

# SPLEEN TRANSCRIPTOME PROFILE OF MUSCOVY DUCKLINGS IN RESPONSE TO INFECTION WITH BACILLUS CEREUS

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**B***acillus cereus* is a Gram-positive, spore-forming associated with food contamination. To our knowledge, no studies have been reported regarding transcriptome analysis of duckling spleen in the context of *B. cereus*. In this study, we carried out RNA-seq-based transcriptome analysis on the spleen of ducklings. Six 1-day-old Muscovy ducklings were equally divided into infected and uninfected control groups with three replicates per group. Ducks in the infected group were inoculated with  $10^5$  CFU *B. cereus* by oral gavage individually. The control group was administered with sterile phosphate buffer saline. Ducks were euthanatized and the spleen was collected on 24 h post-infection (HPI). Key genes upregulated in response to *B. cereus* infection were 60S ribosomal protein L34 (RPL34) and small conductance calcium-activated potassium channel protein 2 (KCNN2) in comparison between the *Bacillus*-infected and uninfected control ducklings. However, five genes were substantially repressed between the aforementioned groups. GO term enrichment analysis suggested that up-regulated and down-regulated DEG significantly enriched in biological processes and molecular functions. Our findings have indicated that multiple genes and pathways may play a crucial role in response to *Bacillus* infection within 24 HPI, offering candidate targets and strategies for prevention and control.

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