Exploring the global transcriptomic response of L. monocytogenes to desiccation on stainless steel

Kragh, Martin Laage; Hansen, Lisbeth Truelstrup

Publication date:
2019

Document Version
Publisher's PDF, also known as Version of record

Link back to DTU Orbit

Citation (APA):
Title: Exploring the global transcriptomic response of *L. monocytogenes* to desiccation on stainless steel

Authors: Martin Laage Kragh and Lisbeth Truelstrup Hansen
National Food Institute, Technical University of Denmark, Kemitorvet, 2800 Kgs. Lyngby, Denmark.

Abstract:

The ability of *L. monocytogenes* to survive desiccation for extended periods on food contact surfaces remains a challenge for the food industry.

The purpose of this study was to further our understanding of the bacterium’s survival by investigating the global transcriptomic response of *L. monocytogenes* to desiccation (43% RH, 15°C) on food grade stainless steel surfaces.

Two strains (a food and an outbreak strain) of *L. monocytogenes* were desiccated (43% RH, 15°C) on stainless steel under conditions simulating a food processing plant. Survivor counts and RNA extracts were obtained after 0 (control), 6, 12, 24 and 48 hours for subsequent rRNA-depleted Illumina TrueSeq RNA library preparations and strand specific Illumina Hiseq 2000 paired end RNA-sequencing. Differentially expressed genes were reported as significant (*p* adjust < 0.05) if log2 fold change were >1 (fold change > 2).

Both strains were reduced by 1.8 – 2.0 log CFU/cm² over 48 hours (from 7.7 log CFU/cm²), with the first log reduction occurring after 6 hours. The number of differentially expressed genes varied among the food (336±20) and outbreak strains (646±32). After commencement of the desiccation, gene expression remained stable over the 48 hours for both strains. A core set of 154 genes were differentially (*p* adjust < 0.05) expressed in both strains throughout the desiccation and included the downregulated cheY and cheA (two component system involved in chemotaxis), the upregulated qoxABCD operon (*sigB* dependent quinol oxidase), and the upregulated phdA (general metabolism related to osmotic stress). In contrast, genes such as *inlH* (internalin H) and *lmo0781-0784* (PTS mannose system) were differentially up- or down- regulated in the strains.

The present study detected novel desiccation associated stress genes in *L. monocytogenes* and revealed strain differences. Taken together this will increase our knowledge of the bacterium’s desiccation-stress response and lead to improved control in food processing plants.