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## Detection of multidrug-resistant *Enterobacterales* isolated from buffalo species

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### Abstract

The study was conducted to investigate the detection of multidrug-resistant *Enterobacterales* isolated in buffalo species during the period of August, 2019 to January, 2020 at the Department of Veterinary Pathology, LUVAS, Hisar. For bacteriological isolation, the samples were collected aseptically from the heart blood, liver, and mesenteric lymph nodes of buffalo species suspected of gastrointestinal tract disorders. The bacterial species were identified through the *Vitek-2* Compact system. Out of 31 Gram negative bacteria, a total 17 different bacterial species were identified. Most of the bacterial species showed multiple drug resistance patterns.

**Keywords:** Buffalo, multidrug, *Enterobacterales*, bacteriological, and vitek-2

### Introduction

Multidrug-resistant *Enterobacterales* (MDRE) are a major cause of hospital-acquired infections associated with high morbidity and mortality, as well as rising the cost of healthcare (Vrancianu *et al.*, 2021) [1]. In several species of *Enterobacteriaceae*, there is an increase in antimicrobial resistance (Karlowsky *et al.*, 2003) [2]. The generic *E. coli*, which is commonly found in raw meat, has the capability to transfer antibiotic resistance to other bacteria residing in the intestine (Dunowska *et al.*, 2006) [3]. Kim *et al.* (2005) [4] reported that enteric bacteria develop resistance to common antibiotics used in human and veterinary medicine, like tetracycline, gentamicin, kanamycin, and streptomycin. In *Enterobacteriaceae*, the *E. coli* serotype (O157:H7) and *Salmonella* caused most of the foodborne illness and were often transmitted through raw meats (Kennedy *et al.*, 2005) [5]. Cogan *et al.* (1999) [6] reported that *Salmonella* could potentially spread on kitchen surfaces during the preparation of the contaminated poultry. The spread of antibiotic-resistant foodborne pathogens threatens the successful treatment of infectious diseases (Andersson, 2003) [7].

### Materials and Methods

The present investigation was undertaken on 38 buffalo carcasses (17 adult buffalo and 21 buffalo calves) suspected of gastrointestinal tract disorders that were brought to the Department of Veterinary Pathology, LUVAS, Hisar for post-mortem during the period of six months (from August, 2019 to January, 2020). The study included the detection of multidrug resistant *Enterobacterales* identified in buffalo carcasses. The isolated microorganisms were subjected to in-vitro antibiotic sensitivity testing using antibiotic discs with appropriate conc. (Table 1) by the single disc diffusion technique (Bauer *et al.*, 1966) [8]. The results were then interpreted on the basis of the inhibition zone as per the manufacturer's recommendations (Hi-Media, India). The bacterial isolates showing resistance to more than three antibiotic groups or combinations were placed in the MDR category (Oteo *et al.*, 2005) [9].

### Results

The results of *in vitro* antibiotic sensitivity are depicted in Table 2. The results revealed that *E. coli* showed maximum resistance to cephalosporin/ $\beta$ -lactamase inhibitors, monobactams,

polymyxins (polymyxin-B), penicillin+ $\beta$ -lactamase inhibitors, followed by fluoroquinolone and aminoglycosides (Table 2). Likewise, the *Salmonella spp.* was found to be most resistant to cephalosporin/ $\beta$ -lactamase inhibitors (except cefepime), monobactams, aminoglycosides (except streptomycin), and penicillin+ $\beta$ -lactamase inhibitors. *Serratia plymuthica* was found to be 100% resistant to cephalosporin/ $\beta$ -lactamase inhibitors, monobactams, and fluoroquinolone, followed by penicillin+ $\beta$ -lactamase inhibitors, but no resistance to polymyxins and aminoglycosides. *Proteus mirabilis*, *Ochrobactrum anthropi*, and *Gardnerella vaginalis* were found to be resistant to most of the antibiotics except aminoglycosides. Polymyxins also showed no resistance against *Proteus mirabilis*. In the case of *Sphingomonas paucimobilis*, which was found to be most resistant to monobactams and the fluoroquinolone group of antibiotics, it showed no resistance to other groups of antibiotics. Likewise, *Stenotrophomonas multophila*, *Pseudomonas mendocina*, and *Pseudomonas aeruginosa* were showed no resistant to most of the antibiotics except monobactams, which showed 100% resistance against *Stenotrophomonas multophila* and were 50% resistant to polymyxins and fluoroquinolone. *Pseudomonas mendocina* was found to be 33.3% resistant to the monobactam group of antibiotics. The multidrug resistance (MDR) pattern of *Escherichia coli* and other *Enterobacterales* was depicted in Tables 3 and 4, which revealed that all isolates of *E. coli*, *Ochrobactrum anthropi*, *Gardnerella vaginalis*, *Proteus mirabilis*, and *Serratia plymuthica* showed MDR patterns, but other *Enterobacterales* did not show any multidrug resistance (MDR) patterns.

### Discussion

The current study was conducted for detection of multi-drug resistant *Enterobacterales* identified in buffalo carcasses (38) including adult and calves. The results revealed that *E. coli* showed maximum resistance to cephalosporin/ $\beta$ -lactamase inhibitors, monobactams, polymyxins (polymyxin-B), penicillin+ $\beta$ -lactamase inhibitors, followed by fluoroquinolone and aminoglycosides. In support of our study, Londhe (2010) [10] also reported the resistance of *E. coli* to cephalosporin but in contrast to our study, Londhe (2010) [10] and Lehreana (2008) [11] reported the sensitivity of *E. coli* to polymyxins and cephalosporin/ $\beta$ -lactamase inhibitors, respectively. More or less similar findings were reported by Dinesh *et al.* (2018) [12] regarding the resistance of *E. coli* to penicillin+ $\beta$ -lactamase inhibitors and aminoglycosides, but in contrast to our study, they found that *E. coli* showed sensitivity towards fluoroquinolone. Brennan *et al.* (2016) [13], in their study in bovine, found that one isolate of *E. coli* was resistant to the  $\beta$ -lactamase and fluoroquinolone groups of antibiotics. The results showed that, *Salmonella spp.* was found to be most resistant to cephalosporin/ $\beta$ -lactamase inhibitors (except cefepime), monobactams, aminoglycosides (except streptomycin), and penicillin+ $\beta$ -lactamase inhibitors. More or less similar results regarding the susceptibility of *Salmonella spp.* were reported by Sushma *et al.* (2016) [14]. The study of sensitivity pattern in *Serratia plymuthica* showed that, it was found to be 100% resistant to cephalosporin/ $\beta$ -lactamase inhibitors, monobactams, and fluoroquinolone, followed by penicillin+ $\beta$ -lactamase inhibitors, but no resistance to polymyxins and aminoglycosides. Likewise, *Proteus*

*mirabilis*, *Ochrobactrum anthropi*, and *Gardnerella vaginalis* were found to be resistant to most of the antibiotics except aminoglycosides. Polymyxins also showed no resistance against *Proteus mirabilis*. Similar findings were reported by Londhe (2010) [10] regarding the susceptibility of *Proteus spp.* to antibiotics. In the case of *Sphingomonas paucimobilis*, which was found to be most resistant to monobactams and the fluoroquinolone group of antibiotics, it showed no resistance to other groups of antibiotics. But in contrast to our study, Cengiz *et al.* (2015) [15] reported the greatest resistance of *Sphingomonas paucimobilis* to gentamicin. In the current study, *Stenotrophomonas multophila*, *Pseudomonas mendocina*, and *Pseudomonas aeruginosa* were showed no resistant to most of the antibiotics except monobactams, which showed 100% resistance against *Stenotrophomonas multophila* and were 50% resistant to polymyxins and fluoroquinolone. *Pseudomonas mendocina* was found to be 33.3% resistant to the monobactam group of antibiotics. The study of multidrug resistance (MDR) pattern of *Escherichia coli* and other *Enterobacterales* revealed that all isolates of *E. coli*, *Ochrobactrum anthropi*, *Gardnerella vaginalis*, *Proteus mirabilis*, and *Serratia plymuthica* showed MDR patterns, but other *Enterobacterales* did not show any multidrug resistance (MDR) patterns. More or less similar results were reported by Shrestha *et al.* (2017) [16] regarding the MDR pattern of total isolated bacterial species.

### Conclusion

In the present study, 61.29% of the of the bacterial isolates exhibit the MDR pattern and are mostly resistant to cephalosporin+ $\beta$ -lactamase inhibitors, monobactams, penicillin+ $\beta$ -lactamase inhibitors, fluoroquinolone, and aminoglycosides. At present, regulation on the misuse of antibiotics should be necessary.

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