacteria) and cis-vaccenic acid  $\text{C}_{18:1n-7}$  (fatty acid evidence in sulfate or sulfur reducing bacteria). These results suggest *Helice formosensis* is an active bioturbator that significantly contributes to lipid contents in biogenic organic matter by enhancing microbial abundance in the environments they inhabit.