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Invasion factor variability as a basis for Listeria monocytogenes highly virulent strain development

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Background & Aim: The gram positive bacterium *Listeria monocytogenes* is a soil-borne human and animal pathogen that circulates in natural foci of infection. It could be transmitted to anthropogenic environment to establish foci of infection at farms and food industry plants. Most of listeriosis cases in humans are caused by a few clonal complexes. Meanwhile, majority of *L. monocytogenes* strains carry the same set of major virulence factors. We suggested that highly virulent strains carry specific variants of major virulence factors. Particularly, the invasion factors of the internalin family, InIA and InIB that provide crossing the intestinal barrier, could be better adapted in highly virulent strains. The purpose of this study was to check this hypothesis on the model of the invasion factor InIB.

Methodology: InlB variability was analyzed on a laboratory collection of 65 *L. monocytogenes* strains and compared with data available from GeneBank. Predominant InlB isoforms were used to complement inlB deletion in EGDe Δ inlB strain. Virulence was assessed in cell invasion assay and a mouse model. Purified InlB isoforms were characterized by SEC and fluorescence.

Findings: Four InlB variants were prevalent among *L. monocytogenes*. Being cloned in EGDe Δ inlB, all variants restored invasion in mammalian cells. After intragastric infection, the strain carrying InlB variant Var14 was the best and showed 40-fold higher loads in the liver, persistance in Peyer's patches and stimulated lower levels of INF-gamma. Var14 was the only InlB isoform that provided perinatal infection. All purified InlB isoforms activated c-Met but differed in kinetics Erk1/2 and Akt signaling pathways InlB isoforms differed in protein stability. Conclusion & Significance: InlB isoforms differently affected *L. monocytogenes* virulence due to differences in their biological and physicochemical properties.

Results: The work supported the hypothesis about virulence factor variability as a basement of highly virulent strains arising.

Recent Publications

- 1. Wiedmann M (2003) ADSA Foundation Scholar Award—an integrated science based approach to dairy food safety: Listeria monocytogenes as a model system. J Dairy Sci. 86(6):1865-75.
- 2. Ragon M, Wirth T, Hollandt F, Lavenir R, Lecuit M, Le Monnier A and Brisse S (2008) A new perspective on Listeria monocytogenes evolution. PLoS Pathog. 4(9):e1000146.
- 3. Nightingale K K, Windham K and Wiedmann M (2005) Evolution and molecular phylogeny of Listeria monocytogenes isolated from human and animal listeriosis cases and foods. J Bacteriol. 187(16)5537-51.
- 4. Sobyanin K, Sysolyatina E, Krivozubov M, Chalenko Y, Karyagina A and Ermolaeva S (2017) Naturally occurring InlB variants that support intragastric *Listeria monocytogenes* infection in mice. FEMS Microbiol Lett. 364(3).

Biography

Svetlana Ermolaeva has her expertise in Molecular Microbiology of soil borne pathogens. Particularly, Listeria monocytogenes and Yersinia pseudotuberculosis are in the focus of her research. Her studies are focused on molecular mechanism of virulence and evolution of these pathogens. Application of physical methods for non-specific eradication of pathogenic microorganisms is the second field of her research.

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