Isolation and Characterization of Novel β-Lactamase Inhibitors Resistant to *Burkholderia pseudomallei* from Environmental Sources of Dhaka, Bangladesh.

Turin Afroz*[1],Afrina Nazmin[2],Nitun Saha Shuvro[3] Aysha Akter Smrity[4], Md Rashedul Islam Emon[5]
[1-5] Bangladesh University of Health Sciences, Dhaka, Bangladesh.
*Correspondence:turinafroze007@gmail.com

Introduction

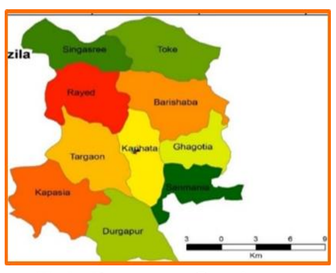
- Only roughly 100 cases of melioidosis have been diagnosed in Bangladesh over the previous 60 years, according to the 3rd South Asian Melioidosis Congress-2023, which was held in October 2023.Approximately 90% of these cases were found at BIRDEM General Hospital.
- An early warning system for newly emerging antimicrobial resistance (AMR) mechanisms is based on environmental origins.
- Antimicrobial therapy and environmental biosafety are seriously threatened by the advent of Burkholderia pseudomallei species resistant to β lactamase inhibitor combinations, including amoxicillin–clavulanate.

Aims

To combat the development of new structure-based β-lactamase inhibitors, this work sought to characterize the phenotype and probable genotype of novel β-lactamase inhibitor-resistant Burkholderia pseudomallei from environmental sources.

Methods

A descriptive type of cross-sectional study was conducted and carried out in the Dhaka Health Laboratory over a period of 3 months ranged from july 2025 to September2025. Burkholderia strains were isolated from the rhizosphere soil of the paddy field in Tok Bazaar, Gazipur, Bangladesh.Phenotypic characterization was the technique used for microbiological analysis based on morphological and biochemical features, including oxidase positivity, motility, and colony pigmentation



Tok Bazaar, Gazipur, Bangladesh

Sample collection

Wrinkled colony

Phenotypic characterization

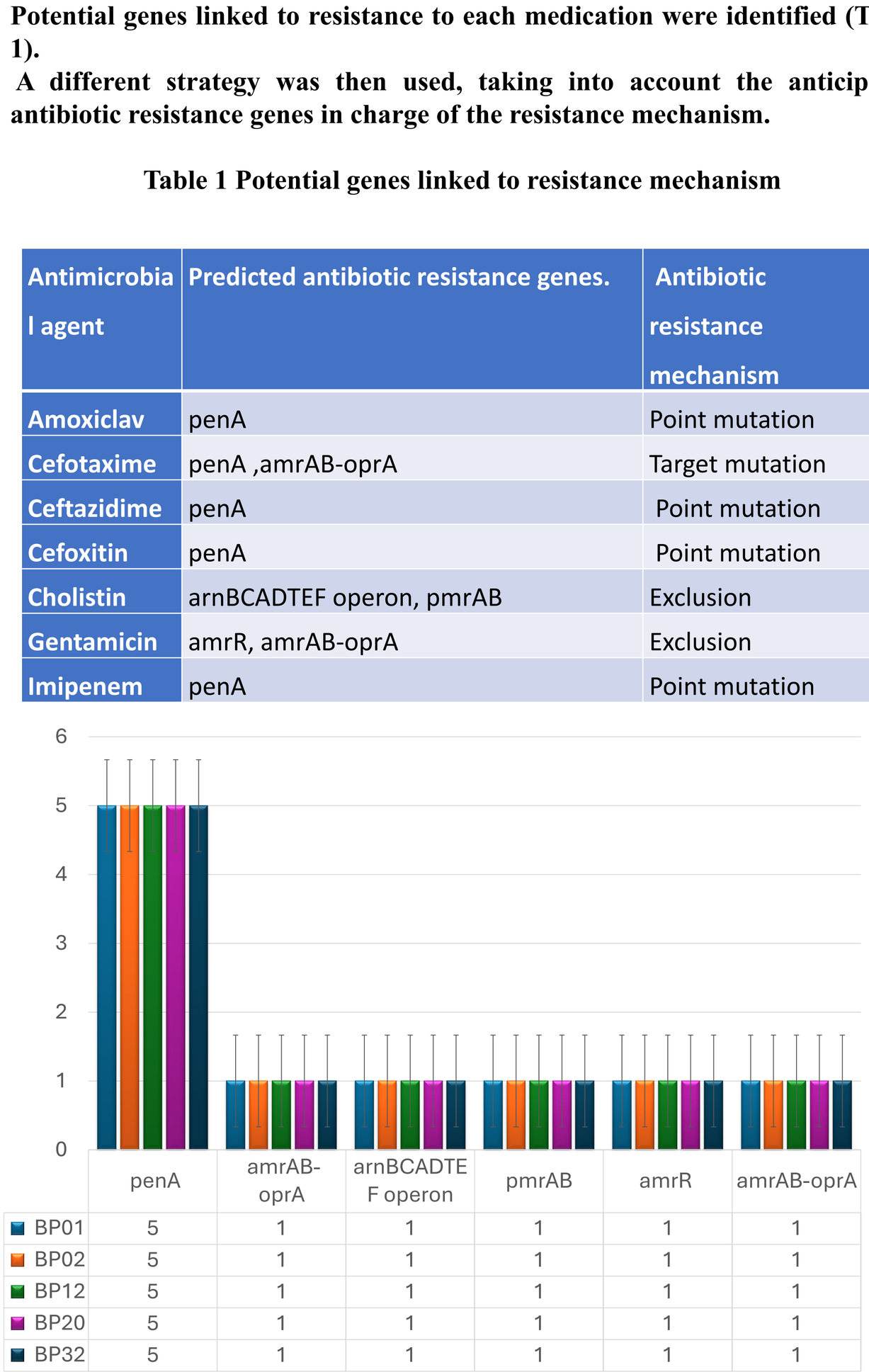
Antimicrobial Susceptibility Test

Results

- Five of the 24 Burkholderia strains that were identified were Burkholderia pseudomallei.
- Complete resistance to amoxiclav, cefotaxime, ceftazidime, cefoxitin, cholistin, imipenem, and gentamicin was among the phenotypic resistance types.
- The predicted genotypic resistance patterns included cefotaxime ceftazidime ,imipenem(penA mutation), cholistin (arnBCADTEF operon, pmrAB), gentamicin (amrR, amrAB-oprA) and amoxicillin–clavulanic acid (penA mutation and amrAB-oprA) .
- Potential genes linked to resistance to each medication were identified (Table 1).
- A different strategy was then used, taking into account the anticipated antibiotic resistance genes in charge of the resistance mechanism.

Table 1 Potential genes linked to resistance mechanism

Antimicrobial agent	Predicted antibiotic resistance genes.	Antibiotic resistance mechanism
Amoxiclav	penA	Point mutation
Cefotaxime	penA ,amrAB-oprA	Target mutation
Ceftazidime	penA	Point mutation
Cefoxitin	penA	Point mutation
Cholistin	arnBCADTEF operon, pmrAB	Exclusion
Gentamicin	amrR, amrAB-oprA	Exclusion
Imipenem	penA	Point mutation



Conclusions

- These findings confirm that penA was the most likely resistance gene and that point mutation was the most common resistance mechanism.
- The research also highlights not only new structure-based β-lactamase inhibitor design but also the need for sequence analysis of the genome of an MDR strain of B. pseudomallei, which advances our understanding of the mechanisms of resistance and will help improve strategies for the selection of more effective treatments and prevention of melioidosis

References

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