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INVESTIGATION AND MOLECULAR CHARACTERIZATION OF SHIGA TOXIN- PRODUCING *E. COLI* O157:H7 FROM MEAT AND DAIRY PRODUCTS IN KIRKUK PROVINCE, IRAQ

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Abstract

Foodborne illnesses have significant repercussions for both society and the economy. Bloody diarrhea, hemorrhagic colitis (HC), and hemolytic uremic syndrome are all diseases that can be caused by Shiga-toxigenic *Escherichia coli* (STEC) (HUS). Consumption of contaminated foods, such as beef and dairy products, is responsible for the spread of the vast majority of infectious diseases in humans. It has been demonstrated that this bacterium can be isolated from a wide variety of foods and can be found in all regions of the world; however, the frequency with which it is discovered varies from one region to another depending on the type of food that is consumed and the techniques that are used to isolate it. This is because the frequency with which it is discovered depends on the kind of food consumed and the techniques used to isolate it. So this study aimed to identify the presence of *E. coli* O157:H7 in beef and cheeses commercially available in the Kirkuk Province of Iraq using various techniques.

A total of 73 food samples, consisting of 43 beef samples and 30 cheese samples, were gathered from various retail shops selling meat and dairy products in and around the city of Kirkuk. After mixing 25 g of each sample with 225 mL of sterile buffer solution and placing the resulting mixture in an incubator for two hours, the results were observed after plating equal aliquots of 1,000 mL onto MacConkey agar and eosin methylene blue (EMB) for a period of 48 hours at a temperature of 44.5 ^{0}C. The isolates were then tested so that the best guess could be made about whether it was Gram-negative enteric bacteria or *E. coli*. During the selective painting process, we used sorbitol MacConkey agar to look for sorbitol-non-fermenting bacteria. Isolates were characterized and determined by subjecting colonies suspected of STEC to a set of tests, and the diagnosis was eventually reached based on biochemical properties. Then we did the serological identification test on the latex slide test method. Finally, STEC molecular detection of *E. coli* O157:H7 isolates was performed by detection of a virulence factor of *E. coli* O157:H7 (stx1 (coding shiga toxin1), stx2 (coding shiga toxin2), eaeA (coding intimin), and hlyA (coding hemolysis) by polymerase chain reaction (PCR) method.

The results showed that due to the absence of fermentation of sorbitol, six samples out of a total of seventy-three samples were identified as having the potential for serotype E. coli O157:H7. The study also showed that (33.33 %) E. coli O157:H7 strains isolated from food samples have Stx1 gene and (33.33 %) of stains isolated from Food samples were have Stx2 gene, while both genes (eae and hly) appeared 100% in all (six) samples.

According to the results of this study, we can conclude that there is a higher risk of cross-contamination of foods in retail meat shops and dairy products because the prevalence of the pathogen is higher in animals. Because cattle serve as a reservoir host for EHEC O157:H7, the level of food contamination is significantly increased. The contents of the intestinal tract is dislodged while handling the carcass. This could lead to the contamination of other types of meat during the slaughtering process and other types of food, including vegetarian food, in the kitchen. This makes it abundantly clear that meat and cheeses must undergo the appropriate handling and processing levels. Precautions must be taken to prevent the spread of contamination from one area to another.

***Key words**: Shiga toxin E.coli, E. coli O157:H7, Foodborne disease, Virulence genes.*