Prevalence and antimicrobial resistance of *Bacillus cereus* isolated from beef products in Egypt

Rejad Shawish1 and Reda Tarabees2,*

1Department of Food Hygiene and Control, Faculty of Veterinary Medicine, University of Sadat City, Sadat City, Egypt
2Department of Bacteriology, Mycology and Immunology, Faculty of Veterinary Medicine, University of Sadat City, Sadat City, Egypt

Abstract

Foodborne pathogens have the main concern in public health and food safety. *Bacillus cereus* food poisoning is one of the most important foodborne pathogens worldwide. In the present study, a total of 200 random beef product samples were collected from different supermarkets located at Menofia and Cairo governorates were examined for the presence of *B. cereus*. In addition, the presence of some virulence encoding genes was evaluated using Multiplex PCR. Finally, the antibiogram testing was conveyed to illustrate the resistance pattern of the confirmed *B. cereus*. The data showed that *B. cereus* was recovered from 22.5%, 30%, 25%, 37.5% and 15% of the minced meat, burger, sausage, kofta, and luncheon respectively. Among the 20 examined isolates 18/20 (90%) were hemolytic. The isolated strains of *B. cereus* were resistant to penicillin G and sensitive to oxacillin, clindamycin, vancomycin, erythromycin, gentamicin, ciprofloxacin, and ceftriaxone. In all, the obtained data showed the importance of emerging *B. cereus* in disease control and prevention programs, and in regular clinical and food quality control laboratories in Egypt.

**Keywords:** Antimicrobial susceptibility, *Bacillus cereus*, Beef products, Multiplex PCR, Virulence genes.

Introduction

Processed beef products such as minced meat, kofta, sausage, burger, and luncheon are gaining common popularity as easily quick prepared meat meals that can solve the problem of the high price fresh meat shortage which is not within the reach of large numbers of low-income families. The contamination of these beef products with the foodborne pathogens is still the main worry for public health, amongst contamination with *B. cereus* is one of the most important foodborne pathogens causing food poisoning among the food consumers all-inclusive.

*B. cereus* is an aerobic spore-forming Gram-positive bacterium normally disseminated in the environment. It is usually isolated from the soil, plant materials, raw meat and processed meat products (Carlin F et al., 2010; Ceuppens et al., 2013). Schedule identification of *B. cereus* is generally comprised isolation on selective media, revealing of motility, hemolysis prototype on blood agar, and acidification of glucose (Stenfors Arnesen et al., 2008).

Although *B. cereus* is implicated in many foodborne illness outbreaks in many countries worldwide, however only a few cases are reported because the symptoms are mostly similar to *Staphylococcus aureus* and *Clostridium perfringens* food poisoning (Stenfors Arnesen et al., 2008; Bottone, 2010; Bennett et al., 2013). *B. cereus* has been incriminated as a cause of two types of food poisoning, emetic and diarrheal syndromes (Drobniewski, 1993).

The pathogenesis of *B. cereus*-induced food poisoning is mostly still indistinct. The microorganism conveys an expansive number of potentially toxic components, including hemolysins, phospholipases, and proteases (Drobniewski, 1993; Beecher, 2001) nevertheless, the precise role of some is still ambiguous. The emetic and the diarrheal syndromes are still the foremost worries for the public health apprehension and the full appreciative of their pathogenesis is imperative. These syndromes are mainly manifested via the release of two core toxins, a heat-labile diarrheal enterotoxin, and heat-stable emetic enterotoxin (Stenfors Arnesen et al., 2008).

The diarrheal syndrome manifested via the release of one or three diarrheal enterotoxins: the tripartite toxins hemolysin BL (HBL) and non-hemolytic enterotoxin (Nhe), the two forms of cytotoxin K (cytK-1 and cytK-2) and possibly enterotoxin T and enterotoxin FM (Moravek et al., 2006). HBL, a three-components toxin, that is encoded by hblD and hblC genes respectively, and a binding component B encoded by hblA gene. The presence of all three components is necessary for the toxin activity (Lindback and Granum, 2006).

*Corresponding Author:* Reda Tarabees. Department of Food Hygiene and Control, Faculty of Veterinary Medicine, University of Sadat City, Sadat City, Egypt. Email: reda.tarabees@vet.usc.edu.eg
The deceptive of *B. cereus* induced food poisoning symptoms and the lack of the clear-cut surveillance statistics in Egypt. This makes the indulgent of the pathogenesis of *B. cereus* food poisoning confusing. Therefore, the current study was undertaken to estimate the incidence of toxigenic *B. cereus* in some beef products collected at the retail level in Egypt using PCR. Additionally, the antibiotic resistance pattern of 20 *B. cereus* isolates was assessed using disc infusion method.

**Material and Methods**

**Sampling**
A total of 200 beef product samples (40 each of minced meat, burger, sausage, kofta, and luncheon) were collected from different supermarkets located at Menofia and Cairo governorates and examined bacteriologically. The presence of toxigenic *B. cereus* was confirmed using PCR based on the presence of virulence encoding genes.

**Preparation of samples**

The collected samples were transferred instantly under full aseptic conditions for bacteriological isolation and identification of *B. cereus*. Briefly, 25 grams of each product were transferred to 225 ml of 0.1% sterile buffered peptone water (Oxoid, UK), then stomached for 2 minutes to provide a homogenate. The homogenate was heat-treated at 80°C for 10 minutes to kill all the vegetative bacteria and recover of the *Bacillus* spores (Rahimi et al., 2013). One ml of the original dilution transferred to a sterile tube containing 9 ml of sterile buffered peptone and incubated at 34°C for 24 hrs as a primary enrichment.

**Isolation and characterization of Bacillus cereus**

The bottles showed turbidity as an indication of *B. cereus* growth were streaked over a dry surface of *Bacillus cereus* selective agar medium (Oxoid, UK) by a bent glass rod and the plates were incubated at 30°C for 24-48 hrs. Suspected typical colonies were later picked up onto sheep blood agar (Oxoid, UK) and incubated at 34°C for 24 hrs to observe hemolysis (Tallent et al., 2012).

Typical colonies of *B. cereus* that showed β hemolysis were further identified based on the biochemical activities (Holbook and Anderson, 1980; Bottone, 2010; Tallent et al., 2012).

**Genotypic characterization of *B. cereus* enterotoxins genes hblC and cytK**

The multiplex PCR was carried out according to Ngamwongsatit et al. (2008). The PCR reactions containing 12.5 μl PCR Master Mix, 1 μl of each primer (0.4 μM hblC and 0.2 μM cytK as final concentration), of 5 μl of DNA templates and RNase-free water was added to a final volume of 25 μl. The PCR conditions were, 94 °C/ 5 min; 30 cycles of (94°C for 45 sec, annealing at 54-56°C for 1 min in case of hblC and at 58°C in case of cytK, elongation at 72°C for 2 min) followed by 72°C for 5 min, 94°C for 45 sec, annealing at 54 and 56°C for 1 min in case of hblC and at 58°C in case of cytK, elongation at 72°C for 2 min and final extension at 72°C for 5 min. The products of PCR were separated by electrophoresis on 1.5% agarose gel (AppliChem, Germany) to determine the fragment sizes. The nucleotides sequences of the primers are shown in the Table 1.

**Antimicrobial susceptibility test**

The antibiotic susceptibility testing was performed using the disc diffusion method (Chon et al., 2012). All the isolates were grown in brain heart infusion broth (Oxoid) for 18 hrs at 34°C and then spread on Mueller-Hinton agar (Oxoid, UK) and left for 15 minutes. Then, eight commercial antibiotic discs (Oxoid, UK) were used: penicillin (10 units), oxacillin (1.0 mg/ml) vancomycin (30 mg/ml), clindamycin (2.0 mg/ml), erythromycin (15 mg/ml), gentamicin (10 mg/ml), Ciprofloxacin (5μg) and Ceftriaxone (30 μg), and the plates were then incubated at 37°C for 18–24 hrs (Chon et al., 2012).

**Results**

**Prevalence of *B. cereus* in the examined beef products**

The data presented in Table 2 showed the prevalence rate of *B. cereus* in the examined beef products. Among the examined beef products, only 52 out of 200 (26%) were positive for *B. cereus*. The highest prevalence rate was recorded in case of beef kofta 15/40 (37.5%), while the lowest rate was in case of beef luncheon 6/40 (15%).

**Genotypic characterization of enterotoxigenic genes using Multiplex PCR**

The data obtained in Table 3 demonstrated the incidence rate of the hblC and cytK enterotoxigenic genes in the examined *B. cereus* isolates. Among the examined isolates, 18/20 (90%) were harbor hblC enterotoxin encoding gene compared with 20/20 (100%) were found to have cytK enterotoxin encoding gene and exhibited a specific band size (Fig. 1).

**Antibiotic sensitivity testing**

The data presented in Table 4 showed the antibiotic resistance pattern of the examined *B. cereus* isolates. A total of 51 isolates were tested for their antibiotic sensitivity prototype against 8 commercial antibiotic discs. The data demonstrated that all the isolates (51/51) were resistant to penicillin G (100%) and sensitive to other antibiotics 51/51 (100%).

**Discussion**

Contamination of meat products with toxigenic *B. cereus* is one of the underestimated foodborne illness worldwide (Ceuppens et al. 2013). In Egypt, there is no accurate surveillance data about the numbers of *B. cereus* induced food poisoning cases. The lack of accurate data may be because of the resemblance of the symptoms with the other foodborne pathogens (Normanno et al., 2007).
The data obtained in the Table 2 demonstrated that the highest incidence rate was recorded in beef kofta and the lowest was in the case of minced meat. This outcome is similar to that obtained by Mohamed and Ghanem (2015), and higher compared with that obtained by Heikal et al. (2006). Conversely, this result is lower than the result obtained by Eid et al. (2008). Processed ready to eat beef products are considered the main source of infection with *B. cereus* and more caution need to be taken in order to minimize the contamination of such products. The selection of fresh and clean flesh, decontamination of the mincing machine, grinders, equipment and knives used in the processing of such products will auspiciously decrease the incidence of *B. cereus* foodborne illness cases among the consumers (FDA, 2012; Torky, 1995, 2004). The higher incidence rate of the *B. cereus* in kofta and minced meat in comparison with luncheon can be explained as luncheon during the processing steps the product was subjected to a high temperature that significantly decreases the number of *Bacillus* spores (Torky, 1995).

Additionally, during the processing of minced meat and kofta, additives, seasoning, and spices were added, these additives are considered a potential risk factor can increase the number of *Bacillus* spores and hence magnitude the incidence of food poisoning. Therefore more consideration should be taken during processing of raw meat and kofta, and only use additives from a trustful source. Moreover, these additives should be regularly tested for the presence of *Bacillus* spores.

The contamination of beef products probably occurred during handling and preparation or post-processing contamination. In addition, keeping the products unrefrigerated for several hours enhances the multiplication of *B. cereus* and hence the liberation of enterotoxin. The study herein was aimed to estimate the accurate incidence rate of toxigenic *B. cereus* and its antibiotic susceptibility pattern in some beef products collected from different localities in Egypt. The data obtained will probably highlight the emergence of *B. cereus* as a serious underestimated cause of foodborne illness and will help in understanding its pathogenesis.

### Table 1. Primers nucleotides sequences used for multiplex PCR amplification of *B. cereus* entotoxins genes.

<table>
<thead>
<tr>
<th>Target gene</th>
<th>Primer</th>
<th>Size in bp</th>
<th>Primer sequence (5'→3')</th>
<th>T°C</th>
<th>Product size in bp</th>
<th>conc(µM)</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>hblC</em></td>
<td>FHblC</td>
<td>19</td>
<td>CCTATCAATACTCTCGCAA</td>
<td>54</td>
<td>695</td>
<td>0.4</td>
</tr>
<tr>
<td></td>
<td>RHblC</td>
<td>20</td>
<td>TTTCCTTGTGTATACGCTGC</td>
<td>56</td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>cytK</em></td>
<td>FCytK</td>
<td>20</td>
<td>CGAGTCACAAGTTGTAACA</td>
<td>58</td>
<td>565</td>
<td>0.2</td>
</tr>
<tr>
<td></td>
<td>R2CytK</td>
<td>20</td>
<td>CGTGTGTAAATACCCCAGTT</td>
<td>58</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

### Table 2. Prevalence rate of *B. cereus* in the examined beef products (40 of each).

<table>
<thead>
<tr>
<th>Beef products</th>
<th>Positive sample</th>
<th>Negative sample</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>No</td>
<td>%</td>
</tr>
<tr>
<td>Minced meat</td>
<td>9</td>
<td>22.5</td>
</tr>
<tr>
<td>Beef burger</td>
<td>12</td>
<td>30</td>
</tr>
<tr>
<td>Beef sausage</td>
<td>10</td>
<td>25</td>
</tr>
<tr>
<td>Beef kofta</td>
<td>15</td>
<td>37.5</td>
</tr>
<tr>
<td>Beef luncheon</td>
<td>6</td>
<td>15</td>
</tr>
<tr>
<td>Total</td>
<td>52</td>
<td>26.5</td>
</tr>
<tr>
<td>Minced meat</td>
<td>No</td>
<td>%</td>
</tr>
</tbody>
</table>

### Table 3. Molecular detection of enterotoxigenic genes of *B. cereus* isolated from examined samples.

<table>
<thead>
<tr>
<th>Target gene</th>
<th>No of examined isolate</th>
<th>Positive isolate</th>
<th>%</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>hblC</em></td>
<td>20</td>
<td>18</td>
<td>90</td>
</tr>
<tr>
<td><em>cytK</em></td>
<td>20</td>
<td>20</td>
<td>100</td>
</tr>
</tbody>
</table>

### Table 4. Antibiotics resistant of *B. cereus* isolated beef products (n=51).

<table>
<thead>
<tr>
<th>Antibiotic tested</th>
<th>Resistant</th>
<th>Intermediate</th>
<th>Sensitive</th>
</tr>
</thead>
<tbody>
<tr>
<td>Penicillin G</td>
<td>51(100.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
</tr>
<tr>
<td>Oxacillin</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>51(100.0)</td>
</tr>
<tr>
<td>Vancomycin</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>51(100.0)</td>
</tr>
<tr>
<td>Clindamycin</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>51(100.0)</td>
</tr>
<tr>
<td>Erythromycin</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>51(100.0)</td>
</tr>
<tr>
<td>Gentamicin</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>51(100.0)</td>
</tr>
<tr>
<td>Ciprofloxacin</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>51(100.0)</td>
</tr>
<tr>
<td>Ceftriazone</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>51(100.0)</td>
</tr>
</tbody>
</table>
Schedule examination of beef products for the presence of Bacillus spores is requisite. Isolation and identification of Bacillus using traditional methods (culturing on selective media and biochemical testing of the confirmed isolates) is still the key element for the confirmation of the infection. The severity of infection with Bacillus is conveyed via the liberation of an array of virulence encoding genes.

Multiplex PCR has emerged as the fast and reliable technique for the confirmation of enterotoxigenic B. cereus (Guinebretière et al., 2006; Ombui et al., 2008). Recently, Ngamwongsatit et al. (2008) have developed and evaluated a group of newly efficient primers used for detection of the genes encoding enterotoxin production in 100% of the tested B. cereus and B. thuringensis strains assuming that, the presence of either gene is an indication for the presence of the whole operon (Ngamwongsatit et al., 2008). In the current work, the existence of the enterotoxin-encoding genes hblC and cytK was assessed in 20 B. cereus isolates using specific primers sets that previously approved by Ngamwongsatit et al. (2008). The data presented in Table 3 and Figure 1 demonstrated that 18 isolates (90%) and 20 isolates (100%) were positive for hblC and cytK gene, respectively. This outcome is in accordance with that obtained previously obtained by Awny et al. (2010). Collectively, emerging of the multiplex PCR as a rapid technique for the affirmation of toxigenic B. cereus in food will probably command the pathogenesis of B. cereus induced-food poisoning in Egypt.

A total of 51 B. cereus isolates were further tested for their antimicrobial susceptibility (Table 4). All the tested isolates were resistant to penicillin G, whereas sensitive to oxacillin, clindamycin, vancomycin, erythromycin, gentamicin, ciprofloxacin, and ceftriaxone. The data obtained herein with the others (Fenselau et al., 2008; Organji et al., 2015; Jawad et al., 2016) showed that B. cereus has a broad range of antibiotic susceptibility and validate the resistance to penicillin G by comparing to susceptibility to clindamycin, vancomycin, and erythromycin.

**Conclusion**

From the obtained data, many conclusions could be drawn, contamination of beef products with B. cereus increase the potential of foodborne infections among the consumers. The cleanliness of the equipment, processing machines, knives, and only use additives from trustful sources are measures significantly will minimize the infection with Bacillus spores. Schedule antibiotic susceptibility testing of B. cereus isolates recovered from beef products will guide choosing the appropriate antibiotic. Also, the data authenticate the significance of counting B. cereus in disease control and prevention programs, and in regular clinical and food quality control laboratories in Egypt.

**Conflict of interest**

The authors declare that there is no conflict of interest.

**References**


Ceuppens, S., Boon, N. and Uyttendaele, M. 2013. Diversity of Bacillus cereus group strains is reflected in their broad range of pathogenicity and diverse ecological lifestyles. FEMS Microbiol. Ecol. 84(3), 433-450.


