RESUMO SIMPLES - PROTOZOÁRIOS E AGENTES TRANSMITIDOS POR VETORES DE IMPORTÂNCIA EM SAÚDE

IL1B AND IL2 EXPRESSION IN BROILER CHICKENS CHALLENGED WITH DIFFERENT LEVELS OF EIMERIA SPP.

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Avian coccidiosis is an intestinal parasitic disease caused by the intracellular protozoan Eimeria spp.. It can cause intestinal epithelial destruction, reduce nutrient absorption, impair weight gain, worsen feed conversion, and increase susceptibility to secondary infections. The total cost associated with prophylaxis, treatment, and production losses due to coccidiosis is estimated to be approximately USD 13 billion annually in the poultry industry. Understanding

the gene expression of cytokines involved in the inflammatory response provides a clearer view of Eimeria spp. infection of broiler chickens, as the expression of pro-inflammatory cytokines, especially IL1β, which acts in the early stages of inflammation, and IL2, which promotes T cell activation and proliferation, serves as an important indicator of the host immune response. In this context, the objective of this study was to evaluate cytokine gene expression dynamics in broiler chickens exposed to different doses of Eimeria spp. One-day-old Coob broilers were orally challenged with the Fortegra® vaccine, containing E. tenella, E. acervulina and E. maxima. Birds received doses that were 10× and 40× higher than the recommended dose. Oocysts were counted using a Neubauer chamber, resulting in inoculated doses of 8.4×10^{6} oocysts for the 10× group and 3.36×10^{7} oocysts for the 40× group, simulating different challenge levels. The animals were divided into three groups: GC (control, PBS), G1 (10× dose), and G2 (40× dose), with 24 birds per group. Four broilers were placed per cage. At 7, 14, and 21 days post-vaccination, eight birds per group were euthanized following the CONCEA guidelines (CEUA No. 1852071223). DNA and RNA were extracted for molecular analysis. DNA samples were used to detect E. tenella, E. acervulina, and E. maxima in the duodenum, jejunum, and cecum. Total RNA (500 ng) was reverse transcribed to cDNA, and PCR assays were performed to evaluate IL1β and IL2 expression. Molecular assays demonstrated the presence of E. acervulina and E. maxima in the duodenum and jejunum of challenged animals. All cecal tissue fragments analyzed in this study from animals challenged with G1 and G2 were positive for qPCR detection of E. tenella and negative for E. acervulina and E. maxima. On day 7 post-infection, IL1β gene expression was significantly downregulated in both challenged groups: 13.37-fold lower in G1 ($p = 0.0011$) and 7.98-fold lower in G2 ($p = 0.0175$). In contrast, IL2 expression was significantly upregulated, being 6.72-fold higher in G1 ($p = 0.0024$) and 12.94-fold higher in G2 ($p < 0.0001$) than in the control. On day 14, IL1β expression showed a marked peak, with an 8.26-fold increase in G1 ($p < 0.0001$) and a 9.40-fold increase in G2 ($p < 0.001$). IL2 expression was also significantly elevated by 5.51-fold in G1 and 5.22-fold in G2 ($p < 0.0001$). On day 21, IL1β expression returned to baseline, with no significant differences ($p > 0.05$). IL2 remained significantly upregulated, reaching 20.78-fold in G1 ($p < 0.0001$) and 12.53-fold in G2 ($p < 0.0001$), with a significant difference between the doses ($p = 0.0170$). These findings demonstrate that Eimeria spp. modulate cytokine expression ofIL1 and IL2 in a dose-dependent manner, offering key insights into immune response dynamics during avian coccidiosis.

Understanding these dynamics is essential because the inflammatory response can cause epithelial damage, directly influencing nutrient absorption and overall performance. This knowledge supports more precise management strategies, including vaccination schedules, rational anticoccidial use, and targeted nutritional interventions to reduce production loss and contribute to the development of effective control strategies.

Palavras-chave: coccidiosis; gallus gallus domesticus; different doses.