

TITLE: GENOMIC ANALYSIS OF LISTERIA MONOCYTOGENES STRAINS ISOLATED FROM FOODS AND CLINICAL SAMPLES.

AUTHORS: ALMEIDA R.M.^{1,2}; JUNQUEIRA, R.M.¹; PANZENHAGEN, P.H.N.³; CONTE-JUNIOR, C.A.³; PEREIRA, R.C.L.¹; REIS, E.M.F.¹; HOFER, C.B.²; VALLIM, D.C.¹

INSTITUTION: 1. LABORATÓRIO DE ZONÓSES BACTERIANAS, INSTITUTO OSWALDO CRUZ, FIOCRUZ, RIO DE JANEIRO, RJ (AV. BRASIL 4365, PAV. ROCHA LIMA, 3º ANDAR, CEP 21040-900, RIO DE JANEIRO – RJ, BRAZIL); 2. FACULDADE DE MEDICINA, HOSPITAL UNIVERSITÁRIO CLEMENTINO FRAGA FILHO, UNIVERSIDADE FEDERAL DO RIO DE JANEIRO, RIO DE JANEIRO, RJ (RUA RODOLPHO PAULO ROCCO, 255 - CIDADE UNIVERSITÁRIA - ILHA DO FUNDÃO, CEP:21941-913, RIO DE JANEIRO – RJ, BRAZIL); 3. PROGRAMA DE PÓS-GRADUAÇÃO EM CIÊNCIA DE ALIMENTOS, INSTITUTO DE QUÍMICA DA UNIVERSIDADE FEDERAL DO RIO DE JANEIRO. (AV. ATHOS DA SILVEIRA RAMOS, 149, CENTRO DE TECNOLOGIA (CT), BLOCO A, 7º ANDAR, CIDADE UNIVERSITÁRIA, RIO DE JANEIRO, RJ).

ABSTRACT:

Listeria monocytogenes causes listeriosis, a serious foodborne illness in high-risk groups such as the elderly, newborns and pregnant women. This pathogen represents a concern for the food industry due to its ability to survive and grow in various environmental conditions (low temperature and high salt concentrations).

The aim of this study was to analyze, by Complete Genome Sequencing (WGS), 48 strains of *L. monocytogenes* isolated from food (21) and clinical (27) samples, from 1975 to 2014 and different States. All strains were deposited in the Listeria Collection (CLIST/LABZOO/Fiocruz). Strains of the following serotypes were used: 4b (27), 1/2b (13), 1/2c (5), 1/2a (2) and 3b (1). The *in silico* analysis was performed using tools built in the BIGSdb-Lm database of the Institute Pasteur/France.

MLST analysis showed the presence of Clonal Complexes: CC3 (15), CC1 (13), CC218 (9), CC9 (5), CC2 (2), CC7 (1), CC59 (1), CC155 (1) and CC315 (1), corresponding to Sequence Types ST3 (14), ST1 (13), ST218 (9), ST9 (4), ST2 (2), ST7 (1), ST59 (1), ST122 (1), ST520 (1), ST1434 (1) and ST1435 (1) respectively. In addition, two new STs were described, ST1434 and ST1435 isolated from ricotta cheese and human blood, respectively. ST1 was associated with hypervirulence and tropism towards the central nervous system (CNS) and ST9 was strongly associated with food but not clinical samples. The genomic island LIPI-1 was found in all strains and 13 of them also had the LIPI-3 Island (all serotype 4b or 1/2b). LIPI-1 and LIPI-3 harbor genes involved in invasion and survival within the host cell. Plasmids were found in 23 strains, six of them with the *bcrA* gene, which confers resistance to benzylkonium chloride. In the chromosome, genes related to resistance against heavy metals (*mco* (6), *mdrL/yfmO* (27), *merR1* (5), *merR2* (5)) and antibiotics (*aacA4* (5), *fosX* (48), *sul* (46), *mprF* (48), *mdrL/yfmO* (27), *norB* (48), *lde* (48)) were also detected.

WGS allowed a deeper analysis of the genetic diversity of *L. monocytogenes* circulating in Brazil, contributing to a better understanding of its virulence and resistance patterns. The sequences are still being analyzed, so the patterns and proportions observed so far may be subject to change.

Keywords: Biocide Resistance, Clonal Complexes, Food-Borne Pathogen, *Listeria monocytogenes*, WGS.

Agency: Capes, CNPq, Fiocruz