

Poster

Genomic Characterization of *Listeria monocytogenes* in Andalucía



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ABSTRACT

Listeria monocytogenes is a Gram positive, foodborne pathogen which can cause a wide range of infections including gastroenteritis, meningitis, and bacteremia. This ubiquitous organism can be isolated from food (milk, meat, and fish products) and food production plants. Ability to surviving *L. monocytogenes* in the environment as well as threat for consumers depends on the presence of virulence genes and genes connected with resistance for sanitizers or antimicrobials.

In this work, *Listeria monocytogenes* whole genome sequencing data from the Sistema Integrado de Epidemiología Genómica de Andalucía (SIEGA) was used to determine the sequence type of isolates based on multi-locus sequence typing (MLST), construct a core single nucleotide polymorphism (SNP) phylogeny and determine the presence of virulence and resistance associated genes.

Overall the work indicates that a genetically diverse range of *L. monocytogenes* strains is present in Andalucía. While some samples have premature stop codons in an important virulence gene (*inlA*), which have been shown to attenuate virulence, others contain different pathogenicity islands (LIPI-3,4) related to a hypervirulent phenotype. With regard to resistance genes, the presence of both genomic islands Survival Stress Islet (SSI-1,2) has been detected in variable proportions, which allows them to survive under different suboptimal conditions. The presence of genes related to resistance to fosfomycin (*fosX*), lincosamides (*lin*), quinolones (*norB*), nicine (*mprF*), and sulfonamides (*sul*) have also been detected in most samples. Also, to a lesser extent, other types of resistance genes have been detected as genes associated with resistance to aminoglycosides (*aacA4*) or associated with resistance to sanitizers and disinfectants (*bcrABC*, *qac*). The genomic characterization of the different samples through bioinformatics tools allows us to track and demonstrate the genetic diversity of the *L. monocytogenes* samples obtained from different sources, giving us information on the pathogenic potential of the samples. These methods have the potential to extrapolate our knowledge of how different genetic mechanisms lead to variation in responses to stress and virulence.

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