

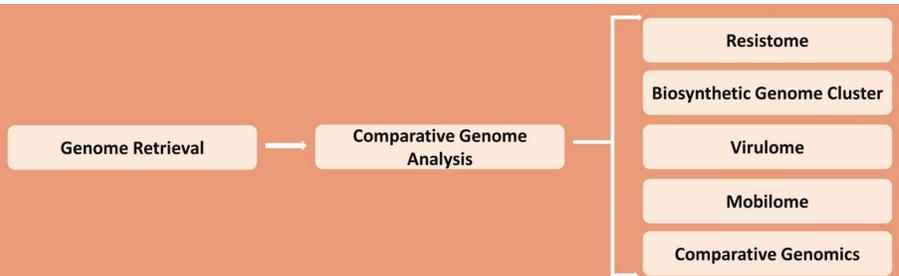
Genomic Insights into *Acinetobacter bereziniae* IJ5: A Comparative Genomics Perspective

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INTRODUCTION & AIM

- Acinetobacter bereziniae*, a widespread environmental organism¹ recently being reported as an emerging nosocomial pathogen capable of causing severe hospital-acquired infections, especially in immunocompromised patients² it is often underreported due to misidentification^{3,4}.
- This study aimed for whole genome sequencing of *A. bereziniae* strain IJ5 (Bangladesh) to characterize its pathogenicity, antimicrobial resistance profile, identify mobilomes, explore virulence-associated features and phylogenomic relation worldwide through comparative genomics.
- Findings contribute to understanding its genomic architecture and highlight the need for regional surveillance.

METHOD



CONCLUSION

- IJ5 has the genome length of 4.4 Mb, comparative genomic analysis revealed that *A. bereziniae* typically has a genome size of 4.4–5.0 Mb.
- Comparative genomic analysis revealed the prominent presence of *adeF*, *qacG*, *vanG*, *vanW*, and *OXA* genes in all *A. bereziniae* strains.
- The IJ5 strain shares conserved secondary metabolite biosynthetic genes and possesses fewer toxin-antitoxin systems compared to other *A. bereziniae* strains, making it possible for future biotechnological exploitation.
- Phylogenomic analysis places IJ5 within a conserved and clinically significant clade, primarily composed of strains mostly from the U.S.A. and fewer Asian strains. The orthologous genome cluster shows a high number of shared core genes and comparatively fewer unique genes in IJ5.
- Future directions include functional studies of resistance genes, investigation of reduced toxin-antitoxin systems, and exploring conserved metabolic pathways for therapeutic or industrial use.

REFERENCES

- Reyes SM, Boletieri E, Allen D, Hay AG. Genome Sequences of Four Strains of *Acinetobacter bereziniae* Isolated from Human Milk Pumped with a Personal Breast Pump and Hand-Washed Milk Collection Supplies. *Microbiol Resour Announc*. 2020 Oct 29;9(44):e00770-20. doi: 10.1128/MRA.00770-20. PMID: 33122407; PMCID: PMC7595943.
- Mo XM, Pan Q, Seifert H, Xing XW, Yuan J, Zhou ZY, Luo XY, Liu HM, Xie YL, Yang LQ, Hong XB, Higgins PG, Wong NK. First identification of multidrug-resistant *Acinetobacter bereziniae* isolates harboring bla_{NDM-1} from hospitals in South China. *Heliyon*. 2022 Dec 24;9(1):e12365. doi: 10.1016/j.heliyon.2022.e12365. PMID: 36699260; PMCID: PMC9868374.
- Al Atrouni A, Joly-Guillou ML, Hamze M, Kempf M. Reservoirs of Non-baumanniil *Acinetobacter* Species. *Front Microbiol*. 2016 Feb 17;7:49. doi: 10.3389/fmicb.2016.00049. PMID: 26870013; PMCID: PMC4740782.
- Bonnin RA, Ocampo-Sosa AA, Poirel L, Guet-Revillet H, Nordmann P. Biochemical and genetic characterization of carbapenem-hydrolyzing β -lactamase OXA-229 from *Acinetobacter bereziniae*. *Antimicrob Agents Chemother*. 2012 Jul;56(7):3923-7. doi: 10.1128/AAC.00257-12. Epub 2012 Apr 16. PMID: 22508298; PMCID: PMC3393453.

RESULTS

Table 1: General features of *Acinetobacter bereziniae* IJ5 strain.

Strain	Biosample ID	Scientific name	Level	Country	Genome size	Scaffold N50	Scaffold L50	Number of contig	Contig L50	Contig N50	GC percent	Probability of being a human pathogen
IJ5	SAMN18145973	<i>Acinetobacter bereziniae</i>	Contig	Bangladesh	4.4 Mb	67.9kb	22	196	67.9kb	22	38%	77.20%

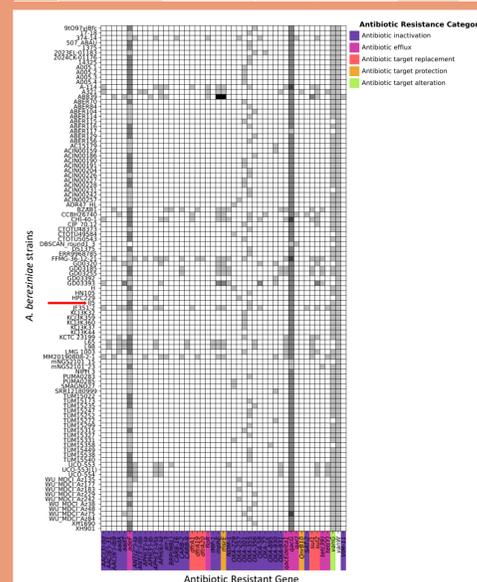


Figure 1: Antibiotic resistance pattern across *A. bereziniae* Strains; grey denotes presence and white denotes absence of ARG gene.

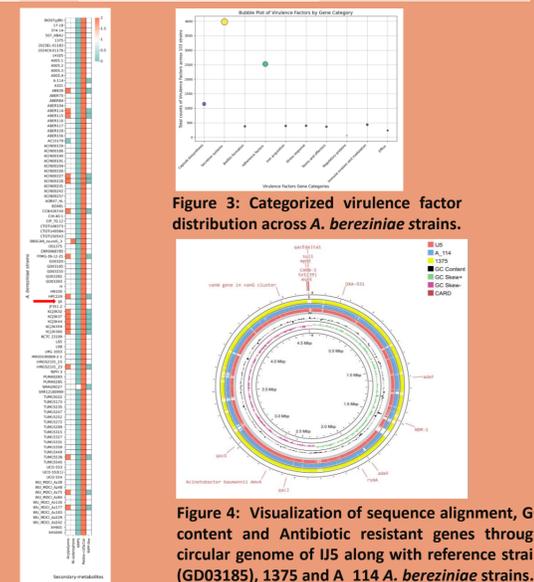


Figure 2: Distribution of BGC across *A. bereziniae* strains; green denotes certain BGC present twice, orange denotes presence of BGC once and white denotes absence of BGC.

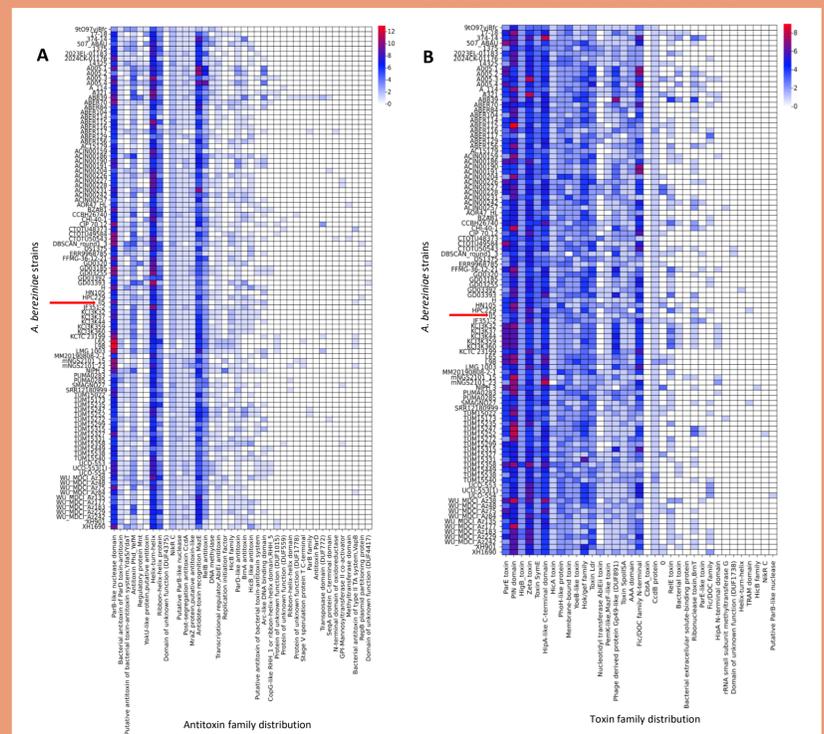


Figure 5: Toxin-Antitoxin system of *A. bereziniae*; (A) Toxin system; blue denotes absence of Toxin system and red denotes presence (B) Antitoxin system; blue denotes absence of Antitoxin system and red denotes presence.

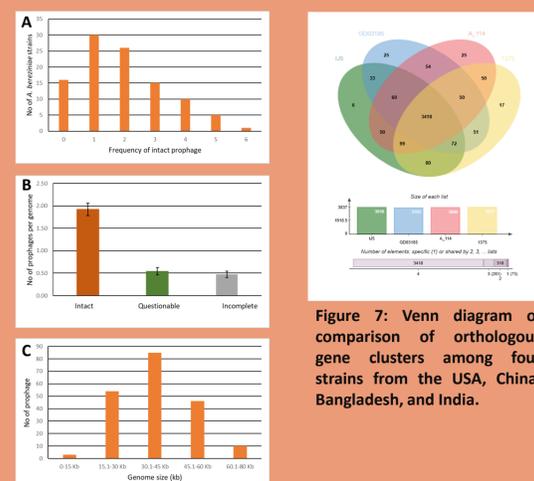


Figure 6: Distribution of (A) Frequency of intact prophage, (B) prophage number, and (C) Genome length of prophages in *A. bereziniae* strains.

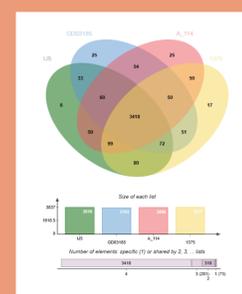


Figure 7: Venn diagram of comparison of orthologous gene clusters among four strains from the USA, China, Bangladesh, and India.

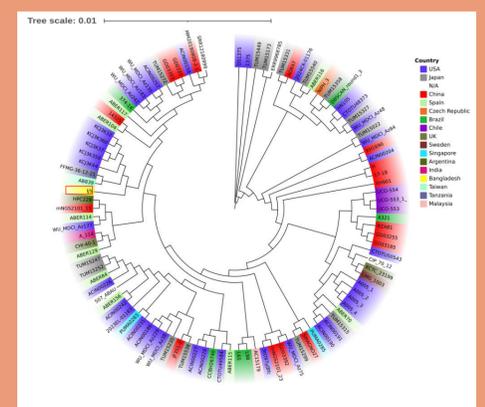


Figure 8: Phylogenomic analysis of globally available *A. bereziniae* strains.