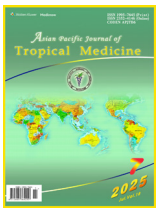

Letter to Editor

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Genetic variabilities of *Acinetobacter baumannii* in a hospital setting using ISSR markers

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Acinetobacter (A.) baumannii is a Gram-negative, non-fermenting opportunistic pathogen increasingly implicated in nosocomial infections, particularly in intensive care units (ICUs). Its ability to acquire multidrug resistance (MDR), including to carbapenems, poses a major public health threat. Infections caused by *A. baumannii*—ranging from pneumonia to bloodstream and wound infections—are difficult to treat and associated with high mortality, especially in critically ill patients[1].

This pathogen's resistance is driven by mechanisms such as beta-lactamase production (*e.g.*, bla*OXA* genes), efflux pumps, porin modifications, and target site mutations. These factors hinder antibiotic efficacy and complicate infection management. Understanding the genetic diversity of *A. baumannii* is essential for effective surveillance and outbreak control. Molecular typing tools like pulsed-field gel electrophoresis (PFGE), multilocus sequence typing (MLST), and whole-genome sequencing have been instrumental in tracking clonal spread and informing infection control, though cost and technical demands limit their routine use[2].

We wish to highlight the genetic diversity of drug resistance of *A. baumannii* isolates from clinical samples in a healthcare setting (Table 1), based on Inter-Simple Sequence Repeat (ISSR) markers. This work is critical given the increasing challenge posed by multidrug-resistant (MDR) *A. baumannii* strains in nosocomial infections.

In our study, eighteen *A. baumannii* isolates were obtained from a tertiary care hospital in Eastern India. Genomic DNA was extracted using the boiling method and subjected to ISSR-PCR using 19 primers, of which 17 yielded clear amplification. Genetic diversity was assessed *via* phylogenetic analysis and principal component analysis.

ISSR primers revealed substantial polymorphism, with ISSR 15 showing the highest resolving power (0.89) and primer index (0.49)[3]. Notably, ISSR 5 and ISSR 13-15 detected the most polymorphic bands, indicating their effectiveness in capturing genomic variation. Unique bands were most frequent in ISSR 1, 3, 6, and 8, further emphasizing genetic heterogeneity (Supplementary Table 1)[4].

The phylogenetic tree (Figure 1) demonstrated distinct clustering patterns among isolates. Isolates S3 and S4 were closely related, while others like S171 and S454 showed substantial divergence. These findings were corroborated by principal component analysis and pairwise similarity matrix scores, highlighting the coexistence of clonal and highly diverse strains within the hospital environment[5,6].

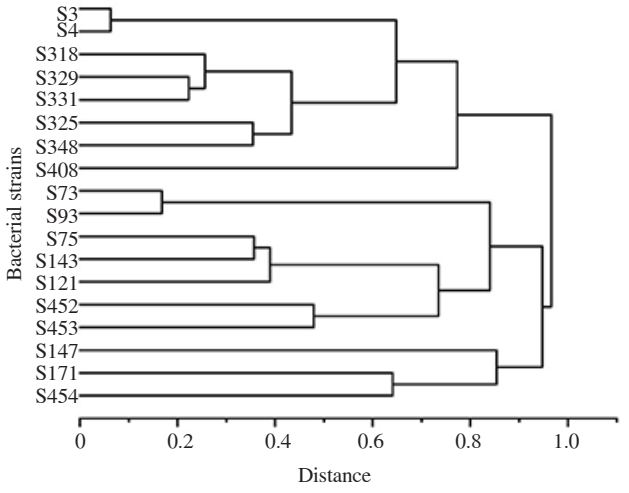

Figure 1. Phylogenetic tree of *Acinetobacter baumannii* strains based on ISSR-PCR data, showing distinct genetic clustering and diversity among clinical isolates.

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Table 1. Antibiotic sensitivity patterns of 18 *Acinetobacter baumannii* with different antibiotic resistant patterns.

Acenetobacter baumanii	Cefoperazone	Meropenem	Levofloxacin	Imipenem	Azithromycin	Chloramphenicol	Colistin	Polymyxin B	Netilmicin	Ampicillin	Cefoxitin	Ceftizoxime	Cefazolin	Tazobactam	Tobramycin	Amikacin	Gentamicin	Ciprofloxacin	Fosfomycin	Sulfamethoxazole	Tigecycline	Minocycline	Doxycycline	Cefuroxime	Tetracycline	Cefixime	Erythromycin
S3	R	R	R	R	R	R	I	I	R	ND	R	R	ND	R	R	R	R	R	S	S	S	S	R	ND	R	R	R
S4	R	I	S	R	R	R	R	I	R	I	R	R	ND	R	R	R	R	S	ND	S	R	R	R	R	R	R	R
S73	I	S	S	S	S	S	I	S	R	S	R	R	ND	S	S	S	S	S	S	S	R	R	R	S	S	R	S
S75	R	R	R	R	S	S	R	S	R	R	R	R	R	R	S	R	R	R	I	R	S	S	R	S	S	S	S
S93	R	R	R	R	R	I	I	I	R	R	R	S	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S
S121	R	R	R	R	S	S	I	I	R	R	R	R	R	R	R	I	R	R	S	R	S	S	R	S	S	ND	ND
S143	S	S	I	S	R	I	I	I	R	S	S	S	S	ND	R	S	S	R	ND	S	S	S	R	R	I	R	R
S147	R	R	R	R	R	R	I	I	R	ND	S	S	S	ND	R	R	R	R	R	R	R	S	S	R	S	R	R
S171	R	R	R	R	R	I	I	R	R	R	S	I	R	R	R	R	R	R	I	R	R	R	I	S	R	R	R
S318	R	R	R	R	R	I	I	I	R	R	S	R	R	R	R	R	R	R	S	R	S	R	R	R	R	R	S
S325	R	R	R	R	R	I	I	I	R	R	R	ND	R	R	R	R	R	R	S	R	S	R	S	ND	ND	R	S
S329	S	R	R	S	S	S	I	I	R	R	R	ND	S	S	S	S	S	R	S	R	S	S	I	S	S	S	S
S331	R	R	R	R	R	S	I	R	R	R	S	R	R	R	R	R	R	R	R	R	ND	R	R	S	R	ND	S
S348	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
S408	R	R	R	R	R	R	I	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
S452	R	R	R	R	R	R	I	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
S453	R	R	R	R	R	R	I	I	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
S454	R	R	R	R	R	S	I	I	R	R	R	ND	R	R	S	R	R	R	S	R	S	R	I	R	R	S	S
S	2	2	2	2	3	6	0	2	0	2	5	3	3	2	4	3	3	2	7	4	8	6	2	6	5	3	8
R	15	15	15	15	15	7	3	5	18	14	13	11	12	14	14	14	15	16	7	14	9	12	13	10	11	13	9
R, %	83	83	83	83	83	38	16	27	100	77	72	72	66	77	77	77	83	88	38	77	50	66	72	55	61	72	50

R: resistant; I: intermediate; S: susceptible; ND: not done.

Such diversity has direct implications for infection control, suggesting multiple sources and possible horizontal gene transfer events[7,8]. Routine genetic surveillance using ISSR markers can offer cost-effective insights into transmission dynamics and resistance evolution, particularly in resource-constrained settings[9,10].

We believe this brief communication adds valuable regional data on *A. baumannii* diversity and supports the utility of ISSR markers in molecular epidemiology.

Conflict of interest statement

The authors decalre that there are no conflicts of interest.

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Authors' contributions

M.C.S developed the concept of this manuscript and P.M performed and wrote the article. D.S corrected the manuscript. All the authors approved the final manuscript.

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