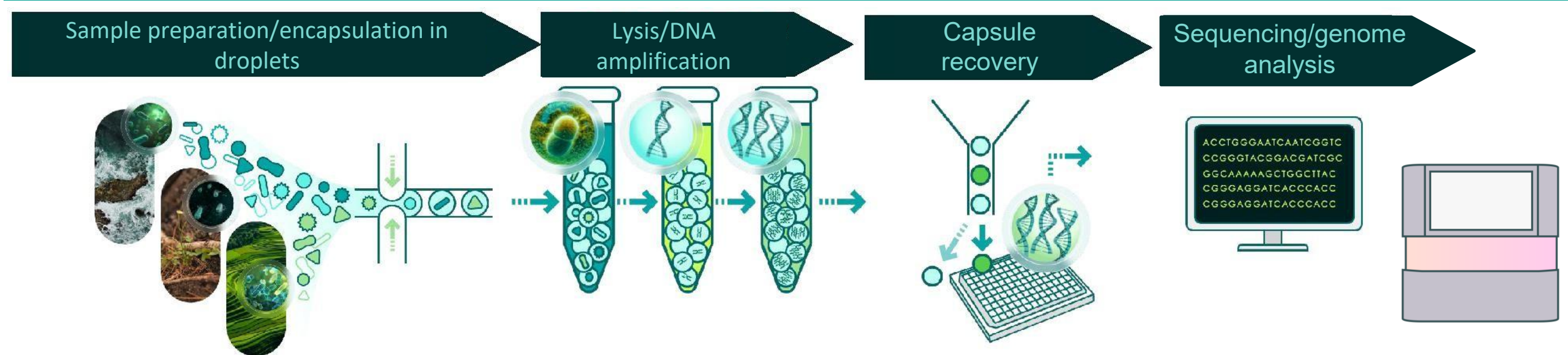


Introduction

Microbes exist in every environment on this planet, and functional genes possessed by microbial dark matter are expected to be applied as resources in diverse fields of industries such as medicine and manufacturing. At bitBiome, we are using bit-MAP®, our proprietary microbial single-cell genome sequencing technology based on the use of droplets, to analyze the vast amount of genetic information possessed by microbial dark matter in any environment at the single-cell level and promote its application to industry. This poster presents examples of bit-MAP® applications across diverse environments.

Microbial single-cell genome sequencing: bit-MAP®

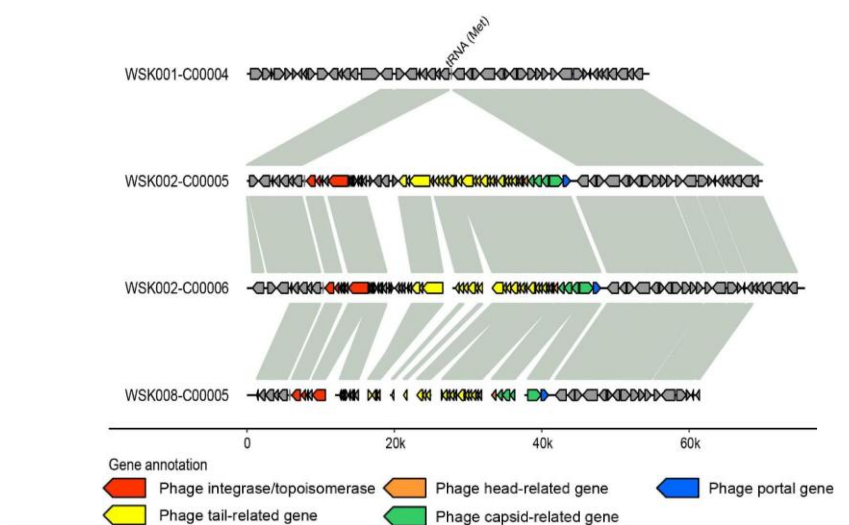


Utilization of microbial single-cell genome sequencing

✓ Linking phages/plasmids to their hosts

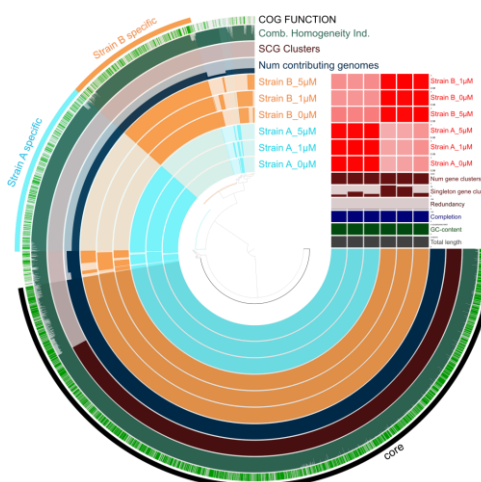
✓ Genome and functional comparison within the same species

✓ Selective bacterial genome acquisition



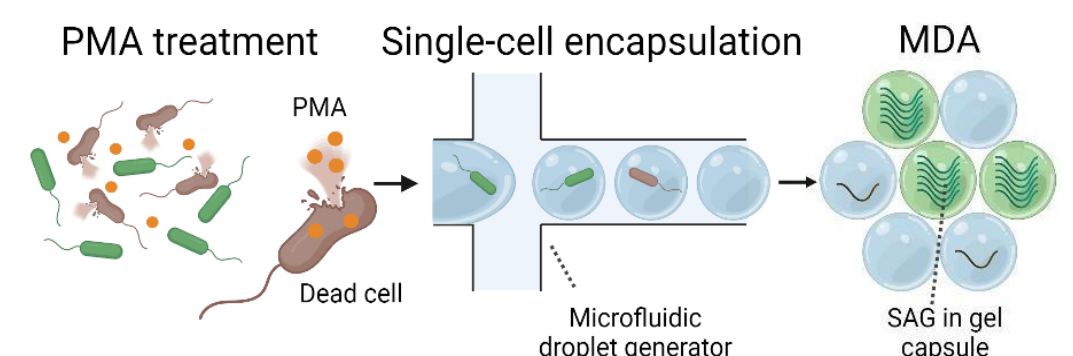
Comparison of phage sequences among the genomes of commensal skin bacteria

Ide et al., 2022. Front. Microbiol.



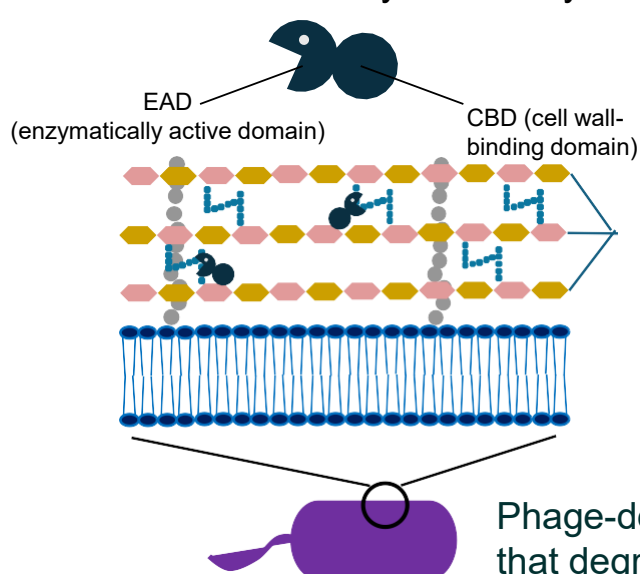
Genome comparison among strains by selective single-cell genomic sequencing of viable bacteria in feces

Hosokawa, et al., 2022 Scientific Report



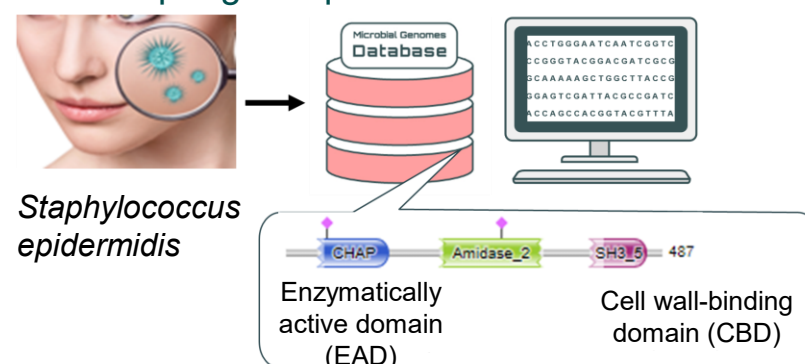
Manufacturing driven by single-cell genome data

Antibacterial enzyme: endolysin



Gene collection/search

Collection of bacterial genome data and phage sequence information



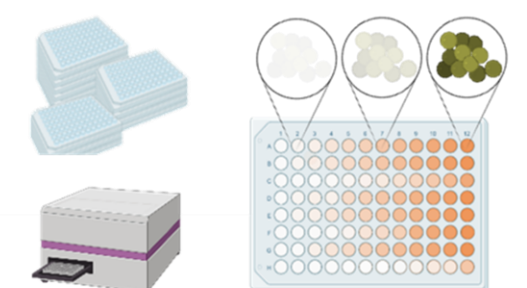
Genetic modification

Protein expression (domain shuffling)

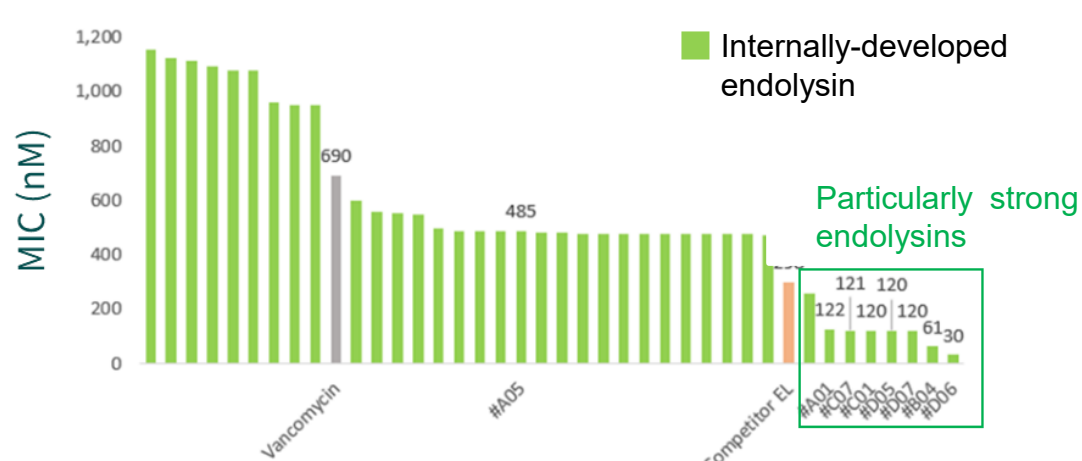


Activity evaluation

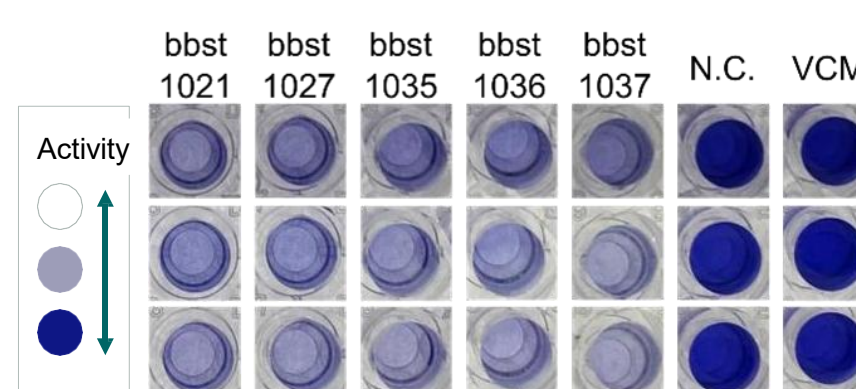
Robotics-based high-throughput screening (HTS)



Obtaining several endolysins with high bactericidal effect



Confirmation of biofilm destruction efficacy



Obtaining endolysin (#C07) that significantly enhances the survival rate of mice with MRSA-induced bacteremia

