

RESULTS OF WHOLE-GENOME SEQUENCING AND PHENOTYPE ANNOTATION OF BACTERIA OF THE GENUS LISTERIA

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INTRODUCTION

The incidence of listeriosis in highly developed countries it ranges from 0.3 to 1.5% [1]. Mortality due to complications of listeriosis infection can reach 30% [2]. Therefore, the fact of contamination of food products with listeria is of great concern. And if earlier it was believed that representatives of the species *L. monocytogenes* possess the largest set of pathogenic factors, then the possibilities of molecular and bioinformatics research methods provide reliable picture with respect to other representatives of the genus *Listeria*, in particular *L. innocua*.

AIM

To study the pathogenic potential of strains of *L. innocua*

METHODS

The classic bacteriological method, mass spectrometry, molecular (whole-genome sequencing), bioinformatics analysis of genetic data were used in the work.

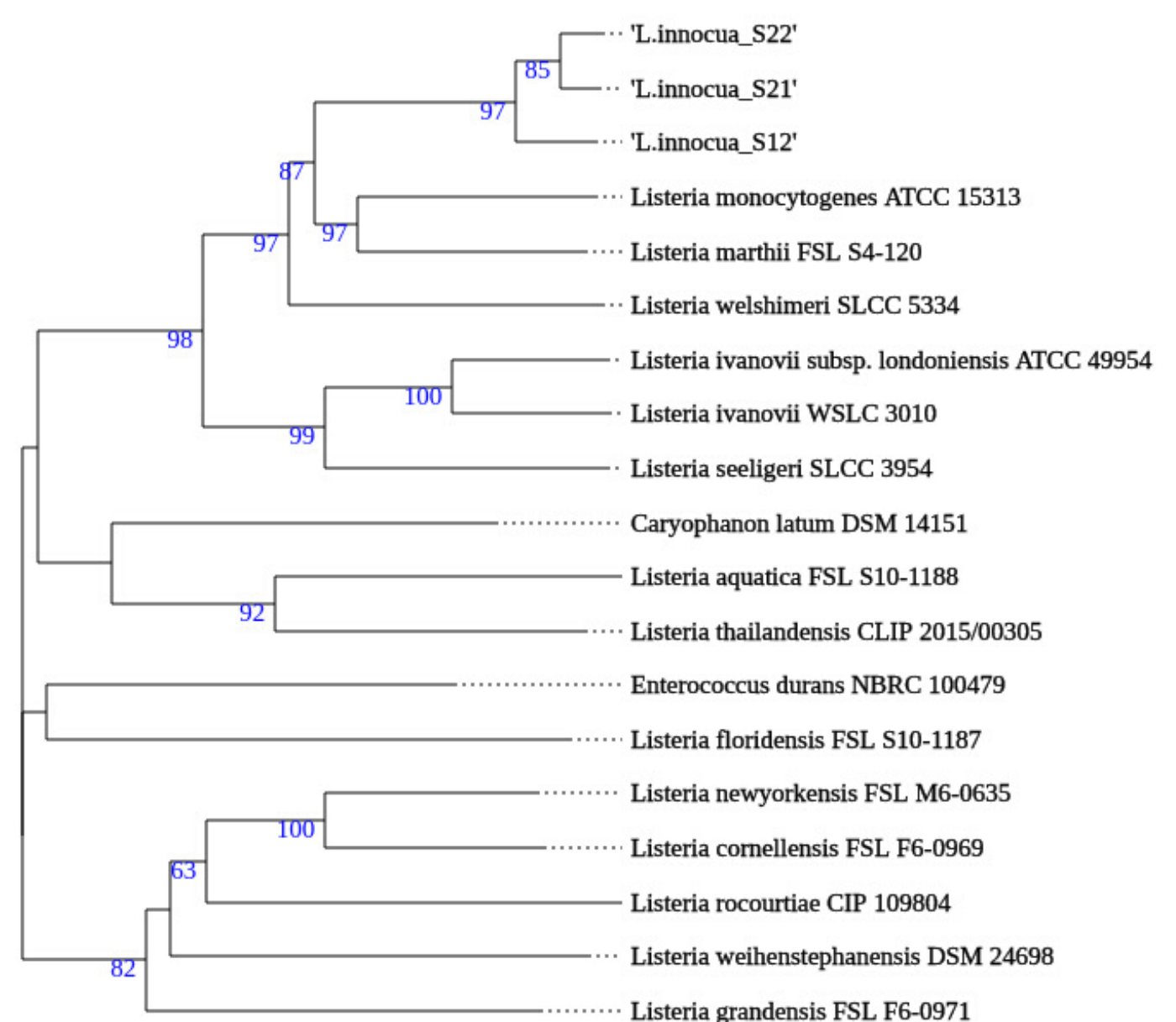
CONCLUSION

The proximity of bacteria in food products, in places of their storage and transportation, can lead to faster transfer of genetic information from representatives of one species to another. At the same time, strains of *L. innocua* acquire pathogenicity and antibiotic resistance factors, which allows them to become hazardous to human health along with strains of the *L. monocytogenes* species.

RESULTS

- L. innocua* have in their genome a number of the virulence gene characteristics which are distinctive to the species *L. monocytogenes*: *clpC*, *prfA*, *ebrB*, *inlJ_1* and *inlJ_2* genes.
- All *L. innocua* strains had the antibiotic resistance genes: from 20 to 30 for each strain. They included genes responsible for resistance to β -lactam antibiotics, fluoroquinolones, aminoglycosides, tetracyclines, macrolides.
- The results of the phylogenetic studies showed a close relationship between the genomes of bacterias *L. monocytogenes* and *L. innocua*.

PHYLOGENETIC RELATIONSHIP OF SELECTED STRAINS OF LISTERIA SPP.



References: [1] Alexandra Moura et al. Atypical Hemolytic *Listeria innocua* Isolates are virulent, albeit less than *Listeria monocytogenes*. *Infect Immun*. 2019 Apr; 87(4): e00758-18.

[2] Glaser P., Frangeul L., Buchrieser C. et al. Comparative genomics of *Listeria* species // *Science*. 2016. Vol. 294. P. 849–852.