

DL: Genomics

Antimicrobial resistance of *Listeria monocytogenes* human strains and correlation to genomic data

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Background:

Studies checking antimicrobial resistance (AMR) of *Listeria monocytogenes* (Lm) are ongoing, coupled with disease surveillance. Lm resistant strains are reported and are increasing. The aim of the work was to investigate AMR of clinical strains of Lm collected from nine regions (mostly in Lombardy and Marche regions) from 2008 to 2020.

Methods:

The dataset consisted of 233 Lm human strains collected from nine regions during the period 2008-2020. All the strains were tested using Sensititre™ Haemophilus Plate (Thermo Scientific, Milano, Italy). Results were expressed according to EUCAST breakpoints for Lm, *S. pneumoniae* and *E. faecalis*. Resistant strains were sequenced using Illumina platform, ABRicate was used to predict antimicrobial resistance genes and plasmids.

Results:

Most of the strains were detected in Lombardy and Marche. The MIC results showed that 11 out of 233 strains were resistant, one to ampicillin, four to tetracycline and six to clarithromycin. Analysing the sequences, all the resistant strains showed to have a common antimicrobial resistant pattern (mprF, norB, FosX, (MLS)lin, lin and lmo0919). Genomic determinants for ampicillin and clarithromycin resistance were not detected. Indeed, only in 3 out of 4 resistant strains tetM was found. Meanwhile, plasmids were detected in 7 strains.

Conclusions:

The distribution of the strains considered in this work did not reflect the real epidemiological situation in Italy, because their origin was mostly from two regions. The emergence of AMR also for Lm needs to be considered. Moreover, official breakpoints for Lm are not defined and to date limited to five antimicrobials excluding clarithromycin and tetracycline, where the pathogen showed resistance. Finally, the incongruence between phenotypic and genomic data suggests that the mechanisms involved in the resistance is not fully known especially for ampicillin. Further investigations are needed to improve the knowledge on Lm AMR.

Key messages:

- Monitoring AMR of *Listeria monocytogenes* is crucial, only effective drug in clinical cases should be used.
- Further investigations are needed to explore the mechanisms involved in antimicrobial resistance of *Listeria monocytogenes*.