Whole-genome sequencing of *Listeria monocytogenes* serotype 4b isolated from ready-to-eat lentil salad in Algiers, Algeria

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Abstract

Listeria monocytogenes is a Gram-positive food-borne pathogen causing a serious threat for public health. Here we announce the whole genome sequence (3 011 693 bp) of *Listeria monocytogenes* serotype 4b, isolated from ready-to-eat lentil salad in Algiers and belonging to sequence type 2, lineage I and clonal complex 2.

Keywords: Algeria, *Listeria monocytogenes*, ready-to-eat, serotype 4b, whole-genome sequencing
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Listeria monocytogenes is a facultatively anaerobic, Gram-positive bacterium that causes two forms of listeriosis: gastroenteritis and invasive infection [1]. *Listeria monocytogenes* is ubiquitously present in the environment. It is often associated with food such as ready-to-eat deli meats and unpasteurized dairy products. Its ability to grow at low temperatures favours its persistence in manufactured food products [2]. Transmission via the faecal–oral route or by ingesting contaminated food turns *L. monocytogenes* into a major concern for food safety and public health. Several historical *L. monocytogenes*-related food-borne outbreaks around the world showed a high mortality rate, particularly in the elderly, pregnant women and immunocompromised individuals [3]. Listeriosis can cause severe symptoms, including septicaemia, meningitis, stillbirths and even death [4].

There are 13 recognized serotypes for *L. monocytogenes* worldwide; however only four of them are of significant concern to human health: 1/2c, 1/2a, 1/2b and 4b, the latter three serotypes are responsible for more than 95% of invasive listeriosis cases [1,5,6]. Historically, the majority of the clinical cases and outbreaks are associated with serotype 4b strains [1,7]. The strain analysed in this study was isolated in 2010 from a ready-to-eat lentil salad according to ISO method 11290 [8,9]. Fraser broth was used for enrichments and Palcam agar for strain isolation. Biochemical identification was then performed using the API Listeria test (Biomérieux, Marcy l'Étoile, France) and subsequently, the strain was serotyped using a multiplex PCR [10]. Genomic DNA was extracted using genomic Tip 20/G (Qiagen, Hilden, Germany) following the manufacturer's instructions. A paired-end 2 × 250-bp sequencing run was performed using an Illumina MiSeq system. The Nextera XT DNA library preparation kit was used to construct libraries from the extracted DNA. Raw sequence reads were trimmed by Trimmomatic v0.36.4 with the following options: trailing: 10, leading: 10, sliding window: 4:20, minlen: 40 [11]. Assembly was carried out using Spades v1.3.1 with default settings [12]. Annotation of assembly was performed using Prokka Rapid prokaryotic genome annotation v1.11 with default settings [13]. Antimicrobial resistance (AMR) gene occurrence was investigated with Resfinder v3.1 with default settings (https://cge.cbs.dtu.dk/services/ResFinder/). Virulence, multilocus sequence typing and PCR-serogroup were investigated using The BIGSdb database for *Listeria* (http://bigsdb.pasteur.fr/listeria).

A total of 263 240 reads of 250 bp were obtained. The genome has a length of 3 011 693 bp, with an average coverage depth of 17×, N50 of 272 618, contains 22 contigs >1000 bp and has a GC% of 38 mol%. Annotation revealed 2974 coding sequences (CDS), 58 tRNA and 2880 hypothetical proteins. This strain was found to

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belong to PCR-serogroup: IVb (3), sequence type: 2, lineage: I and Clonal complex: CC2. The antimicrobial resistance gene *fosX* was found in addition to 55 virulence genes. None of the known *prfA* alleles corresponds to our *prfA*, the closest one was *prfA* with 99% identity [4].

To best of our knowledge, this is the first genome of *Listeria* spp. reported in Algeria. This whole genome has been deposited at GenBank under accession number GCA_006348975.1 and its raw reads are at Sequence Read Archive under accession number SRR9099607.

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Conflicts of interest

There is no potential conflict of interest or financial disclosure for any authors.

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