COMPARISON OF *Cronobacter sakazakii* DETECTION BY USING RAPID METHOD (PCR) WITH CLASSICAL CULTURAL METHOD IN INFANT FORMULA

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Cronobacter sakazakii which was reclassified in 2007, is an opportunist pathogenic bacteria belongs to Enterobacteriaceae family and causes meningitis, septicaemia and necrotic enterocolitis in new-borns and immunosuppressive babies. The bacteria can be isolated from various food and environmental samples. However, because of the several *Cronobacter sakazakii* endemics of babies, isolation from infant formulas prepared in new-born units of the hospitals, received a great scientific attention.

Cronobacter sakazakii was mostly isolated from dehydrated infant formula which are used for babies which cannot receive breast milk. The bacteria has a severe prognosis and several cases has resulted with death (mortality rate is 42%).

The main cause of high pathogen contamination risk in dehydrated formula is that, these products are not heat processed after hydrating and needs a significant care during preparation.

In our country 20% (approximately 1 million) of the 0 to 3 year old kids consume infant or advanced formula. This forces the research area to develop and validate sensitive and reliable methods for detection of *Cronobacter sakazakii*.

Although legal authorities generally rely on classical cultural methods, PCR is consider as an alternative method because of its high accuracy and sensitivity.

Making a decision for choosing an appropriate alternative method is based on the evaluation results of the verification/validation of the methods. For this, performance of an alternative method should be evaluated in reference to an international standard method.

The aim of our study was to verify the performance of the alternative rapid PCR method (BAX® System) with classical cultural method for detection of *Cronobacter sakazakii* in infant formula containing single and multiple competitive flora, in compliance with the requirements of ISO 16140. For this, infant formula samples were divided into two groups. The first group was spiked with *Cronobacter sakazakii* (ATCC 29544) and *E.coli* (ATCC 25922) to form a single competitive flora while the other group was spiked with (*Cronobacter sakazakii* (ATCC 29544), *E.coli* (ATCC 25922), *C.freundii* (ATCC 8090), *S.enteriditis* (ATCC 13076) and *S.epidermitidis* (ATCC 12228) to form a multiple competitive flora. The spiking of *Cronobacter sakazakii* was made in three different levels. The samples were then analyzed with two methods and validation parameters of LoD, false negative, false positive, relative specifity and sensitivity of the two method were calculated.