A first molecular characterization of *Listeria monocytogenes* isolates circulating in humans from 2009 to 2014 in the Italian Veneto region

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**SUMMARY**

Listeriosis is a disease usually associated with the consumption of low-processed ready-to-eat food products contaminated by *Listeria monocytogenes*. In Italy, listeriosis has an incidence of 0.19-0.27 cases per 100000 persons. Since detailed information concerning the molecular characterization of listeriosis in the Italian Veneto region is currently lacking, we analyzed 36 *L. monocytogenes* clinical isolates collected between 2009 and 2014. Results show that the serotype 1/2a was the most represented among the tested samples. No antimicrobial resistance was detected in selected isolates representing the main pulsotypes.

**Key words:** *Listeria monocytogenes*, Listeriosis, Pulsed-field gel electrophoresis (PFGE), Genotyping, Antimicrobial resistance.

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the clinical cases. The most prevalent pulsotype clustered three isolates (samples 22, 24, 25-26) that were temporally and geographically related to the provinces of Treviso and Vicenza. It has also been shown that one pulsotype (samples 19 and 20) could be attributed to an event of maternal-foetal transmission, considering that the two samples were isolated from clinical samples collected in the same hospital from a mother and her newborn. This pulsotype was also detected in sample 15 collected nine months before from an elderly woman, but no relation was found with samples 19 and 20.

Finally, 18 isolates representative of the different pulsotypes were randomly selected and tested for their susceptibility to the following antimicrobials: ampicillin, linezolid, penicillin, ceftriaxone, erythromycin, cefotaxime, meropenem, levofloxacin, clindamycin, doxycycline, teicoplanin, daptomycin, trimethoprim/sulfamethoxazole, moxifloxacin, vancomycin, using the Sensititre ARIS® 2X system (Thermo Fisher Scientific) and following the European Committee on Antimicrobial Susceptibility Testing (EUCAST) breakpoints. All the selected Lm strains analyzed were susceptible to the tested antimicrobials; indeed, only a minority of clinical antibiotic-resistant Lm strains have been described in the literature so far (Camargo et al., 2017).

Overall, genotyping with PFGE did not show a particular relation between the collected isolates, suggesting multiple origins for Lm strains involved in infections that required admission to hospitals. Furthermore, antimicrobial resistance was not detected in the selected isolates representing the different pulsotypes. However, implementation of surveillance with molecular typing of Lm isolated from food and humans is needed for a rapid identification and control of outbreaks, and to trace the origin of infection. Furthermore, improvements to the genotyping approach, i.e. PFGE combined with other molecular techniques (e.g. multilocus sequence typing) could represent a strategy for an in-depth genetic characterization of Lm isolates.
Competing interests
The authors declare that there is no conflict of interest regarding the publication of this article.

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References


