summary

The present study was designed for isolation of *Bacillus cereus* and detection the prevalence of three types of toxin genes (*EM1,HB1,cerAB*) ,and then draw the phylogenetic tree by using restriction fragment length polymorphism(RFLP) method on (*cer AB*) gene .

The samples were collected from different source(stool, food, hospitals environments , clinical instruments) . A total of 200 samples during the period September 2012 to February 2013 were collected.

All samples were cultured on blood agar to observed the hemolysis, and submitted to cultural and biochemical tests. The results revealed that :100/200 (50%) of samples were gave positive growth for *Bacillus cereus* .as the following: 50(50%) from stool, 20 (66.66%)from food, 15(75%)from hospitals environments, 15 (30%) from clinical instruments.

The study revealed that *B. cereus* were the more common isolated pathogens from the total collected specimens as compared with other pathogens.

Forty isolates were submitted to molecular detection of *B. cereus* (*BC1*), and three types of it's toxin genes (*HB1,EM1,cerAB*) by using Polymerase chain reaction assay (PCR).

The result showed that 38 of 40 (95 %) of isolates which were tested by cultural and biochemical test have *BC1* gene, while (85%) of these isolates have *HB1* gene .The results revealed also that no isolates have *EM1* gene ,While *cerAB* gene were detected in 36 out of 40 isolates (90%) .

The restriction fragment length polymorphism for product of polymerase chain reaction RFLP of the *cerAB* gene was used to investing the genomic diversity for differential of 36 isolates from 40 of *B. cereus*.

The products of PCR were cutting with *Rsa*I endonucleases. The Results for 36 isolates revealed that isolates have 4-7 fragments. In combination, we could differentiate 6 different groups among 36 isolates analyses.