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Preliminary screening of ESBL-producing *Escherichia coli* and *Klebsiella pneumoniae* carriage among migrant communities in Klang Valley, Malaysia

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ABSTRACT

Economic migrant workers are crucial for a country's development but may also contribute to transboundary transmission of antimicrobial resistance (AMR). This study aimed to investigate the silent carriage of ESBL-producing *Escherichia coli* (ESBLEC) and *Klebsiella pneumoniae* (ESBLKP) among economic migrants from Indonesia, Bangladesh and Nepal residing in Klang Valley, Malaysia. Between December 2023 and May 2024, 263 study participants of Indonesian, Bangladeshi, and Nepalese migrant communities were recruited and rectal swabs collected. Swabs were then cultured on CHROMagar™ ESBL; presumptive ESBL-positive strains were confirmed and antimicrobial susceptibility-tested using a VITEK 2 system. ESBL genotyping was also performed on confirmed isolates. A total of 67 and five strains were confirmed as ESBLEC and ESBLKP, respectively. Both ESBLEC and ESBLKP strains showed similar resistance to penicillin and 3rd generation cephalosporins, though more ESBLKP strains were resistant to 4th generation cephalosporins. More ESBLEC strains were resistant to ciprofloxacin. No carbapenem-resistant strains were detected. The $bla_{\text{CTX-M-1}}$ gene family was predominantly found in ESBLEC strains from all three nationalities, while ESBLKP strains frequently harboured bla_{TEM}, $bla_{\text{CTX-M}}$, and bla_{SHV} genes. The prevalence of ESBL-producing strains was highest among Bangladeshi participants (n = 16, 31.4 %), followed by Indonesians (n = 47, 29.7 %) and Nepalis (n = 9, 19.1 %) working in domestic or manufacturing sectors. These findings highlight the public health risks of high ESBLEC and ESBLKP carriage in healthy migrant workers, which may impact recruitment and retention, leading to labour shortages and higher costs. Screening and increased awareness are crucial to limit the spread of these pathogens.

1. Introduction

Economic migrant workers crossing international borders play important roles in a country's development. At the same time, human migration is an integral factor towards the dissemination of infectious diseases, including infections by bacteria that are resistant to antibiotics. Antimicrobial resistance (AMR) was first identified as a major global health challenge by the World Health Organization (WHO) in 2016 during the 71st United Nations General Assembly. In 2019, a systematic analysis of the global burden of bacterial infections estimated a total of 4.95 million deaths due to AMR, where *Escherichia coli* and *Klebsiella pneumoniae* were identified as two bacterial species associated with deaths attributable to AMR [1]. A more recent study reiterated the importance of these two pathogens [2].

E. coli and *K. pneumoniae* are members of the *Enterobacterales* order that predominantly reside in the human gut. In locations where sanitation and hygiene practices are below par, these bacteria can cause faecal contamination of food products and be transmitted unknowingly between humans [3]. Human-environment transmission may also occur. In addition, both bacteria are common nosocomial pathogens that cause infections in hospitals [4]. Due to the ubiquitous nature of these bacteria in the gut and the issue of antibiotic misuse, many strains of *E. coli* and

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K. pneumoniae are now resistant to first-generation beta-lactams, a common class of antibiotics used to treat bacterial infections. Alarmingly, recent reports show increasing reports of these bacteria producing Extended-Spectrum Beta Lactamases (ESBL) enzymes, which render them resistant to the killing effects of newer generations of beta-lactams [5]. bla_{TEM}, bla_{SHV} and $bla_{CTX\text{-}M}$ are the more common ESBL genes detected in ESBL-producing Enterobacterales, with the $bla_{CTX\text{-}M}$ gene variants dominating in recent years [6].

Patients infected with ESBL-producing bacteria face limitations in treatment options. The situation further compounds AMR when carbapenem, a broad-spectrum antibiotic that should be reserved for serious infections, is prescribed to these patients. Similar to antibiotic-susceptible strains, ESBL-producing *E. coli* (ESBLEC) and *K. pneumoniae* (ESBLKP) can be carried in the guts of healthy individuals (carriers), transmitted between individuals, and cause invasive infections. Indeed, high ESBLEC and ESBLKP colonization rates in the community have been associated with increased incidence of hospital infections caused by these pathogens.

In Malaysia, infections caused by ESBLEC and ESBLKP have been increasing since 2019. The National Surveillance of Antimicrobial Resistance (NSAR 2023) documented a rising trend in penicillin and cephalosporin (1st to 4th generation) resistance in both *E. coli* and *K. pneumoniae* strains isolated from patients in the country from 2007 to 2023. By 2023, more than 70 % of *E. coli* isolates were resistant to penicillin, while cephalosporin resistance ranged from 13 % to 28 % based on data from 2007 to 2023. Similarly, *K. pneumoniae* exhibited cephalosporin resistance rates between 13 % and 27 % over the same period, underscoring a persistent and concerning trend in antimicrobial resistance.

While these reports mainly comprise of hospital cases recorded in local Malaysians, information about community carriage of these pathogens in the migrant workforce remains unavailable. Worryingly, the increasing trend of ESBLEC and ESBLKP isolation coincides with the significant influx of economic migrants from Indonesia, Bangladesh, and Nepal to Malaysia since the year 2000 [7], where Indonesian workers started arriving in the country in 2000, followed by Bangladeshis in 2007, and Nepalis in 2017. According to the 2019 Labor Force Survey, Malaysia was the largest importer of human labour in East Asia in 2018, with 2.18 million foreign workers out of a labour force of 14.7 million [8]. Coincidentally, a high prevalence of ESBL cases has been reported in Indonesia, Bangladesh, and Nepal [9]. A tricycle project in Indonesia noted that 40 % of 100 pregnant women were carriers of ESBL [10]. In addition, pooled prevalence rates of ESBL were 21 % (95 % CI: 15 %–27 %) in Bangladesh [11] and 29 % (95 % CI: 26 %–32 %) in Nepal [12]. Human mobility such as economic migration (which will involve a longer duration compared to short-term travel) [5] is undoubtedly one of the risk factors for the dissemination of AMR [13]. In light of the increasing reports of ESBLEC and ESBLKP cases in Malaysia, it is important to better understand ESBLKP and ESBLEC carriage within the migrant communities in Malaysia, as occupational health needs for migrants remain lacking, despite their contribution to the economy [14].

In this study, we collected rectal swabs from Indonesian, Bangladeshi, and Nepali economic migrants working in the Klang Valley, Malaysia to investigate the carriage of both ESBLEC and ESBLKP in these communities. Antibiotic susceptibility testing and genotyping of ESBL genes were also carried out. Demographic data and information about antibiotic awareness and the migration process from study participants were collected and analysed.

2. Materials and methods

2.1. Study setting and sample collection

The study was conducted between December 2023 and May 2024 on economic migrant communities originating from Indonesia, Bangladesh, and Nepal residing in the Klang Valley, a densely populated urban area in Malaysia where migrants live and work alongside Malaysians. Potential participants were informed about the study via WhatsApp messaging originating from migrant community leaders via a liaison from the North South Initiative (NSI), a Malaysian-based social justice, non-governmental organisation. This pilot-based study employed a minimum sampling size of 30 participants per nationalities, with a study power of 80 % and an effect size ranging from moderate to large [15]. Inclusion criteria for the participants were: (1) Indonesian, Bangladeshi or Nepali citizenship, (2) working and residing in Klang Valley, Malaysia, (3) 18 years old and above (4) provided written consent for participation in the study. Participants who did not fulfil the inclusion criteria were excluded from the study.

Sample collection was performed at the NSI headquarters in Klang Valley, Malaysia. Participants were firstly briefed about the study. Individuals who agreed to participate in the study filled out a consent form and provided demographic information, details of previous antibiotic usage, household information, and history of hospitalization. Subsequently, rectal swabs (one swab per participant) were collected and transported to the testing laboratory using a modified Amies transport medium (Vacutest Kima, Italy). Swabs were kept at room temperature and processed for bacterial culture within 24 h post-collection.

2.2. Bacterial culture, isolation of ESBLEC and ESBLKP

Rectal swabs were cultured on CHROMagar™ ESBL (CHROMagar, France) and incubated under aerobic conditions for 24 h at 37 °C. Mixed-growth colonies were colony-purified and subcultured on CHROMagar™ ESBL (CHROMagar, France) and incubated at 37 °C for another 24 h. Identification of ESBLEC and ESBLKP was carried out according to the manufacturer's instruction, i.e., pink colonies were presumptively identified as ESBLEC, while blue colonies (with or without a red halo) were presumptively identified as ESBLKP.

2.3. Confirmation of ESBLEC, ESBLKP, and antimicrobial susceptibility test

Identification of presumptive ESBLEC and ESBLKP strains were confirmed using a VITEK 2 system (bioMérieux, France.) The system was also used to perform antimicrobial susceptibility testing on confirmed isolates. Antibiotics tested were penicillin (AMP), cefuroxime (CFU), cefotaxime (CTX), ceftriaxone (CRO), ceftazidime (CAZ), cefepime (FEP), amoxicillin/clavulanate (AMC), piperacillin/tazobactam (TZP), ampicillin/sulbactam (SAM), amikacin (AMK), gentamicin (GEN), ciprofloxacin (CIP), ertapenem (ETP), imipenem (IMP) and meropenem (MEM).

2.4. ESBL genotyping

DNA was extracted from ESBLEC and ESBLKP strains using the boiling method [16]. ESBL genotyping was carried out according to the protocol described by Ogutu et al. (2015) [17]. Briefly, bacterial colonies were boiled in sterile distilled water at 98 °C for 10 min, followed by centrifugation at 15,000×*g* for 5 min at 4 °C. The supernatant was used as the DNA template for two sets of multiplex PCR: Set 1 targeted bla_{TEM}, $bla_{CTX\text{-}M\text{-}1}$, and $bla_{CTX\text{-}M\text{-}9}$; Set 2 targeted bla_{SHV} and $bla_{OXA\text{-}1}$.

2.5. Statistical analysis

Data analysis was performed using the Statistical Package for Social Sciences (SPSS) version 22 (IBM Corp., Armonk, NY, USA). Categorical variables were summarized as frequencies. Chi-square test and Fisher's exact test were employed, where applicable, to compare differences in ESBL carriage based on accommodation type, hospitalization within six months prior to sampling, antibiotic prescription within six months prior to sampling, and antibiotic resistance across migrant nationalities,

where a p-value of <0.05 was considered to be statistically significant.

3. Results

3.1. Participant demographics, antibiotic awareness and migration information

A total of 263 healthy volunteers participated in this study and consented for sample and information collection. After sample processing, only 256 samples were included in the study; seven samples were excluded due to missing swab samples, duplication in sample collection and incomplete consent forms. Demographics of all participants are shown in Table 1. The median age of the participants was 39 years old for Indonesians, 29 years old for Bangladeshis, and 30 years old for Nepalis. Majority of the Indonesian participants were females (n = 99, 62.7 %), while most Bangladeshi and Nepali participants were males (n = 43, 84.3 % and n = 37, 78.7 %, respectively). Indonesian migrants were predominantly employed as domestic labourers (n = 130, 82.3 %), while Bangladeshi migrants worked mostly in the manufacturing (n = 18, 35.3 %) and construction (n = 16, 31.4 %) sectors. Nepali participants were largely employed in the manufacturing sector (n = 24, 51.1 %).

The majority of the participants completed secondary education. Among the 256 participants, 88.3 % were working beyond their home country for the first time. Additionally, 77.7 % (n = 199) were living in shared accommodation while working in Malaysia. Interestingly, about half of the migrant participants (Indonesians, n = 83, 52.5 %; Bangladeshis, n = 24, 47.1 %; Nepalis, n = 18, 38.3 %) had been working in Malaysia for 1–5 years. A majority of the participants had not taken antibiotics and had not been hospitalized in the 6 months prior to sample collection.

Table 1
Participant demographics, antibiotic awareness and migration information.

	Country of origin, n(%)		
	Indonesia	Bangladesh	Nepal
Number of participants	164 (100)	51 (100)	48 (100)
Number of rejected samples (Due to missing samples, duplicates and incomplete consent forms)	6 (3.7)	0 (0)	1 (2.1)
Number of samples included into the study	158 (96.3)	51 (100)	47 (97.9)
Gender			
Male	56 (35.4)	43 (84.3)	37 (78.7)
Female	99 (62.7)	8 (15.7)	8 (17.0)
N/A	3 (1.9)	0 (0)	2 (4.3)
Age			
Less than 20 years old	2 (1.3)	0 (0)	0 (0)
20–29 years old	38 (24.1)	26 (51.0)	21 (44.7)
30–39 years old	34 (21.5)	15 (29.4)	19 (40.4)
40–49 years old	53 (33.5)	8 (15.7)	3 (6.4)
Above 50 years old	19 (12.0)	1 (2.0)	0 (0)
N/A	12 (7.6)	1 (2.0)	4 (8.5)
Working sector			
Domestic workers	130 (82.3)	2 (3.9)	1 (2.1)
Manufacturing	3 (1.9)	18 (35.3)	24 (51.1)
Construction	3 (1.9)	16 (31.4)	5 (10.6)
Food and beverages	8 (5.1)	5 (9.8)	1 (2.1)
Others	8 (5.1)	4 (7.8)	11 (23.4)
N/A	6 (3.8)	6 (11.8)	5 (10.6)
First time working beyond home country			
Yes	141 (89.2)	47 (92.2)	38 (80.9)
No	16 (10.1)	4 (7.8)	8 (17.0)
N/A	1 (0.6)	0 (0)	1 (2.1)
Accommodation in Malaysia			
Alone	31 (19.6)	8 (15.7)	16 (34.0)
Sharing	126 (79.7)	43 (84.3)	30 (63.8)
N/A	1 (0.6)	0 (0)	1 (2.1)
Working duration in Malaysia			
Less than 1 year	3 (2.0)	6 (11.8)	0 (0)
1–5 years	83 (52.5)	24 (47.1)	18 (38.3)
Above 5 years	60 (38.0)	21 (41.2)	22 (46.8)
N/A	12 (7.6)	0 (0)	7 (14.9)
Hospitalized 6 months prior to sample collection			
Yes	3 (1.9)	4 (7.8)	5 (10.6)
No	153 (96.8)	47 (92.2)	42 (89.4)
N/A	2 (1.3)	0 (0)	0 (0)
Prescribed antibiotics 6 months prior to sample collection			
Yes	12 (7.6)	13 (25.5)	15 (31.9)
No	134 (84.8)	36 (70.6)	30 (63.8)
Not sure	8 (5.1)	1 (2.0)	0 (0)
N/A	4 (2.5)	1 (2.0)	2 (4.3)
Education			
No formal education	1 (0.6)	5 (9.8)	2 (4.3)
Primary education	43 (27.2)	12 (23.5)	12 (25.5)
Secondary education	99 (62.7)	24 (47.1)	28 (59.6)
Tertiary education	13 (8.2)	10 (19.6)	5 (10.6)
N/A	2 (1.3)	0 (0)	0 (0)

3.2. Isolation of ESBLEC and ESBLKP strains from CHROMagar™ ESBL

A total of 69 rectal swab cultures produced pinkish colonies on CHROMagar™ ESBL (presumptive ESBLEC), while 22 swab cultures produced blue colonies (presumptive ESBLKP). Two individuals carried both ESBLEC and ESBLKP. A representative colony from each presumptive ESBLEC and ESBLKP were stocked as strains and used for further investigations.

3.3. ESBLEC and ESBLKP identification and antibiotic susceptibility testing via a Vitek 2 system

All presumptive ESBLEC strains (n = 69) were identified as *E. coli*. On the other hand, only 5 (22.7 %) presumptive ESBLKP strains were identified as *K. pneumoniae*; the remaining presumptive ESBLKPs were identified as *Enterobacter* sp. (n = 7, 31.8 %), *Citrobacter* sp. (n = 3,13.6 %), *Serratia* sp. (n = 3, 13.6 %), *Stenotrophomonas* sp. (n = 4, 18.2 %) and were subsequently excluded from the study. Two (3.0 %) of presumptive ESBLEC tested as susceptible to 3rd generation cephalosporins (CRO and CAZ) and were excluded from the study. ESBLEC carriage was the most prevalent in the Bangladeshi participants (n = 16, 31.4 %), followed by Indonesians (n = 43, 27.2 %) and Nepalis (n = 8, 17.0 %) (Fig. 1). On the other hand, of the five ESBLKP confirmed strains, none were detected in Bangladeshi participants. All ESBLEC and ESBLKP were resistant to AMP and at least one 3rd generation cephalosporin (Fig. 2(a) and (b)). Moreover, all ESBLKP strains were resistant to the 4th generation cephalosporin FEP and were mostly resistant towards antibiotics from the beta lactam – beta lactamase inhibitor group. Nonetheless, 62.7 % ESBLEC (n = 67) were resistant to CIP compared to 40.0 % ESBLKP (n = 5). No carbapenem resistance was detected among all the strains.

3.4. ESBL genotyping

All ESBLEC and ESBLKP strains harboured ESBL genes. $bla_{\text{CTX-M-1}}$ was predominantly present in ESBLEC isolates from all participants. bla_{SHV} was not detected in the ESBLEC isolates. Interestingly, strains from Indonesian participants frequently harboured more than one ESBL gene (Table 2). ESBLKP isolates from Indonesia and Nepal exhibited similar ESBL genotypes, with each isolate harbouring bla_{TEM}, $bla_{\text{CTX-M}}$, and bla_{SHV} genes, and none harbouring the $bla_{\text{OXA-1}}$ gene (Table 2).

3.5. Association between ESBL carriage, antibiotic susceptibility and demographic variables

Among participants with ESBL carriage, 75.0 % lived in shared accommodations (n = 54), 16.7 % had taken antibiotics prior to sampling (n = 12), and 6.9 % had been hospitalized within six months before sampling (n = 5). However, no significant differences were observed when comparing these variables between ESBL carriers and non-carriers (p > 0.05). Interestingly, the distribution of strains according to the

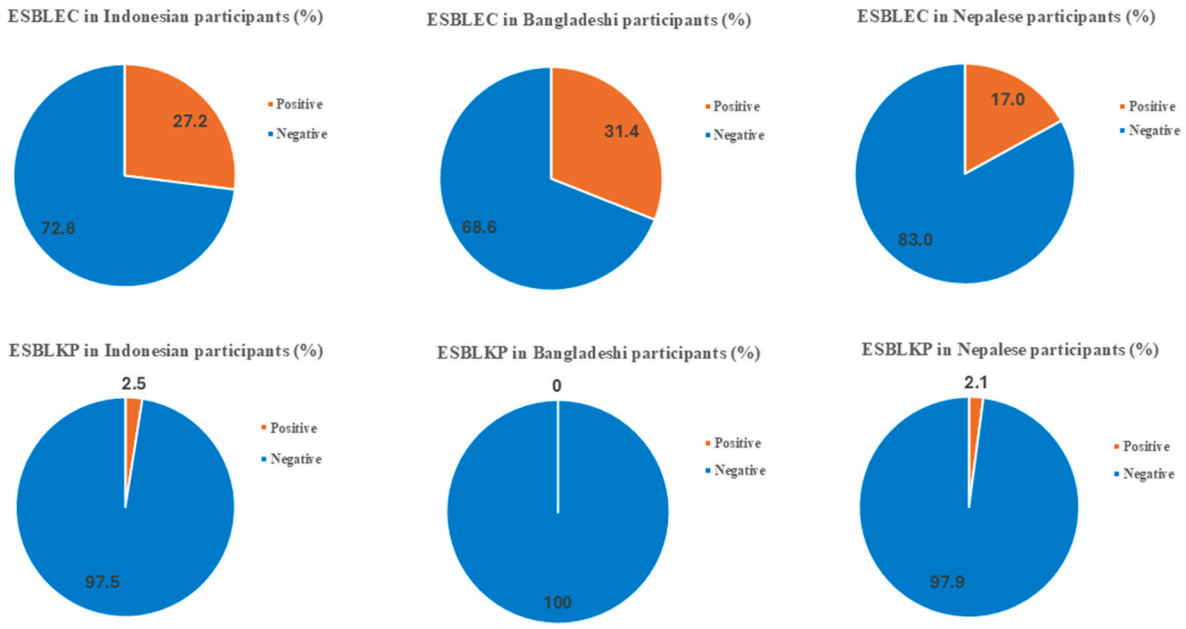

Fig. 1. Carriage of ESBLEC and ESBLKP according to migrant nationalities.

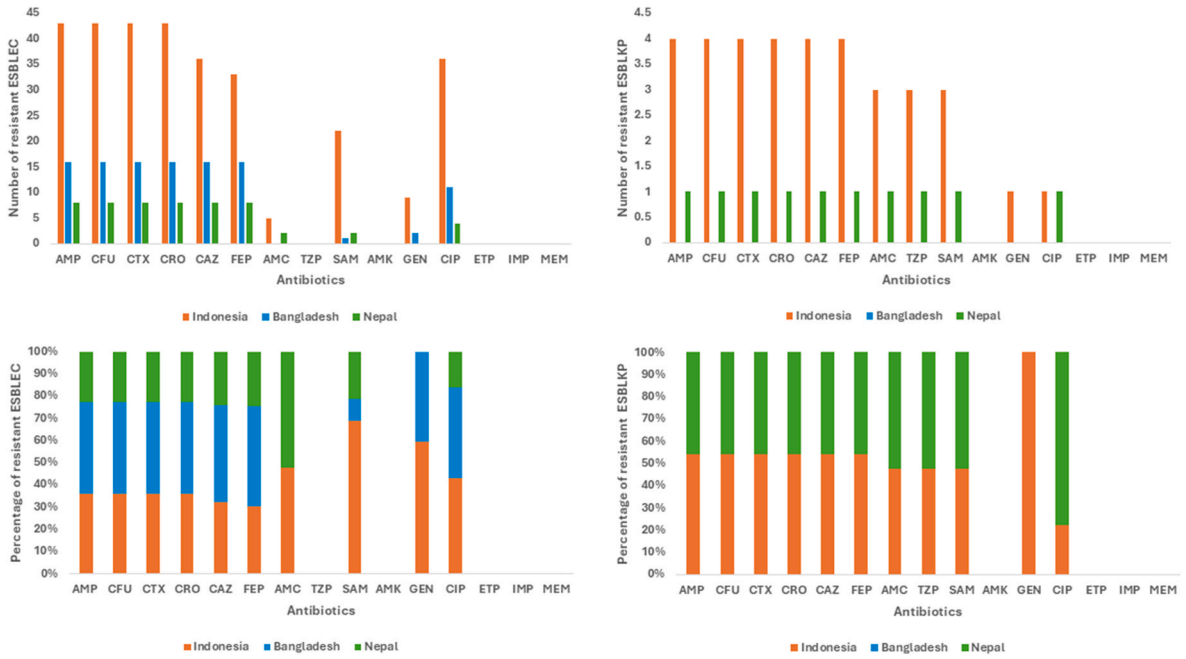

Fig. 2. a) ESBLEC strains resistant to tested antibiotics; b) ESBLKP strains resistant to tested antibiotics; c) Distribution of ESBLEC according to antibiotic resistance; d) Distribution of ESBLKP according to antibiotic resistance.

migrants' nationality appeared to be similar for AMP and cephalosporin resistance. However, resistance to FEP and SAM was significantly different between strains from Indonesian and Bangladeshi migrants ($p < 0.05$). Notably, more strains from Indonesian migrants were resistant to SAM, GEN, and CIP (Fig. 2(c) and (d)) but these differences were not significant.

4. Discussion

Antibiotics play a crucial role in the management of bacterial infections. However, antibiotic misuse and limitations in access to clean water and sanitation have driven the spread of AMR, especially in lower-income countries (LICs). Economic hardship and lack of opportunities in their home countries have persuaded residents of LICs commonly involved in economic migration, to seek greener pastures abroad. This has been more prominent in recent years with increased geopolitical instability coupled with easy access to transportation across geographical regions [5].

In this study, we set out to determine the silent carriage of ESBLEC and ESBLKP in Indonesian, Bangladeshi, and Nepali economic migrant workers residing in Klang Valley, Malaysia. In our cohort of participants, we observed an interesting gender demarcation in the economic activities they participated in. Most Indonesian participants were females and worked as domestic helpers; Bangladeshis were predominantly males who were evenly distributed between the construction and manufacturing sectors while Nepali migrants, mainly males, were

Table 2
ESBL genotyping for ESBLEC and ESBLKP strains.

	ESBLEC, n(%)			ESBLKP, n(%)		
	Indonesian (n = 43)	Bangladeshi (n = 16)	Nepali (n = 8)	Indonesian (n = 4)	Bangladeshi (n = 0)	Nepali (n = 1)
ESBL gene						
bla_{TEM}	22 (51.2)	2 (12.5)	3 (37.5)	4 (100)	0 (0)	1 (100)
$bla_{CTX\text{-}M\text{-}1}$	39 (90.7)	14 (87.5)	8 (100)	4 (100)	0 (0)	1 (100)
$bla_{CTX\text{-}M\text{-}9}$	3 (7)	2 (12.5)	0 (0)	0 (0)	0 (0)	0 (0)
bla_{SHV}	0 (0)	0 (0)	0 (0)	4 (100)	0 (0)	1 (100)
$bla_{OXA\text{-}1}$	12 (27.9)	1 (6.3)	2 (25.0)	0 (0)	0 (0)	0 (0)
ESBL profile						
$bla_{TEM} + bla_{CTX\text{-}M\text{-}1}$	11 (25.6)	1 (6.3)	2 (25.0)	0 (0)	0 (0)	0 (0)
$bla_{TEM} + bla_{CTX\text{-}M\text{-}9}$	2 (4.7)	1 (6.3)	0 (0)	0	0 (0)	0 (0)
$bla_{CTX\text{-}M\text{-}1} + bla_{OXA\text{-}1}$	5 (11.6)	1 (6.3)	1 (12.5)	0	0 (0)	0 (0)
$bla_{CTX\text{-}M\text{-}9} + bla_{OXA\text{-}1}$	1 (2.3)	0 (0)	0 (0)	0	0 (0)	0 (0)
$bla_{TEM} + bla_{CTX\text{-}M\text{-}1} + bla_{OXA\text{-}1}$	6 (14)	0 (0)	1 (12.5)	0 (0)	0 (0)	0 (0)
$bla_{TEM} + bla_{CTX\text{-}M\text{-}1} + bla_{SHV}$	0 (0)	0 (0)	0 (0)	4(100)	0 (0)	1 (100)
bla_{TEM}	1 (2.3)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
$bla_{CTX\text{-}M\text{-}1}$	17 (39.5)	12 (75.0)	4 (50.0)	0 (0)	0 (0)	0 (0)
$bla_{CTX\text{-}M\text{-}9}$	0 (0)	1 (6.3)	0 (0)	0 (0)	0 (0)	0 (0)
bla_{SHV}	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
$bla_{OXA\text{-}1}$	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)

involved in manufacturing. This might be due to the Medan Agreement of 1984, which sought to streamline Indonesian labour recruitment for Malaysia. Sulistyowati (2011) [18] noted that Indonesians were drawn to low-wage jobs in domestic work, agriculture, construction, and services, which were less appealing to local Malaysians. On the other hand, the 2015 Government-to-Government program between Malaysia and Bangladesh expanded worker participation in manufacturing, plantations, and construction, which were more suitable for males [19]. For Nepalese workers, the Malaysian Migrant Workers Policy of 1992 and a bilateral agreement in 2019 focused on meeting the demand in the manufacturing sector [20]. Migrant workers are often engaged in jobs requiring economic interaction, such as domestic work and the food and beverage industry that may introduce ESBL-producing pathogen transmission risks; however, their social interactions outside of work may be more limited due to workplace confinement and societal barriers. For most of the participants, Malaysia was their first and only foreign work experience destination with many having lived for a considerable length of time in the country.

Asymptomatic global cumulative (2003–2018) pooled prevalence of ESBLEC carriage has been reported to be 16.5 %, with the highest rate in South-East Asia (27 %; 95 % CI 2.9 %–51.3 %) [21]. ESBLKP carriage prevalence is generally lower than that of ESBLEC [22] which mirrors the trend in our study, where we observed a higher prevalence of community ESBLEC. We could not compare the antibiotic susceptibility profiles of our strains with the ones from Malaysians as, to our knowledge, there are currently no published reports of ESBL carriage amongst Malaysians, making direct comparisons challenging. Nonetheless, we found that the strains from this study generally retain susceptibility towards non-cephalosporin antibiotics, except for Indonesian ESBLECs, which were mostly resistant to SAM, GEN, and CIP. These three antibiotics are first-line antibiotics prescribed in general practitioner clinics, where these clinics are the most common access to healthcare services for the migrant population in Malaysia [23]. As the antibiotic selection pressure is higher in hospitals compared to the community, ESBL strains isolated from asymptomatic carriers are typically susceptible to more antibiotics [24].

The significant differences in resistance to FEP and SAM between strains from Indonesian and Bangladeshi migrants ($p < 0.05$) likely reflect differences in antibiotic usage patterns and stewardship practices in their countries of origin. In Indonesia, the implementation of pre-approval policies has reduced the use of restricted broad-spectrum antibiotics and increased reliance on narrow-spectrum agents like SAM—potentially explaining the observation of more strains being resistant to SAM [25]. Conversely, Bangladesh has experienced a sharp increase in overall antibiotic consumption, particularly third-generation cephalosporins such as CTX, which accounted for over 33 % of national antibiotic use. This overuse of broad-spectrum agents is associated with the rise of ESBLs [26] and may underlie more FEP resistance seen in Bangladeshi strains. Additionally, prescribing behaviours influenced by physician experience, local guidelines, and healthcare setting can vary significantly, even within the same country. These factors likely contribute to intra- and inter-country variability in resistance patterns [27].

Genes that code for ESBLs are diverse and grouped into several families [28], where the more common ESBLs in ESBLECs and ESBLKPs are from the TEM, SHV, and CTX-M families. We identified $bla_{CTX\text{-}M\text{-}1}$ as the most prevalent ESBL gene among our strains, a finding that aligns with previous studies in Malaysia [29], Indonesia [30], Bangladesh [31], and Nepal [32]. This gene family contains the highest number of variants [33] and has successfully achieved global dissemination since first described in 1986 [34]. Indeed, the “globalization” of CTX-M enzymes is documented by the detection of these genes even in food, animals, and the environment. Human migration has been postulated to have contributed to the dissemination of $bla_{CTX\text{-}M}$ genes.

High prevalence of ESBL carriers among migrant communities in Malaysia could pose significant challenges to public health and the economy. ESBL infections are strongly associated with preceding carriage [35]. Treating ESBL infections often requires carbapenems that will further drive antibiotic selection pressure in patients and the environment. In addition, ESBL-carrying patients require longer hospital stays [36] and will strain healthcare budgets, especially for migrant workers lacking comprehensive insurance. The spread of ESBL-producing bacteria among migrants contributes to community-wide AMR, increasing the burden on public health resources and necessitating costly interventions like screening and preventive measures [37]. ESBL carriage and infection may affect the recruitment and retention of migrant workers, potentially leading to labour shortages and higher recruitment costs. Limited access to healthcare exacerbates health issues related to ESBL carriage, perpetuating a cycle of poor health and economic disadvantage among lower-income migrant workers [14].

Importantly, beyond human transmission, ESBL carriage affects animal and environmental health. While surveillance of ESBL-producing pathogens is well-established in humans - especially for hospital-associated cases, the importance of One Health ESBL surveillance has begun to gain traction [38]. Environmental sources, particularly surface water, have emerged as key reservoirs of resistant bacteria, with *E. coli* carrying genes such as bla_{TEM} commonly detected [39], alongside

significant levels of antibiotic residues [40]. While long-term migration has been identified as a driver of global AMR dissemination [41], short term travellers to high-prevalence regions can return as carriers [42], exacerbating the spread of ESBL-producing pathogens. In recent years, hotter, wetter climate compounded the dissemination of these pathogens across geographical regions [43]. Altogether, these factors collectively underscore the need for integrated, cross-sectoral strategies to effectively monitor the spread of the ESBL pandemic [44].

Long-term management of ESBL infections may require significant investments in healthcare infrastructure, impacting national budgets and economic planning. Addressing these issues requires a multi-faceted approach that includes improving healthcare access for migrant workers, investing in preventive measures, and promoting effective antibiotic stewardship. These strategies are crucial for mitigating both the health and economic impacts of ESBL infections. In the context of Malaysia, integrating ESBL screening into the Mandatory Notification of Communicable Diseases under Section (2) of the Prevention and Control of Infectious Diseases Act 1988 would enable systematic monitoring and more effective public health interventions. Additionally, developing educational materials in migrants' native language on AMR awareness and responsible antibiotic use could help promote prudent antimicrobial consumption. These measures would support early detection, reduce transmission, and improve AMR management in our migrant communities.

This study has several limitations. The small sample size may limit the generalizability of the findings, as no prior studies exist for reference. Consequently, the study may be underpowered - though the data can inform future sample size calculations. Selection bias was also a concern, as only three migrant communities - Indonesian, Bangladeshi, and Nepali - were included. Additionally, geographical bias was present, as data collection was limited to the Klang Valley. Consent bias might have further influenced the results, as undocumented migrants or those hesitant to participate may have been underrepresented. To address biases, several measures were taken to enhance the representativeness of the study. Recruitment was not restricted to a single occupational sector, and collaboration with NGOs improved outreach.

This study also lacked an assessment of the acceptance or acceptability of rectal swabbing among the migrant communities. While all participants provided informed consent, we did not formally evaluate their perceptions, comfort levels, or cultural sensitivities regarding the sampling procedure. Furthermore, in terms of inclusion criteria, our study did not include any temporal parameters, which may have introduced potential bias into the results. Antibiotic usage and hospitalization history was also not traceable to any individual to preserve study participant anonymity. Future investigations could implement anonymized coding systems to track trends while preserving privacy, incorporating temporal inclusion criteria may help reduce bias, and a post-sampling questionnaire could be used to assess participant acceptance and the overall acceptability of the sampling process.

5. Conclusion

There is a high prevalence of ESBL silent carriage in our migrant community residing in Klang Valley, Malaysia. Given the rising incidence of ESBLEC and ESBLKP in the country, along with the increasing number of migrant workers, our study highlights the urgent need for screening programs for ESBL-producing bacteria in this population. Currently, data on such screens are lacking, making our findings particularly valuable for understanding and addressing the high prevalence of ESBL carriage in our migrant community.

CRediT authorship contribution statement

Muhammad Azreen Mat Husin: Writing – original draft, Validation, Software, Resources, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Adrian Anthony Peirera:** Writing – review & editing. **Thana Seelan:** Writing – review & editing. **Ramliza Ramli:** Writing – review & editing, Supervision. **Ilana Lopes Baratella da Cunha Camargo:** Writing – review & editing, Supervision. **Sheila Nathan:** Writing – review & editing. **Hui-min Neoh:** Writing – original draft, Validation, Supervision, Software, Resources, Project administration, Methodology, Investigation, Funding acquisition, Formal analysis, Data curation, Conceptualization.

Informed consent statement

Informed consent was obtained from all subjects involved in the study.

Institutional review board statement

Ethics approval for the study was granted by the Universiti Kebangsaan Malaysia Research Ethics Committee (UKM PPI/111/8/JEP-2023-201).

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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