RESULTS

Identification of Campylobacter jejuni in a sample. The 16s rRNA POST PCR product was sequenced using DTCS Quick Start Kit. Sequencing fragments were purified by ethanol precipitation and sequenced using DTCS Quick Start Kit and GeXP System. After quality based trimming, the 18s rDNA sequence of the beverage contaminant and its alignment results in NCBI. The microbial contaminant was initially identified as an Escherichia coli - pathogenic sample was obtained from Takara, Japan. Genomic DNA was extracted by a quick spin in boiling water bath for 15 minutes. The microbial contaminant was then sequenced using DTCS Quick Start Kit and GeXP System. After quality based trimming, the 18s rDNA sequence was BLASTed against the 16s rRNA database at NCBI website. Alignment results (Figure 6) showed query sequence has high homology to pathogenic bacteria and non-pathogenic bacteria. The sample is known to be non-pathogenic, the sample is identified as an E. coli species.

Identification of E. coli in a sample. A non-pathogenic bacteria sample was obtained from Takara, Japan. Genomic DNA was extracted by a quick spin in boiling water bath for full length 16s rDNA was amplified and sequenced using DTCS Quick Start Kit and GeXP System. Consensus sequence was created in Gene Studio (Figure 7) and submitted to NCBI for BLAST search. Search results (Figure 8) showed the query sequence has high homology to pathogenic bacteria species. Since the sample is non-pathogenic, the sample was identified as an E. coli species.

CONCLUSIONS

• Sanger Sequencing is more specific and reliable than traditional microbial identification methods such as culture typing.

• Capillary Electrophoresis analysis of ribosomal RNA gene sequence on GenomeLab GeXP Genetic Analysis System is simple, fast and accurate.