

# Prof. Jang-Cheon Cho

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**Biography:** *Jang-Cheon Cho* is a full professor in the Department of Biological Sciences at Inha University (Korea), where he has served as a faculty member since 2005. He obtained his Ph.D. in 2000 at Seoul National University, Korea. His *research* interests lie in the area of aquatic microbiology, ranging from marine environments to freshwater ecosystem, with special focuses on cultivation of majority of the uncultured bacteria, microbial taxonomy of oligotrophic marine bacteria and their genomes, and isolation of bacteriophages infecting abundant groups of bacteria. He had been an associate editor of *IJSEM* (2010-2015), *Journal of Microbiology* (2009-2011), and *Journal of Microbiology and Biotechnology* (2012-2014). He has been serving as an editor for *Microbes and Environment* (2012~), *Journal of Microbiology and Biotechnology* (2016~), and *BisMis* (2015~).



## Cultivation of bacteriophages from aquatic ecosystems and virome reanalysis

Viruses, obligate parasites, are the smallest and the most abundant biological entities, which thrive on earth with approximately  $10^{31}$  particles. Most viruses in the ecosystem are believed to be bacteriophages (phages) that are particularly found in aquatic environments where phage particles can encounter their host cells while freely floating. Therefore, diverse researches on phages have been specifically performed in marine environment, the largest reservoir for phage particles, such as isolation of the most abundant marine bacteriophages, pelagiphages and *Puniceispirillum* phage HMO-2011 and a verrucophage known to infect the phylum *Verrucomicrobia*. These successful stories tell us that cultivation of major prokaryotic strains are prerequisite for taming marine viruses since the cultivation of bacterial and archaeal strains is the only way of isolating viruses that infect prokaryotic cells. On the contrary, freshwater bacteriophages have been understudied, representing that only few of freshwater cyanophages have been identified and the rest of the phages remain largely unknown. Therefore, both the bird's eye view (virome analyses) and microscopic view (individual phages) for freshwater phages are in need. First, in order to investigate the viral community distribution, we have performed viral metagenomic studies on an oligotrophic lake. Most of the contigs obtained from the virome study revealed to be most closely related to marine-origin bacteriophages, which indicated the lack of identified freshwater phages, leading to limited interpretation of freshwater viral community. Second, along with the viral metagenome analyses, we have isolated novel freshwater bacteriophages from the same freshwater lake. As a result, we were able to successfully isolate phages infecting bacterial members of the class *Betaproteobacteria*, such as the family *Methylophilaceae*. When the newly identified phage genome was considered, resolution of virome interpretation has improved, that one of the most frequently found contigs was discovered to be related to our newly isolated bacteriophage. Considering that phages infecting the most abundant bacterial groups in freshwater, such as *acI* and *acIV* groups, are still unknown, stable cultivation of those bacterial groups, subsequent isolation of their phages, and interpretation of virome data using the phage genomes will be next goals in the freshwater phage ecology.