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WHOLE GENOME SEQUENCING FOR SURVEILLANCE OF LISTERIA MONOCYTOGENES IN ITALY

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Aim: Molecular typing of foodborne pathogens represents an essential tool for epidemiological surveillance, outbreak detection and infectious diseases control. In this work, we performed molecular characterization, by Whole Genome Sequencing (WGS), of *Listeria monocytogenes* (L.m.) clinical strains isolated in Italy, in 2020.

Methods: Two hundred twenty four L. m. clinical strains, isolates in Italy in the framework of listeriosis surveillance, were collected. The sequencing was carried out on a IonTorrent S5 platform and the analysis performed automatically on the bioinformatics platform based on the ARIES analysis system and the IRIDA data collection platform, at Istituto Superiore di Sanità.

Results: The serogroups mainly associated with cases of listeriosis were IVb and IIa, followed by IIb. Most of the strains belonged to Lineage I, the remaining to Lineage II. Strains were divided into 34 Sequence Types (ST) / Clonal Complexes. Specifically, strains were mainly distributed among ST1, ST2 and ST5, all belonging to Lineage I. The phylogenetic analysis of the genomes allowed the identification of 19 clusters, most of which was composed of a number of strains ranging from 2 to 6. Two clusters, 4 and 90, were composed of 13 and 15 strains, respectively.

Conclusions: Molecular characterization of the 224 strains isolated in 2020, compared with the genomic sequences of all L. m. present in the database, since 2010, allowed to follow the dynamics of the circulation of the strains in Italy both timely, for the prompt identification of possible outbreaks, and retrospectively allowing to identify persistent outbreaks.