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Global Transcriptome Analysis of Lactobacillus animalis NP51 exposed at different Temperatures

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Lactobacillus animalis NP51 is a bacterium of interest in food industry because of its ability to inhibit foodborne pathogens and spoilage. The addition of this microorganism as probiotic to animal feed is generally recognized as safe (GRAS) for use in cattle. The aim of this study was to use RNA-seq to determine the transcriptional profile of Lactobacillus animalis NP51 at different temperatures 25°C (environment temperature), 39°C (host temperature-bovine), and 45°C (animal feed temperature). The bacterial strain was grown overnight at 37°C for 18h; overnight cultures were diluted into fresh medium and incubated at 25, 39, and 45°C until mid-logarithmic phase was reached. Total RNA extracted from two biological replicates of each temperature was rRNA depleted; individually bar-coded RNA-Seq libraries were prepared and sequenced on a MiSeq instrument. Raw data sets were assembled using de novo assembly. DNAStar Array Star software was used to analyze transcript levels. To obtain the quantitative amounts of expression, host temperature was set up as control. By comparing 25°C to the control, 572 genes were identified as differentially expressed, 488 genes showed reduced expression while 84 increased expression. At 45°C, 54 genes were differentially expressed, 23 showed reduced expression and 31 showed increased expression. The differentially expressed genes at both temperatures include the down-regulation of PTS gene expression, used for the uptake of carbohydrates; the late competence protein ComGA required for the competence-related block in chromosome replication, and the upregulation of the EmrE multidrug resistance protein. This study provides important information about the transcriptional differences of Lactobacillus animalis NP51 at low and high temperatures providing the basis for the characterization of genes with a potential role in the inhibition of foodborne pathogens.