Summary

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The study was conducted during the period from January 2016 to May 2017. Clinical samples were collected from women suffering from miscarriage before 24 weeks of gestation,the samples were collected under specialized medical supervision.

The number of samples taken was 92 clinical samples from Babylon Teaching Hospital of Gynecology and Pediatrics and 83 clinical samples from Maternal and Children Hospital in Al- Qadisiyah provinice. Food samples were randomly collected from supermarkets in different areas of Babil and Qadisiyah governorates, which included 69 samples of cheese, 58 frozen red meat, 51 frozen chicken meat samples.

Listeria monoytogenes were isolated using a selective media *L. monocytogenes*, with the addition of a supplement that helps to grow *L. monocytogenes* and inhibit the growth of other types of bacteria. The isolates were identified using microscope and biochemical tests. The results showed that the isolation rate of *L. monoytogenes* was 13 (3.68%) of the total number of 353 isolates and 6 (3.42%) isolates out of 175 clinical samples and 7 (3.93%) isolates out of 178 food samples, In Babil province 3 (3.26%) isolation from the total of 92 samples and in Al-Qadisiyah province 3 (3.61%) of the total of 83 samples. 3 (4.35%) of total 69 samples of cheese, 2 (3.92%) of 51 chicken meat samples and 2 (3.44%) of 58 red meat samples were isolated.

The results of this study demonstrated that the most age group was exposed to *L. monoytogenes* infection (26-30), which represented 3 of total 6 (5.17%). The women were most infected with bacteria during the first three months (less than 12 weeks of gestational age) 5 of total 6 (5.15%) were the most infected patients of rural areas 4 of total 6(4.39%).

PCR technique was used to confirm the diagnosis of *L. monoytogenes* isolates by detecting the virulence genes (*hlyA, prfA, inlA, actA, plcA, iapA*), as the percentage of the appearance of these genes was 100% for all isolates of *L. monoytogenes*.

DNA sequencer technique and phylogenetic tree analysis were based on *hlyA* gene sequence clearly detection *L. monocytogenes*, could be the reliable option to indicate presence of *L. monocytogenes.* In the present study, we identified 5 isolates of *L. monocytogenes* from clinical and food samples based on hlyA gene sequence. Using MEGA 6 software, and UPGMA tree analysis (Unweighted Pair Group Method with Arithmetic Mean).

Our results demonstrate the relationship between the local isolates with the other Gene Bank isolates, and also showed a genetic affinity in the isolates of *L. monocytogenes* isolated from food samples compared to the clinical isolates. Also showed a higher probability of transition substitution mutation than transversion substitution mutation within the sequence of gene between local isolates and globally recognized isolates.