B021

Effects of Interspecies Hydrogen Transfer Between Sulfidogen and Methanogen on the Anaerobic Corrosion of Iron Coupon

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We attempted to figure out the involvement of hydrogen on microbial metal corrosion using a co-culture system composed of *Desulfovibrio desulfuricans* and *Methanococcus maripaludis*. *D. desulfuricans* was grown on Postgate medium C and D with iron coupon, and weight loss and hydrogen production were measured after 3-week incubation. Hydrogen was produced approximately 10 times higher in medium D than in medium C, and a modified medium C omitting sulfate also showed 47% higher corrosion rate than in regular medium C Exogenously added hydrogen into the medium D showed 4 times higher corrosion rate (1 1 mg/cm^2/d) than that of medium C (0 28 mg/cm^2/d), and acetate production was doubled in medium D Coculture of *D. desulfuricans* and *M. maripaludis* containing iron coupon showed significantly less corrosion than that of the *D. desulfuricans* alone culture in medium C. The results suggested that the produced hydrogen by *D. desulfuricans* was consumed by *M maripaludis* to produce CH_4 as the metabolic end products Therefore, *M maripaludis* is considered to play an important role to reduce the microbial corrosion by removing hydrogen acting as an effective accelerator of iron corrosion

B022

Genome Probing Microarrays for Monitoring the Neonatal Gastrointestinal Microflora.

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Gastrointestinal microflora influence the human health and disease significantly Conventional selective culture plating methods or 16S rRNA-PCR based methods for detecting the fecal microflora have been reported to get some limitations such as 'Great plate count anomaly' and PCR bias. In this study, we constructed a novel format of microarrays, i e genome-probing microarrays (GPMs) for specific, sensitive, and high-throughput monitoring the intestinal microflora. Especially, in order to describe the development of the intestinal microorganisms from initial acquisition and subsequent succession of bacteria in the neonatal gastroin-testinal track from diet, whole genomes of more than 120 predominant neonatal bacteria were printed in one slide of GPM. Here we present the result of GPM technology as a powerful tool used for detection of intestinal microflora of breast-fed infants and formula-fed infants in species level

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B023

Simultaneous Detection of Virulence Factors by Multiplex PCR in *Aeromonas spp.*

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430 presumed *Aeromonas* spp were isolated from a trout farm, diseased trout fish, and stream which is selected as control. Isolated strains were identified by restriction fragment length polymorphism analysis (RFLP) of PCR-amplified 16S-rDNA To examine the relationship of pathogenicity of identified strains and virulence genes, 6 genes were simultaneously detected by multiplex PCR assay 6 genes code for aerolysin, serine protease, glycerophospholipid-cholesterol acyltransferase (GCAT), lipase, nuclease and lateral flagella and reported as virulence factors. Finally, *Aeromonas sobria* was dominant in fish farm and diseased fish. Genes coding for aerolysin and nuclease were mainly detected in this species In natural water samples, which were considered as the experimental control, *A. caviae, and A. veronii* were dominant. So at least in investigated fish farm, genes coding for aerolysin and nuclease were relate to fish disease. This study is available to minimize human health risk and to monitor species composition and virulence genes of *Aeromonas* in fish farm, rapidly.

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B024

Analysis of Bacterial Community Structure in Water and Sponge from the Lake Baikal

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In Lake Baikal, the ratio of Eubacteria number to total bacteria number was from 41.20 to 72.81% at all depths. The ratios of each group in 0, 5, 10, 25, 50, 100m water samples were 3.1~8.1% for α-group, 2 1~8 9% for β-group, 2.1~11 2% for γ-group, 2 9~10 7% for *Cytophaga-Flavobacterium* group and 22.6~46.3%, for other Eubacteria. We applied to sponges by different pretreatment One was sonicated after squeezing, the other was just sonicated. In sponges, the ratio of Eubacteria number to total bacteria number was from 40.7 to 60 3% The Eubacteria ratio of squeezing samples were higher than just sonication The ratios of each group in sponge samples were 2 9~5 7% for α-group, 3.1~4.1% β-group, 3 3~4.3% for γ-group, 2 8~3 8% for *Cytophaga-Flavobacterium* group and 26 0~47.1% for other Eubacteria. The bacterial numbers in Lake Baikal were lower than other lakes and there values decreased along depth, Moreover among the bacterial community, the other Eubacterial group showed higher proportion Also in sponges took on a similar phase with Baikal water This mean that the bacterial community is different from other lakes and probably to have a specific composition