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Characterization of *Bacillus sp*. probiotics available for aquaculture use

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The use of probiotics in aquaculture is proving to be effective in improving disease resistance, nutrition and/or growth of cultured organisms. Three strain of *Bacillus sp*. was isolated from the intestinal tract of fish and identified by conventional biochemical characteristics and 16S rDNA gene sequence analysis. We studied the probiotic properties of *Bacillus sp*. The strains studied exhibit antibacterial activity against the different pathogenic tested. Adherence assays revealed that the isolates are fairly adherent. The challenge test on axenic Artemia culture showed that the protection against pathogenic Vibrio was improved. On the basis of these results, we can suggest that the strains studied can be used as potential probiotic candidates for the culture of *Artemia*.

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Diversity of methanogenic Archaea and sulfate-reducing bacteria are not affected by carbon source and sulfate amount in anaerobic microcosms

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Sulfate-reducing bacteria compete with methanogens during anaerobic digestion in the presence of sulfate. This study aimed to characterize the anaerobic microbial diversity and function during biomethane generation from sulfate-containing wastewaters under different operational conditions. Microcosms were prepared using an anaerobic sludge sample and different carbon sources (formate, butyrate, propionate, acetate and trimethylamine). Varying amounts of sulfate was provided to establish carbon/sulfate ratio of 0.5, 1.5 and 5. Methane, volatile fatty acid and sulfate concentrations in microcosms were measured using gas and ion chromatography systems. High-throughput sequencing of 16S rRNA genes for bacteria and Archaea and functional genes encoding dissimilatory sulfite reductase and methyl-coenzyme M reductase was carried out for taxonomic and functional characterization. The highest methane amount was measured in the acetate microcosms (1184-1307µmol), regardless of the carbon/sulfate ratio applied. It was followed by propionate (869-1214 µmol); butyrate (656-770 µmol), trimethylamine (466-602µmol) and formate (251-402µmol), suggesting the sulfate amount had little effect on the methane generation from each carbon source. Sequence analysis revealed the strong dominance of Methanobacterium genus across all microcosms (42-62%) irrespective of the operational conditions. Similarly, SRB composition did not change in the microcosms where Deltaproteobacteria super cluster and Desulfoarculus dominated. The results indicate that acetate leads to the highest methane amount and restricted populations are active during methane production from sulfate-containing wastewaters. The activity rather than diversity of these populations change during methane production from sulfate-containing wastewaters. Therefore, it may be possible to manipulate anaerobic reactors to enhance methane generation by providing optimum conditions.

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