LARGE-SCALE GENOME SEQUENCING OF MARINE PHAGES TO ANALYZE THEIR DISTRIBUTION AND GENOMIC DIVERSITIES IN SURUGA BAY, JAPAN

Yohei Nishikawa*†[1,2], Ryota Wagatsuma[2], Katsuhiko Mineta[2,3,4], Takashi Gojobori[4,5],
Masahito Hosokawa[2,6,7], and Haruko Takeyama‡[2,6,7]

[1]Biomanufacturing Process Research Center, National Institute of Advanced Industrial Science and Technology (AIST), Ibaraki – Japon
[2]Research Organization for Nano and Life Innovation, Waseda University, Tokyo – Japon
[3]Graduate School of Science and Technology, Shizuoka Institute of Science and Technology, Shizuoka – Japon
[4]Marine Open Innovation (MaOI) institute, Shizuoka – Japon
[5]Department of Life Sciences, National Cheng Kung University, Tainan 701 – Taïwan
[6]Graduate School of Advanced Science and Engineering, Waseda University, Tokyo – Japon
[7]Institute for Advanced Research of Biosystem Dynamics, Waseda University, Tokyo – Japon

Résumé

One milliliter of seawater contains up to 10ˆ8 phages, which vastly overwhelms the number of bacteria. These marine phages play a crucial role in maintaining the balance and diversity of marine ecosystems by regulating cell numbers, cycling of organic matter, and modulating horizontal gene transfer through the infection of host bacteria. Despite these significant ecological roles of marine phages, most phages remain challenging to culture in laboratory settings. Thus, a lot of research has focused on genome-based analysis. However, in conventional metagenome-based sequencing, a large part of the phage genomes has been lost during the assembly process. To address this problem, our research has developed an accurate and high-throughput genome sequencing platform at a single-particle level utilizing microfluidic droplets. This platform enables the collection of diverse sequences of environmental DNA phages, revealing genomic micro-diversities within the same phage species(1). In this study, we applied this platform to conduct large-scale phage genome sequencing on seawater samples collected from various locations, seasons, and depths in Suruga Bay, the deepest bay in Japan. Consequently, we obtained over 4,000 medium- or high-quality viral single-amplified genomes (vSAGs), most of which represent novel phage sequences. Currently, these novel vSAGs are being used for the analysis of phage distribution within Suruga Bay and comparative genomics within the same phage species. In this presentation, these latest findings are presented, as well as the practicality of microfluidic droplets in single-cell and single-particle analysis.

(1) Nishikawa Y., Takeyama H., et al., The ISME Journal, 18:1, 2024, 10.1093/ismejo/wrae124

---

[*] Intervenant

[†] Auteur correspondant: yohei-nishikawa@aist.go.jp

[‡] Auteur correspondant:

Mots-Clés: Phage, Genome, Single particle genomics, Droplet microfluidics, Single cell