

## **Antibiogram and MDR Pattern of the Bacterial Isolates from German Cockroaches (*Blattella germanica* L.) at RMCH, Rajshahi, Bangladesh**

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Received 1 November 2022, accepted in final revised form 13 December 2022

### **Abstract**

German cockroaches, *Blattella germanica* L. are the most dangerous pests in hospital environments which cause diseases like food poisoning, dysentery, and diarrhea. Antibiogram and multidrug resistance (MDR) patterns of the bacterial isolates from the cockroaches inhabiting three Wards of Rajshahi Medical College Hospital, Rajshahi, Bangladesh, were determined. A total of 52 bacterial isolates, 26 from the cuticle and 26 from the gut, comprising 20 (38.5 %) from the Neuromedicine ward, 18 (34.6 %) from the Orthopaedic ward, and 14 (26.9 %) from the Surgery ward, were used for biochemical assays and diagnostic characteristics, where seven Gram-negative rod species were identified. *E. coli* (n=8 or 40 %), *Klebsiella* spp. (n=5 or 28 %) and *Klebsiella* spp. (5 or 35 %) constituted the most dominant bacteria from the three wards respectively. Antibiogram of the bacterial isolates against 18 commonly used antibiotics revealed that *Serratia*, *Klebsiella*, *Escherichia*, and *Pseudomonas* were resistant to Cefazidime, whereas *Salmonella*, *Enterobacter*, and *Proteus* were sensitive to the drug. Results of the present study suggest that the German cockroaches might serve as reservoirs for pathogenic and MDR bacteria, which in turn could be responsible for the spread of common food-borne diseases in hospital patients, their attendants, and health professionals.

**Keywords:** Antibiogram; Multidrug resistance (MDR); German cockroaches; Gram-negative; Pathogenic bacteria.

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doi: <http://dx.doi.org/10.3329/jsr.v15i2.62557> J. Sci. Res. **15** (2), 559-570 (2023)

### **1. Introduction**

Cockroaches are one of the most well-known pests of household, commercial, and healthcare establishments, as they not only contaminate food by shedding droppings and germs that can cause food poisoning, but they also spread bacteria, fungi, and other harmful microbes in infested regions [1]. They are reported to carry a wide range of bacterial species that they pick up from the environment in which they inhabit, and they can be found in nearly all human dwellings, particularly in areas where food is stored, processed, cooked, or served [2]. The German cockroach (*Blattella germanica* L.) and the

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American cockroach (*Periplaneta americana* L.) are the most significant and objectionable pests found in hospitals and healthcare facilities, apartments, homes, and food-handling establishments worldwide [3]. They usually come in close contact with human beings and are carriers of human pathogenic bacteria on the external areas of their bodies or in their digestive tracts [4]. Gram-negative bacteria in the cuticle and gut of three cockroaches, including *B. germanica* has been reported earlier in Bangladesh and other countries [5-8].

The emergence and spread of multidrug-resistant (MDR) bacteria at an increased rate in recent years is of public health concern [9]. Hospital cockroaches can play a significant role in the dissemination of such bacteria between the environment and human beings. MDR bacteria such as *E. coli*, *Pseudomonas* sp., and *Klebsiella* sp. were found in cockroaches collected from hospitals and homes in Malaysia [10]. From the external body surface and alimentary tract homogenates, bacterial genera including *Klebsiella*, *Enterobacter*, *Pseudomonas*, *Salmonella*, *Staphylococcus*, *Escherichia*, and *Shigella* were isolated and identified in Ethiopia [11], where MDR was seen in all the bacterial species. The prevalence of *Staphylococcus aureus* in *P. americana* collected from restaurants and households in Chittagong City, Bangladesh [12], and the prevalence of *Salmonella* spp. and their MDR profile among the street food items in Chittagong urban areas [13] have been reported. Vector characteristics and MDR bacteria found in *B. germanica* from hospitals, food restaurants, and residential areas of Dhaka City have been investigated [14]. In Ethiopia, however, food-borne illness was found to be associated with five bacterial species from the gut of cockroaches [15]. Recently, antibiotic resistance properties and distribution of virulence factors in the pathogenic bacteria isolated from hospital cockroaches have been reported in Iran [16,17], Saudi Arabia [18], and Spain [19].

Despite the abundance of cockroaches in and around Rajshahi City Corporation areas, there is little information about their role as mechanical transmitters of Gram-negative bacteria. There have been few studies on the carriage of MDR and pathogenic bacteria by *B. germanica* in hospitals, restaurants, and other city areas. Therefore, the principal aim of the present investigation was to: (1) isolate bacteria from the cuticle and alimentary tract of the sampled cockroaches from three randomly chosen wards of Rajshahi Medical College Hospital (RMCH) at Rajshahi, Bangladesh; (b) identify them using morphological, Gram-staining and biochemical techniques; and (c) determine antibiogram profile and MDR pattern of the bacterial isolates in response to 18 commonly used antibiotics in the study area. The findings of this investigation would help assess the role of pathogenic and MDR bacteria inhabiting the experimental cockroaches that pose a potential threat to hospital patients, their attendants, and the health professionals in the study area, as well as similar habitats in the country.

## **2. Materials and Methods**

### **2.1. Test insects**

Neuromedicine Ward (NMW), Orthopaedic Ward (ORW), and Surgery Ward (SRW) of the Rajshahi Medical College Hospital (RMCH) at Rajshahi, Bangladesh, were chosen at random for the collection of experimental cockroaches (Fig. 1a). The sources of the test insects were food cabinets, cupboards, and washrooms of the aforesaid wards. Of about 50 adult cockroaches of both sexes caught by hand picking with surgical gloves and kept in sterile screw-capped 250 ml jars, five intact and live cockroaches were chosen at random from each of the wards. Immediately after collection, the sampled insects were transported to the Genetics and Molecular Biology Laboratory, Department of Zoology, University of Rajshahi, for identification and microbiological analyses. The cockroaches were first killed using chloroform-soaked cotton in a sterile jar and then identified using a standard taxonomic key [20]. The dead cockroaches were then placed individually in sterile test tubes for microbiological investigations [14,21]. The experiments were conducted from July 2021 to December 2021.

### ***2.2. Isolation and characterization of the microbes from the samples***

The external body surface of the cockroaches was washed for two minutes with a 0.5% physiological saline solution (9.0 g/L NaCl; Saloride®, Beximco Pharmaceuticals Ltd., Bangladesh), and the wash was considered as an external body homogenate. After cleaning, the cockroaches were first immersed in 70 % ethanol for five minutes to disinfect, then in the sterile saline solution again to remove any signs of ethanol. Using a dissecting microscope, an alimentary tract of the cockroaches was dissected out aseptically with sterilized dissecting needles. In between dissections, the instrument was soaked in ethanol and flamed. The excised intestine was homogenized in 5 ml sterile saline solution following the procedures described earlier [14,22].

A total of 52 homogenates, originating from 26 external body surfaces and 26 alimentary tract washes, were numbered from M1 to M52 and processed for further analysis. The homogenates comprised 20 bacterial isolates from NMW, 18 from ORW, and 14 from SRW. About 10 µL loop full of each homogenate was cultured onto eosin methylene blue (EMB), MacConkey (MAC), and xylose lysine deoxycholate (XLD) agar media using the spread plate technique and then incubated at 37 °C for 24 h. These provided presumptive identification of the bacterial species by their size, color, form, margin, and elevation characteristics (Table 1). Isolated colonies were sub cultured on nutrient agar media to obtain pure cultures. The characteristics of the isolated colonies were recorded after observing bacterial growth on all plates.

### ***2.3. Microscopic examination and identification of bacterial isolates***

For the identification of the bacteria, microscopic observations (Fig. 1b-f) followed by morphological and growth characteristics coupled with biochemical and carbohydrate tests (Fig. 1g) were performed. The bacterial species were identified according to *Bergey's Manual of Systematic Bacteriology* [23].

#### **2.4. Determination of antibiogram profile and MDR pattern**

The antibiotics, manufactured by the reputed pharmaceutical companies, were procured from the Model Medicine Market, Laxmipur, Rajshahi, and the following concentrations were employed: Amoxicillin (AMO, 30 µg/disc), Amoxiclav (AMC, 30 µg/disc), Ampicillin (AMP, 10 µg/disc), Azithromycin (AZM, 15 µg/disc), Cefixime (CEF, 10 µg/disc), Ceftazidime (CEZ, 30 µg/disc), Cephadrine (CED, 30 µg/disc), Ciprofloxacin (CIP, 5 µg/disc), Doxycycline (DOX, 30 µg/disc), Erythromycin (ERY, 15 µg/disc), Gentamicin (GEN, 10 µg/disc), Kanamycin (KAN, 30 µg/disc), Levofloxacin (LEV, 5 µg/disc), Nalidixic acid (NAL, 30 µg/disc), Neomycin (NEO, 30 µg/disc), Penicillin (PEN, 10 µg/disc), Rifampicin (RIF, 5 µg/disc) and Tetracycline (TET, 30 µg/disc). The antibiogram profile of the bacterial isolates against the above-mentioned 18 commonly used antibiotics was determined *in vitro* (Fig. 1h) employing the standard disk diffusion method [21,24], and the MDR pattern of the isolates was interpreted using the manufacturer's guidelines, where disc distances of 5-9 mm were considered resistant (R), 10-14 mm intermediate (I) and  $\geq 15$  mm sensitive (S).

### **3. Results and Discussion**

#### **3.1. Cultivation, identification, and isolation of the bacteria**

Gram-negative bacteria respond to EMB, a modestly selective stain; MAC is a selective and differential culture medium used to isolate enteric Gram-negative bacteria, whereas XLD is a selective growth medium used to isolate certain pathogenic microbes from clinical and food samples. Here, the identity of the bacterial isolates was further confirmed by Gram staining and biochemical and carbohydrate tests (Table 2). Thus, seven Gram-negative bacteria species belonging to *Escherichia*, *Klebsiella*, *Serratia*, *Salmonella*, *Pseudomonas*, *Enterobacter*, and *Proteus* were identified, colony characteristics of which were as follows: *E. coli* produced a distinctive metallic green sheen whereas *Klebsiella* species produced an off-white color on the EMB agar medium. On the MAC agar medium, on the other hand, *E. coli*, *Klebsiella*, and *Enterobacter* species grew pink while *Serratia marcescens* produced red; *Pseudomonas* and *Proteus* species produced off-white, but *Salmonella* species produced pale pink color colonies. In the XLD medium, *E. coli* colonies were yellow in color, and *Klebsiella* colonies grew pink.

Table 1. Colony characteristics of bacterial isolates from *B. germanica* grown on solidified agar media (n=52; RMCH, Bangladesh).

Isolate numbers (Wards)	Size	Colour	Form	Margin	Elevation	Presumptive identification
<b>EMB agar medium (n=13)</b>						
M28, M29, M30, M31, M32 (NMW); M46 (ORW); M8, M9, M10, M11, M12 (SRW)	Small	Metallic green	Regular	Entire	Raised	<i>Escherichia coli</i>
M48, M50 (ORW)	Small	Off white	Regular	Entire	Raised	<i>Klebsiella</i> spp.
<b>MacConkey agar medium (n=33)</b>						
M15, M16, M17, M18 (NMW); M35, M36 (ORW); M1, M2, M3, M4 (SRW)	Medium	Red	Regular	Entire	Raised	<i>Serratia marcescens</i>
M19, M20 (NMW); M37 (ORW) M5, M6 (SRW)	Small	Pink	Regular	Entire	Raised	<i>Klebsiella</i> spp.
M22 (NMW); M38, M39 (ORW); M7 (SRW)	Large	Off white	Irregular	Serrated	Raised	<i>Pseudomonas</i> spp.
M23, M24 (NMW); M40, M41 (ORW)	Small	Pink	Regular	Entire	Raised	<i>Escherichia coli</i>
M21, M25 (NMW); M42, M43, M44 (ORW)	Large	Pale pink	Regular	Entire	Raised	<i>Salmonella</i> spp.
M26 (NMW); M45 (ORW)	Small	Pink	Regular	Entire	Raised	<i>Enterobacter</i> spp.
M27 (NMW); M47, M51 (ORW)	Large	Off white	Irregular	Serrated	Raised	<i>Proteus</i> spp.
<b>XLD agar medium (n=6)</b>						
M33 (NMW); M49 (ORW); M13 (SRW)	Medium	Yellow	Regular	Entire	Raised	<i>Escherichia coli</i>
M34 (NMW); M52 (ORW); M14 (SRW)	Medium	Pink	Regular	Entire	Raised	<i>Klebsiella</i> spp.

NMW= Neuromedicine Ward; ORW= Orthopaedic Ward; SRW= Surgery Ward; Isolated bacteria were presumptively identified by biochemical tests (Table 2); RMCH= Rajshahi Medical College Hospital.

### 3.2. Prevalence of the bacterial isolates

Hospital ward-wise distribution of bacterial isolates showed that 20 (38 %) came from NMW, 18 (35 %) from ORW, and the remaining 14 (27 %) from SRW, where the predominant *E. coli* comprised 30.8 % followed by *Klebsiella* (25 %), *Serratia marcescens* (19%), *Salmonella* (9.6 %), *Pseudomonas* (7.7 %), and the least prevalent 3.8% each for *Enterobacter* and *Proteus* species (Table 3). The cuticle and gut components of the bacterial isolates revealed a similar trend where *E. coli* was the predominant species, composed of 35 % external body surface and 27 % alimentary tract, while *Enterobacter* and *Proteus* were the least common bacteria, both of which comprised 4 % of the isolates (Table 4).

Table 2. Growth response on three agar media, Gram staining, biochemical and carbohydrate tests of the bacterial isolates from *B. germanica* (n=52; RMCH, Bangladesh).

Hospital wards and Isolate numbers	Growth on			Biochemical tests							Carbohydrate tests				Presumptive identification	
	EMB agar	MAC agar	XLD agar	Gram stain	Motility	H <sub>2</sub> S	Indole	Citrate	Catalase	Oxidase	KOH	Glucose	Fructose	Galactose		Lactose
Neuromedicine Ward (n=20)																
M15, M16	-	+	-	-	+	-	+	+	+	+	+	+	-	-	+	<i>Serratia marcescens</i>
M17, M18, M19, M34	+	+	-	-	+	-	-	+	+	-	+	+	+	+	+	<i>Klebsiella</i> spp.
M21	-	+	-	-	+	-	-	-	+	-	-	+	+	+	+	<i>Pseudomonas</i> spp.
M22, M23, M29, M30, M31, M32, M33	+	+	+	-	+	-	+	+	+	-	+	+	+	+	+	<i>Escherichia coli</i>
M20, M24	-	+	-	-	-	-	-	+	+	-	+	+	+	+	-	<i>Salmonella</i> spp.
M25, M27, M28,	-	+	-	-	+	-	+	+	+	+	+	-	-	-	+	<i>Enterobacter</i> spp.
M26	-	+	-	-	+	-	-	+	+	-	+	+	+	+	+	<i>Proteus</i> spp.
Orthopaedic Ward (n=18)																
M35, M36	-	+	-	-	+	-	+	+	+	+	+	+	-	-	+	<i>Serratia marcescens</i>
M37, M48, M49, M50, M52	+	+	-	-	+	-	-	+	+	-	+	+	+	+	+	<i>Klebsiella</i> spp.
M38, M39	-	+	-	-	+	-	-	-	+	-	-	+	+	+	+	<i>Pseudomonas</i> spp.
M40, M41, M47, M51	+	+	+	-	+	-	+	+	+	-	+	+	+	+	+	<i>Escherichia coli</i>
M42, M43, M44	-	+	-	-	-	-	-	+	+	-	+	+	+	+	-	<i>Salmonella</i> spp.
M45, M46	-	+	-	-	+	-	+	+	+	+	+	-	-	-	+	<i>Enterobacter</i> spp.
Surgery, Ward (n=14)																
M1, M2, M3, M4	-	+	-	-	+	-	+	+	+	+	+	+	-	-	+	<i>Serratia marcescens</i>
M5, M6, M10, M11, M14	+	+	-	-	+	-	-	+	+	-	+	+	+	+	+	<i>Klebsiella</i> spp.
M7	-	+	-	-	+	-	-	-	+	-	-	+	+	+	+	<i>Pseudomonas</i> spp.
M8, M9, M12, M13	+	+	+	-	+	-	+	+	+	-	+	+	+	+	+	<i>Escherichia coli</i>

EMB= Eosin methylene blue; MAC= MacConkey; XLD= Xylose lysine deoxycholate; + = bacterial growth, - = no bacterial growth; RMCH= Rajshahi Medical College Hospital.

### 3.3. Antibiogram profiles and MDR pattern of the bacterial isolates

Results on the antibiogram profile and MDR patterns of the bacterial isolates from *B. germanica* against 18 commonly used antibiotics are presented in Tables 5 and 6, respectively. *Escherichia*, *Salmonella*, *Enterobacter*, and *Proteus* species each were resistant to half of the antibiotics tested (9 or 50 %), whereas *Klebsiella*, *Serratia*

*marcescens*, and *Pseudomonas* species were resistant to the majority of the antibiotics (10 or 55.6 %). Eight out of 18 antibiotics, viz., Amoxicillin (AMO), Amoxiclav (AMC), Ampicillin (AMP), Cefixime (CEF), Cephadrine (CED), Erythromycin (ERY), Penicillin (PEN) and Rifampicin (RIF), were 100 % resistant to all seven bacterial isolates under study. Thus, the overall MDR pattern of the bacterial isolates revealed 52.3 % resistance, 42.1 % sensitivity, and 5.6 % intermediate response toward the tested antibiotics.

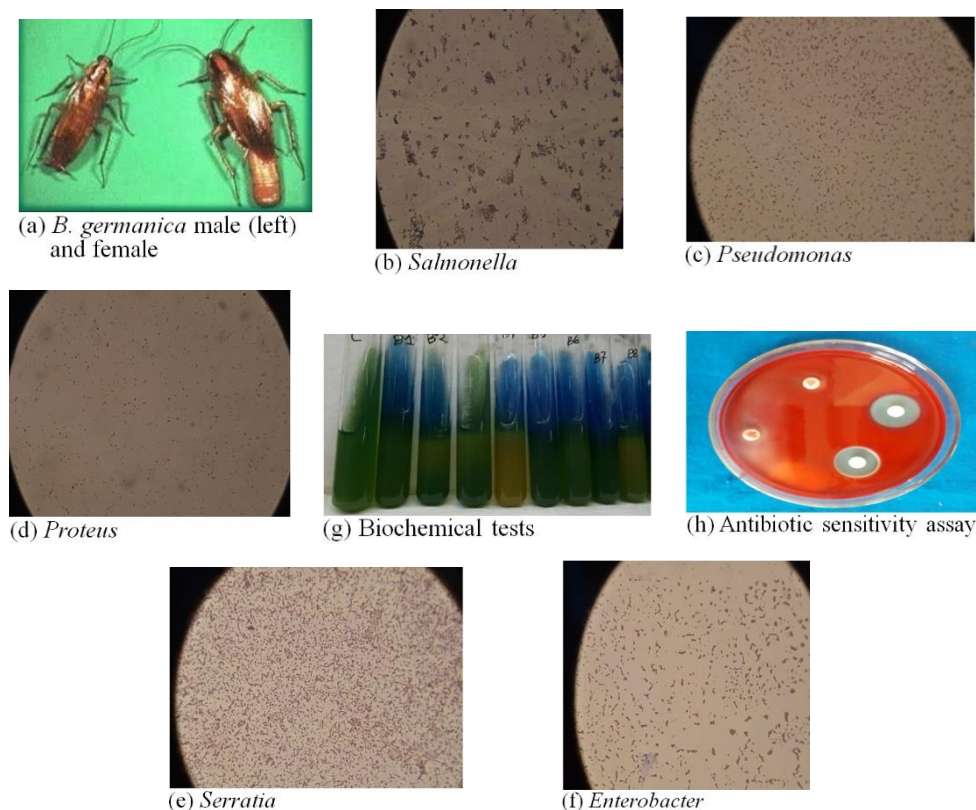


Fig. 1. (a) Experimental insects, (b-f) Bacterial species, (g) Biochemical tests; (h) Antibiotic sensitivity assay.

Table 3. Distribution of bacterial isolates from *B. germanica* collected from three hospital wards (n=52; RMCH, Bangladesh)

Bacterial species	NMW	ORW	SRW	Total
<i>Escherichia coli</i>	8 (50%)	4 (25%)	4 (25%)	16 (30.8%)
<i>Klebsiella</i> spp.	3 (23.1%)	5 (38.5%)	5 (38.5%)	13 (25%)
<i>Serratia marcescens</i>	4 (40%)	2 (20%)	4 (40%)	10 (19%)
<i>Salmonella</i> spp.	2 (40%)	3 (60%)	-	5 (9.6%)
<i>Pseudomonas</i> spp.	1 (33.3%)	2 (50%)	1 (33.3%)	4 (7.7%)
<i>Enterobacter</i> spp.	1 (50%)	1 (50%)	-	2 (3.8%)
<i>Proteus</i> spp.	1 (50%)	1 (50%)	-	2 (3.8%)
Total (%)	20 (38%)	18 (35%)	14 (27%)	52 (100%)

NMW=Neuromedicine ward; ORW=Orthopaedic ward; SRW=Surgery ward; RMCH=Rajshahi Medical College Hospital.

Table 4. Distribution of bacterial isolates from the external body surface and alimentary tract of *B. germanica* (n=52; RMCH, Bangladesh).

Bacterial species	No. bacterial isolates		Total
	External body surface	Alimentary tract	
<i>Escherichia coli</i>	9 (35 %)	7 (27 %)	16
<i>Klebsiella</i> spp.	6 (23 %)	7 (26 %)	13
<i>Serratia marcescens</i>	4 (15 %)	6 (23 %)	10
<i>Salmonella</i> spp.	3 (11 %)	2 (8 %)	5
<i>Pseudomonas</i> spp.	2 (8 %)	2 (8 %)	4
<i>Enterobacter</i> spp.	1 (4 %)	1 (4 %)	2
<i>Proteus</i> spp.	1 (4 %)	1 (4 %)	2
Total (%)	26 (50 %)	26 (50 %)	52 (100 %)

RMCH= Rajshahi Medical College Hospital.

Isolates M15, M17, M22, M26, M38, M43, and M45 were chosen at random for the bacterial species of *Serratia*, *Klebsiella*, *Escherichia*, *Proteus*, *Pseudomonas*, *Salmonella*, and *Enterobacter*, respectively; R= Resistant to antibiotics ((disc distances 5-9 mm)); I= Intermediate responses (10-14 mm); S= Sensitive to antibiotics (15-20 mm); RMCH = Rajshahi Medical College Hospital.

Table 5. Antibiotic susceptibility patterns of the bacterial isolates from *B. germanica* (n=7; RMCH, Bangladesh).

Antibiotics used	<i>E. coli</i>	<i>Klebsiella</i> spp.	<i>Serratia marcescens</i>	<i>Salmonella</i> spp.	<i>Pseudomonas</i> spp.	<i>Enterobacter</i> spp.	<i>Proteus</i> spp.
Amoxycillin (30 µg)	R	R	R	R	R	R	R
Amoxyclave (30 µg)	R	R	R	R	R	R	R
Ampicillin (10 µg)	R	R	R	R	R	R	R
Azithromycin (15 µg)	I	R	I	R	R	S	R
Cefixime (10 µg)	R	R	R	R	R	R	R
Ceftazidime (30 µg)	R	R	R	S	R	S	S
Cephadrine (30 µg)	R	R	R	R	R	R	R
Ciprofloxacin (5 µg)	S	S	S	S	S	S	S
Doxycycline (30 µg)	S	S	S	S	S	S	S
Erythromycin (15 µg)	R	R	R	R	R	R	R
Gentamicin (10 µg)	S	S	S	S	S	S	S
Kanamycin (30 µg)	I	I	S	S	S	S	I
Levofloxacin (5 µg)	S	S	S	S	S	S	S
Nalidixic acid (30 µg)	S	S	S	S	S	R	S
Neomycin (30 µg)	S	S	S	S	S	S	S
Penicillin (10 µg)	R	R	R	R	R	R	R
Rifampicin (5 µg)	R	R	R	R	R	R	R
Tetracycline (30 µg)	S	I	R	S	S	I	S

Table 6. Antibiotic susceptibility pattern of the bacterial isolates from *B. germanica* against 18 commonly used antibiotics (n= 52, RMCH, Bangladesh).

Bacterial species	Antibiotic sensitive n (%)	Antibiotic intermediate n (%)	Antibiotic-resistant n (%)	No. Antibiotic discs tested	No. Bacterial isolates n (%)
<i>Escherichia coli</i>	7 (38.9)	2 (11.1)	9 (50.0)	18	16 (100.0)
<i>Klebsiella</i> spp.	6 (33.3)	2 (11.1)	10 (55.6)	18	13 (100.0)
<i>Serratia marcescens</i>	7 (38.9)	1 (5.5)	10 (55.6)	18	10 (100.0)
<i>Salmonella</i> spp.	9 (50.0)	0 (0.0)	9 (50.0)	18	5 (100.0)
<i>Pseudomonas</i> spp.	8 (44.4)	0 (0.0)	10 (55.6)	18	4 (100.0)
<i>Enterobacter</i> spp.	8 (44.4)	1 (5.6)	9 (50.0)	18	2 (100.0)



<i>Proteus</i> spp.	8 (44.4)	1 (5.6)	9 (50.0)	18	2 (100.0)
Total	53	7	66	126	52
Percentage	42.1	5.6	52.3	100.0	100.0
Range (min-max)	33.3-50.0	0.0-11.1	50.0-55.6	-	-

RMCH = Rajshahi Medical College Hospital.

Cockroaches are common in hospital environments because they latter provide optimum temperatures, humidity, and convenient food sources. According to a previous study, 98 % of cockroaches found in medical facilities had illnesses in their integuments or digestive systems [25]. Cockroaches provide a source of harmful germs in medical settings [26,27] because they are the major carriers of causative agents from all families of viral, bacterial, protozoan, and helminthic infections [22,28]. Moreover, these insects can transmit disease factors in addition to complying with the human environment [1]. A total of 32 bacteria, including *Salmonella* and *Shigella*, 15 species of fungi and molds, 7 intestinal helminth parasites, two protozoans, and a virus, were isolated from cockroaches and their feces [29,30].

It has been hypothesized that the microbial gut flora of cockroaches living in polluted environments produces substances to thwart bacterial infections [31]. Here we report seven Gram-negative bacteria species belonging to *Escherichia*, *Klebsiella*, *Serratia*, *Salmonella*, *Pseudomonas*, *Enterobacter*, and *Proteus* from the cuticle and gastrointestinal tract of the sampled *B. germanica*. Antibiogram profiles of the bacterial isolates suggest that all of them belong to MDR strains. The presence of these bacteria in hospital wards indicated that they could constitute a major health risk to humans and associated animals like cats and rodents because urinary tract, biliary tract and peritoneal infections, wound infections, sepsis, gastroenteritis, and pneumonia are all possible illnesses caused by these microbes [32,33].

Similar to the present results, cockroaches from hospitals in Iran were found to carry *E. coli*, *Enterobacter*, *Klebsiella*, *Pseudomonas*, *Salmonella*, and *Shigella*, which were resistant to a number of antibiotics [34]. The present bacteria genera on the cuticle and gut of *B. germanica* are similar to those found in earlier studies of cockroaches in India [35], Bangladesh [14], and Nigeria [36]. Recently, it has been reviewed in Germany that cockroaches can disseminate potentially pathogenic bacteria *via* feces and other deposits in places like hospitals and kitchens [37]. To the best of our knowledge, however, this is the first prevalence report of *Serratia marcescens*, a Gram-negative rod, in the gut of *B. germanica* from Bangladesh.

Antibiotics are used to assess their effectiveness against pathogenic bacteria [38]. It is conceivable that bacterial species associated with hospital cockroaches are prone to develop resistance to commonly used antibiotics in the study area. Of 18 antibiotics used in this study, only six, *viz.*, CIP, DOX, GEN, LEV, NAL, and NEO, were sensitive to the bacterial isolates. So, the majority of the bacteria were resistant to about 67% of the antibiotics used. Similar antibiotic resistance to the bacteria associated with cockroaches has been reported by previous studies [6,14,36,39,40]. The current data suggest that German cockroaches might pose a serious health threat to communities surrounding the

study area, as the isolated bacterial strains were found to be resistant to a variety of antibiotics.

MDR is a critical public health issue, as decreasing antibiotic effectiveness leads to higher patient mortality, longer hospital stays, and higher healthcare expenses [41]. It is one of the most pressing issues confronting global public health today. The situation is particularly serious in developing countries, as bacterial infections that cause human diseases are also those where antibiotic resistance is most visible. A limited number of studies on MDR bacteria carried by cockroaches exist, and most of them focused mainly on resistant or opportunistic diseases. In hospitals and other urban environments, antibiotic-resistant human diseases were shown to be carried by cockroaches and houseflies [28,30,42,43], suggesting that the insect gut may potentially function as a mixing ground for MDR bacterial genes [44].

Cockroaches and houseflies might act as vectors that disseminate MDR to humans *via* direct contact, human food contamination, and horizontal gene transfer [45]. A couple of very recent reports from Iran [17] and Spain [19] showed the importance of *B. germanica* as reservoirs and transmission vectors for MDR pathogens because they form the main threat to global health nowadays, and annually, a lot of patients die in hospitals due to infections with MDR bacteria, especially *Staphylococcus aureus* [18]. So, the irrational use of antibiotics needs to be banned and/or restricted in both human and animal medicine prescriptions to prevent the emergence of MDR bacterial species in the community. Moreover, potential factors associated with cockroaches that contributed to this high MDR of the isolates deserve further investigation.

#### **4. Conclusion**

*B. germanica* seen in hospital areas might be linked to the spread of MDR pathogenic bacteria, thus potentially increasing the risk of human infections. It is therefore recommended that appropriate measures be made to control *B. germanica* and other cockroach species and monitor the sensitivity pattern of infections transmitted by them. The possibility of eradicating cockroaches from patient care units should also be considered. The current results indicate that *B. germanica* may constitute a health danger to communities living near cockroach populations. In order to control cockroaches and other vector insects, effective preventive and control measures, in addition to good environmental practices and procedures, must be employed to reduce vector-borne diseases in men in the hospital and healthcare facilities in the study area.

#### **Acknowledgments**

The work was partly funded by a research grant from the Faculty of Biological Sciences, RU, to MKM.

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