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Dr. Satoru Suzuki, Professor, Environmental Microbiology, Center for Marine Environmental Studies (CMES), Ehime University was born in Hokkaido in 1956. He received his B.Sc. in Food Science from the Faculty of Fisheries, Hokkaido University in 1980. In 1985, he obtained Ph.D. in Virology and Biochemistry from the Graduate School of Pharmaceutical Sciences, Hokkaido University. He was in the University of Alberta, Edmonton, as an Alberta Heritage Foundation for Medical Research Postdoctoral Fellow from 1985 to 1987. He served as an Assistant Professor in Hokkaido University (1987 to 1992) and Associate Professor in Kochi University (1992 to 2000) and then moved to Ehime University in the year 2000 as the Professor, Environmental Microbiology. His major field of interest is environmental microbiology with emphasis on biochemistry and molecular biology. He has received Young Investigator Award from the Japanese Society of Fish Pathology in 1999 and JSME Prize for the Best Publication from the Japanese Society of Microbial Ecology in 2001. He has authored 108 original publications in English and 5 books in English and Japanese as of January, 2008.

Response of Microbes to Chemical Contaminants

— From Molecular Level to Community Level —

Our group focuses on marine microbes which play an integral role in the microbial food web, and act as a buffer to ecological stress and chemical pollutants. Studies include advanced research on the microbial loop and molecular ecology of marine microbes. Results from these studies can be used to develop technology to improve marine industries related to aquaculture and seawater utilization, and monitoring of human and ecosystem health. Our current projects include the following:

1) Ecology of Resistant Bacteria for Anthropogenic Chemicals

Antibiotics and organometal contamination in the ocean induces serious problems. Antibiotics themselves are not toxic, but the contamination by antibiotics can select for drug-resistant bacteria in the environment. Drug resistance genes can further be transferred and spread to various bacterial species, resulting in multi-drug resistant bacteria. Drug resistant bacteria may also occur by exposure to various chemicals other than antibiotics. The occurrence of drug-resistant bacteria and dynamics of gene transfer is a newly discovered environmental risk of chemical pollution. We are focusing on the molecular ecology of antibiotics resistance and tributyltin resistance in environmental bacteria, and how this transfer of resistance and gene degradation occurs in different environments. Water, sediment cores and biological samples are all being analyzed.

2) Biochemistry of Dissolved Proteins in Seawater

The formation of dissolved organic matter (DOM) is an initial step in the microbial loop. Primary production of DOM by photosynthesis is a "*de novo*" pathway in DOM production. Also, degradation of biomolecules is another DOM-producing pathway ("salvage pathway"). Of the macromolecules, proteins are most important, because they supply a good balance of C and N through the salvage pathway to the microbial loop and primary production. However, the sources and fates of dissolved proteins in the ocean are not clearly understood. What types of dissolved proteins are in seawater? ... We are currently profiling dissolved proteins in seawater using liquid chromatography equipped with tandem mass spectrography. What organisms and mechanisms degrade proteins in seawater? ... To discover this we are examining proteolytic activities in seawater. How do proteins change in seawater? ... We are using membrane proteins of *Pseudomonas aeruginosa* as model proteins for the study of protein degradation. You

might ask "why *P. aeruginosa* proteins?"

....Please check my papers, or e-mail me (S. Suzuki).

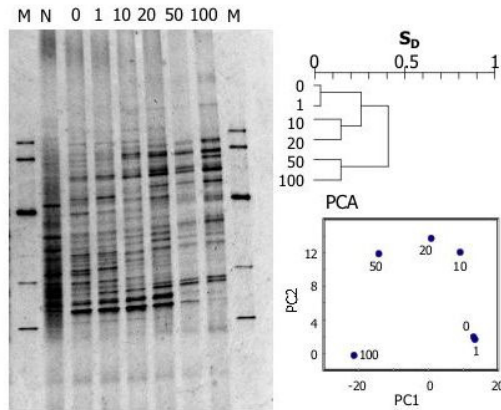


Fig. 1. Effect of tributyltin (TBT) on microflora of Mekong River sediment. Dose dependent changing of community structure was occurred by high concentration of TBT.

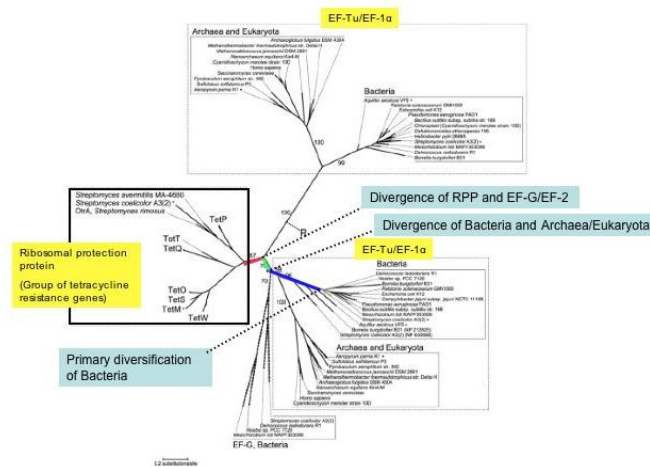


Fig. 2. Composite phylogenetic tree of tetracycline (TC) resistance gene (RPP gene) and EF-genes. RPPs were derived through duplication and divergence of the ancient GTPase before the divergence of the three super-kingdoms.