Identify and Analyze the Antibiotic Resistant Isolate from Fresh Produce

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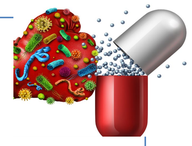
Introduction

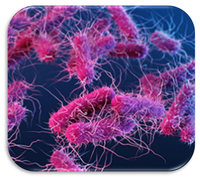


Antibiotic-resistant bacteria also refer to as **superbug** are strains of bacteria that have evolved and developed resistance against antibiotic drugs that were once used to treat them. The development of new antibiotics then bacteria gain resistance has led to an ongoing and never-ending battle between us and these bacteria. According to the CDC, more than 2.8 million people get infected every year, and 38,000 people die from this. Thus, it poses a public health concern, particularly for those with weaken immunity.

The **extended-spectrum beta-lactamases (ESBL)** producing are bacteria that have developed resistance against commonly used Beta-lactam antibiotics; While **Carbapenem-resistant Enterobacterales** are those that have developed resistance against third generation antibiotics that are used to treat infection caused by bacteria like ESBL.

The Center for Disease Control and Prevention (CDC) has identified them as:

Serious Threat



Extended-spectrum beta-lactamases (ESBL) producing

Urgent Threat

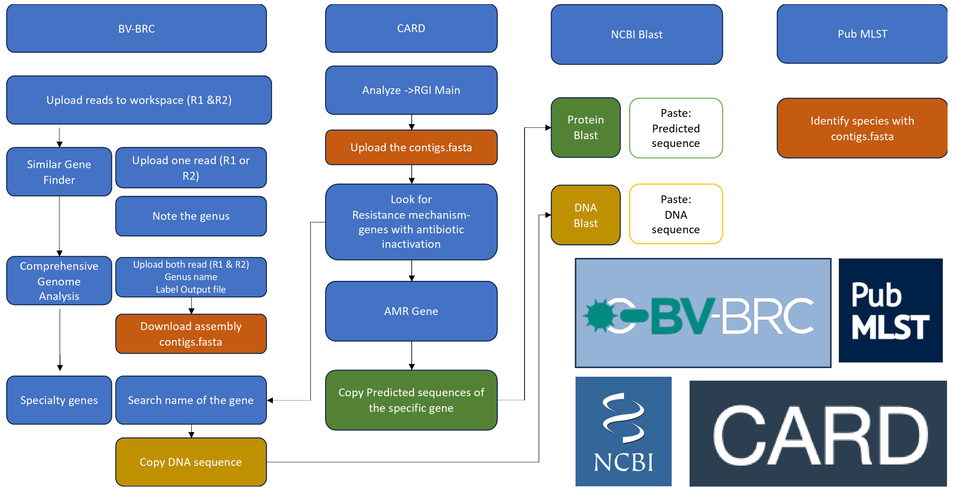
Carbapenem resistant Enterobacterales

Report has been found that outside of U.S, these antibiotic resistant bacteria, like extended-spectrum beta-lactamases (ESBL) producing can be spread to human through contaminated food and water source, but not much is known about how they are spread in the U.S. However, the fresh produce we eat can be reservoir for these antibiotic resistance bacteria. Thus, it is essential to gain a better understanding of the antibiotic resistant bacteria isolated from these fresh produce. Espically when consider the fact that we consume most of the fresh produce raw.

Bioinformatic analysis is a common tool that is widely use in modern biology and medical research. It is a powerful and robust computation approach tool that combines computer science, mathematics, physics and biology. It helps to provides in-depth interpretation and analysis of the biological data through the interdisciplinary knowledges. And is an efficient and effective way for data analysis with the large database for matching and need little to no need of human monitoring when data was processed. For instance, bioinformatic analysis can be used to process and match the sequenced genomic reads to its massive database and provide a wide range of information, from identifying the organism as whole down to the genomes. Additionally, it can be used to provide mathematical and statistical analysis of the biological data, such as understanding the biodiversity of the dataset.

Tools such as **BVBRC, CARD, NCBI Blast, and PubMLST** help to provide bioinformatic analysis and interpretation of the sequenced genomic reads. The generation of various figures such as phylogenic tree, circular view of genomes and tables helps to provide better understanding of the unknown antibiotic resistant organism and its characteristics.

Method



Result

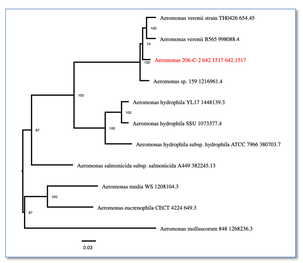


Fig 1. Phylogenic Analysis of the Isolate 206-C-2 from BV-BRC

The isolate 206-C-2 was identified mostly closely to *Aeromonas veronii*.

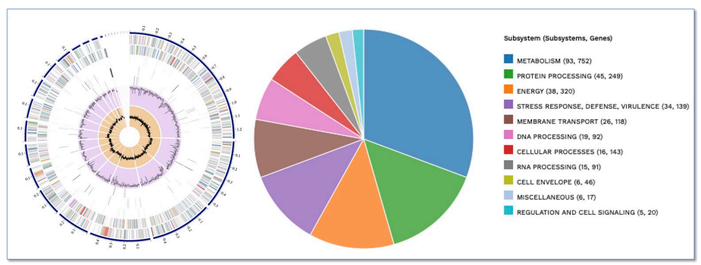


Fig 2. Circular view of genome annotation (left) and subsystem analysis (right) of 206-C-2 from BV-BRC. Outer to inner rings shows the contigs, forward strand, reverse strand, RNA genes, antimicrobial resistance genes, virulence factors, GC content and GC skew. The colored genes on the forward and reverse strand has specific function as shown in the subsystem analysis.

There were 25 contigs and an average GC content of 58.79%.

Table 1. Antimicrobial Resistance Genes of 206-C-2 from BV-BRC that used k-mer-based AMR genes detection method

Antibiotic activation enzyme	KatG
Antibiotic inactivation enzyme	ChpA family
Antibiotic target in susceptible species	Alr, Ddl, dxr, EF-G, EF-Tu, folA, Dfr, folP, gyrA, gyrB, Iso-tRNA, kasA, MurA, rho, rpoB, rpoC, S10p, S12p
Antibiotic target protection protein	QnrB family
Antibiotic target replacement protein	fabV
Efflux pump conferring antibiotic resistance	MacA, MacB, MdtL, TolC/OpmH
Gene conferring resistance via absence	gldB
Protein altering cell wall charge conferring antibiotic resistance	GdpD, PgsA
Regulator modulating expression of antibiotic resistance genes	H-NS, OxyR

Table2. Specialty genes of 206-C-2 Matched with Specific Sources Obtained from BV-BRC

	Source	Genes
Antibiotic Resistance	CARD	9
Antibiotic Resistance	NDARO	2
Antibiotic Resistance	PATRIC	38
Drug Target	DrugBank	40
Drug Target	TTD	7
Transporter	TCDB	32
Virulence Factor	PATRIC_VF	17
Virulence Factor	Victors	30

Table 3. Resistance Gene Identifier Result of 206-C-2 from CARD.

ARO Term	AMR Gene Family	Drug Class	Resistance Mechanism	% Identity of Matching Region	% Length of Reference Sequence
OXA-912	OXA beta-lactamase, OXA-12-like beta-lactamase	penam	antibiotic inactivation	99.62	100
adeF	resistance-nodulation-cell division (RND) antibiotic efflux pump	fluoroquinolone antibiotic, tetracycline antibiotic	antibiotic efflux	43.71	99.06
adeF	resistance-nodulation-cell division (RND) antibiotic efflux pump	fluoroquinolone antibiotic, tetracycline antibiotic	antibiotic efflux	48.65	97.64
rsmA	resistance-nodulation-cell division (RND) antibiotic efflux pump	fluoroquinolone antibiotic, diaminopyrimidine antibiotic, phenicol antibiotic	antibiotic efflux	92.73	101.64
qacJ	small multidrug resistance (SMR) antibiotic efflux pump	disinfecting agents and antiseptics	antibiotic efflux	36.89	101.87
cphA3	CphA beta-lactamase	carbapenem	antibiotic inactivation	99.21	100

Objective

The aim of this study was to further analyze the sequenced isolate (206-C-2) sampled from the fresh produce that was confirmed to have carbapenem resistance. Various bioinformatic analysis tools was used, which include BVBRC, CARD, NCBI Blasts, and PubMLST . They were used to identify the isolate confirmed with antibiotic resistance and further analysis of its resistant genes.

Conclusion

Based on the confirmation with the different bioinformatic analysis tools, the isolate **206-C-2** was most closely identified with ***Aeromonas veronii*** with 25 contigs and GC content of 58.79%. Depends on the database that was used, the number of genes with antibiotic resistance varies, CARD identified 9 genes, NDARO 2 genes, PATRIC 38 genes. The further analysis with CARD indicated that gene named OXA-912 and cphA3 sued antibiotic inactivation as the resistance mechanism against penam and carbapenem, respectively.

Future Research

To identify and gain better understanding of all the isolates that were sequenced. Additional bioinformatic analysis will be carried out with other isolates that were confirmed to have antibiotic resistance. Along with identification of unique isolates for further analysis and research which provide more valuable information than the commonly known ones.

Acknowledgement

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Reference

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