Development of PCR-based methods for monitoring *Enterobacteriaceae* family members in food using the *gyrB* gene

Leite, A.M.O; Asensi, G.F.; Del Aguila, E.M., Silva, J.T. and Paschoalin, V.M.F.

Departamento de Bioquímica, Instituto de Química, Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brasil.

Enterobacteriaceae family members are of special microbiological interest because of their pathogenic and non-pathogenic relationships with the human gastrointestinal tract and warm-blooded animals. Some species are indicators of fecal contamination and also may be responsible for the occurrence of foodborne diseases. The analysis of bacterial community using molecular methods, such as PCR amplification of the 16S RNA gene in combination with denaturing gradient gel electrophoresis (DGGE), is commonly performed in microbial ecology. However, the comparison of genome sequence carried out previously indicated that the *gyrB* gene is more discriminative than 16S RNA in the classification of closely related species of bacteria. Two different primers were designed to amplify sequences from *gyrB* gene, only for a prevalent group of enteric bacteria, which might be useful to perform phylogenetic studies and to study of the bacterial communities in the food chain. The applicability and specificity of these primers were evaluated by performing PCRs using DNA templates obtained from 15 reference strains, among them 10 genera belonging to the *Enterobacteriaceae* family. As expected, amplicons of the predicted size were obtained for the target group, whereas, the reference strains, that are not members of that family, did not showed any amplification.

Supported by CNPq and FAPERJ.