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Kragh, Martin Laage; Hansen, Lisbeth Truelstrup

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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 ($p_{\text{adjust}} < 0.05$) if log2 fold change were $>1$ (fold change $>2$).

Both strains were reduced by $1.8 - 2.0 \log \text{ CFU/cm}^2$ over 48 hours (from 7.7 log CFU/cm$^2$), 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 ($p_{\text{adjust}} < 0.05$) 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.