

B025

Measurement of Active Bacteria by Quantitative Direct Viable Count Method in Lake Paro and Lake BaikalJai Kyou Hur^{*}, Eun young Seo, Ji Ho Kim, and Tae Seok Ahn*Department of Environmental Science, Kangwon National University*

Quantitative direct viable count(qDVC) method is modified original direct viable count(DVC) method, it is able to quantitative analysis about active bacteria. Glycine cultivation and freeze-thaw treatment is used to quantitative analysis, bacterial cell change into spheroplast during that process. For confirm of qDVC method's effectiveness, this method apply to active($\geq 90.0\%$) *Escherichia coli* and above 80.0% were detected. The number of active bacteria in natural samples were also determined, and the results were compared with the ratio of viable cells determined by the qDVC method, qDVC cell is higher than other techniques. This results also represented L. Paro and L. Baikal samples. It is concluded that the qDVC procedure can easily discriminate between viable cell and others. This procedures provides very useful information about freshwater environmental samples. However, the qDVC procedure should be modified for each ecosystem since glycine cannot interfere with the synthesis of peptidoglycan for cell wall formation in some environmental bacteria. So future studies included substrate concentration, culture time, condition of antibiotics for suitable to each ecosystem.

B026

The Analysis of the Activated Sludge in S municipal WWTP by Various ParametersSun Ja Cho^{1*}, Yong Ju Jung², Gui Sook Nam³, and Sang Joon Lee²¹*Department of Microbiology, Pusan National University,*²*Department of Microbiology, Pusan National University,*³*Korea Agricultural and Rural Infrastructure Corporation*

We intended to analyze the sludge of S municipal WWTP biologically which have operated by activated sludge process in Busan, Korea. The experimental period was from April 2004 to January 2005. The parameters to estimate sludge were MLSS, SVI, the numbers of bacteria and fungi per gMLSS and the area-ratio of each group to total eubacteria by FISH technique. The temperature in aeration tank was the range of 9.6 - 27.3°C, pH was 6.4 - 7.0, the concentration of DO was 1.2 - 5.1 mg/L and MLSS was 1,040 - 2,720 mg/L and the SV₃₀ was 17.5 - 75%.

The numbers of microbes per gMLSS were $3.1 \sim 1.52 \times 10^6$ CFU and $1.1 \sim 10.5 \times 10^4$ CFU fungi by plate agar method, a cultivation method. By cultivation-independent method, FISH and DAPI, the eubacteria-ratio to whole biomass was up more 90%, and α -, γ -, β -proteobacter were occupied 55.8 ~ 70.7% to total eubacteria in order.

The ratio of ammonia-oxidizing bacteria and nitrite-oxidizing bacteria were 12 - 15% to the whole eubacteria. The ratio of each group to eubacteria were not big variation on month, but β subclass proteobacter was comparatively higher percent when water temperature was low.

B027

Analysis of Bacterial Community of Oral Cavity in Jeju ResidentsByoung-Jun Yoon^{1*}, Dong-Heon Lee¹, Youn-Hwa Kim², Cha Soo Heo¹, and Duck-Chul Oh¹¹*Department of Life Science, Cheju National University,*²*Department of Dental Hygiene, Ulsan College*

This study was aimed to investigate the bacterial community of oral cavity in the Jeju residents. 16S rDNA clonal library for the bacterial community was constructed using the 16S rDNA PCR products. A total of 407 clones was examined by amplified rDNA restriction analysis(ARDRA) using *Hae*III. 106 different RFLP types were detected from 160 clones. The 106 clones from 106 different RFLP types were selected and sequenced. About 500-600bp length 16S rDNA sequences of selected clones were determined, and analyzed clones revealed that bacterial community in oral cavity of Jeju resident is composed of bacteria belonging to five groups in the level of phyla; Proteobacteria(46%), Firmicutes(25%), Bacteroidetes(17%), Fusobacteria(7%), and Actinobacteria(2%). Based on the sequence data in this study, the predominant bacterial groups of oral cavity in Jeju residents consisted of 28 genera. There was no significant difference between groups by age in bacterial diversity.

B028

The Biological Treatment of Paper Mill Wastewater using *Pseudomonas* sp.Min-Woo Yun^{1*}, Soon-Bok Lee², Jin-Soo Kim², Dong-Hyo Kang², and Sang-Seob Lee¹¹*Department of Biological Engineering, Kyonggi University,*²*Research Institute of Nuxian, ³Busan Metropolitan City Environmental Installations Corporation*

The pulp and paper industry generates quantities of wastewater. Their chemical oxygen demands (COD_{Mn}) can be as high as 1,100 mg/l. It is not easy to treat paper wastewater because of various type of xenobiotic chemicals. Nowadays, the paper mill wastewater was treated by both biological treatment and chemical treatment. However, problems are that biological treatment could not properly work and chemical treatment is very expensive to maintain.

In this study, the paper mill wastewater from Y paper mill in Kyonggi-do was only treated by activated sludge with two *Pseudomonas* sp. which have high removal efficiency for xenobiotic chemicals. We made the lab-scale reactor which consists of an influent, two aerobic culture tanks, and an effluent. Two *Pseudomonas* sp. mixture were inoculated 0.3g/l(w/w) into first aerobic tank at the every 7 days. The conditions of reactor were MLSS 4000mg/l, SRT 30 days, HRT 48 hours and then DO 2.0mg/l, 3.0mg/l at each aerobic tank. In results, the COD_{Mn} of effluence was 33.5mg/l and removal efficiency was as high as 93.1%. Then we confirmed how many *Pseudomonas* sp. are in the activated sludge by in situ hybridization.