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Poster Abstracts

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PHENOTYPIC AND GENETIC CHARACTERISTICS ASSOCIATED WITH LISTERIA MONOCYTOGENES FOOD CHAIN ISOLATES DISPLAYING ENHANCED AND DIMINISHED COLD TOLERANCE

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Abstract Content: The potentially fatal human pathogen *Listeria monocytogenes* (*Lm*) is most recognized for its ability to contaminate foods and grow during refrigerated storage. Given the importance of preventing *Lm* from reaching dangerous levels in food, little is known about the genetic and physiological differences between strains with varied cold tolerance. The objective of this study was to determine if *Lm* isolates with enhanced cold tolerance, exhibit other high risk characteristics that may add to their survival and/or pathogenicity. To accomplish this, 166 predominantly food/food plant *Lm* isolates were tested in brain heart infusion broth, for their ability to tolerate cold (4°C), salt (6% NaCl, 25°C), acid (pH 5, 25°C), and desiccation (33% RH, 20°C) stress. Isolates were considered tolerant or sensitive if they exhibited survival characteristics > or < than the mean ± 1SD. Remaining isolates were classified as intermediate. Draft whole genome sequencing was performed to elucidate potential genotype/phenotype correlations. Evidence for several overlapping geno- and phenotypes were observed. Notably, isolates with a wildtype invasion gene, *inlA* (n=119), had faster ($p < 0.000$) growth rates at 4°C than strains with a truncated version (n=47). Cold tolerant isolates were more likely to be tolerant to the other three stresses than intermediate and cold sensitive isolates. Similarly, cold sensitive isolates were more likely to be sensitive to the other stresses. Cold tolerant isolates had shorter ($p = 0.012$) lag phases in salt than cold sensitive isolates, and a positive correlation ($p = 0.002$, $r = 0.239$) existed between growth rates of isolates under salt and acid stress. A whole genome single-nucleotide-variants (SNVs) phylogeny revealed closely related cold tolerant and sensitive isolates, suggesting that minor genetic differences (ie. SNVs), are likely responsible for phenotypic differences. This study highlights that *Lm* isolates displaying high risk factors exist in food processing environments, and emphasizes a need for more research regarding the evolution of these strains.

Disclosure of Interest: None Declared

Keywords: acid stress, cold stress, *Listeria monocytogenes*, salt stress, whole genome sequencing