中文題目：新興多重抗藥希瓦氏菌的比較基因體研究
英文題目：Comparative genomic analysis of emerging multidrug-resistant *Shewanella algae*

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Background:

Multi-drug resistant *Shewanella algae* has emerged rapidly worldwide, which poses a challenge to public health. Despite there is a growing body of reports that identified resistance determinants to various antibiotics, the resistome remains largely unknown. Advances in sequencing technology and bioinformatics permit the analysis of resistome on a scale previously impossible. As part of our continued efforts to address this challenge, the study aims to construct the resistome identified in globally obtained whole genome sequences using comparative genomic analysis.

Materials/methods:

A global collection of multidrug-resistant *Shewanella algae* genomes from various source were included in the study. We used alignment-based approaches with a multiple-database-based annotation protocol to improve resistance gene detection. Tools that used assembled sequences as inputs include CARD, ARDB, ARG-ANNOT, ResFinder, and HMP. Queries with best hits were validated using ARGDIT and IMG to the consistency of annotations between different databases. For comparative analysis of the resistance genes in different genomes, the identified drug resistance genes in the type strain ATCC 51192 were aligned against investigated *Shewanella algae* genomes, using BLASTX under the following criteria: alignment coverage of a minimum of 50% at an E-value < 10E-5. Whole genome average nucleotide identity analyses based on modified algorithm using orthologous genes were performed.

Results:

The genome size of the tested strains was ~4.7 Mbp, covering >90% of the total estimated size of the reference genome. The overall G+C% content was ~53.0%, and there were 4,100–4,200 coding sequence. All isolates with different multidrug resistance profiles harbored numerous antibiotic resistance coding genes, include chromosome encoded carbapenem-hydrolyzing oxacillinase genes, *qnrA* gene and efflux pump operons. Phylogenetic analysis based on average nucleotide identity values indicated diverse sequence types.

Conclusions:

We have developed a whole genome sequence based pipeline for integrating resistome analysis of *Shewanella algae* genomic data and identified core resistome in multi-drug resistant *Shewanella* *algae*. Our study provides new insights into the intrinsic and acquired drug resistance determinants in *Shewanella algae*, which will be helpful for better understanding the evolution of antibiotic resistance in this emerging pathogen.

Keywords:
***Shewanella algae*, Multidrug-resistant organism, whole genome sequencing, comparative genomics**