

## Determinants of Stress Resistance in Local Foodborne *Listeria monocytogenes* Strains as Revealed by Functional and Comparative Genomics

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### Abstract

**Introduction:** The ability to survive environmental stress is a key factor in the transmission and pathogenicity of *Listeria monocytogenes*. Environmental stress resistance and food survival ability of *L. monocytogenes* are extremely variable among strains. Comparative genomic analysis and functional annotation can identify unique genetic elements and proteomic products associated with *L. monocytogenes* from different food processing environments. This study sought to identify the genetic determinants of stress resistance and their functional roles in local foodborne *L. monocytogenes* strains.

**Methodology:** Whole genome sequences of two local isolates of *L. monocytogenes* strains were compared with genomes of previously sequenced *L. monocytogenes* isolates from food processing environments. Possibly unique genomic regions and predicted proteomes. Gene ontology (GO), clusters of orthologous groups (COG) and KEGG orthology (KO) analysis were used for functional annotation.

**Results and Discussion:** The study is expected to identify and elucidate possibly unique genetic elements influencing the stress resistance of local strains. An understanding of genetic differences allows the identification of possible relationships with specific phenotypic traits.