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Molecular regulation of adhesion and biofilm formation in Bacillus licheniformis high and low biofilm producers using RNA-Seq

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Bacillus licheniformis is a dominant spore-forming microbial contaminant of the dairy industry throughout the world. A variety of studies suggest that the ability of this species to form biofilms is the key reason for its widespread prevalence. However, despite its apparent prevalence and spoilage potential, there is no information regarding the molecular determinants involved in biofilm formation by B. licheniformis. We used the transcriptome sequencing (RNA-seq) technology to reveal over- and underrepresented transcripts in the transition from the planktonic (logarithmic culture) to the biofilm state (24 h old) in a high and low biofilm forming B. licheniformis dairy strains. Genes, representing 28.3 % and 36.3 % of the whole B. licheniformis gene content were upregulated in the biofilm state as compared to the planktonic state in high and low biofilm producers, respectively. The gene expression patterns of several groups of genes differed significantly (P<0.05) under the two growth conditions The genes related to chemotaxis proteins (CheA, CheB, CheC, CheD, CheV, CheW, CheY, MotA, MotB) and flagellar assembley were exclusively upregulated in the planktonic phenotype as compared to biofilms in both strains. In terms of Kyoto Encyclopedia of Genes and Genomes (KEGG) based pathways, metabolic pathways were significantly (P < 0.05; Q-values < 0.05) downregulated in the planktonic state as compared to the biofilm state in both strains which shows that biofilm formation is an energetically expensive process. Lipid and sugar metabolism seemed to play an important role in the matrix production. Overall, several genes involved in adhesion, matrix production and matrix coating were either absent or less expressed in the biofilm state of low biofilm producer as compared to the high biofilm producer. Interestingly, the genes related to sporulation and extracellular polymeric substances were concomitantly expressed in the biofilm state of both strains which suggests that sporulation is coupled with the biofilm formation in this species similar to B. subtilis. Collectively, our results provide a comprehensive insight into biofilm formation in B. licheniformis that will be helpful for future research into mechanisms and targets..

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