Identification of *Listeria* species isolated in Tunisia by Microarray based assay: results of a preliminary study.

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Abstract:

Microarray-based assay is a new molecular approach for genetic screening and identification of microorganisms. We have developed a rapid microarray-based assay for the reliable detection and discrimination of *Listeria* spp. in food and clinical isolates from Tunisia. The method used in the present study is based on the PCR amplification of a virulence factor gene (*iap gene*). The PCR mixture contained cyanine Cy5-labeled dCTP. Therefore, the PCR products were fluorescently labeled.

The presence of multiple species-specific sequences within the *iap* gene enabled us to design different oligoprobes per species. The species-specific sequences of the *iap* gene used in this study were obtained from GenBank and then aligned for phylogenetic analysis in order to identify and retrieve the sequences of homologues of the amplified *iap* gene analyzed. 20 probes were used for detection and identification of 22 food isolates and clinical isolates of *Listeria* spp (*L. monocytogenes*, *L. ivanovi*), *L. innocua*, *L. welshimeri*, *L. seeligeri*, and *L. grayi*). Each bacterial gene was identified by hybridization to oligoprobes specific for each *Listeria* species and immobilized on a glass surface.

The microarray analysis showed that 5 clinical isolates and 2 food isolates were identified listeria monocytogenes. Concerning the remaining 15 food isolates; 13were identified listeria innocua and 2 isolates could not be identified by microarray based assay. Further phylogenetic and molecular analysis are required to design more species-specific probes for the identification of *Listeria* spp. Microarray-based assay is a simple and rapid method used for *Listeria* species discrimination.