TITLE: MOLECULAR CHARACTERIZATION OF *LISTERIA MONOCYTOGENES* STRAINS ISOLATED FROM HUMAN AND FOOD SOURCES BY WHOLE GENOME SEQUENCING

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ABSTRACT:

Listeria monocytogenes causes listeriosis, a severe foodborne disease in high-risk groups as elderly, newborns and pregnant women in which case fatality is usually up to 20-30%. This pathogen represents a significant concern for food industry due its ability to survive and growth in diverse environment conditions (low temperature and high salt concentrations). Whole Genome Sequencing (WGS) analysis has emerged as an important methodology for the characterization of L. monocytogenes isolates regarding the presence of genes involved in virulence and the study of its genetic diversity. In this study, 21 L. monocytogenes isolates from serotype 4b (n=10), 1/2c (n=5), 1/2b (n=3), 1/2a (n=2) and 3b (n=1) were obtained from clinical samples (n=13) and ready-to-eat food (n=8) in Brazil and deposited in the Listeria Collection (Coleção de Listeria - CLIST) of Instituto Oswaldo Cruz/FIOCRUZ. In silico analysis was performed using tools built in the BIGSdb-Lm database of Institut Pasteur/France. Multi-locus sequence typing (MLST) identified 9 sequence types (ST) in which the most frequent were ST1 (n=5), ST3 (n=4) and ST9 (n=4). In addition, two new ST were described, ST1434 and ST1435 isolated from ricotta cheese and human blood, respectively. Sequence types most found in this study correspond to most common reported worldwide (ST1 and ST9), ST1 has been associated with hipervirulence and central nervous system (CNS) tropism and ST9 were strongly associated with food but not with clinical samples. Genomic islands LIPI-1, LIPI-3 and LIPI-4 were identified in all L. monocytogenes strains analyzed. LIPI-1 and LIPI-3 harbor genes involved with invasion and survivor inside the host cell, while LIPI-4 accounts for the hypervirulence and enhanced CNS and maternal-neonatal tropism. The Whole Genome Sequencing has been shown to be a powerful tool for characterization of the genomic elements of virulence and in the study of genetic diversity of L. monocytogenes isolates circulating in Brazil, contributing to the understanding of virulence and lineages better adapted to cause disease and to survive in food.

Keywords: Listeria monocytogenes, Virulence, Foodborne pathogen, WGS, Molecular typing.

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