

## Evaluation of primer sequence targeting *invA* gene of *Salmonella* sp. by in silico PCR

### ABSTRACT

In silico PCR via algorithm and computer simulation aim to provide an easy way to analyse and obtain the theoretical PCR results we may expect from DNA, by using up to date bacterial genomes sequences. In this study, primer set *invA*-F and *invA*-R targeting *Salmonella* invasion gene, *invA*, was evaluated by in-silico PCR amplification against prokaryotic genome of major foodborne pathogens. A total of 127 strains of bacterial genome sequences from *Salmonella* sp.(27), *Escherichia* sp.(59), *Listeria* sp.(26) and *Campylobacter* sp.(15) were used as DNA templates in the PCR simulation analysis. The primer set simulatively amplified a single band of 285 bp PCR product with all 25 strains of *Salmonella enterica* subsp. *enterica*, whereas no amplification is produced with *Salmonella bongori* and *Salmonella enterica* subsp. *arizonae*. There was no cross-reaction obtained with other bacterial genomes indicated that the primer set is specific to *Salmonella enterica* subsp. *enterica* only. PCR experiments using *invA*-F and *invA*-R that was carried out in the laboratory had successfully amplified the 285 bp amplicons using DNA from *S. Typhimurium*, *S. Enteritidis*, *S. Polarum* and *S. Gallinarum*.

**Keyword:** In silico; Polymerase chain reaction; *InvA* *Salmonella*; Amplification